

## Diversity of latex properties in French Guianan trees- DILATE

PI : Yannick ESTEVEZ & Christopher BARALOTO

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**Abstract :** DILATE is a multidisciplinary exploratory project at the frontier between biochemistry, ecology and ecophysiology to study natural latex produced by French Guianan woody plants. The main objective is to determine whether variation of physicochemical properties in latex may be correlated to some inherent functional traits among contrasted plant communities. We will survey tens of species in diverse angiosperm lineages and across contrasting forest habitats to integrate for the first time physical and chemical properties of tropical plant latexes including: (i) NMR and IR spectroscopy (nature and structure of the polymer), (ii) electronic microscopy (particle size), (iii) water content, and (iv) proteins content. . The project will have high impact in terms of original databases generated for this potentially important but understudied plant trait, and for an important collaboration between chemical and ecological teams of the Labex who have not worked much together as yet.

## Parasites, disease and the global spread of cane toads: how do parasites impact amphibian health and biological invasions? - ERH

PI : Crystal GRAHAM

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**Abstract :** The « enemy release hypothesis » (ERH) posits that release from native competitors, predators, and parasites facilitates invader success in a new environment. However, the ERH remains to be fully experimentally tested, particularly in vertebrates. To comprehensively test the ERH biogeographical comparisons (involving native and invasive ranges) combined with controlled laboratory experiments are required. The cane toad (*Rhinella marina*) provides an ideal model organism in which to test the impacts of parasites and diseases on invasion success and amphibian health across a global geographical scale. *Rhinella marina* is a toxic amphibian native to Central and South America but has been introduced to almost 100 locations worldwide. Because of its extensive and well documented invasion history (presenting replicated natural experiments), high population densities, and status as a model species for amphibian research, it presents a perfect study system. I propose to trace the geographical path of toad invasions back to their native origins to comprehensively test the ERH using geographical population comparisons and infection experiments. The geographical comparisons will build on an extensive dataset I have collected in its most notorious invasive population in Australia and serve as a backdrop for reciprocal infection experiments to test whether introduced toads are differentially affected by their original parasites compared to native populations. For this proposal, I will compare parasitism in native populations (French Guiana, Guyana, Panama) with invasive populations (Australia, Hawaii, Florida, Bermuda) to provide an unparalleled geographical framework for my laboratory experiments testing the ERH using toads from these same populations. Specifically, I will compare relative toad density, body condition, and reproductive rates between native and invasive ranges to investigate population fitness. Further, I will compare parasites of cane toads in their native vs invasive ranges to investigate whether parasite-release is driving toad success. Further I will examine which parasites are most likely to be introduced during an invasion. I expect toad fitness will be positively correlated with distance (and number of translocations) from the toad's native range. However, I predict that the release from parasite pressure and the loss of immunogenetic diversity (associated with

bottlenecking events during successive translocations to new ranges) will render invasive toads more susceptible to infection with native range parasites. This geographic comparison will enhance our understanding of the factors that facilitate species invasions, potential pathways for introduced parasites, and the role of parasites and diseases in suppressing wildlife health.

## **Are bromeliad roots absorptive? A Preliminary study on fungal association in bromeliads – FunBrom**

PI : Céline LEROY

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**Abstract :** One critical challenge for plants is to maintain an adequate water and nutrient supply under fluctuating environmental conditions. In canopy habitats, epiphytic plants have evolved remarkable morphological and physiological adaptations for attaining and retaining water and nutrients. Whereas the benefits of arbuscular mycorrhizal fungi (AMF) to plants growing on the forest floor are well described, little is known about the associations AMF form with plants in the forest canopy. Bromeliads are one of the most diverse groups of epiphytes found in the entire tropical and subtropical zones of the Americas. A unique feature of this family is that many species are capable of absorbing water and nutrients directly from atmospheric sources thanks to their foliar trichomes, reducing the roots to a purely mechanical support function, attaching the plant to the substrate.

Fun-Brom aims to characterize the occurrence and diversity of fungal associations in bromeliad roots and to consider the extent of the role of roots and fungi in plant performance. We propose to analyze patterns of fungal diversity according to the ecological types and ontogeny of the bromeliads by combining morphological and Next Generation Sequencing approaches. Moreover, we will conduct in situ and greenhouse experiments in order to characterize the role of roots and fungal associations in bromeliad performance. Fun-Brom project will give us a new highlight of fungal diversity in bromeliads and more generally in an understudied forest compartment. Discovering fungal associations may challenge the current perception of bromeliad nutrition and understanding the diversity of nutritional pathways and mechanisms of alternation between them is crucial to construct predictions of bromeliad responses to climate change.

## **The Guianese evolutionary project on economics for social insects- GUEPES**

PI : Seirien SUMNER

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**Abstract :** There is a major – unsolved – mystery about social wasps throughout South America, which challenges fundamental ideas in evolutionary biology. We believe French Guiana can and must be in the frontline of an exciting attempt to solve it. One of the fundamental equations at the heart of evolutionary biology – ‘Hamilton’s rule’ – states that altruistic behaviour can evolve, if directed towards relatives. This insight explains the extraordinary cooperative phenomena we see in the living world, including the grouping of close relatives into social colonies. This cooperative grouping has reached its pinnacle in ‘eusocial’ societies, where subordinate workers sacrifice their own chance of reproduction in order to help raise close relatives. However, in the paper-wasps of South America, a radical behaviour has recently been discovered (1). So-called ‘drifting’ wasps are moving between multiple nests: they help raise the brood on a network of nests rather than just their own. This means that they are, for much of the time, raising the brood of distant relatives at the expense of

close relatives. This extraordinary behaviour demands an explanation, because it challenges central ideas in social evolution. Polistes wasps in French Guiana nest in clusters of nearby nests. This presents a unique opportunity to dissect this remarkable behaviour. Using cutting-edge technology, this project will employ radio-tagging – attaching tiny radio-tags to hundreds of wasps, and stationing radio-antennae at each nest – to understand the mystery, and find a solution to this striking and urgent enigma. The GUEPES project is an interdisciplinary mission to unify economics and evolution on the biodiverse Guiana Shield.

## Is ecological speciation a major driver of diversification in tropical leaf-mining insects?- LEAFMINE

PI : Jérôme MURIENNE & Carlos LOPEZ VAAMONDE

*EDB Toulouse & INRA Orléans*

**Abstract :** A large proportion of all known terrestrial species are tropical flowering plants and their associated herbivorous insects. Therefore, understanding the mechanisms of diversification of those groups would explain the evolution of much of our extant terrestrial biodiversity. A popular explanation for the enormous diversity of phytophagous insects and plants is ecological speciation, a process by which a shift in host plant within an ancestral species causes the divergence into two new sister species, each adapted to feed on different host plants [1]. However, the relative importance of host plant shifts in the speciation process of herbivorous insects is an area of debate. In this project we will assess for the first time the frequency of ecological speciation via host shifts for tropical leaf-mining moths of the family Gracillariidae. We will assess host plant range of the community of Gracillariidae at the Paracou research station using a combination of lab rearing and DNA barcoding of larvae and their host plants. In addition, we will test whether host plant DNA can be amplified from the gut contents of adult moths collected at light using NGS technology. We will then generate a fossil calibrated multigene molecular phylogeny for over one hundred species to reconstruct the frequency of host plant shifts (niche) in relation to speciation events.

## Sound of orgy: the acoustics of Amazonian explosive breeding amphibians- ORGY

PI : Elodie COURTOIS

*CNRS Guyane*

**Abstract :** A significant part of Amazonian animal species produce sound during communication and navigation acts. The sound emanating from these singing species constitute an original facet of tropical biodiversity that can be sampled locally or regionally over long time periods with autonomous audio sensors. Community or landscape sound can be analysed with adequate signal procedures to estimate acoustic diversity complexity and to potentially serve as a proxy of diversity dynamics. A major key element of the tropical acoustic diversity arises from the vocalisations of amphibians. In particular, several frog and toad species exhibit a striking acoustic collective behaviour by emerging and calling in massive number in a limited area and during a very brief period (1-2 nights). This flash collective reproduction phenomenon, known as explosive breeding, gather thousands of individuals belonging to up to 12 species forming a very intense and complex chorus. Surprisingly, very few is known on the causes and consequences of these unique acoustic events. Our project aims at coupling environmental and acoustic monitoring on five explosive breeding sites in French Guiana to reach the following goals: (i) to identify the main abiotic factors that may elicit such

massive and synchronised emergence of several species at the same time, (ii) to test through a niche analysis whether species have over-dispersed vocalisations within the acoustic space they have to share, and (iii) to explore whether recent acoustic indices can help in tracking remotely and automatically the occurrence and the composition of these explosive breeding events. The expected results will shed light on the origin and structure of a remarkable diversity pattern particularly vulnerable to the global climate changes. Eventually, the project covers topics, such as species interaction and biodiversity monitoring, directly in line with the ecosystem processes and biodiversity aims of the CEBA.

## Predicting the spread of Infectious mycobacteria communities among French Guiana food web - PRIMEWEB

PI : Rodolphe GOZLAN

*MIVEGEC, Cayenne*

**Abstract :** Many of the approximately 250 known human emerging infectious diseases are directly linked to regions of tropical rainforest, of these many originate from freshwater aquatic systems. As urbanisation, population encroachment and deforestation increase across the globe, their effect on tropical ecosystems can be dramatic, the loss of function and collapse in food webs can often lead to opportunistic, highly fecund species being able to take hold and flourish in a more restricted niche space. Such shifts in community organization invariably lead to a change in the dynamics of tropical water-borne diseases. In addition, the effects of land-use and deforestation have primarily been concerned with established vector-borne diseases, notably malaria and leishmaniasis. However, to understand the change in more generalist EID's (e.g. some bacteria), it is necessary to assess in detail the shifts in communities that arise from land-use changes.

Here based on a comprehensive investigation of tropical freshwater aquatic communities, across a gradient of land-use, a set of state-of-the-art techniques (e.g. stable isotope analysis, High-Resolution Melting Analysis) will be employed to build detailed structural pictures of freshwater communities, hosts but also of a range of bacterial infectious agent belonging to the genus *Mycobacterium* and responsible for both human and wildlife diseases. Our understanding of human infection from mycobacteria predominately stems from two species, *M. tuberculosis* and *M. leprae* responsible for tuberculosis and leprosis respectively. Most other mycobacteria are classed as "opportunistic" pathogens. However, we have currently no understanding of the spatial distribution and abundance of these *Mycobacterium* spp. communities among aquatic food web and across freshwater ecosystems.

Thus it is impossible to appreciate if the observed distributions of human disease agent within host food webs (e.g. *M. ulcerans* - MU - responsible for Buruli ulcer cases in French Guiana) are essentially driven by intraspecific adaptations to specific functional hosts or if their current distribution patterns are influenced by competition with other wildlife infectious agents occupying similar ecological niches.

Specifically we will test if the distribution of MU in aquatic food web reveals the distribution of other mycobacteria in space and time but also if mycobacteria specific of human, amphibian and fish diseases occupy ecological niches functionally similar. In addition, we will characterise the role and impact of socio-economic drivers of land-use and deforestation on the distribution and abundance of the different groups of mycobacteria.

This project proposal is therefore a great unifying framework to better understand 1) the ecological niches of generalist pathogen communities in tropical food webs and 2) the underpinning dynamic of human and wildlife disease emergence. The project proposal could lead to a significant breakthrough in ecological medicine, linking in an integrative framework, processes of microorganism competition, (aquatic), food web organisation and impact of socio-economic drivers. Such approach to microbial

ecology is novel and show international leadership.

### **Integrating state-of-the-art genomic and morphological tools to disentangle the biogeography of the long-nosed armadillo species complex (genus *Dasybus*) - TATU2**

PI : Frédéric DELSUC

*ISEM, Montpellier*

**Abstract :** With their Pan-American distribution, long-nosed armadillos (genus *Dasybus*) constitute an understudied model for Neotropical phylogeography. Our project aims at deciphering the taxonomy of the seven extant species with special focus on the biogeography of the widespread nine-banded armadillo (*D. novemcinctus*). Preliminary analyses based on two mitochondrial genes showed that this ubiquitous species might in fact form a species complex with notably a highly divergent lineage in French Guiana. Following from these unexpected results, we used an integrative taxonomy approach coupling next-generation sequencing with cutting-edge 3D-geometric morphometric techniques for species delimitation. In year 1, we collected geometric morphometric data for 51 skulls borrowed from international museums, and for newly collected individuals in French Guiana using  $\mu$ CT-scans. Preliminary analyses of this data set revealed the distinctiveness of Guianan specimens, which have much more dome-shaped skulls than others.

These very promising results need to be completed by more extensive geographical and taxonomic sampling. From the molecular side, we now have collected and sequenced a total of 289 individuals for the mitochondrial D-loop marker. This provides a database from which we chose a first set of 48 representative samples for solution-based target enrichment of 1034 carefully selected single-copy nuclear exons in all classically described species and the distinct mitochondrial lineages revealed within *D. novemcinctus*. This first NGS experiment is currently ongoing and should also allow assembling the complete mitogenomes. These data will constitute a necessary first step towards understanding the phylogenetic relationships and biogeography of long-nosed armadillos. However, in this second year, we need to collect more morphological and molecular data to determine the taxonomic status as well as to circumscribe the geographical distribution of the Guianan lineage that likely represents a new species.

### **Risk assessment of the emergence of zoonotic viruses as a result of the invasion of *Ae. albopictus* in the Amazonian rainforest - TIGERAMAZON**

PI : Frédéric DELSUC

*MIVEGEC, Montpellier*

**Abstract :** Epidemic transmissions of Emerging Infectious Diseases (EIDs) have increased in the last 30 years mainly as a result of social, demographic and environmental transformations. Mosquito-borne diseases (MBDs) are among the most serious EIDs, for example Dengue viruses (DENV) and Chikungunya viruses (CHIKV), which are responsible for recent epidemics and outbreaks around the world. Recently, these traditionally “tropical” MBDs have spread into temperate areas as a consequence of globalization and increased transcontinental exchanges, which have fostered the diffusion of viruses and vector mosquitoes. In this context, local emergence of any arboviral disease can rapidly translate into a global threat. *Aedes* (*Stegomyia*) *albopictus* is an invasive mosquito species with origins in the forested areas of Southeast Asia and which has spread across the world.

This species spread to South America in 1985 in Brazil, and subsequently established itself in Argentina, Paraguay, Colombia, and Venezuela, but mainly throughout Brazil. This invasion has potential health consequences as *Ae. albopictus* is known to support the development and transmission of more than 25 arboviruses under laboratory conditions, and has now been recognized as a primary epidemic vector of DENV, CHIKV and Zika virus. In Brazil, *Ae. albopictus* is mainly reported in periurban and rural environments, sometimes close to the Amazon rainforest. To date, little study has been made of its capacity to invade forest environments in Brazil and elsewhere in South-America. In the tropical areas, and particularly in Central Africa, the species has colonised sylvan environments where it interacts with wildlife and potentially with zoonotic pathogens. Such a situation generates a new risk for the transfer of emerging viruses from wildlife to humans. The main goal of this project is to assess this risk in the Amazon forests. For this purpose we will investigate penetration of *Ae. albopictus* in forested areas of Brazil. We will also study its blood-feeding behaviour and collect *Ae. albopictus* to screen for sylvan arboviruses.

### **Diversity, distribution and host specificity of three model symbionts in hummingbirds - TROCSYMB**

PI : Christophe Thebaud & Javier Pérez Tris

*EDB Toulouse & Universidad Complutense de Madrid*

**Abstract :** Hummingbirds are a unique environment for symbionts due to their high metabolic rates, extreme flight aerodynamics and small size. Here we want to explore the diversity and host specificity of avian blood parasites, feather mites and Avipoxviruses of this exclusive radiation of birds in the lowland rainforest of French Guiana. As hummingbirds have the highest metabolic demands in the vertebrate world and this is associated with erythrocyte adaptations, we hypothesize that their parasites will be specialized with exceptional host exploitation strategies. Furthermore, the fast wing movement of hummingbirds, with over 60 wing beats per second, poses a challenge for the distribution and persistence of feather mites. These symbiotic organisms have adapted to a specialized lifestyle on the feathers of most bird species in the world. By studying mite diversity and spatial distribution on hummingbird wings, we aim to uncover unique morphological and behavioral adaptations to this singular habitat. Finally we want to explore the prevalence and diversity of skin lesions caused by Avipoxviruses in hummingbirds, which are likely to be particularly affected by these infections due to their very small size compared to other birds. This comprehensive analysis of the symbionts of hummingbirds from French Guiana will contribute to the discovery of new species and symbiotic lifestyles, giving an excellent opportunity to improve our understanding of the evolution of host-symbiont interactions in megadiverse environments.

### **Undergrowth Acoustic Communication of “Earless” Frogs - UACEF**

PI : Antoine Fouquet

*CNRS Guyane*

**Abstract :** Acoustic communication depends on an efficient emission, propagation and reception of the signal. The system fails if one of these elements is disrupted. However, some frogs lacking a middle ear are still able to hear. The aim of this study is to get insights on how frogs lacking a middle ear behave and use sound to communicate. We will address this question using the acoustic communication system of the minute toad *Amazophrynella minuta*, a diurnal bufonid that lives in the French Guyana rainforest, as a model system. The acoustic propagation environment and the acoustic behavior of the toad will be studied using a double array of microphones. Acoustic

stimulation under natural conditions will be employed to test its sensitivity and to decode its calls. Finally, we will investigate the neural mechanisms of this system by measuring the evoked neural responses to sound, either free-field sound (loudspeaker) or local sound stimulation by earphones attached to the body wall or head region. This study will shed light on the evolutionary processes that led to the loss of the middle ear.

## Validating methods for quantifying the drought response of tropical trees, and implications for modeling - WILT

PI : Isabelle Marechaux

*EDB, Toulouse*

**Abstract :** Tropical forests are expected to experience an increase in drought intensity and frequency under climate change. It is critical to better quantify and model their ability to withstand or adapt to these changes. However only limited amount of data on the physiological responses of tropical trees to drought is currently available. Leaf water potential at turgor loss point ( $\pi_{tip}$ ) and the vulnerability of xylem to cavitation (as measured by  $P_{50}$ ) both are good proxies of ecological drought tolerance in tropical trees and they are good candidates to parameterize and improve predictions of both mechanistic and statistical forest models. However, established links between these species parameters of drought tolerance and tree response patterns to drought are still lacking. Here we propose to explore these links, by measuring on the same trees,  $\pi_{tip}$  and  $P_{50}$  on the one hand, and variation of tree hydraulic state as soil dries on the other hand, through measurements of leaf pre-dawn water potential, leaf midday water potential, stomatal conductance and sap flow at both the beginning and the end of the dry season. To this end, we will take advantage of the newly established COPAS instrument (Nouragues station, French Guiana) that enables easy access to canopy trees, and of the already acquired expertise in the group. We will then assimilate field-measured traits into several modelling frameworks. These models will be used to assess how drought-related water stress may modify tropical forest functioning.

## Traditional knowledge and technological properties of construction timbers in French Guiana: from old knowledge to new uses - WoodUses

PI : Jacques Beauchêne

*EcoFog, Kourou*

**Abstract :** Studies of local knowledge related to nature in French Guiana are numerous on medicinal plants, but much fewer studies are dedicated to technical plants like the uses for basketry, dugout or long bow. At the same time, a lot of studies show that local people have very important ethnobotanical and ethnoecological lore, e.g. more than 1100 species are known and named by Wayãpi people. Nevertheless wood as building material, a major traditional use, has never been studied. One year ago, we started a research in order to better understand traditional uses in building. We cross, in a multidisciplinary study, an ethnobotanical approach of local knowledge with a technological approach in wood sciences. First, the field surveys highlighted that the technological properties of woody species traditionally used are poorly known by scientists and foresters because of their low exploitable diameter. Finally, the first technological tests emphasize that some of woody species used for traditional housing have very interesting mechanical proprieties (high specific modulus of elasticity). These results led us to explore these exceptional woods to make a higher added-value products for niche market such as in musical instrument making. The violin bows are of special interest in this context because wood properties are essential to the final quality, and

because historic tropical woods used by bow makers are more and more difficult to stock up. The aim of the project is to focus on a deeper exploration of woody species used by Amerindian community and characterize their properties on a large number of specimens. Thanks to this project, the challenge is to go up to the evaluation of the potential of these woods for highly technical use, through the production of violin bows to be tested by specialized bow makers craftsmen and musicians.