

DNA from air for biodiversity surveys

PI : Pierre TABERLET

LECA, Grenoble

Abstract : DNA metabarcoding is now routinely implemented for assessing biodiversity using water, soil, and sediment samples, not only for microorganisms, but also for plants and animals. Airborne particles have also been used for assessing microorganisms diversity (bacteria, archaea, fungi). However, they had never been used to assess plant and animal biodiversity, despite a few mentions in the literature showing that plant and animal cell remains are present in the air. Here, we propose to test if airborne particles can provide biodiversity information about plants and animals. We suggest to carry out this pilot experiment in the Nouragues field station (CNRS), using the COPAS that will allow to sample at different level of the forest (ground, canopy, above canopy levels).

Testing collective evolution in Neotropical trees

PI : Myriam HEUERTZ

BIOGECO, Cestas

Abstract : Theoretical models predict that inter-specific hybridization could represent a key factor in the maintenance of highly diverse communities. COLLEVOL will put this prediction to the test by focussing on an under-studied component of tropical forest tree biodiversity: the capacity of related tree species to hybridize and thereby to experience collective evolution, i.e., joint gene pool dynamics. Hybridization research is especially timely in tropical rainforests because current climate and habitat change can profoundly affect interspecific gene flow through habitat fragmentation or phenology changes. We select a taxonomically abundant clade of the Lecythidaceae in French Guiana (FG) containing two systems with high levels of suspected hybridization, the (*Lecythis*) *Corrugata* and the (*Eschweilera*) *Parvifolia* clades. We will generate a ddRAD genome scan on a core collection of sympatric species of these clades and outgroups at four geographic locations, and will build a microsatellite data set in a wide-range collection to address the following specific objectives: 1/ construct a phylogenetic hypothesis based on plastid and nuclear genomic data, 2/ infer the recent/current gene flow relationships in each location, delimit species and infer the phylogeographic history including introgression in the *Corrugata* and *Parvifolia* clades, 3/ test neutral and adaptive facets of collective evolution, identifying enlarged effective population sizes (e.g., delaying extinction of rare taxa) and characterizing the genomic fraction of candidate genes under selection along with their putative function and putative selective drivers. Solid estimates of phylogenetic relationships and population genetic history and a highly replicated study design (for geographic sites, genomic markers and focal clades) are ideally suited to tease apart alternative explanations for allele sharing, namely incomplete lineage sorting vs. hybridization and introgression. We thus expect to discover the first empirical evidence for collective evolution in tropical forest trees, characterizing the impact of proximal evolutionary processes for the maintenance of highly diverse communities.

The Role of colouration in structuring dragonfly communities

PI : Julien RENOULT

ACTE, Paris

Abstract : Communication mediates interactions between organisms, and as such it is expected to play a fundamental role in both the phylogenetic diversification of lineages and in determining patterns of species co-occurrence. Yet community-level studies have mainly focused on noncommunicative traits to understand the links between the ecological and evolutionary processes

that underlie species assemblages. In the DRAGON project, we will investigate the determinants of species assemblage at different spatial scales in Guyanese dragonflies and damselflies (Odonata) emphasising the role of socio-sexual visual signals. We will test a hypothesis where habitat openness and competitive exclusion antagonistically select on dragonfly colouration and determine assemblages at the habitat and community scales, respectively. The project relies on the collaboration between a visual ecologist, a community ecologist and a field odonatologist. DRAGON will allow centralising observations and constituting a database of occurrence and ecology for a group of insects 1) the Amazonian diversity of which has remained largely unexplored, and which are increasingly recognized as 2) key indicators of freshwater ecosystems and as 3) important Service Provider Units in pest control. DRAGON will also require the development of new, state-of-the-art techniques to analyse differences and similarities in visual phenotypes, which we expect will be very influential in visual ecology and evolutionary biology more generally. Overall, the DRAGON project will make significant advances in both our knowledge of the Amazonian biodiversity and in fundamental questions in ecology and evolution.

Evolutionary venomomics of ants

PI : Niklas Tysklind

ECOFOG, Kourou

Abstract : Venoms target many major physiological pathways and tissues, and thus form a rich source of novel molecular probes, therapeutics and biopesticides. Given the great species diversity of ants (Hymenoptera: Formicidae) with more than 13,000 described species (1) and huge potential for novel chemical compounds, ant venoms may be considered to be a new frontier in the search for bioactive peptides and structural protein novelty. Despite such potential, the limited amounts of venom found in ants has hindered in-depth exploration of ant venoms. These limitations can now be overcome by recent developments in “integrated venomomics” where the individual venom toxins are inferred at the transcript level and confirmed by mass spectrometry. This integrated venomomics strategy has revolutionised the field of toxinology in snakes (2), cone snails (3) and, spiders (4) but has never been applied to investigate ant venoms. By combining transcriptomic and proteomic analyses we propose to explore and characterise the diversity of venoms on a suite of Neotropical ant species. Besides their bioprospecting potential, the rich diversity of ants and their contrasting associated ecological traits, provide a creative playground for testing hypotheses on the molecular evolution of venoms. The selective pressures for fast acting venoms in arboreal ants compared to terrestrial ants will be tested in three genera of the subfamily of Ponerinae (i.e. Anochetus, Odontomachus and, Neoponera), where the great biochemical diversity of their venoms has been highlighted by recent proteomic studies(5-7). The inclusion of a fourth non-ponerine genus, Pseudomyrmex, will allow testing whether the non-predatory use of venom, and the reduction of microbial exposure of an arboreal life, has led to reduced complexity of venom transcriptomes/peptides. This proposal aims to explore this intriguing yet poorly understood toxin diversity in great detail using an innovative multidisciplinary approach that combines ecology, transcriptomics, proteomics, and bioinformatics.

Disentangling the factors shaping gut microbiota diversity across arthropod predators

PI : David DUNEAU & Lucie ZINGER

EDB, Toulouse

Abstract : Since the technical revolution of high-throughput sequencing, the role of gut microorganisms on their host fitness has become the focus of active research. In insects, this has

profound implications for better controlling vector born diseases and, more basically, to better understand the evolutionary history of insect-microbiota associations. Yet, most studies remain fairly descriptive and fail to disentangle the ecological and/or evolutionary processes shaping the insect gut microbiota. In the GUMDROP project, we will determine the respective role of host life history traits, host taxonomy and geographic location on the diversity and composition of the gut microbiota in predatory arthropods. We will conduct an in situ approach in French Guiana tropical forests by sampling specimens with contrasted life history traits and distributed across the phylogeny of arthropods. We will combine this approach with a feeding experiment to test the robustness of the association between the hosts and their microbiota. We believe the GUMDROP project to be at the forefront of what is currently published about insect gut microbiota, especially in tropical areas.

Cascading effects of hummingbird malaria across multilayer ecological networks

PI : Christophe THEBAUD & Javier PEREZ-TRIS

EDB, Toulouse & University of Madrid

Abstract : Ecological relationships involve a complex array of bipartite interactions between organisms, such as mutualism, parasitism or predator-prey relations. All these intermingle to form multilayer ecological networks, in which the outcome of an interaction may have cascading effects on the ecological function of the species associated to the different interactions they maintain with other organisms. However, most research on ecological interactions has been conducted under the monolayer paradigm, which neglects the connections among bipartite ecological networks, thereby providing an oversimplified representation of the structure of biodiversity and the processes that drive its evolution. This project will represent a first step to initiate a research line that analyzes the impact of malaria parasites on hummingbird performance, and the cascading consequences of such impacts upon the role of hummingbirds as (i) mutualists of plants (pollinators), (ii) vehicles for transportation of phoretic plant parasites (flower mites), (iii) vectors of venereal plant diseases, and (iv) hosts of mucosal avian viruses. By embracing this seldom adopted multilayer network paradigm, we expect to make a breakthrough in the understanding of the processes underlying the architecture of biodiversity, as well as the ecological factors that may modulate important ecosystem services such as pollination in Neotropical rainforest.

Microbial community structures in French Guiana ticks: a multi-level study of their origin, diversity and drivers

PI : Olivier DURON

MIVEGEC, Montpellier

Abstract : Understanding how intra-host microbial communities are shaped is one of the most current challenging tasks of microbiology and infectious disease science. Here we propose to address this issue in a medically important group of arthropods, ticks, for which we know little in French Guiana. To spread and persist within tick populations, bacteria typically use a large panel of lifestyle strategies: while some species are vertebrate pathogens, moving from through infectious (horizontal) transmission, some others rather behave as endosymbionts, undergoing maternal (vertical) transmission. This creates a complex web of interactions and dispersion patterns offering an excellent opportunity to tackle questions about the origins, structures and drivers of host-associated bacterial communities at different hierarchical and spatial scales. To this aim, we will first create a tick collection sampled under a metapopulation/metacommunity framework from both anthropic and non-anthropic landscapes. For facilitating tick identification, we will concomitantly develop for

the first time a molecular barcoding system focused on French Guiana tick species. Second, we will finely inventory bacterial diversity through 16S rDNA high throughput sequencing coupled with Multi-Locus Typing Systems (MLST) for some focal bacterial genera. Third, we will characterize bacterial community structures and their drivers. We will combine bioinformatics and statistical tools with critical testing of ecological theory in order to integrate non-pathogenic and pathogenic forms into a more conceptual framework closed to community ecology. We will thus investigate on changes in bacterial community structure with tick species and/or spatial distance and/or hierarchical scales and/or local environments and/or vertebrate hosts on which ticks were collected. Overall, this knowledge is of ecological and evolutionary importance, but also of medical importance since it may directly use to assess the health risks associated to ticks in French Guiana, e.g. Q fever, Brazilian spotted-fever or tick-borne typhus diseases.

Soil responses to drought and nutrients

PI : Clément STAHL & Elodie COURTOIS

EcoFoG Kourou & LEEISA, Cayenne

Abstract : Interactive effects of resources limitation (water and nutrients) on soil functioning remain poorly studied in tropical ecosystem. Understanding the impact of drought events and changes in nutrients availability on belowground microbial communities (structure and activity) is needed to clarify their importance on ecosystem functioning under climate changes. In this project, we propose to conduct an experiment under semi-natural condition in order to disentangle the effect of drought and nutrients availability on soil microbial diversity and activity. We will mimic predictions from global climate models (changes in nutrient stoichiometry and increase drought) by contrasting several treatments with or without rainfall exclusion and with or without nutrients addition (Nitrogen and/or Phosphorus). We will realize a set of measurement before and after treatment in order to characterize changes on belowground microbial communities. More specifically, we will (1) assess microbial community structure and diversity using DNA based technics and (2) estimate microbial activity by determining soil greenhouse gas exchange and enzyme activity. We will follow this experiment during several months (before and after treatment) in order to assess both the immediate effects of drought and nutrients addition on soil functioning and also the capacity of resilience of microbial communities.

Seeking the sources of terrestrial biodiversity in French Guiana by enhancing the fossil record

PI : Pierre-Olivier ANTOINE

ISEM, Montpellier

Abstract : French Guianan terrestrial ecosystems result from a complex history, notably in terms of biogeography. Yet, mostly due to dense vegetation cover and intense soil weathering, the pre-Holocene French Guianan sedimentary record has never been investigated for its paleontological potential. SOURCE aims at unearthing fossil specimens in the field (either animals, plants, or fungi) for documenting past continental biodiversity in the territory of French Guiana, in order to reconstruct hypothetical paleoenvironmental conditions for such a past biodiversity, and to initiate a comparison with coeval assemblages previously described in adjacent regions. In that purpose, the team will scrutinize late Cenozoic fluvial terraces known to crop out along the Maroni River, during an 8 day-trip by boat in October 2016. This may allow for both unearthing macroscopic fossil remains and sampling soft sedimentary rocks for microvertebrates, microfossils, pollen, and spores. Any specimen unearthed during the SOURCE project is then likely to be used in order to give access to an unforeseen window on the sources of French Guianan biodiversity, to provide first-hand data for reconstructing past environmental conditions in French Guiana, and to replace it in the broader context of regional/global climatic and environmental changes recorded throughout the late

Cenozoic. In that sense, SOURCE is an obligate risk-taking first step in order to characterize the source(s) of French Guianan terrestrial biodiversity. The SOURCE team includes paleontologists with an strong experience of interdisciplinary fieldwork (vertebrate and invertebrate paleontology, palynology, and geology) in Amazonia and a renowned practice for scientific outreach, by interacting with scholars, students, pupils, and with civil society.

Mechanisms underlying the evolution of an exaggerated sex-specific trait

PI : Abderrahman KHILA

ENS, Lyon

Abstract : Understanding the origin of the remarkable biodiversity in nature is an important goal in biological studies. On this line, sexual selection is a major contributor of phenotypic diversity, often resulting in the evolution of extravagant phenotypes. Many examples can be observed in nature, including the evolution of exaggerated morphological traits that grow disproportionately larger than other body parts. Despite longstanding interests in the evolution of exaggerated phenotypes, little is still known about the environmental factors responsible for the exaggeration and hyper-variability of these traits. In this proposal, we study an original natural system, the pond skater *Microvelia longipes* found in French Guiana, to understand how various facets of selection can shape phenotypic diversity in nature. This species is characterized by a striking variation in the length of male legs, whereby leg length in some males is exaggerated. Preliminary lab experiments have underlined the role of these exaggerated legs in male-male competition as well as their high nutrient sensitivity compared to other body parts. We aim to develop a multilevel functional approach that combines evolutionary and behavioral ecology, comparative genomics and transcriptomics, to study the origin and evolution of an exaggerated sex-specific phenotype that characterizes this species. To achieve this, we will conduct an exhaustive field investigation of natural populations of *M. longipes* to understand the evolution of this sex-specific exaggerated trait. The project is structured around three aims. Aim (1) what is the specific function associated with the exaggerated trait in nature? Aim (2) what are the costs and benefits associated with the trait, including fitness components. And aim (3) what are the potential factors responsible for the origin of leg length exaggeration in *M. longipes*? This project will provide significant insight into the environmental mechanisms underlying the evolution and maintenance of exaggerated traits. In addition, results from this project will establish a new model system, from French Guiana, to study handicap theory, phenotypic plasticity, and the role of the selective environment in shaping animal diversity. Results from this project will provide a fresh and unbiased insight into the mechanisms underlying species diversification within the context of their ecological environment.