

Ant nesting habits impact on venom peptide activities - ANTPEP

PI : Alain DEJEAN

EcoFog, Kourou

Abstract : Protecting the Amazonian biodiversity has evident scientific and economic importance, including the pharmacological and structural diversity of natural products. The ANTPEP project is a natural continuation to studies on *Pseudomyrmex* predatory behavior and their venom toxicity and composition based on the nesting habits of the species compared (i.e., terrestrial and arboreal species, and, among the latter, plant-ants or obligate inhabitants of myrmecophytes that shelter these ants in hollow structures). The studied terrestrial species possesses 87 linear peptides; the arboreal species possesses 23 peptides, including three with disulfide bonds; and the plant-ant has 26 peptides, including five with disulfide bonds and three dimeric peptides. Our aim is to evaluate the bioinsecticide activities of purified peptides from the *Pseudomyrmex* crude venoms. Cytotoxic bioassays, based on flow cytometry technology, will be conducted on insect primary cell cultures. We propose to determine the mechanism of action (cell cycle, apoptosis, intracellular Ca²⁺ and Cl⁻ concentrations) on purified peptides to highlight a structure-activity relationship. The prospects include sequencing the peptides with insecticidal activities and conducting new pharmaceutical trials to determine which peptides have antimicrobial properties.

Camouflage of conspicuous signals in the Dendrobatidae poison frogs - CAMO

PI : Innes CUTHILL

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Abstract : Aposematism, or warning signals, are used by a wide range of conspicuously coloured toxic animals to advertise their unpalatability to predators. In theory a predator will remember the association between the phenotype and the toxicity and leave the prey unharmed. However, in nature things are rarely so simple and aposematic species do fall prey to predators naïve to the association, or to specialised predators immune to the defence. Indeed, recent research has shown that avian predators may be able to regulate their intake of toxins and balance the associated costs against nutrient gain. Therefore, maximal conspicuousness may not be the best survival mechanism as it increases the encounter rate with potential predators. Our recent unpublished work has demonstrated that the arrangement of aposematic patterning may be determined by principles described in the camouflage literature, in order to switch between conspicuousness and crypsis dependent on context and the viewing distance of the observer. The often asymmetric and disruptively distributed patterns of the poison frog, *Dendrobates tinctorius*, implies that aposematism is not maximised for long distance signalling, and that camouflage is favoured at greater viewing distances. This makes it an ideal model system for testing our hypothesis. We aim to establish the signalling properties of *D. tinctorius* in relation to observer viewing distance and background.

Comparative analysis of physiology and parasitism of neotropical birds - COMPAREBIRDS

PI : Philipp HEEB
EDB, Toulouse

Abstract : Tropics are hotspots of biodiversity, and a part of this extreme diversity resides in cryptic life-history trait variations among species. Our current understanding of the physiological factors governing life-history evolution in birds is heavily biased by studies carried in the temperate zones. Life histories of tropical birds remain poorly explored and are currently based on a handful of species studied. We propose a research project that aims at widening our knowledge on tropical birds by collecting multiple physiological and parasitological parameters from a significant number of avian taxa. With the use of phylogenetic comparative analyses, our main goal is to understand how different components of the immune system, telomere dynamics and stress hormones are shaped by tropical environments. Furthermore, by examining the microbial and parasite communities infecting birds we will be able to explore the degree in which phylogeny shapes the associations between the levels of antigen exposure and their anti-bacterial host responses. In summary, this study will greatly expand current knowledge on the relationships between physiological and parasitological characteristics of the Neotropical avifauna.

Ecological Genomics of species divergence in *Heliconius* butterfly – EcoGenHel

PI : Brian COUNTERMAN
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Abstract : This proposed study aims to further our understanding of the rich biodiversity of French Guiana by uniquely combining genomic techniques with mathematical Ecological modeling. This will offer the first fine scale study of the spatial distribution of population genomic variation and how it directly relates to isolating barriers within and between (*Heliconius*) species. Species distribution models are traditionally been used to determine the relative importance of environmental and ecological factors on patterns of species distributions. However here we propose to use these models in a fundamentally different way, one that offers a better understanding of how different reproductive isolating barriers influence genomic divergence during the incipient stages of speciation. By implementing modeling into a landscape genomic approach we are afforded the ability to measure the relative contribution of different isolating barriers to genomic divergence. Leveraging the collaborative nature of *Heliconius* community we will then be able to place these data into a larger genomic and evolutionary context that will ultimately contribute to resolving one of the most amazing adaptive radiations.

Hydraulics and Sap of Trees from the Amazonian Tropics - HydroSTAT

PI : Damien BONAL & Louis SANTIAGO

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Abstract : Tree mortality during drought has been documented in forests worldwide. However, we still do not understand why tropical trees show diverse responses to drought, with some species suffering high mortality rates during drought while other species do not. This proposal combines measures of xylem vulnerability with osmotic potential of xylem, phloem and laticifers for an overall physiological picture of species-specific drought resistance. Trait databases will be used to evaluate plant hydraulic strategies with respect to axes of ecological strategy variation. The data will be related to species composition in forest plots across French Guiana to determine whether species distribution patterns across precipitation gradients are related to drought resistance.

Adaptation at innate immune genes in Primates: divergence and polymorphism in New World Monkeys - IMMUNOPRIM

PI : Emilie LECOMPTE

EDB, Toulouse

Abstract : Wildlife populations evolved under environmental pressures which impacts the inter- and intra-specific variability of the genome. Pathogens engage with their host a permanent conflict and are assumed to be important drivers of genetic diversification among and within host species. As a result of this evolutionary dynamics between host and parasites, organisms have evolved sophisticated innate and adaptive immune system. Immune function genes are likely to experience strong parasite-driven selective pressures. Wildlife immunogenetics has mainly focused on adaptive immunity. But these genes account only a fraction of the variation among individuals in pathogen susceptibility. The evolutionary ecology of innate immune genes remains poorly understood. The objectives of the project are to 1/ identify, for some innate immune genes, variations of the evolutionary rate and signature of selection in Primates lineages and 2/analyze using haplotypes the structure and the genetic variability of two sympatric New World Monkeys species to identify the level of polymorphism and possible signature of selection on the innate immune genes. This will allow us to better understand the genetics of immune adaptation in Primates at different timescales.

Monitoring Incipient Speciation of *Drosophila* in Amazonia - MONISPEC

PI : Wolfgang J. MILLER

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Abstract : The MONISPEC program is aimed to monitor and record the tempo and mode of the ongoing speciation process in Amazonian *Drosophila* species belonging to the neotropical willistoni

species group in their natural habitats of French Guiana in real-time. We furthermore aim to compare their natural speciation dynamics to our experimental speciation data obtained under artificial conditions in our laboratory performed with the classic neotropical *Drosophila* lab strains that were originally sampled by Dobzhansky in the 1960s. Systematic collections from the Guiana region 50 years ago have uncovered the coexistence of four different *Drosophila paulistorum* semispecies with overlapping habitats, but due to the expression of complete sexual isolation against each other they never interbreed in the wild. Forced inter-semispecies crosses under lab conditions, however, give rise to hybrid offspring that suffer high embryonic F1 mortality and complete hybrid male-sterility. We recently have demonstrated that sexual isolation of this species group is caused by the mutualistic, strictly maternally-transmitted, intracellular bacterium named Wolbachia, which causes bi-directional cytoplasmic incompatibilities in forced inter-semispecies hybrids. Moreover we found that Wolbachia of *D. Paulistorum* specifically localizes to defined brain regions associated with female mate recognition. These observations strongly imply that Wolbachia can manipulate and orchestrate natural host sexual behavior by priming the neuronal pheromone-perception/interpretation circuit in female flies. Hence the neotropical *Drosophila*-Wolbachia symbiosis system provides an excellent biological model for deciphering the sexual isolation mechanisms that trigger incipient speciation at both levels, i.e., pre- and postzygotically.

Gene flow and riverine barriers in the Guiana Shield: a multitaxon test across the Oyapock River – MUStARd

PI : Antoine FOUQUET & Luciano NAKA

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Abstract : One of the most striking biogeographic features of Amazonia is that rivers often delimit the distributions of animal species. Therefore, it is not surprising that the first model proposed to explain the origin of Amazonian biodiversity invoked rivers. According to the riverine barrier hypothesis, rivers could act as barriers, structuring biological populations and ultimately promoting speciation. Despite its long-standing history, empirical support for this hypothesis remains controversial. In this proposal, we aim to study the current role of rivers as barriers in three different groups of animals: birds, frogs, and harvestmen (Arachnida). Because the permeability of riverine barriers may depend on the characteristics of the rivers and on the dispersal ability of focal species, we will test the level of gene flow across the lower, middle, and upper Oyapock River in selected taxa with high and low dispersal capabilities. The rivers of the Guiana Shield (GS) run over Precambrian rocks and are thus more channeled and supposedly have more stable courses over time than the large white water rivers of the Amazonian floodplain, where a weak support for the riverine barrier hypothesis has been recovered. Therefore, GS rivers can be expected to represent efficient long-term barriers to gene flow for terrestrial species. Previous studies have substantiated the correspondence between the course of the rivers in the GS and phylogeographic breaks and distribution boundaries in frogs and birds. We will sample frogs, birds and harvestmen species on both margins of the Oyapock River from its headwaters to the estuary, and examine the genetic structure using one mtDNA loci for 10 species of each group and genome wide NGS data for a subset of the species of each group. These data, which will represent the first of the kind across any Amazonian river, will be used to test if

levels of gene flow increasing towards the headwaters, and whether the pervasiveness of a riverine barrier varies according to specific traits expected to provide different dispersal abilities.

The adaptive value of a novel marker of drug susceptibility in Amazonian *Plasmodium falciparum* parasites – PlasmoDynEvol

PI : Stéphane PELLEAU & Lise MUSSET

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Abstract : *Plasmodium falciparum* malaria is a deadly disease endemic in French Guiana. After decades of treatment with chloroquine, parasites acquired high level of resistance and this drug was abandoned. Since then, parasites progressively regained susceptibility to this molecule. In this project we will use transfection experiments to validate the contribution to the current chloroquine susceptible phenotype of a candidate mutation we recently identified. We will then question the adaptive value of this genotype in order to understand why it spread in the parasite population. We will test different hypotheses of adaptation by proposing different mechanisms by which this genotype might increase fitness: increased growth rate, increased capacity to produce sexual forms (transmission advantage), decreased susceptibilities to the drugs used after chloroquine withdrawal, or competitive advantage of parasites harboring the mutant allele vs. the wild-type in mixed culture. Therefore, in addition to the biological validation of a new genetic marker of drug susceptibility, this work will help to provide inferences about the dynamics and mechanisms of *P. falciparum* evolution, a crucial issue regarding the public health importance of this pathogen in French Guiana.

Reconsidering protective ant-plant mutualisms from a nutritional perspective - ProNut

PI : Jérôme ORIVEL

EcoFog, Kourou

Abstract : Myrmecophytism is a common mutualism in tropical rainforests wherein plants provide ants with a nesting site and/or food resources in exchange for protection from herbivores and competitors. Yet, recent observations suggest that some myrmecophytic plants also benefit from recycling nutrient-rich ant waste. Moreover, some evidence indicates that microorganisms may mediate this nutritional interaction. Although these findings may completely modify our vision of the outcomes that drive the evolution of myrmecophytism, our knowledge of plant nutrition by ants is still too weak to draw broad conclusions. The aim of the present project is to reconsider myrmecophytism from a nutritional perspective. We propose to analyze nutrient flows between seven broadly distributed species of myrmecophytes in French Guiana, 11 ant partners and the associated microbiome using both correlational and experimental approaches. Moreover, we will conduct fine scale morphological and ultrastructural analyses of the plants to search for the specific structures that permit nutrient uptake. Using this information, we expect to be able to reconsider the evolution of myrmecophytism in response to both protective and nutritional selection pressures.

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

PI : Frédéric DELSUC

Institut des Sciences de l'Evolution, Montpellier

Abstract : With their Pan-American distribution, long-nosed armadillos (genus *Dasybus*) constitute an understudied model for Neotropical biogeography. Our project aims at deciphering the evolutionary history of the seven extant species with special focus on the biogeography of the widespread nine-banded armadillo (*D. novemcinctus*). Our analyses based on two mitochondrial genes and a nuclear locus show that this ubiquitous species might in fact form a species complex with notably a highly divergent lineage restricted to French Guiana. Following from these surprising results, we will use an integrative approach coupling next-generation sequencing with cutting-edge 3D-geometric morphometric techniques. Solution-based target enrichment will be used to obtain both complete mitochondrial genomes and genomic data for 1047 carefully selected single-copy nuclear exons and flanking sequences in 96 representative individuals. In parallel, geometric morphometric measures will be collected for specimens available in museums and for newly collected individuals in French Guiana. These data should allow resolving the phylogenetic relationships of long-nosed armadillos, determining the taxonomic status of French Guiana populations, and reconstructing in details the biogeography of *D. novemcinctus* with focus on the role of the Guiana shield. These data will constitute a necessary first step towards understanding the exceptional adaptive potential of this species distributed across a wild diversity of habitats and environments across the continent.

Evolutionary history of mammal-trypanosome associations in the Guiana Shield – TRYPShield

PI : Miguel PINTO

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Abstract : Comparative biology studies of host-parasite associations (e.g., phylogenetics, phylogeography, and coevolution of immunity and infection) are not common because of difficulties in accessing representative samples and acquiring relevant genetic data. However, study of evolutionary associations between mammals and their trypanosome parasites are now highly feasible because of advances in DNA sequencing, an abundance of genomic resources for mammals and trypanosomes, and comprehensive tissue collections as available for the Guiana Shield. With these advantages, I propose to meet the following four key objectives: Objective 1: Survey mammalian trypanosomes from the Guiana Shield using preserved tissues. Objective 2: Determine the phylogenetic relationships and biogeographic origins of the mammalian trypanosomes of the Guiana Shield. Objective 3: Analyze host associations and phylogeographic patterns of *T. cruzi* in this

complex biogeographic region. Objective 4: Understand genetic aspects of the evolutionary arms-race between mammals and trypanosomes. It is expected that the results may constitute a valuable model for understanding the joint evolutionary history of hosts and parasites. The methods applied in this research can be extrapolated to other organisms, in particular to blood-borne parasites that cannot be cultured easily and to hosts not easily encountered in the wild. The laboratory and analytical methods used in this project will provide a new spin to the use of traditional biodiversity tissue repositories; with the new DNA sequencing technologies and the available genomic information, is becoming possible to do work that a few years ago was restricted to model species only.