

PhDays
2019

6 & 7 Juin
Centre IRD
Amphithéâtre des Plantes

Pour s'inscrire



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Thursday 6th June

9h30 – Opening

**Session 1 : Diseases control and prevention for plants and Human
chairman: Mathilde HUTIN**

9h35 – Risk assessment of arboviral diseases transmission using an epidemiological biomarker of human exposure to Aedes bites in Abidjan, Côte d’Ivoire – **Hubert ZAMBLE Bi Zamblé – MIVEGEC**

9h55 – Cassava Bacterial Blight in Côte d’Ivoire – **Michaëlle Andrée Célestine TOURE – IPME**

10h15 – Effet de l’allèle de résistance aux insecticides L1014F du gène VGSC sur le rythme d’activité des anophèles vecteurs du paludisme – **Amadou Sékou TRAORE – MIVEGEC**

10h35 – Coffee break.

10h55 – Report and characterization of bacterial diseases caused by Xanthomonas oryzae in Senegal – **Hamidou TALL – IPME**

**Session 2 : Usage and conservation of biodiversity
chairman: Marion PICARD**

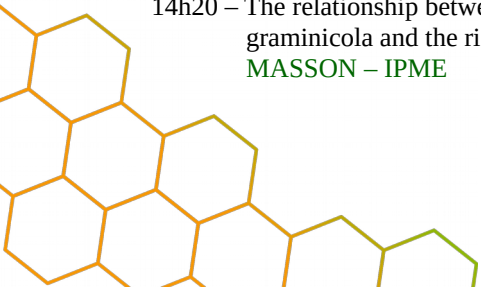
11h15 – Evolutionary cradles and museums of plant diversity in tropical Africa – **Léo-Paul DAGALLIER – DIADE**

11h35 – Characterization of microbial diversity implicated in phytostabilisation in a context of rehabilitation of the former Kettara mine, Morocco – **Najoua MGHAZLI – HSM**

11h55 – Lunch break.

14h00 – Effet de la gestion des résidus d’abattage sur la biodiversité du sol et ses fonctions associées dans les replantations d’hévéa en Côte d’Ivoire – **Aymard KOUAKOU KOUAKOU – ECO&SOLS**

14h20 – The relationship between the plant parasitic nematode M. graminicola and the rice root microbiome – **Anne-Sophie MASSON – IPME**





Session 3 : Evolution and adaptation through different models
chairman: Thomas VAIN

14h40 – Evolutionary history of a plant root parasite: *Meloidogyne graminicola* – Ngan PHAN THI – IPME

15h00 – Coffee break

15h20 – Evolutionary history of the savanna palm species *Borassus aethiopicum* (Coryphoideae) in West Africa – Mariano Joly KPATENON – DIADE

15h40 – Adaptation of Burkholderia to different types of interactions with rice: comparative genomics and transcriptomic approach – Adrian WALLNER – IPME

16h00 – Differential codon usage preferences are conserved in in-paralogous genes throughout Chordata – Fanni BORVETO – MIVEGEC

Friday 7th June

Session 4 : Mechanisms of development and interaction
chairman: Kevin BELLANDE

9h35 – Nucleoporin MLP1 is a non-canonical actor of ploidy maintenance in Trypanosomatid parasites – Akila YAGOUBAT – MIVEGEC

9h55 – Impact of AP2/ERF transcription factors on rice panicle development – Ai My LUONG – DIADE

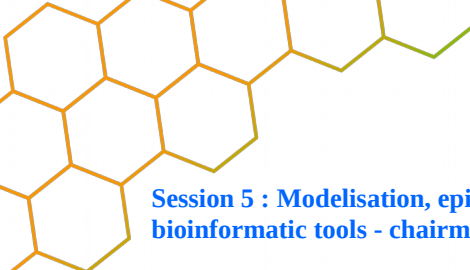
10h15 – Investigating the role of G-quadruplex binding proteins in the maintenance of genome integrity in malaria parasites – Pratima GURUNG – DIMNP

10h35 – Coffee break.

10h55 – Dynamics of cell division patterns and their role on germ cell fate acquisition during ovule primordium development in Arabidopsis – Elvira HERNANDEZ LAGANA – DIADE

11h15 – Comparative analysis of rice sensing of plant-beneficial Burkholderia – Eoghan KING – IPME





Session 5 : Modelisation, epidemiology and development of bioinformatic tools - chairman: Marie SIMONIN

11h35 – Socio-cultural dynamics associated with the propagation of Xpm in cassava crops in the Colombian Caribbean – **Dario PEREZ – IPME**

11h55 – Lunch break.

14h00 – Impact of future climate change on species providing Non-Timber Forest Products in tropical Africa: Consequences on their distribution and economic consequences – **Eldys AMOUSSOU – DIADE**

14h20 – COUSIN (COdon Usage Similarity INDEX): A normalized measure of Codon Usage Preferences – **Jérôme BOURRET – MIVEGEC**


14h40 – Analysis and modeling of trajectories of drifting fish devices in tropical ocean areas and estimation of beaching risk – **Taha IMZILEN – MARBEC**

15h00 – Coffee break.

15h20 – Ebola virus at the human-wildlife interface and animal reservoir of Ebola virus in DR Congo - **Placide MBALA KINGEBENI – TransVIHMI**

15h40 – Thermal pace-of-life strategies improve phenological predictions in ectotherms – **Quentin STRUELENS – CEFE**

16h20 – Prize giving ceremony



Thursday 6th May

- **Session 1 : Diseases control and prevention for plants and Human – chairman: Mathilde HUTIN**

- 9h35 – Risk assessment of arboviral diseases transmission using an epidemiological biomarker of human exposure to Aedes bites in Abidjan, Côte d'Ivoire – **Hubert ZAMBLE Bi Zambélé**^{1,2,3}, Andre SAGNA^{2,3}, Maurice ADJA A.^{2,4}, Negnorogo COULIBALY^{2,4}, Anne POINSIGNON³, Franck REMOUE³. – **MIVEGEC**

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4. UFR Biosciences, University of Felix Houphouët Boigny, Abidjan, Côte d'Ivoire

Human exposure to Aedes' bites, therefore to the risk of arbovirolosis, is not uniform and current entomological tools are unable to measure this contact at the individual level. Identifying the most vulnerable people or neighborhoods would make the fight against Aedes more focused and effective. The aim of this study was to evaluate the heterogeneity of children's exposure to Aedes stings in urban areas in Africa using the specific salivary biomarker (anti-Nterm-34kDa IgG).

A cross-sectional study was conducted in November 2015 on 813 children aged between 9 months and 14 years residing in three neighborhoods of Abidjan: Anoumambo, Bromakoté and Petit-Bassam. The ELISA technique allowed to measure Aedes aegypti's Nterm-34kDa salivary peptide IgG antibody level on sera collected.

Our results showed that children residing in Bromakoté and Petit-Bassam had a higher level of specific IgG responses compared to those in Anoumambo ($P < 0.0001$). In addition, young children in the 1-5 age group had higher specific IgG levels than those in the 11-14 age group ($P = 0.031$).

The anti-Nterm-34kDa IgG is a relevant indicator that health authorities could use to target populations most at risk of arbovirolosis in urban areas.

Keywords: Aedes; arbovirolosis; urban; salivary biomarker, Abidja.

- 9h55 – Cassava Bacterial Blight in Côte d'Ivoire – **Michaëlle Andrée Célestine TOURE – IPME**

The aim was to survey the widely used varieties and point out the most vulnerable to Cassava Bacterial Blight (CBB). It was also to assess cassava farmers' knowledge on climate change and CBB for a better management. The information were collected through surveys in the seven agro-ecological zones (AEZ) of Côte d'Ivoire in 2017. A total number of 302 farmers were interviewed. Fields were assessed for the frequency of varieties presence, severity index (SI), disease incidence (DI) and high severity index (HSI) of CBB. The results indicated that most of the farmers were illiterate. They were able to identify changes occurred in climate and their impacts on cassava. Deforestation and fire bushes were mostly designed as factors of climate change and the adoption the displacement of planting dates was their best adaptation strategy to the changes. Concerning CBB, it was unknown by them. For the varieties, three of them were predominately recorded and are locally known as Akama, Yace and Yavo. Yavo was found more susceptible than Akama and Akama than Yace to CBB. These results constitute a base for the measures of farmers' and the varieties vulnerability to climate change and CBB evolution.

Keywords: Climate change, Cassava Bacterial Blight, Varieties, Côte d'Ivoire, Farmers.

- 10h15 – Effet de l'allèle de résistance aux insecticides L1014F du gène VGSC sur le rythme d'activité des anophèles vecteurs du paludisme – **Amadou Sékou TRAORE – MIVEGEC**

Le paludisme, en dépit des efforts de lutte, reste un problème majeur de santé publique en Afrique subsaharienne. En l'absence de vaccin, l'utilisation massive des moustiquaires

imprégnées d'insecticide (MII) demeure le principal moyen de prévention du paludisme. L'efficacité des MII à réduire la transmission repose sur le fait que les anophèles vecteurs piquent principalement au milieu de la nuit, et empêchent ainsi le contact homme-vecteur.

Mais des études récentes montrent un changement du comportement de piqûre des vecteurs en réponse à l'utilisation des MII, avec la présence de plus en plus de moustiques piquant à des heures précoces ou tardives de la nuit, lorsque les personnes ne sont plus sous leurs moustiquaires. Chez les anophèles à l'instar d'autres insectes, maints comportements sont contrôlés par des horloges endogènes circadiennes, déterminant leur occurrence au bon moment au cours de la journée. Aussi, on a observé que les mutations du gène *VGSC* conférant une résistance aux insecticides peuvent perturber certains comportements des moustiques. Il est donc pertinent vérifier si les mutations du gène *VGSC* pourraient avoir un impact sur les rythmes d'activité des anophèles vecteurs.

Pour appréhender le comportement de piqûre décalé observé sur le terrain chez les anophèles vecteurs, nous avons donc comparé au laboratoire l'activité de locomotion de la F1 issue d'une population naturelle d'*Anopheles gambiae* s.l afin d'identifier des différences dans la structure temporelle de l'activité selon la présence ou absence de la mutation L1014F.

Mots clés : Anophèle, Paludisme, Rythme, Résistance.

- 10h35 – Coffee break.
- 10h55 – Report and characterization of bacterial diseases caused by *Xanthomonas oryzae* in Senegal – **Hamidou TALL – IPME**

Xanthomonas oryzae PV. *oryzae* (*Xoo*) was reported in Senegal in the 1980s by Trinh et al. But no strain of *Xoo* was isolated and no other report was made. However, *Xanthomonas oryzae* PV. *oryzicola* (*Xoc*) has not been reported in Senegal so far. The selection of BB and BLS resistance genes is based on their efficacy against the most virulent *Xoo* and *Xoc* breeds in the region. The absence of studies on *Xanthomonas* in Senegal means that no strategy has been pursued to control these diseases. We aim to confirm Trinh's observations. To do this, surveys were conducted in the main rice growing areas between 2014 and 2016. Leaf samples were collected and analyzed. After bacterial isolation, a PCR multiplex was used to confirm the presence of *Xanthomonas oryzae* PV. *oryzae* and *oryzicola* at different sites in each region. IRBB lines were used to identify the *Xoo* breed. We also assessed the presence of *Tal3C*, *Tal2g*, *AvrXa18*, *AvrXa1* and *AvrXo1* on *Xoc* strains. We plan to look at genetic diversity of *Xanthomonas* by VNTR analysis.

Keywords: Report, characterization, Senegal, races, rice, *Xanthomonas oryzae*.

- **Session 2 : Usage and conservation of biodiversity - chairman: Marion PICARD**
 - 11h15 – Evolutionary cradles and museums of plant diversity in tropical Africa – **Léo-Paul DAGALLIER**, Steven Janssens, Olivier J. Hardy, Jan J. Wieringa, Gilles Dauby, the RAINBIO consortium, Thomas L.P. Couvreur – **DIADÉ**

Uncovering where species diversify and persist over evolutionary time is fundamental to better understand the biodiversity and for conservation. Here, for the first time, we identify cradles and museums of angiosperm diversity across tropical Africa, one of the most biodiverse and unique places on Earth.

Regions containing significant concentration of young (neo-) and old (paleo-) endemic taxa were identified by analyzing the distribution of over 1700 genera combined with a novel time-calibrated phylogenetic tree.

At the generic level, phylogenetic diversity and endemism are mainly concentrated in the biogeographically complex region of Eastern Africa. We show that mountainous areas are both

centers of neo- and paleo-endemism. The lowland rain forest of the Guineo-Congolian region is characterized by widespread and old lineages.

We show the vital role played by mountains acting simultaneously as cradles and museums of tropical African plant biodiversity. In contrast, lowland rain forests act mainly as museums of diversity. Further refining our comprehension of the processes shaping African biodiversity, potentially at the species level, will be important to confirm our results.

Keywords: Plants, endemism, tropical Africa, biogeography, evolution, conservation

- 11h35 – Characterization of microbial diversity implicated in phytostabilisation in a context of rehabilitation of the former Kettara mine, Morocco – **Najoua MGHAZLI, Dr. BRUNEEL Odile – HSM**

Mining activities generate high quantities of polluting waste. When sulphide minerals are present in these wastes, they can form –in the presence of water and oxygen- acidic effluents, rich in metals and metalloids, known as acid mine drainage. The former Kettara mine (Morocco), produced more than 3 million tons of mineral waste deposited in the environment. A scenario of rehabilitation of this mine comprise the deposit of an alkaline phosphate layer on top of Kettara acid tailing to limit the infiltration of water and to neutralize acid mine formation. Revegetation of the site is the final step. However, the mining substrates are generally of poor quality to allow the installation and the growth of plants in semi-arid area, with a destructured soil, very rich in phosphate and possibly contaminated with metals and metalloids.

Microorganisms could strongly accelerate the process of phytostabilisation. They are also strongly involved in plant growth. Other organisms can also be implicated on the mobilization-immobilization of metals and metalloids in the soil.

In our study, microbial communities present in the phosphate layer were characterized using Illumina-MiSeq sequencing in order to identify these communities. Among those microorganisms, some have plant growth promoting traits and can be beneficial for the establishment of a vegetative cover.

Keywords: Microbial diversity, Phosphate mine, Illumina sequencing, Kettara mine.

- 11h55 – Lunch break.
- 14h00 – Effet de la gestion des résidus d’abatage sur la biodiversité du sol et ses fonctions associées dans les replantations d’hévéa en Côte d’Ivoire – **Aymard KOUAKOU KOUAKOU, Dr Alain BRAUMAN – ECO&SOLS**

Ce projet se situe dans la problématique générale de substitution de modes culturels basés sur des intrants chimiques par des modes de gestions plus durables, basés sur la gestion des résidus organiques. Ces modes alternatifs doivent être évaluées notamment sur les aspects biodiversité et les fonctions-services associées. Le modèle choisi est l’hévéaculture qui constitue un modèle pertinent pour mesurer l’impact des pratiques agricoles. En effet, les fortes pressions foncières et demandes en caoutchouc naturel ont conduit les planteurs à privilégier les modes intensifs de culture. L’objectif de cette thèse est de déterminer si l’apport de matière organique après replantation, peut améliorer le fonctionnement biologique du sol. Notre hypothèse est que la vitesse de résilience du système sol suite à la perturbation due à l’abatage, sera d’autant plus rapide que la quantité de résidus d’abatage sera importante. Cette hypothèse sera testée sur deux plantations d’hévéa situées en Côte d’Ivoire dans des contextes pédo-climatiques différents. L’étude de la biodiversité concernera la macrofaune, la mésofaune (collembolés), la microfaune (nématodes) et les microorganismes. En parallèle le fonctionnement du sol sera suivi avec le kit de terrain BIOFUNCTOOL (mesures liées au cycle du carbone, de l’azote et au maintien de la structure des sols).

Mot clés : Matière organique, Biodiversité fonctionnelle, Restauration, Sol.

- 14h20 – The relationship between the plant parasitic nematode *M. graminicola* and the rice root microbiome – **Anne-Sophie MASSON**, Hai HO BICH², Marie SIMONIN¹, Hue NGUYEN THI³, Pierre CZERNIC¹, Lionel MOULIN¹, Stéphane BELLAFFIORE¹ – **IPME**

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². Vietnam Academy of Science and Technology, Hanoi, Vietnam

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Meloidogyne graminicola, also known as the rice root-knot nematode, is the most damaging plant parasitic nematode, especially on rice in Asia. This obligate soilborne parasite creates galls that disturb the root morphology and physiology. It also impacts the interactions in the communities of root-associated bacteria that are essential for the plant health. Therefore, it is important to uncover the relationship between *M. graminicola* and the rice root microbiome. During this event, I will present results obtained from a survey we conducted in Northern Vietnam in 2017. We collected infected and non-infected roots from naturally infested rice fields. Using a metabarcoding approach, the results show that the structure, the diversity and the predicted functions of the bacterial communities are modified by *M. graminicola* infection. Such a shift in the rice root microbiome could be responsible for the host susceptibility in the field. In order to control this pest, using resistant cultivars in combination with agroecological practices could increase the soil resilience to this plant pathogen.

Keywords: microbiome, biocontrol, interaction, microbial ecology, gall-inducing nematodes, rice.

- **Session 3 : Evolution and adaptation through different models - chairman: Thomas VAIN**

- 14h40 – Evolutionary history of a plant root parasite: *Meloidogyne graminicola* – **Ngan PHAN THI** – **IPME**

M. graminicola (Mg), commonly named as the rice root-knot nematode (RKN), is one of the most prevalent plant-parasitic nematodes in rice agrosystems. Mg distributed worldwide, mainly in Asia and America, recently found in Europe and Africa. However, Mg was recently discovered (ca. 40-50 years ago) and still poorly documented. Understanding of its origin, genomic structure, and intraspecific diversity would offer a better knowledge of how this nematode successfully damaged rice in many different environments. Previous studies on nuclear ribosomal DNA (nrDNA) suggested a close phylogenetic relationship between *M. graminicola*, *M. oryzae* and *M. exigua* despite their different modes of reproduction, main host and geographical distribution. In order to clarify the evolutionary history of these species and to explore their molecular intraspecific diversity, we sequenced the genome of 12 *M. graminicola* isolates, representing populations of worldwide-spread origins, and two South American isolates of *M. oryzae*. High heterozygosity in their nuclear genome plus the detection of divergent homologous genomic sequences suggest a hypothesis of the hybrid origin of that both species. *kmer* analysis point out to a distinct ploidy level in each species, compatible with a diploid *M. graminicola* and a triploid *M. oryzae*. Phylogenetic analyses of mitochondrial genomes and three nuclear genomic sequences confirm close relationships between these two species, with *M. graminicola* being a putative parent of *M. oryzae*. Similar approaches should be done also in *M. exigua*. The hypothesis of hybrid origin of *M. graminicola* should be improved in the whole genome level. A reference genome sequence for *M. graminicola* is necessary for the detection of divergent homologous in whole genome sequences and for comparative analysis between *M. graminicola*, *M. oryzae* and *M. exigua*. Furthermore, Fluorescence *in situ* hybridization will be used to detect the presence of divergent copies on chromosomes of *M. graminicola*. In addition, comparative mitogenomics of those 12 *M. graminicola* isolates with a Chinese published isolate reveals only 15 polymorphisms that are phylogenetically non-informative. This low intraspecific diversity, coupled to a lack of phylogeographic signal, suggests a recent worldwide expansion of *M. graminicola*. To confirm this, investigating intraspecific diversity among Mg isolates at the genome-wide level is necessary. In parallel, a study on the evolution clock of Mg will add a specious knowledge about the evolutionary history of Mg species.

Keyword: Evolution.

- 15h00 – Coffee break
- 15h20 – Evolutionary history of the savanna palm species *Borassus aethiopum* (Coryphoideae) in West Africa – **Mariano Joly KPATENON – DIADE**

A large part of the species' distribution area in Africa is found in the continent's savannah areas. These savannahs have also been subjected to different climatic fluctuations known in the past. However, these vast tracts of land are home to several species that have been little studied until now. *Borassus aethiopum* Mart, a savannah palm, which stands out in the vegetation due to its large size is naturally distributed in tropical African regions not covered by large vegetation. This palm is widely exploited by local populations because it offers multiple socio-economic services. Very few studies have been conducted on this slow-growing species, and those that are known focus on its morphological features and therapeutic properties. In my PhD work I will reconstruct the evolutionary dynamics of *Borassus aethiopum*. To achieve this aim, an intra-specific sampling of *Borassus* palm across west African has been done. A total of 133 nuclear genes were sequenced for 90 individuals leading to good inter and intra specific variability useful for phylogeographic analyses. The genetic structure will be inferred using clustering approaches. Molecular dating will be performed using BEAST and fossil data to reconstruct the temporal dimensions of this species evolution. These different results will allow me to infer the evolutionary dynamics of this important savanna palm species.

Keywords: Evolution, phylogeny, phylogeography, *Borassus aethiopum*.

- 15h40 – Adaptation of *Burkholderia* to different types of interactions with rice: comparative genomics and transcriptomic approach – **Adrian WALLNER – IPME**

The microscopic soil population is immensely diverse. A multitude of organisms, bacteria, fungi, oomycetes and insects compete for their niche and the available nutrients. Members of the genus *Burkholderia* are perfectly adapted for this environment and are found in all kinds of soils all over the world. They can intimately interact with every type of soil inhabitant, either as symbionts or pathogens but are also highly studied for their biocontrol and bioremediation abilities. With a few exceptions *Burkholderia* harbor a genome of significant size, which allows them to adapt to various conditions and environments. Beyond the genus, this versatility can be observed intraspecifically. Different strains, belonging to the same species can be observed in water, air, soil, the rhizosphere, the plant endosphere, on animals and as human opportunists.

Throughout my thesis, I aim at studying the diversity within the *Burkholderia* genus at a genomic level. Using a transcriptomic approach and Tn-seq I will examine a subset of *Burkholderia* species with focus on their adaptation to plants. As *Burkholderia* count among the few plant endophytes carrying a type 3 secretion system, I strive to explore the involvement of this macromolecular system in the adaptation of endophytic bacteria to their host plant.

Keywords: plant-bacteria interaction, comparative genomic, transcriptomic, Tn-Seq.

- 16h00 – Differential codon usage preferences are conserved in in-paralogous genes throughout *Chordata* – **Fanni BORVETO, Ignacio G. Bravo – MIVEGEC**

The Polypyrimidine Tract Binding protein 1 (PTB, also known as PTBp1) functions mainly as a splicing regulator and found in most chordate species. It has two paralogs that seem to be tissue restricted: PTB2 (aka nPTB) – in neurons - and PTB3 (aka ROD1) - in hematopoietic cells - which are identical up to 70-80% to PTB1. We used the PTBp1-2-3 gene of 60 diverse chordate species in order to study the phylogeny, codon usage bias and how the two are related. The phylogenetic reconstruction of these sequences shows three well defined branches, one for each paralog, where the inner structure of each branch respects the species tree. This indicates that the appearance of paralogs took place before the emergence of the different chordata clades. The codon usage analysis of these sequences revealed that independently of the species and its taxonomic clade, the three paralogs have distinct codon

usage preferences. In fact, the GC3 content of PTB1 is very high, while PTB2 is A-T rich in all species. PTB3 also shows an A-T rich profile, although less marked than PTB2.

Our results suggest that a sustained constrained directional mutational landscape has differentially shaped codon usage preferences of in-paralogs in chordates. We think this directional selection is compatible with Ohno's model of evolution by gene duplication, where duplicates accumulate mutations, which then permits the gene to acquire new functions or maintain the original function in different conditions.

Keywords: Codon usage bias, Evolution, protein synthesis, Information transfert fidelity.

Friday 7th May

- **Session 4 : Mechanisms of development and interaction - chairman: Kevin BELLANDE**

- 9h35 – Nucleoporin MLP1 is a non-canonical actor of ploidy maintenance in Trypanosomatid parasites – **Akila YAGOUBAT**¹, Slavica Stanojic¹, Laurence Berry⁴, Lucien Crobu¹, Nada Kuk¹, Patrick Bastien^{1,2}, Artur Scherf^{2,3}, Yvon Sterkers^{1,5} - **MIVEGEC**

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Trypanosomatids are a group of divergent eukaryotes of medical and economical relevance. Nuclear pore complexes (NPCs) are large multiprotein complexes embedded in the nuclear envelope. The primary function of NPCs is the nucleo-cytoplasmic transport; however, recent research indicates that nucleoporins (NUPs), which are the structural units of NPCs, are emerging as important regulators in other core processes including chromosomal segregation and transcription. Twenty-five NUPs were identified in the Trypanosomatids. Here using CRISPR-cas9, we localized the nucleoporin MLP1 at the nuclear basket of nuclear pores in *T. brucei* and *Leishmania* sp. RNAi knockdown of TbMLP1 led to a severe growth reduction associated with abnormal nucleus and kinetoplast pattern and aneuploidy shown by FISH and flow cytometry analysis. Two days post induction of knockdown, less than 50% of cells remained disomic, as soon as 8 hours post induction, 70% of cells divided asymmetrically; the total number of homologs was odd, suggesting a defect in the regulation of DNA replication and/or chromosome segregation. Our results revealed that TbMLP1 is required to maintain diploidy in *T. brucei*. The role of Mlp1 in DNA replication or chromosome segregation will be further explored by molecular combing and by following the distribution of kinetochores during mitosis, respectively.

Keywords: Trypanosoma, aneuploidy , nuclear pore complex , replication/segregation.

- 9h55 – Impact of AP2/ERF transcription factors on rice panicle development – **Ai My LUONG**, Otho Mantegazza, Thomas Harrop, Carole Gauron, James Tregear, Hélène Adam and Stéphane Jouannic - **DIADÉ**

Panicle architecture is among the most important agronomic traits, which directly relate to rice yield. Grain number, panicle length, primary branch number and secondary branch number are the major components of rice panicle structure. In plants, *AP2/ERF* genes encode transcriptional regulators involved in many developmental and physiological processes. An *in silico* analysis of two RNA-seq datasets of the genus *Oryza* led to the identification of 86 *AP2/ERF* genes expressed during rice panicle development at early stages. Some of these genes might play a role in determining the inter-specific diversity of rice panicle development. For a better understanding of panicle development regulation to improve the rice yield, we

characterize *AP2/ERF* genes of potential interest through functional analysis. Another purpose will be to enhance knowledge of molecular mechanisms involved in the meristem establishment during panicle development, this being a key determinant of panicle architecture. The study results will allow to identify the key factors of rice panicle growth that could be targeted for improvement in breeding programs.

Keywords: rice, panicle, AP2/ERF, gene function, evolution.

- 10h15 – Investigating the role of G-quadruplex binding proteins in the maintenance of genome integrity in malaria parasites – **Pratima GURUNG**¹, Elodie Gazanion¹, Vincent Guitard¹, Satya Pandey², Katrin Paeschke², Patrizia Alberti³, Serge Urbach⁴, Laurent Lacroix⁵, Jose-Juan Lopez-Rubio^{1*} – **DIMNP**

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³. Nucleic Acid Structures, Telomeres and Evolution, MNHN, CNRS UMR 7196, INSERM U1154, Sorbonne University, 43 rue Cuvier, 75231 Paris, France.

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Plasmodium falciparum, a malaria-causing parasite, manifests a complex life cycle involving various morphologically and functionally distinct forms within two different hosts - human and *Anopheles* mosquitoes. The enrichment of G-quadruplex forming motifs in the genome of these AT-biased parasites in the telomeric and sub-telomeric regions, where the virulence genes are present, points towards a role of these motifs in the maintenance of genome integrity and antigenic variation. However, there is a lack of experimental evidence to support this hypothesis. Here, we provide the first comprehensive survey of the G4-interactome to investigate the role of G4-mediated regulatory mechanisms in *Plasmodium*. Using a combination of unbiased (in silico methods) and biased approaches (Yeast one-hybrid and DNA pull-down assay), we have identified ~154 putative G4 interacting proteins in *Plasmodium falciparum*. The orthologs of most of these proteins were shown to interact with G4s, thus strengthening our results. Furthermore, to explore how these candidates contribute to G4-mediated regulatory processes, we have selected some candidates to perform functional studies following validation of their binding properties. Collectively, this study will shed light on this understudied epigenetic regulatory mechanism. Given their essential role in parasite development this study will likely generate new targets for antimalarial drugs.

Keywords: Gene regulation, Malaria, genome integrity and DNA G-quadruplexes

- 10h35 – Coffee break.
- 10h55 – Dynamics of cell division patterns and their role on germ cell fate acquisition during ovule primordium development in *Arabidopsis* – **Elvira HERNANDEZ LAGANA**¹, Ethel Mendocilla-Sato², Célia Baroux², Daniel Grimanelli¹ and Daphné Autran¹ – **DIADE**

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In *Arabidopsis*, the female germline develops from a single subepidermal precursor within the ovule primordium known as the Megaspore Mother Cell (MMC). In recent years, multiple studies have revealed genetic and epigenetic factors implicated in the control of MMC fate acquisition and unicuity. Yet, the role of key morphological cues such as cell division patterns regulating these processes is very poorly understood. By taking advantage of high-resolution microscopy techniques, we have generated a large set of 2D and 3D quantitative data allowing

us to provide evidence that cell proliferation is spatially and temporally controlled within the ovule primordium. Additionally, we found that the tendency of ovules to form supernumerary MMCs is associated with specific alterations of cell mitotic activity within this organ.

Keywords: Plant reproduction, development, microscopy

- 11h15 – Comparative analysis of rice sensing of plant-beneficial *Burkholderia* – **Eoghan KING**, Lionel MOULIN and Pierre Czernic – **IPME**

In the context of plant-pathogen and plant-mutualists interactions, the underlying molecular bases associated with host colonization are well described. However it is not the case for non-mutualistic beneficial interactions or associative symbiosis. Particularly little is known about the transcriptional regulations associated with the “immune tolerance” of crop plants towards beneficial microbes. In this context, the study of the *Burkholderia*-rice model is very promising to describe the molecular mechanisms implicated in associative symbiosis. Indeed several species of the *Burkholderia* genus can colonize rice tissues and have beneficial effects. We produced the transcriptome at 7 dpi of rice plants inoculated with two rice root-associated *Burkholderia* (*B. vietnamiensis*, *B. kururiansis*) through RNA-Seq and proceeded to their comparative analysis. This study revealed that extensive transcriptional regulations occur in leaves throughout the establishment of the interaction at the root level. However important differences were observed, although the studied *Burkholderia* species are phylogenetically closely related, especially the defense response of rice roots during bacterial colonization were very different. We were also able to identify hormonal signaling pathways showing opposite regulations in leaves depending on the inoculated species of which the expression of related genes was analyzed throughout the establishment of the interaction.

Keywords: Rice, *Burkholderia*, Endophyte, RNA-Seq

- **Session 5 : Modelisation, epidemiology and development of bioinformatic tools - chairman: Marie SIMONIN**

- 11h35 – Socio-cultural dynamics associated with the propagation of *Xpm* in cassava crops in the Colombian Caribbean – **Dario PEREZ** – **IPME**

Cassava is a primary crop for food security of thousands of people in the world. In Colombia, the Caribbean region contributes about half of the total production of cassava at the national level, despite the region's socioeconomic difficulties and phytosanitary problems. A major threat to this crop staple production is Cassava-Bacterial-Blight (CBB), which is a disease caused by the bacterial pathogen *Xanthomonas phaseoli* pv. *manihotis* (*Xpm*) able to cause irreversible damage to the plant and impeding growth and productivity. Cassava is mainly propagated by cuttings, which are often distributed from nurseries or exchanged between farmers.

Our objective is to analyze the impact of the social organization and agricultural practices on the exchanges of cassava material by farmers and their effects on CBB dynamics. We will document the sociocultural practices impacting the distribution of *Xpm* in cassava crops, taking as a case study the exchange network of cassava cuttings in peasant and indigenous communities in the Colombian Caribbean. Participant observation will be done to inform individual sociodemographic characteristics, management practices of cassava crop, and perceptions about the incidence of *Xpm*. In addition, cassava leaves will be sampled *in situ* to diagnose the distribution and diversity of *Xpm* in the Caribbean.

Keywords: Agrobiodiversity, Biocultural memory, Economic botany, Local knowledge

- 11h55 – Lunch break.
- 14h00 – Impact of future climate change on species providing Non-Timber Forest Products in tropical Africa: Consequences on their distribution and economic consequences – **Eldys AMOUSSOU** – **DIADÉ**

Climate change (CC) poses new challenges in biodiversity conservation because it influences environmental factors. CC will affect all the levels of biodiversity, from genes to ecosystems.

Tropical rain forests are the most diversified ecosystems on the earth. In Africa, they have a great importance because of their diverse ecosystem services. Indeed, they contribute to the local economy through the exploitation of Non-Timber Forest Products (NTFP) and they participate in the global climate regulation. Evaluating the adaptation and resilience capacities of rain forests is thus essential to improve conservation policies and develop strategies to deal with climate change.

The global objective of this project is to understand the impact of future CC on the flora of Africa through the prediction and the evaluation of their impact on species providing NTFP. Especially this thesis will consist in:

- Modelling the different scenario of NTFPs species spatial dynamics in response to the future CC for different future time periods (2055, 2085)
- Realizing a typology of species (“winners” or “losers”) regardless of the magnitude of the change in climatic suitability
- Modelling the scenario of evolution of tropical biodiversity using the scenario of deforestation in tropical Africa
- Testing the role of protected areas in the mitigation of the consequences of CC on PFNL species
- Evaluating the economic impact of climate change on NTFPs at local and global level in Africa and
- Determining the role of climate change in the actual and future structuration of the genetic diversity of some tropical species.

We will develop a multidisciplinary approach: an approach of modelling of ecological niche that will be re-crossed with economic data on the utilization of species.

Keywords: Climate change, ecological niche modelisation, non-wood forest products, Tropical forests.

- 14h20 – COUSIN (COdon Usage Similarity INdex): A normalized measure of Codon Usage Preferences – **Jérôme BOURRET – MIVEGEC**

Codon Usage Preferences (CUPrefs) describe the unequal usage of synonymous codons at the gene, genomic region or genome scale. Numerous indices have been developed to measure the CUPrefs of a sequence. We introduce a normalized index to calculate CUPrefs called COUSIN for COdon Usage Similarity INdex. This index compares the CUPrefs of a query against those of a reference dataset and normalizes the output over a Null Hypothesis of random codon usage. COUSIN results can be easily interpreted, quantitatively and qualitatively. We exemplify the use of COUSIN and highlight its advantages with an analysis on the complete coding sequences of eight divergent genomes, two of them with extreme nucleotide composition. Strikingly, COUSIN captures a hitherto unreported bimodal distribution in CUPrefs in genes in the human and in the chicken genomes. We show that this bimodality can be explained by the global nucleotide composition bias of the chromosome in which the gene resides, and by the precise location within the chromosome. Our results highlight the power of the COUSIN index and uncover unexpected characteristics of the CUPrefs in human and chicken. An eponymous tool written in python3 to calculate COUSIN is available for online or local use.

Keywords: bioinformatics, Codon Usage Bias, whole-genome analysis, methodology

- 14h40 – *Analysis and modeling of trajectories of drifting fish devices in tropical ocean areas and estimation of beaching risk* – **Taha IMZILEN – MARBEC**

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Over the last decades, purse seine fishing companies have massively invested in drifting fish aggregating devices (dFADs) to increase fishery productivity. However, the use of these devices is associated to a number of potential negative impacts, in particular, beaching events of dFADs in coastal environments which contribute to marine debris and ghost fishing, and pose a threat to sensitive marine habitats, such as coral reefs.

A number of proposals have been made to reduce these negative impacts, including by selective placement and timing of deployments to avoid areas with a high probability of

beaching or by physically removing beached dFADs from landing sites. All of these potential mitigation measures depend on a detailed understanding of where and when beaching events occur. Here, we have done a global retrospective analysis of trajectory data from dFADs deployed by French purse-seiners over the period 2007-2017. Results indicate that not only has the number of beaching events increased in recent years, but the fraction of all deployed dFADs that beach has also increased in the period 2007-2013. We hypothesize that this is because the very large number of deployed dFADs has led to an increasing number of dFADs not being fished upon, giving them more time to beach. We identify coastal hotspots for beachings, and in particular beachings in coral reefs. By backtracking from beaching areas, we identify deployment areas that have a high probability of leading to a beaching event within 3 months. Though many beachings occur in remote areas, a significant number are sufficiently close to a port capable of carrying out a dFAD clean-up operation if proper incentives can be put in place to sustain such operations.

Keywords: Fish aggregating device, Fisheries, Oceanography, Surface currents, Lagrangian transport.

- 15h00 – Coffee break.
- 15h20 – Ebola virus at the human-wildlife interface and animal reservoir of Ebola virus in DR Congo – **Placide MBALA KINGEBENI – TransVIHMI**

Ebola virus, formerly responsible for sporadic epidemics between 10 and 15 years apart in remote rural areas of central and western Africa, is becoming more prevalent in large urban areas. Between 2017 and 2018, DR Congo experienced three epidemics, the last being in progress for about seven months. Although studies on several animal species have shown the presence of antibodies against Ebola antigens or a part of Ebola virus genome-like, the reservoir of this virus is still unknown. We have set up a project in three African countries (DRC, Guinea and Cameroon) to understand how the virus is circulating in wildlife and during inter-epidemic periods in humans living near areas previously affected by the Ebola virus disease. We analyzed 4022 bats (1736 frugivores and 2199 insectivores) and 2611 non-human primates (2258 small monkeys and 353 bonobos) for antibodies to Ebola virus antigens by Luminex technology and detection of Viral RNA by RT-PCR. We also confirmed the 2018 epidemics in the DRC and responded quickly to pertinent public health issues during the current outbreak by sequencing using Illumina technology, as about 50% of confirmed cases could not be linked solely by epidemiological methods.

Keywords: Ebola virus, wild fauna, human, Democratic Republic of the Congo.

- 15h40 – Thermal pace-of-life strategies improve phenological predictions in ectotherms – **Quentin STRUELENS**^{1,2}, François Rebaudo³, Reinaldo Quispe⁴, Olivier Dangles² – **CEFE**

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An advance in phenology—the timing and duration of biological events—of numerous species has been widely recorded and linked to climate change. Phenological variability within a population is widespread in nature and arises from underlying differences in performance, metabolism or behavior among individuals. The “pace-of-life syndrome” explains differences in performance by characterizing slow and fast individual strategies within a population, but has yet to be explored under a phenological context. We hypothesized that taking into account thermal pace-of-life strategies in development rate models would improve phenological predictions in ectotherms. To test our hypothesis, we reared populations of the quinoa moth

(*Copitarsia incommoda*) at several temperatures (4619 phenological observations), and by individually following each individuals, we characterized the proportion of slow and fast individuals within the populations. We then integrated the observed thermal pace-of-life strategies in development into a predictive phenological model through the transformation of the commonly used thermal performance curve into a thermal performance probability. The predictive power of our models were evaluated by confronting the predicted phenology with the observed one, through a cross-validation process. We finally explored our models by generating data for a virtual species with various life-history traits.

Keywords: Ecology, Agroecology, Socio-ecosystem dynamics, Tropical Andes.