CeMEB - Scientific Day (September 24th, 2020)

Scientific basis of Exploratory Research projects (call for project 2017 – no.1)

9:20-9:40	PI	Unit
	Florent Liégeois	**MIVEGEC**
Partners	**Serge Morand**	**ISEM**
AWARE	**zimbAbWe bAt viRusEs screening**	
Key words	**Emerging viruses, Bats, phylogeny, Host-virus interaction**	
Abstract	Viral outbreaks represent a major health challenge for human societies. The last two decades have been marked by dramatic viral epidemics that have heavily impacted human health, social relations and the globalized economic system. To date, the COVID-19 pandemic is still unresolved. Three of these emergent episodes are the result of cross-species transmission of Coronavirus (SARS-CoV-1, Mers-CoV and SARS-CoV-2). SARS-CoV-1 and Mers-CoV were initially transmitted to mammals (civets and dromedaries respectively) by bats before infecting humans. The SARS-CoV-2 probably originates from bats. In this context, the identification and characterization of viral populations circulating in bat colonies is an essential step in the implementation of sentinel surveillance and the development of detection tools for these microorganisms. The CeMEB AWARE Project "Bat virus screening in Zimbabwe" is part of this approach. Bats habitats of different species (frugivores and insectivores) have been selected. Human populations living near these colonies are exposed to the faecal and urinary excreta of these animals either through the collection of guano in the caves or through the establishment of agricultural crops under the trees sheltering some of these bats. The faeces were collected and tested with molecular tools for the detection of different viral families.	

9:40-10:00	PI	Unit
	Guilaume CASTEL	**CBGP**
Partners	**François CHEVENET**	**MIVEGEC**
PALADIN	**PuumALA DIversity & evolutioN**	
Key words	**Puumala virus, diversity, evolution, phylogeography**	
Abstract	The PALADIN project aimed to better understand the circulation, diversity and evolution of a zoonotic virus in France, the Puumala virus (PUUV), responsible for cases of nephropathia epidemica (NE). The virus circulates mainly in an endemic zone comprising the north-eastern quarter of the country, but its presence is probable outside this zone. During the project, trapping of bank voles, the PUUV's exclusive reservoir, took place in four regions considered to be non-endemic for the NE. Serological and virological analyzes allowed the detection of the virus in the Morvan massif for the first time. Phylogenetic analyzes have determined that viral isolates from this region are genetically very similar to those from another previously identified non-endemic region, the Sologne forests. Phylogeographic analyzes were carried out using the PastView software (www.pastview.org), designed, produced and published as part of the PALADIN project. PastView integrates a set of inference and visualization tools to help identify evolving scenarios. Three main routes of independent dispersion of PUUV have thus been identified on a European scale. At the French level, we propose a scenario of the evolutionary history of the various identified clusters of PUUV.	

10:00-10:20	PI	Unit
	Guillaume Charrière	**IHPE**
Partners	**Olivier Duron** **Jean-Christophe Auguet**	**MIVEGEC** **MARBEC**
AMIBADAPT	**Exploring marine AMoebae and their endosymbionts as an environmental intracellular ADAPTive niche for pathogen emergence**	
Key words	**Free-living amoebae, endosymbionts, marine environments, pathogen emergence**	
Abstract	Amoebae are heterotrophic protists which feed on bacteria by phagocytosis. As a result of this predation, some bacteria have developed resistance or escape strategies, and in some cases, can even behave like endosymbionts. During the AMIBADAPT project, we explored the diversity of marine amoeba in the Mediterranean coastal marine environment and the endosymbiotic bacteria associated with them to assess their potential role as a reservoir for pathogenic bacteria. Following a sampling campaign, 18s barcoding analyzes of the diversity of amoebae revealed that the majority of amoebae present in this environment belong to two distinct taxonomic groups, the Paramoebae and the Vannellae, the benthic diversity being greater than the planktonic diversity, and the benthic composition tending to be specific to the sampling site. By carrying out 16s barcording analyzes on clonaly isolated amoebae, we have identified associations between some of these amoebae with bacteria belonging to Chlamydiae, Vibrionaceae, Legionellaceae and Rickettiaceae. We were able to confirm further the association of Vibrionaceae with amoeba of the genus Vannella by FISH, and the first phylogenetic data indicates that these vibrios are related to groups of pathogenic vibrios in the Splendidus clade, and they may represent a distinct taxonomic group which is still poorly characterized. In the coming years, we will investigate further the interactions between marine amoebae and their association with vibrionaceae and their related pathogenic neighbors.	

10:45-11:05	PI	Unit
	Mélanie DEBIAIS-THIBAUD	**ISEM**
Partners	**Emilie FARCY**	**MARBEC**
SKEL'ESTRO	**Effect of (xeno)estrogens in skeleton development: a comparative approach in chondrichthyan and teleost fishes**	
Key words	**Skeleton development, vertebrates, fish, (xeno)estrogen, evolution, estrogen signaling**	
Abstract	Of natural or synthetic origin, estrogenic compounds are waterborne environmental contaminants able to interact with the endocrine system at very low concentrations (ng/L to µg/L). The Skel'estro project has questioned investigated the potential impact of these compounds on the skeletogenesis at early developmental stages in two vertebrate species: a teleost fish (the european seabass *Dicentrarchus labrax*) and a cartilaginous fish (the lesser spotted catshark *Scyliorhinus canicula*). The first objective was to determine and characterize the genetic actors involved in estrogenic regulation of skeletogenesis. In a second step, experimental exposures were performed to evaluate their impact on skeleton mineralization and on gene expression patterns. In the case of the seabass which is a bony fish, we detected transcriptional activation in chondrocytes, osteoblasts and osteoclasts at the initiation of ossification. These observations correlate with higher bone development in the case of exposure with 0,4 and 40 ng/L of 17-beta-estradiol or 1,6 µg/L bisphenol-A (BPA, a known xenoestrogen). Similar perturbations are still to evaluate in the catshark. This complementary collaboration led to better understanding of several biological aspects in both species: characterization of skeletogenesis-related genes and their genomic loci; description of accessible phenotypic traits for skeletal development in early stages; functional tests of estrogenic compounds in the regulation of development.	

11:05-11:25	PI	Unit
	Aurélie CELERIER	**CEFE**
Partners	**Maeva ORLIAC**	**ISEM**
PYGMHIPPOCOM	**Olfactory and acoustic communication in the pygmy hippopotamus**	
Key words	**Olfaction, Hearing, Evolutionary history Behaviour, Anatomy, CT scan, Cetartiodactyla**	
Abstract	Communication is a relatively well-documented theme among cetaceans, but this field remains almost unexplored among hippos, their current closest relatives. In particular for the endangered pygmy hippopotamus (Choeropsis liberiensis, for which there is no data on the involvement of hearing or olfaction in communication. The aim of this behavioral and morphological study is to explore the anatomical supports and functional characteristics of these two sensory modalities. The morphological observations made by CT scan at ear level (tympanic bubble, ossicles of the middle ear, structures associated with the cochlear canal, innervation and irrigation of the cochlea) highlight adaptations of the auditory system to the amphibious lifestyle. They also indicate specialization in low frequency perception in accordance with behavioral findings indicating a vocal repertoire and low frequency perception optimum. The morphological description of the cribriform plate of the ethmoid bone (surface, shape, number, size and distribution of foramina) gives a first image of peripheral olfactory innervation in this taxon. At the same time, the ethological study shows that these animals are able to perceive and discriminate the odors of their conspecifics. Being solitary and territorial, these data should be considered in a context of spatial and sexual competition. Thus, our pioneering study brings new fundamental knowledge on the sensory abilities of these semi-aquatic mammals and opens broader perspectives concerning amphibious communication in cetartiodactyls.	

11:25-11:45	PI	Unit
	Pierre-André Crochet	**CEFE**
Partners	**Frédéric Veyrunes**	**ISEM**
SPECISEX	**Investigating the role of sex chromosomes in reproductive isolation and speciation**	
Key words	**Speciation, introgression, hybrid zones, genomics, RADseq, reptiles, karyotype, sex chromosomes, systematics**	
Abstract	The aim of the project is to examine whether the divergence of sex chromosomes facilitates the evolution of reproductive isolation. To test this hypothesis, we will collect data on hybridization and introgression in several secondary contact zones to examine whether the evolutionary lineages that differ in their sex chromosomes show higher levels of reproductive isolation compared with lineages that do not differ in sex chromosomes. We have selected two species complexes within the genera Podarcis and Acanthodactylus (lizards family Lacertidae) as models, because we have preliminary data suggesting multiple independent contact zones in these complexes. During the project, we essentially established the feasibility of the project by developing the karyotyping, since it was the first time that lizard karyotypes were performed on the Cyto-Genomics platform (Julie Perez, ISEM) and we had never carried out a RADseq project on lizards in Montpellier either. The two methodological components of the project were successfully developed in Montpellier during this project and we obtained extremely encouraging preliminary results. Despite a comparable amount of speciation, the Podarcis species show a remarkable uniformity in sex chromosomes while on the contrary the Acanthodactylus species have revealed a remarkable diversity of ZW sex chromosomes, from tiny and homomorphic to large and very heteromorphic. In addition, the RADseq analyzes confirmed a very strong reproductive isolation in Podarcis, and in Acanthodactylus we also identified several instances of speciation between lineages that differ strongly in their sex chromosomes. To reach the objectives of the project, we still need to characterize the karyotypes of a few lineages and continue the acquisition of genomic data to assess the level of reproductive isolation in all contact zones. When this is done, we will have karyotypes and measures of admixture in about twenty secondary contact zones, allowing us to examine the link between reproductive isolation and the degree of differentiation of ZW chromosomes.	

11:45-12:05	PI	Unit
	Catherine Girard	**ISEM**
Partners	**B. Meyer-Berthaud**	**AMAP**
MARCON	**Biotic responses of faunas and floras to abiotic changes in deep time**	
Key words	**Marine and continental ecosystems, survival strategies, Devonian**	
Abstract	The MARCON project was aimed at better understanding the abiotic changes associated with the Devonian/Carboniferous (D-C) boundary event 360 million years ago, as well as the timings and processes of the biotic responses. For this purpose, the diversity and disparity of the ancient communities had to be estimated in order to target marine and continental ecosystems in the same integrative approach and determine whether their responses were synchronous or not. The analyses revealed geographical, temporal and especially morphological diversification of the floras and faunas. For floras, a systematic replacement of spore-yielding plants and a significant morpho-anatomical diversification of trees and reproductive structures in the lignophyte clade are observed. For marine fauna, the increasing complexity of the geometry of their mouthparts is interpreted as a possible response to competitors who are diversifying as a result of the D-C crisis.	

13:30-13:50	PI	Unit
	Elena Kazakou	**CEFE**
Partners	**Marie-Pierre Chapuis**	**CBGP**
DINER	**exploring Domestication Impacts on plaNt-insEctbacteRia interactions**	
Key words	domestication, *Locusta*, bacteries, plant defences	
Abstract	Domestication modified growth rate and nutrient contents of crop plants to fit human needs. It has also eventually reduced defence against herbivores, and inadvertently impacted leaf microbial communities, which could interfere with plant-insect interactions. Hence, domestication affected herbivores life history and behaviour in several ways. Examining whether and how selection of specific plant attributes can alter herbivores behaviour through phylosphere modifications is crucial in the agroecological context. We explored these potential cross-effects with a wheat-locust-system. We hypothesized that modern wheat cultivars are less resistant to herbivory and better fill the nitrogen requirements for locusts than ancient cultivars. We expected modern wheat cultivars to decrease the gregarious behaviour of locusts, promoting coherent migrations. To test these hypotheses, we select 20 cultivars from the domestication history of tetraploid wheat Triticum turgidum in two experiment. The first experiment was set-up on the CEFE campus (platform Labex “terrain d’experience CEFE”) and was composed of two treatments “Control” (C) and “Herbivory with locusts” (H). Several traits were measured: Resistance traits related to structural defences, Resistance traits related to chemical defences, tolerance traits related to plant growth, Traits related to nutritional values. The second experiment was a cafeteria realised in the UMR CBGP were the locust’s preferences for the 20 genotypes were estimated. Our results showed that selection of productive cultivars during domestication and modern selection has a negative effect on plant defence efficiency. Modern wheat cultivars better fill the nitrogen requirements for herbivore growth and survival. Contrary to pour hypotheses, we found that accessions that herbivory effects were higher in wild accession than in ancient mostly due to the higher leaf production of the ancient accessions. Finally we demonstrated that induced effects of herbivory on plant traits will differ during domestication.	

13:50-14:10	PI	Unit
	Joannès GUILLEMOT	**Eco&Sols**
Partners	**Xavier MORIN** **Eric NICOLINI**	**CEFE** **AMAP**
DIVTROP	**What biological mechanisms link biodiversity to tropical forest functioning? A tree experiment in Brazil**	
Key words	**above-belowground relationships, carbon and nutrient cycling, forest restoration, Mata Atlântica, tree diversity, soil (micro)organisms**	
Abstract	Tree diversity influences key ecosystem processes and services currently supplied by forests, but the relationships between forest biodiversity and ecosystem functioning remain poorly understood, especially in the tropics. Moreover, the effects of diversity on ecosystem functioning rely on complex feedback loops between tree and soil that needs to explored in an integrated framework. In this context, the DIV-TROP project gathered a multidisciplinary team to design and implement a new tree diversity gradient experiment in the Mata Atlântica biome, southern Brazil. The MataDIV experiment indeed aims to provide both new knowledge on tropical forest functioning and scientific bases to forest restoration programs. MataDIV includes a manipulation of tree diversity (from monocultures to 6-species mixtures), nutrient fertilization and through fall exclusion to explore the interactive effects of tree diversity, soil fertility and water stress on ecosystem functioning. An extensive soil characterization of the experiment was conducted before planting, as a “t=0” reference to quantify the interactions between tree diversity and soil functioning, and the way these interactions build with time. The soil physicochemical properties and the diversity (i.e. functional diversity, species diversity and species richness) of soil bacterial and fungal communities were characterized, and their variations across the experiment and the soil profiles were explored. MataDIV is a long-term multidisciplinary research platform that will aim at fostering innovative collaborations in the years to come.	

14:10-14:30	PI	Unit
	Doyle McKey	**CEFE**
Partners	**Philippe Hinsinger**	**Eco&Sols**
FUNRAFI	**Functioning of soils under wetland raised-field agriculture**	
Key words	**agroecology, biodiversity-based agriculture, self-organization, soil engineers, wetland**	
Abstract	In different parts of the world, farmers make raised fields in wetlands to provide flooding-intolerant crops with well-drained soils. Raised-field agriculture has attracted most scientific interest in the Neotropics, where long- abandoned vestiges of pre-Columbian raised fields cover large areas. Ironically, little is known about wetland raised-field agriculture where it is practiced today, notably in Africa. In Mossaka, Congo Republic, we conducted the first detailed study of how wetland raised fields are built and maintained, and how their soils function. Soil profiles in raised fields of different ages and different phases in the field/fallow cycle showed that addition of topsoil and plant biomass during field construction, and periodic addition of these materials after fallows, leads to great activity of soil meso- and macrofauna, creating well-drained, porous soils. Mineralization of decomposing organic matter in subsurface layers leads to high N and P availability for 1-2 years following field construction or rehabilitation. As fields age, and with increasing depth in soil, nutrient availability decreases and soil physical properties become less favourable for plant growth. In less than 40 years, bioturbation and decomposition erase stratigraphic traces of field construction and management. Our results open new questions into the ecology of wetland agriculture, and suggest new lines of inquiry into the geoarchaeology of pre-Columbian raised fields.	

14:30-14:50	PI	Unit
	Éric Garnier	**CEFE**
Partners	**Errol Véla**	**AMAP**
FUNBIOME	**Plant FUNctional BIOgeography in the Mediterranean**	
Key words	**Biogeography, climatic change, drought, environmental gradients, functional diversity, plant traits, scientific and data syntheses**	
Abstract	Understanding how biodiversity and its various dimensions relate to the environment lies at the roots of ecology and is required to address key pending challenges in ecology, such as: the prediction of changes in the composition of vegetation and ecosystem services in responses to global change components or the understanding and prediction of vegetation distribution from local to global scales. Many ecological models thus strongly depend on reliable quantifications of such relationships. Yet our understanding of these relationships remains fragmentary and inconsistent, seriously impeding our capacity to answer pressing ecological questions and predict how ecological systems respond to changes, be they natural or human-induced, local or global. The overall ambition of the FUNBIOME project is to fill this knowledge gap, which is key to identify which species and ecosystems are at risk in a changing world. By generating advances on how the functional dimension of biodiversity relates to components of global climatic changes such as temperature and drought across the Mediterranean Biogeographic Region, the project contributes to the advancement of basic knowledge in a Region which is both a biodiversity and a climatic hotspot.	

15:20-15:40	PI	Unit
	Guila Ganem	**ISEM**
Partners	**Carine Brouat**	**CBGP**
DRANGE	**Environmental and evolutionary Drivers of species distributions and RANGE limits**	
Key words	**Population genomics, Niche modelling, aridity, demography, adaptation, rodents, Africa, RAD-seq, RNA-Seq**	
Abstract	We aimed to address the environmental and evolutionary drivers of the distribution and range limits of two sister species having evolved in contrasted environmental conditions (arid versus mesic). We sampled the two species across a gradient of aridity, and from the core to the edge of their overlapping distributions. We performed Rad-sequencing across populations. It enabled us to ascertain the taxonomy of the species complex, and to determine within and between species divergence and evaluate hybridization in the contact zones. Preliminary analyses indicated no sign of recent hybridization and relatively little introgression between the species. They also suggested smaller population sizes of the mesic species at contact zones compared to core areas. Genetic differentiation was significant among populations of both taxa. The next step (which has been postponed due to the Covid-19 pandemics) is to conduct comparative analyses of the past demographical dynamics of both species within core and edge populations. We also applied 3 types of widely used SDMs to model the species potential ranges under current and future climatic conditions (at the 2070 horizon), and used one extreme climate scenario (MIROC RCP 8.5) to explore potential variations under climate change. Our preliminary results indicate that the way absences or pseudoabsences are chosen has a very important impact on the model projections. For example, a strategy that relies solely on optimizing predictive power usually selects precipitation variables only for the arid species, and potentially misses some of the dynamics that are linked to the temperature gradients in the region. The type of statistical model used had a smaller influence on the results, and ensemble forecasting was usually adequate to find consensus between predictions.	

15:40-16:00	PI	Unit
	Yunne Shin	**MARBEC**
Partners	**Philippe Verley**	**AMAP**
USBIO	**Uncertainty in Scenarios of BIOdiversity**	
Key words	**Biodiversity scenarios, ecosystem models, uncertainty analyses, global changes**	
Abstract	Scenarios are invaluable tools to guide long term strategic policies, prompt management actions and increase public awareness on future threats to biodiversity. To increase scenarios impacts on policies and trigger appropriate management responses, USBIO aimed at developing a framework to quantify the uncertainty linked to future projections of biodiversity. Based on the expertise of a group of scientists skilled in modelling and statistics, working in terrestrial and marine ecosystems, developing diverse scenarios of global changes, USBIO was able to review a range of dedicated methods to address uncertainty in biodiversity scenarios. Specific case studies in marine and terrestrial realms allowed to address different sources of uncertainty (parameter, structural, internal variability) and ultimately to formulate some generic guidelines that could be transferred to the broader scientific community.	