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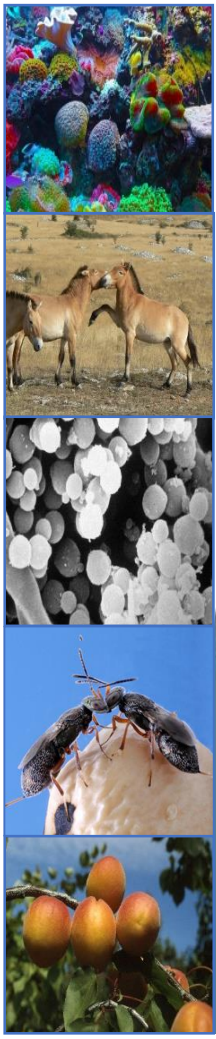

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Diversity and evolution of genetic sex determination in fish

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Abstract

Sex determination evolution in teleost fishes is amazingly dynamic with coexistence of both environmentally- and genetically-driven sex determination systems. In species with genetic sex determination, both classical male (XX-XY) and female (ZZ-ZW) heterogametic systems can be found in closely related species, and even sometime in different populations of the same species. There are also species with more complex genetic sex determination systems relying on polygenic sex determination with or without multiple sex chromosomes. In addition, master sex determining genes controlling the genetic sex determination gene network, and in fine the individual sexualization, are also subject to frequent changes. This presentation will focus on how new genomics resources (genome and transcriptome assemblies), tools (sequencing methodologies, bioinformatics) and approaches (whole genome sequencing, RAD-sequencing, Pool-sequencing) have deeply changed the sex determination research field and how they can be used to better understand the amazing diversity of sex chromosomes and master sex determining genes. Examples will be taken from diverse clades of teleost fishes to illustrate the frequent turnovers of sex determination systems, the variability of sex chromosome differentiation, and the diversity of master sex determining genes and their related mechanisms of action. We will also report on recent results showing that supernumerary B chromosomes can drive sex determination in some fish species and thus could be considered as a new class of unusual sex chromosome (B-Sex).

*Speaker

First evidence of long-lasting association between viruses and the Black soldier fly, Hermetia illucens

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Abstract

Understanding viral diversity is as essential for food security as for human health. Indeed viruses also impact plant and animal used as food. This brings particular economical risks to the burgeoning insect as food and feed industry, promoting more sustainable proteins. In insect farming, viruses cause negative economic impacts to long-established species like honey bees or crickets. More recent models used in the insect industry, such as black soldier flies (*Hermetia illucens,* BSF) may also face viral diseases. but lack of knowledge about any pathogens of BSF, leaves the industry unaware of any potential threats from viruses. There are however increasing reports of symptoms and mortality issues in BSF farms, many of which could fit viral diseases. As traces of contemporary and past viral infections can be mined in transcriptomics and genomic datasets, we undertook a bioinformatic approach to explore publicly available BSF data. A novel EVE discovery pipeline uncovered several endogenous viral elements (EVEs) in 3 BSF genomes. Some EVE sequences were found in all three BSF genomes, indicating ancient integration in the BSF genome. Moreover, using Virsorter2, CheckV and BLAST on assembled contigs and scaffolds, we uncovered several viral sequences associated with multiple genomic and transcriptomic datasets. In particular, transcriptomic data led to the genome assembly of an uncharacterized virus related to a group of EVE sequences. Phylogenetic analysis of this undescribed virus genome sequence placed it in the viral family, *Totiviridae*. Thus we referred to this viral sequence as Hermetia illucens Toti-like virus 1 (HiT virus 1). Of note, a short sequence that is highly similar to one group of these EVEs is expressed in BSF, suggesting possible antiviral activity. Altogether, the results suggest that HiT virus 1 is an exogenous virus producing an active infection, and that related viruses have long been associated with BSFs.

*Speaker

Intra-annual shifts and deterministic assembly of root endospheric microbial communities of the grapevines

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Abstract

Microbial communities provide numerous ecological functions to plants and are essential for plant health and crop production. Understanding dynamics of how microorganisms assemble is therefore one of the pressing challenges in microbial ecology. Many studies have characterised microbial assembly through spatial analyses and have emphasized existing local heterogeneities even at small geographical scales. However, temporal dynamics of microorganisms remain under-investigated despite their significant importance in microbial assembly and therefore, on plant resistance and *fitness*. Here, we focused on the root-microbiota endosphere, because of the intimate link with plants. We sampled 25 fields across a single vineyard at 3 dates (September 2018 and 2019; June 2019) for two types of cultivar to investigate temporal changes and signatures of specific plant stages. We showed remarkable preserved temporal patterns between the two cultivars with very similar microbial communities between the two September dates. In Particular, we found higher Actinobacteria and lower Glomeromycota richnesses in September. Moreover, we demonstrated a high proportion of non random bacterial assembly of the root endosphere, indicating deterministic impact of the plant or the environment in microbial recruitment. Our study suggested the importance of long-term microbial ecology monitoring, within and between years, in understanding complex microbial assembly rules.

*Speaker

Recent advances in bivalve-microbiota interactions for disease prevention in aquaculture

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Abstract

In bivalves, no clear-cut functional role of microbiota has yet been identified, although many publications suggest that they could be involved in nutrition or immunity of their host. In the context of climate change, integrative approaches at the crossroads of disciplines have been developed to explore the environment-host-pathogen-microbiota system. Here, we attempt to synthesize work on (1) the current methodologies to analyse bivalve microbiota, (2) the comparison of microbiota between species, between host compartments and their surrounding habitat, (3) how the bivalve microbiota are governed by environmental factors and host genetics and (4) how host-associated microbes act as a buffer against pathogens and/or promote recovery, and could thereby play a role in the prevention of disease or mortalities.

*Speaker

Macroecology & macroevolution of the oceanic plankton

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Abstract

Plankton are a core component of marine ecosystems with exceptional taxonomic and ecological diversity, yet their global distribution patterns, as well as the historical and contemporary processes driving these patterns, remain poorly understood. I will present research in my group using *Tara* Oceans metabarcoding data aimed at better characterizing the patterns and drivers of ocean plankton diversity. I will first present a global study of eukaryotic plankton biogeography comparing the biogeography of 70 major groups of eukaryotic plankton and showing how body-size and ecological function shape biogeography through the joint roles of transport and the environment. Next, I will present phylogenetic methods that allow understanding how historical events of speciation, extinction and trait evolution shaped present-day diversity patterns, as well as some applications on planktonic groups. I will highlight the difficulties and promise of carrying these types of analyses on the oceanic plankton.

[*]Speaker

Microbial community assembly in a mosaic of marine lichens

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Abstract

Lichens have long been perceived as organisms resulting from symbiosis between a fungus and a photosynthetic partner (an algae or a cyanobacteria). However, many attempts at axenic culture of mycobiont and photobiont have shown the importance of the associated microorganisms in the establishment of the symbiosis. However, how these microorganisms are assembled in lichens, and particularly in seaside lichen mosaics, remains a mystery to this day. In order to answer these questions, we determined, through metabarcoding methods, the composition and distribution of the microbial communities in 6 different lichen species (*Tephromela atra, Ochrolechia parella, Anaptychia runcinate, Xanthoria aureola, Diploschistes caesioplumbeus, Buellia* sp.) assembled in mosaic on a seaside rock. This analysis revealed the presence of the same photobiont (*Trebouxia jamesii*) in almost all lichen except *Xanthoria* (which presented Trebouxia arboricola as a main photobiont). All the lichen presented their respective mycobiont as the most abundant organisms. All lichen species were dominated by *Alphaproteobacteria*. Overall, multivariate analysis revealed a structure of the microbiome per lichens species. On top of the metabarcoding analysis, a survey of the metabolome of the lichen was performed. It showed a majority of fatty acids (anteiso 15:0, 16-methyl 17:0, 18:2 n-6), orcinol and benzoic acid. The comparison between the microbiome and the metabolome revealed the presence of taxon/metabolite associations specific to lichen species. Most lichens had their mycobiont and some bacteria correlated to one or two metabolites. Only *Ochrolechia* did not show any metabolite/taxon association.

*Speaker

High-quality genome assemblies of corals highlight the specifics of their long lifespan

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Abstract

During the last decade, several coral genomes have been sequenced allowing a better understanding of these symbiotic organisms threatened by climate change. Scleractinian corals have an important ecological role and are an essential element of the reefs, which shelter a great diversity of species. Here we generated two coral genomes, Porites lobata and Pocillopora meandrina with unprecedented contiguity that allowed us to study the functional organization of these genomes. We annotated their gene catalogue and reported a relatively higher gene number than that found in other corals. This finding is explained by a high number of tandemly duplicated genes, which are generally difficult to assemble and annotate, especially using short-read technologies. These duplicated genes, which originate from multiple and distinct events in the coral lineage, belong to gene-families linked to the immune system and disease-resistance which we suggest to be a functional consequence of their long lifespan.

*Speaker

Coral associated microorganisms from communities to genomes

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Abstract

Coral reefs, among the most diverse ecosystems on earth, support a high biodiversity of fishes and corals that show well defined patterns of biogeography and richness both at the local and ocean scale. These animals strongly rely on associated microorganisms for health and nutrition, but the diversity of the reef microbiome and its distribution across reefs remains poorly studied. Here we tested whether reef microorganisms showed global patterns of biogeography and diversity. The Tara Pacific expedition systematically collected 3 coral genera, 2 fish species and plankton in 96 different reefs from 32 islands across the Pacific Ocean. A total of 5392 microbial communities analyzed by 16S rRNA metabarcoding revealed a large diversity of microorganisms, which represents up to 16% of the estimated earth microbial diversity. The global patterns of microbial diversity were different from the ones known for macroorganisms, they varied between and within the 3 biomes (coral, fish and plankton), and geographically. We further used metagenomes to get a functional insight into the reef microbiome. Assembled genomes of *Endozoicomonas*, the most common coral associated bacteria, revealed metabolic diversity and niche adaptation across the Pacific Ocean. The use of both metabarcoding and metagenomics proved to be an efficient approach to uncover patterns of microbial ecology at scales ranging from the organism to the ocean. Our Pacific Ocean study provides new insight into the global diversity of the coral reef ecosystem and the factors driving the distribution of its microbial world

*Speaker

MetaPDOcheese : Nature and role of biotic drivers of microbial communities in traditional cheeses

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Abstract

PDO cheeses are generally considered as high quality, non-standardised products whose sensory richness arises from a variety of milk production and processing conditions. These practices would contribute to shaping microbial biodiversity and to the selection of ecotypes of environmental species that have adapted to the dairy environment. We seek to demonstrate this hypothesis by characterising the biotic and technological drivers of the cheese microbiota across the French PDO production areas. As a beneficiary of France Genomique major sequencing projects in 2017, MetaPDOcheese is the first large-scale study of the microbiota in all French PDO cheeses.

Massive sequencing of "taxonomic marker" gene amplicons was used to describe the bacterial and fungal diversity of 1,145 cheeses and 390 milks originating from 44 PDO areas. A database consolidating all the technical information associated with the samples was also created.

Up to 289 bacterial genera and 820 species, as well as 175 fungal genera and 333 species were identified from $>$ 1 billion sequences generated from the 2,306 cheese samples (cores and rinds). Up to 549 genera and 1,230 bacterial species, as well as 671 genera and 1,367 fungal species were identified from $>$ 180 million sequences generated from the milk samples. A core microbiome comprising several tens of bacterial and fungal taxa was identified in milk. The milk's microbiota differed according to the dairy species. The core microbiome in cheese was limited to one fungal species (*Geotrichum candidum*) at 100% prevalence. A core microbiome was identified across each cheese family, mainly composed of species potentially added as starters for cheese making and ripening. The cheeses microbiota differed in terms of community richness and composition between the 7 cheese families and within families, according to PDO labels. Secondary structuring factors, such as the ripening duration, were also highlighted across each cheese family.

*Speaker

Uncharted biosynthetic potential of the ocean microbiome

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Abstract

Microbes are phylogenetically and metabolically diverse, and have been a rich source of bioactive compounds and biotechnological applications1,2. Yet capturing this diversity and exploring its biosynthetic potential in natural environments remains challenging since the vast majority of microbial life has not yet been cultivated3. For the open ocean, current genomic data resources leave at least two-thirds of global metagenomic data unaccounted for4,5. Thus, the ocean microbiome remains largely uncharted as a reservoir for new biosynthetic enzymes and natural products. Here, we reconstructed > 25,000 draft genomes, including

*Speaker

from > 2,500 uncharacterized species, from globally-distributed ocean microbial communities, and combined them with _˜10,000 genomes from cultivated and single cells. Mining this resource revealed _˜40,000 putative biosynthetic gene clusters (BGCs), many from unknown phylogenetic groups. Among these, we discovered within a sparsely sampled and uncultivated bacterial phylum a new BGC-rich lineage (*Candidatus* Eudoremicrobiaceae) to include the most biosynthetically diverse microbes detected in the open oceans. By integrating metatranscriptomic data, we shed light on the ecology of this newly identified group of bacteria, and hypothesize a role for BGC products in structuring transcriptional states of environmental populations. Furthermore, we experimentally characterized several *Ca.* Eudoremicrobiaceae biosynthetic pathways, and identified an unusual (poly-phosphorylated) metabolite with low-micromolar protease inhibitory activity and a suite of biosynthetic enzymes, including a novel maturase, that synthesize a highly modified peptide. Together, this work illustrates how microbiomics-driven strategies enable prospecting for candidate bioactive compounds and new enzymology in underexplored microbes and environments.

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Biogeographical patterns and determinism of soil fungal alpha-diversity in France

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Abstract

The fungal kingdom has been diversifying for more than 800 million years and has colonized a large number of habitats on Earth. With 2 to 6 million species mostly found in soils, this heterotrophic kingdom is probably the second most diverse one among *Eukaryota* after animals. Fungi are major ecological players that support various ecosystem functions across trophic levels. The FungiMic-RMQS project aims to explore the soil fungal diversity on a wide scale in France using a metabarcoding approach (18S rDNA) and the French Soil Quality Monitoring Network. Based on this unique dataset in the world (2,200 soil samples), we described the spatial distribution of fungal diversity at the scale of mainland France and also environmental drivers by tackling biogeographical patterns and ecological concepts (intermediate disturbance hypothesis). Early results based on alpha-diversity (Hill numbers) show that total fungal richness at the territory scale includes 136,000 unique OTUs. Environmental parameters explain about 20% of the variance of fungal richness, with soil characteristics as the first environmental filter and then climatic conditions, land management, and spatial descriptors. We also present heterogeneous and spatially structured alpha-diversity maps across the French territory. We conclude our study with a discussion on the distribution of r/k strategists across land uses based on the prediction of rDNA gene copy numbers *per* OTU.

*Speaker

Carbon Fixing Unknowns: Exploring small green algae 'dark matter'

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Abstract

Despite its importance for human well being, marine plankton remains poorly characterised and understood. This is particularly due to its high diversity in terms of taxonomy and function. Recent metagenomic studies have revealed that marine plankton is far more diverse than previously thought (Carradec et al. 2018, Duarte et al. 2020), with hundreds of thousands of genetically distinct taxa and more than 150 million genes documented, however more than half of the planktonic 'omic' sequences have still unknown taxonomy and/or function, especially in terms of sequences with eukaryotic origin. These unprecedented amounts of data on planktonic communities call for the need of innovative data-driven methodologies to quantify and observe their biogeographic importance. Focusing on carbon dioxide fixation in the Chlorophytes of the class Prasinophyceae, we investigate the link between environmental variability of Carbon parameters and pathway specific genes and gene transcripts across the Tara Ocean sampling stations. In this case study we want to explore the potential of putative C4 biochemical carbon fixation which could be of ecological importance as it bypasses photorespiration (Karlusisch et al. 2021). Using a curated sequence collection of eukaryotic metagenomic assembled genomes and the application of sequence similarity networks we explore this planktonic 'dark matter'. The obtained network is composed of 1,219,858 protein functional clusters, including 4,446,560 proteins with roughly 60% unknown sequences. Through the analysis of protein families including known as well as unknown sequences the oceanic distribution of function-related processes can be quantified. Including unknown sequences in microbiome analysis is necessary in order to assess the full functional potential of

*Speaker

single organisms as well as microbial communities. With the correlation to global environmental parameters we demonstrate the potential importance of these previously discarded sequences and provide a case study for the exploration of sequencing unknowns at a global scale.

Massive invasion of genes by selfish genetic elements in Paramecium germline genomes

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Abstract

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Ciliates are unicellular eukaryotes with both a germline genome and a somatic genome in the same cytoplasm. The somatic macronucleus (MAC), responsible for gene expression, is not sexually transmitted but develops from a copy of the germline micronucleus (MIC) at each sexual generation. In the MIC genome of *Paramecium tetraurelia*, genes are interrupted by tens of thousands of unique intervening sequences, called Internal Eliminated Sequences (IESs), that have to be precisely excised during the development of the new MAC to restore functional genes. To understand the evolutionary origin of this peculiar genomic architecture, we sequenced the MIC genomes of nine *Paramecium* species (from ˜100 Mb in *P. aurelia* species to > 1.5 Gb in *P. caudatum*). We detected several waves of IES gains, both in ancestral and in more recent lineages. While the vast majority of IESs are single-copy in present-day genomes, we identified several families of mobile IESs, including non-autonomous elements acquired via horizontal transfer, that generated tens to thousands of new copies. These observations provide the first direct evidence that transposable elements can account for the massive proliferation of IESs in *Paramecium*. The comparison of IESs of different evolutionary ages indicates that, over time, IESs shorten and diverge rapidly in sequence while they acquire features that allow them to be more efficiently excised. We nevertheless identified rare cases of IESs that are under strong purifying selection across the *aurelia* clade. The cases examined contain or overlap cellular genes that are inactivated by excision

*Speaker

Fishing for the microbiome of tropical tuna

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Abstract

Tuna represent a significant part of the global fish and seafood economy and have a major nutritional and societal value in coastal developing countries. Although the consumption of tuna poses a risk of food poisoning through the development of pathogenic bacteria, the composition of their microbiome, and its main determinants such as species, sex, or geographic location still remain unknown. Using metabarcoding and metagenomic approaches, we examined the taxonomic composition of bacterial and viral communities present in the skin mucus, gut and liver of the two most consumed tuna species worldwide (i.e. Skipjack and Yellowfin), from individuals caught in the Atlantic (Ivory Coast) and Indian Oceans (Reunion Island). Overall, the composition of the tuna bacteriome was not influenced by the fish sex, however it was clearly species-specific in the gut microflora and site-specific in the skin mucus. Interestingly the liver was found to host a unique bacterial community, which composition varied with species and sampling site. Although a specific bacteriome was identified within each organ, several taxa including *Mycoplasma*, *Cutibacterium* and *Photobacterium* spp were found to be common to the gut, liver and skin mucus microflora. Whatever the organ considered, tuna virome exhibited a large diversity, mainly dominated by eukaryotic viruses, which represented on average 67% of the taxonomically assigned sequences while phages accounted for only 33%. The virome composition showed significant differences between the three organs, but remained totally independent of the sex and tuna species. We observed the presence of specific viral families inferred to each organ, some of them being previously identified as fish and/or human pathogens (*Iridoviridae, Parvoviridae*, *Alloherpesviridae*, *Papillomaviridae*). Overall, these results suggest that the body of tuna is composed of several microbial niches harboring diversified bacterial and viral communities, whose ecological interactions, circulation and role toward the host organism should be further investigated.

*Speaker

Genomic signatures of clonality in the deep water kelp Laminaria rodriguezii

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Abstract

The development of population genomic approaches in non-model species allows for renewed studies of the impact of reproductive systems and genetic drift on population diversity. Here, we investigate the genomic signatures of partial clonality in the deep water kelp *Laminaria rodriguezii*, known to reproduce by both sexual and asexual means. We compared these results with the species *Laminaria digitata*, a closely related species that differs by different traits, in particular its reproductive mode (no clonal reproduction). We analysed genome-wide variation with dd-RAD sequencing using 4077 SNPs in *L. rodriguezii* and 7364 SNPs in *L. digitata*. As predicted for partially clonal populations, we show that the distribution of FIS within populations of *L. rodriguezii* is shifted toward negative values, with a high number of loci showing heterozygote excess. This finding is the opposite of what we observed within sexual populations of *L. digitata*, characterized by a generalized deficit in heterozygotes. Furthermore, we observed distinct distributions of FIS among populations of *L. rodriguezii*, which is congruent with the predictions of theoretical models for different levels of clonality and genetic drift. These findings highlight that the empirical distribution of FIS is a promising feature for the genomic study of asexuality in natural populations. Our results also show that the populations of *L. rodriguezii* analysed here are genetically differentiated and probably isolated. Our study provides a conceptual framework to investigate partial clonality on the basis of RAD-sequencing SNPs. These results could be obtained without any reference genome, and are therefore of interest for various non-model species.

*Speaker

Genome-wide evolutionary responses of European oaks since the Little Ice Age

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Abstract

The pace of tree microevolution during the Anthropocene warming is largely unknown. We used a retrospective approach to monitor genomic changes in oak trees since the Little Ice Age (LIA). Allelic frequency changes were assessed from whole-genome pooled sequences for four age-structured cohorts of sessile oak (*Quercus petraea*) dating back to 1680, in each of three different oak forests in France. The genetic covariances of allelic frequency changes increased between successive time periods, highlighting genome-wide effects of linked selection. We found imprints of parallel linked selection in the three forests during the late LIA, and a shift of selection during more recent time periods. The changes in allelic covariances within and between forests mirrored the documented changes in the occurrence of extreme events (droughts and frosts) over the last three hundred years. The genomic regions with the highest covariances were enriched in genes involved in plant responses to pathogens and abiotic stresses (temperature and drought). These responses are consistent with the reported sequence of frost (or drought) and disease damage ultimately leading to the oak dieback after extreme events. They provide support for rapid adaptive evolution of long-lived species during recent climatic changes.

*Speaker

during development, suggesting conserved regulatory mechanisms. Similar to the evolution of introns in eukaryotes, the evolution of *Paramecium* IESs highlights the major role played by selfish genetic elements in shaping the complexity of genome architecture and gene expression.

Genomics of endogenous symbiotic viruses in parasitoid wasp-insect host interactions

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Abstract

Interactions between organisms shape eco- and agrosystems. Parasitoid wasps play an important role in environments by regulating populations of their insect hosts which can be pests of plants. Among certain parasitoid wasps, remarkable parasitic strategies, involving the endogenization of viruses, have evolved. Indeed, multiple events of viral domestication have been described in the genomes of certain Braconidae and Ichneumonidae wasps. Each event taking a different evolutionary trajectory and leading to different -sometimes convergent- virulence strategies involving the production of non-replicative viruses or virus-like-particles, essential for wasp parasitism success. The fate of non-replicative viruses in the insect hosts in which they are injected is also fascinating, as these viruses have an impressive capacity to integrate in all tissues of parasitized hosts. They have in consequence been mediators of horizontal-gene-transfers between different insect species, the scale and consequences of which have yet to be evaluated both in natural ecosystems and in the context of biological control in agriculture.

*Speaker

Disentangling the effects of genotype, environment, and symbiotype on coral holobiont gene expression across the Pacific

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Abstract

Assessing adaptation and acclimation capacities of coral holobionts is crucial for anticipating the impact of climate change on coral reefs. Whereas local and controlled investigations of coral acclimatization are increasingly common, *in situ* studies at ocean-wide scales remain scarce. In this context, the Tara Pacific Expedition was launched in order to quantify standing genetic diversity and assess adaptive potential of corals to environmental shifts on a global scale. We analyzed metagenomic and metatranscriptomic sequence data from 103 colonies of the reef-building coral *Pocillopora meandrina* sampled from 11 islands across the Indo-Pacific Ocean. Genome-wide single nucleotide polymorphism analysis identified five major host lineages and indicated the potential for thermally-driven ecological speciation in *Pocillopora* corals. In addition, we observed strong host-symbiont fidelity across the Pacific Ocean except in islands where recent and/or historical heat stress may have induced a symbiont shift towards more thermo-resistant *Durusdinium*. Host expression profiles were primarily influenced by both genetic lineage and the environment and were significantly correlated with historical sea surface temperatures. In contrast, symbiont expression profiles were less dependent on environmental context and were primarily driven by algal genotype. Comparative functional analysis of genes that were co-regulated between the *Pocillopora* host and dinoflagellate symbiont identified regulation of apoptosis, oxidative damage repair, ATPase-coupled proton transport, and amino acid metabolism as some of the most strongly enriched gene ontology categories among co-expressed genes. The expression profiles of these genes were also strongly correlated with historical sea surface temperatures, suggesting potential thermal adaptation of the environmental stress response (ESR). Overall, our results demonstrate the role of transcriptomic plasticity in local adaptation of the host, the primacy of genotype for symbiont expression, and the role of the ESR in maintaining *Pocillopora* holobiont integrity across environments. Our data provide a reference for the biological state of corals across the Indo-Pacific and demonstrate the power of large-scale genomic and transcriptomic analyses to provide new insights into corals' capacities for resistance, adaptation, and resilience to environmental change.

*Speaker

Genome-wide patterns of bracovirus chromosomal integration into multiple host tissues during parasitism

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Abstract

Bracoviruses are domesticated viruses found in parasitic wasp genomes. They are composed of genes of nudiviral origin involved in particle production and proviral segments encoding virulence genes necessary for parasitism success. During particle production, proviral segments are amplified and individually packaged as DNA circles in nucleocapsids. These particles are injected by parasitic wasps together with their eggs into host larvae. Bracovirus circles of two wasp species were reported to undergo chromosomal integration in parasitized host hemocytes, through a conserved sequence named Host Integration Motif (HIM). Here, we used bulk Illumina sequencing to survey integrations of *Cotesia typhae* bracovirus circles in the DNA of its host, the maize corn borer (*Sesamia nonagrioides*) seven days after parasitism. First, assembly and annotation of a high-quality genome for *C. typhae* enabled us to characterize 27 proviral segments clustered in proviral loci. Using these data, we characterized large numbers of chromosomal integrations (from 12 to 85 events per host haploid genome) for all 16 bracovirus circles containing a HIM. Integrations were found in four *S.*

*Speaker

nonagrioides tissues and in the body of a caterpillar in which parasitism had failed. The 12 remaining circles do not integrate but are maintained at high levels in host tissues. Surprisingly, we found that HIM-mediated chromosomal integration has occurred at least six times accidentally in the wasp germline during evolution. Overall, our study furthers our understanding of wasp-host genome interactions and supports HIM-mediated chromosomal integration as a possible mechanism of horizontal transfer from wasps to their hosts.

Vertical transmission of the gut microbiota in termites: evidence from a host-population based approach

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Abstract

To consider the 'holobiont' (i.e., the host and its symbionts) as a unit of selection in evolution, there must be a continuity of partnerships between the host and symbionts throughout generations. Vertical transmission of the microbiota (i.e., from host parent to offspring) constitutes an efficient mechanism ensuring such a continuity, but so far, empirical evidences of this transmission mode have remained insufficient, especially in non-model systems in which microbiota are highly diverse.
During this talk, I will present the results of a host-population based approach we designed to test the hypothesis according to which gut symbionts of termites are vertically transmitted. Gut symbionts of termites are highly diverse and are essential for host nutrition. Vertical transmission in termites can be defined as the transfer of a symbiont from a parental colony to a descendant colony. To be transmitted, a symbiont must be present in the winged individual hosts leaving the parental colony because only these reproductives can found a descendant colony and therefore can pass the symbionts to the next generation.
In our studies, we first developed a theoretical model postulating that the prevalence of a given symbiont taxon in host populations only depends on its vertical transmission rate. We then tested the model by studying the diversity of gut microbiota in two populations of the termite *Reticulitermes grassei*, by sequencing amplicons of 18S and 16S rRNA genes. The data set allowed us to estimate for each symbiont: (i) its prevalence in host populations, and (ii) its vertical transmission rate based on its frequency among reproductives. Results showed that most symbiont taxa fit the model, suggesting that vertical transmission is the principal mechanism ensuring the stability of host-microbiota associations in termites.

*Speaker

Endogenization of dsDNA viruses as a widespread source of adaptation in endoparasitoid species.

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Abstract

Modern genomic sequencing approaches have revealed abundant endogenous viral elements (EVEs) within eukaryotic genomes. These sequences can sometimes provide the recipient genomes with major evolutionary advantages: this is known as viral domestication (dEVEs). For instance, in some cases, the endogenized viral genes may protect its host from parasitoid attack, or from other virus infection as observed in mosquitos. In other cases, membrane fusion properties from viruses have been repeatedly co-opted by three very different eukaryote clades: mammals, viviparous lizards, and parasitoid wasps. In mammals and lizards, those genes derive from retroviral elements and are involved in the placental synthesis. In some endoparasitoid wasps, the same viral fusogenic propriety has been domesticated following ancestral dsDNA viral genome integrations. Those endogenized viral genes are used by the wasps as a delivery tool to inject virulence factors, essential to the developmental success of their offspring. So far, five independent cases of such viral domestication in parasitoid wasps have been described in a limited set of wasps families, within the huge diversity of the Hymenoptera order. In the present project, we aim to characterize the diversity of these viral domestication events at the scale of the Hymenoptera order. To do so, we developed a bioinformatic pipeline that look after endogenization involving all categories of donor viruses (ssDNA,dsDNA,ssRNA, dsRNA). This pipeline also includes an assessment of the evolutionary history and selective pressure of viral integration events. It allowed us to highlight new cases of viral domestication that are likely to be involved in the reproductive success of wasps. Quantitatively, these data also suggest that (i) dsDNA viruses are more frequently endogenized and domesticated than other viruses, and (ii) that endoparasitoid lifestyle is more prone to integration and domestication of viruses compared to their ectoparasitoid or free-living counterparts. The reasons underlying this pattern will be discussed.

*Speaker

Following the Adaptive Path of Apricot Domestication using Population Genomics

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Abstract

The specific traits that have recently evolved in domesticated organisms under strong and recent human-driven selection provide unique opportunities to understand adaptive processes as it leaves footprints in the genome. Here we studied the evolutionary history and selection footprints in apricots (Armeniaca section) using a population genomics approach based on the short-read sequencing of the genomes of nearly 600 accessions. We showed that Chinese and European apricots formed two differentiated gene pools, resulting from independent domestication events from distinct wild Central Asian populations. Consistent with large effective population sizes and outcrossing in fruit trees, we found a relatively low proportion of the genome affected by selection. In addition to improving our fundamental knowledge on the processes of fruit tree domestication, we unraveled the origin of resistance to sharka, the most detrimental viral disease affecting stone fruit trees, despite the absence of the pathogen within the ancestral populations. We are currently studying the variability of response to virus infection of wild apricot trees among the Central Asian forests, to identify resistance genes and document their natural diversity.

*Speaker

Mosaic genomes of bananas

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Abstract

Banana is a major crop that derives from hybridizations between Musa species and subspecies that diverged in Southeast Asian regions and archipelagos. Diploid and triploid hybrids with seedless parthenocarpic fruits were selected by humans and thereafter dispersed through vegetative propagation. We sequenced 161 accessions, including banana cultivars and representatives of Musa diversity, in Illumina WGS. Methods based on multivariate analysis and SNP clustering allowed to identify several ancestral groups as contributors to these cultivars, including one species not previously shown to be largely involved and two uncharacterized genetic pools that have yet to be identified. Complex chromosome mosaics involving at least three and up to seven ancestral groups were found, highlighting a much more complex origin than expected with multiple hybridization steps. The triploid Cavendish banana cultivar that represent 50% of the world production had contributions from six ancestral groups including the two uncharacterized genetic pools. Using the sequence data and genotyping-by-sequencing data from 11 progenies, we characterized seven large reciprocal chromosome translocations and showed that they emerged in different ancestral groups of Musa. Most diploid and triploid cultivars analyzed were structurally heterozygous for 1 to 4 translocations. All translocations induced a recombination reduction of variable intensity and extent. The translocated chromosomes were found preferentially transmitted in many cases, this may have favored their colonization. Impact of genome architecture on genetic analysis of agronomic traits will be illustrated.

*Speaker

New ways to improve the narrow genetic diversity of the polyploid crop Brassica napus (oilseed rape)

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Abstract

Brassica napus (oilseed rape) is a recent allotetraploid species resulting from the interspecific hybridization and genome doubling of the diploid species *B. rapa* (turnip) and *B. oleracea* (cabbage). This crop is notably used for human and animal consumptions as well as to produce biofuel. Due to its polyploid origin but also to the selection of few characters involved in seed quality, its genetic diversity has been severely eroded. It is thus crucial to rapidly improve its diversity. The current challenge for the long-term maintenance of this crop, which is the second oilseed crop in the world, is to produce new varieties resistant to diverse biotic stresses but also adapted to the new climatic constraints due to global warming. To that purpose, we recently collected both landraces and wild populations (100 per species) of its parental diploid species from the North of France to the South of Algeria. These populations growing in highly contrasted environments were sequenced and will notably be used to identify novels sources of resistance to various a(biotic) stresses by taking advantage of the recent genome assemblies of several *Brassica* species. In addition, the efficient use of all this diversity requires optimal crossing strategies to introgress small regions carrying the favourable alleles within oilseed rape genome. To that purpose, our research group investigates novel ways to modify the strict regulation of homologous recombination. We notably demonstrated that an allotriploid hybrid, resulting from a cross between oilseed rape and one of its diploid parent (*B. rapa*), increases the homologous recombination frequency (x3) but most interestingly enables the formation of crossovers all along the chromosome, especially in normally cold recombination regions (pericentromeres). We are currently performing epigenomic and transcriptomic analyses to explore their role in this unique recombination pattern. All these studies will open new avenues for oilseed rape breeding.

*Speaker

Genome dynamics in Rhodnius species, vectors of Chagas disease

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Abstract

Triatominae are kissing bugs vectors of *Trypanosoma cruzi*, the causative agent of Chagas disease, endemic in Latin America. Some *Rhodnius* species are domiciliar vectors and are mainly found in human dwellings in some countries and some others are only found in their natural environments where they feed on animals. To study genome dynamics, we have sequenced, assembled, and annotated coding sequences for 9 *Rhodnius* species. We found a mean of 10647±565 putative coding sequences. We estimated a mean gene family rate which across the phylogeny (0.0028 gains and losses/gene/million years) but highlighted more losses than gains that suggests strong genomics contractions The study of ortholog groups within the genus *Rhodnius* seems to show a greater diversity of genes in sylvatic species compared to that in domiciliary species. To correlate genome contractions and genome size, we also used flow cytometry to estimate the genome size for six *Rhodnius* species and compared the results with the estimates obtained from k-mer distributions in genome sequences. *R. prolixus* display the largest genome size (510Mb), *R. neivai, R. nasutus, R. milesi* and *P. tertius* have smaller genomes (472-493Mb) but *R. robustus* has the smallest (428kb). Compared to Triatoma species, the *Rhodnius* species have smaller genome sizes with a smaller heterogeneity. The potential adaptive trait of the dynamics of the genome in *Rhodnius* and genome size is therefore discussed.

*Speaker

The dual role of recombination suppression in the formation of inversion polymorphisms

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Abstract

Inversion polymorphisms are well known for their role in suppressing recombination between differentiated haplotypes. They are commonly associated with adaptive variation, e.g. in climate adaptation, host-pant adaptation, microhabitat segregation, and may also be linked to ecological speciation. Recombination suppression is supposed to be key in allowing the formation of differentiated haplotypes governing concerted changes in multiple so-called coadapted traits that can coexist within populations. Yet neither the formation of differentiated haplotypes nor their long-term maintenance is easily explained, first because the effects of recombination suppression in maintaining together coadaptation is also making adaptive evolution ineffective and may lead to degeneration, but also because coadaptation does not explain polymorphism unless certain conditions on the selective regime are met. I will present here the case of an inversion polymorphism controlling wing-pattern mimicry in a butterfly, with a fine dissection of positive and negative selection acting on the different inversion genotypes. This allows us to understand better the dual roles of recombination suppression on the maintenance of complex adaptive polymorphisms.

*Speaker

What can we learn from genome scans about the genetic basis of hybrid fitness?

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Abstract

Predicting and understanding the factors underlying the fitness of hybrid crosses is a key aim both for the applied study of crops and domesticated animals, as well as the fundamental study of genetic and evolutionary processes. One way to identify loci involved in hybrid fitness breakdown is to perform genome scans on hybrid individuals and look for outliers that may be indicative of incompatibilities. What can these genome scans tell us about the genetic architecture of hybrid fitness, and can we feel assured that outliers are indeed associated with incompatibilities? We present some analytical work, verified by simulations of hybrids under a Dobzhansky-Muller incompatibility model and Fisher's geometric model to explore this question. Our preliminary results suggest that large-effect loci show up as outliers in genome scans under both models, and that outlier loci need not be the main contributors to fitness breakdown in hybrids.

*Speaker

The root-knot nematode Meloidogyne incognita shows surprising adaptability despite clonal reproduction and low variation at the genome level

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Abstract

The most devastating nematodes to worldwide agriculture are the root-knot nematodes with *Meloidogyne incognita* being the most widely distributed and damaging species. Despite its supposed obligatory clonal reproduction, this species can overcome resistance genes and adapt to new hosts and environments. Clonal reproduction has been suspected based on cytological observations but, so far, never confirmed by population genomics data. At the species level, *M. incognita* is highly polyphagous with thousands of host plants. However, the host range varies among different *M. incognita* isolates that may present distinct and more restricted host compatibilities. We sequenced the genomes of 11 isolates across Brazil, with different host ranges to assess the mode of reproduction and how genome variations associate with biological traits, including agronomic culture, and geographical distribution. By aligning the genomic reads, we identified SNPs and small-scale insertions/deletions. Analysis of linkage disequilibrium and 4-gametes test, showed no sign of meiotic recombination, confirming the clonal mode of reproduction of *M. incognita*. We showed that there are relatively few

*Speaker

point variations between the different isolates, and these variations show no significant association with either the host range, the geographical origin of the samples or the host plant on which they have been collected. We then explored the impact of transposable elements (TEs) on genome plasticity. We found variation in the TE content across different isolates and that they have been recently active with isolate-specific TE insertions, including within genic and upstream regulatory regions. Variations in TE contents across the isolates recapitulates the variations observed at the SNP level and are thus also not correlated with the biological traits under investigation. Overall, these results suggest that multiple independent gains and losses of parasitic abilities and adaptations to different environmental conditions account for the broad host spectrum and wide geographic distribution of *M. incognita*.

The European Reference Genome Atlas, 200.000 genomes to revolutionise biology

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Abstract

In 2020, a large community of European scientists came together to initiate a new project with an ambitious aim: to sequence the genome of all known eukaryote species living in Europe. Under the umbrella of the Earth BioGenome Project, ERGA will generate genomes of high ("reference") quality, with all chromosomes completely assembled. The overarching aim of ERGA, alongside other projects of similar scale (The Darwin Tree of Life in the UK, The Vertebrate Genome Project) is to better understand and preserve biodiversity, provide a foundation for advanced ecosystemic studies, better understand genome biology and evolution, and fuel innovative technologies based on genomics. From field sampling to sequencing, assembly, annotation and data storage and distribution, the task of orchestrating the work of dozens of laboratories and genome centres in Europe is formidable. Technical difficulties abound, especially concerning the requirements for high quality DNA for sequencing, often from microscopic species. Assemblies will be challenged by the high genomic variability shown by specimen or potential polyploidy. Genome annotations will remain a cornerstone for future studies, and will be made especially complex in taxa with few resources. Despite these difficulties, within the first year of its existence, the ERGA initiative has established governing bodies and launched a pilot project focused on several dozen species to establish protocols and strategies. By connecting all living forms in one Tree of Life through their genome inherited from common ancestors, systematically sequencing biodiversity will likely stimulate new approaches to investigate biological problems

*Speaker

10 years of data evolution in genomics

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Abstract

Over the last few decades, genomics has gone through several technological scaling changes not found in other fields of biology. The data acquisition challenge associated with these changes makes it difficult to monitor the latest methodological developments. Researchers need to think continuously not only about the best genomic solution to answer their questions, but also about how the data will be analysed, stored and shared. As technology has improved, so have the skills needed to work in genomics. Today, principal investigators must be experts in experimental design, limitations and accessibility of genomic technologies, notebooks, github repositories, FAIR principles...

The rapid evolution of genomics over the last decade makes it difficult to predict where we will be in the next ten years. However, it is clear that genomics will be part of our daily lives, from the laboratory bench to our homes. This is why we now need to think about how to make the results and applications of our research more accessible and transparent so that everyone can understand how genomics will be used in our daily lives.

*Speaker

De novo Sequencing and Assembly of Complex Genomes

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Abstract

Reconstructing plant genomes is a difficult task due to their often large sizes, unusual ploidy and large numbers of repeated elements. However, the field of sequencing is changing very rapidly, with new and improved methods released every year. With the rise of long-read and long-range technologies, the delivery of chromosome-scale assemblies is now possible for almost all species. This presentation will show the advanced techniques already existing in the field and illustrate their application to generate high-quality assemblies.

*Speaker

De novo assembly of complex genomes, comparing long read sequencing technologies and data processing strategies.

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Abstract

SeqOccin is regional project aiming at increasing third generation long read technologies expertise of the local Genotoul sequencing and bio-informatic platforms. The covered topics are genome assembly, large variation and methylation calling as well as metagenomic analysis. In this frame, both Oxford Nanopore and PacBio sequencers have been tested on farm animal and plant species including cow, pig, quail and corn. Our aim is to provide our users with simple and computer efficient solutions to process long reads. In the first project phase, regarding genome assembly, we have compared sequencing technologies, assembly and polishing software packages as well as strategies. Our analysis confirm that repeats can have a massive impact on genome assembly metrics modifying N50 by an order of magnitude. It showed that long high quality reads were able to build mega base long repeated genomic regions. While comparing error prone and high quality long read assembly metrics we also saw differences in assembly size and completeness. HiFi Assembly lengths getting closer to flow cytometry genome size evaluations. Working with HiFi reads renders also genome polishing optional and therefore limits polishing induced chimeric genome content and reduces processing time.

*Speaker

Discovering multiple types of DNA methylation from bacteria and microbiome using nanopore sequencing

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Abstract

Bacterial DNA methylation occurs at diverse sequence contexts and plays important functional roles in cellular defense and gene regulation. Existing methods for detecting DNA modification from nanopore sequencing data do not effectively support de novo study of unknown bacterial methylomes. In this work, we observed that a nanopore sequencing signal displays complex heterogeneity across methylation events of the same type. To enable nanopore sequencing for broadly applicable methylation discovery, we generated a training dataset from an assortment of bacterial species and developed a method, named nanodisco (https://github.com/fanglab/nanodisco), that couples the identification and fine mapping of the three forms of methylation into a multi-label classification framework. We applied it to individual bacteria and the mouse gut microbiome for reliable methylation discovery. In addition, we demonstrated the use of DNA methylation for binning metagenomic contigs, associating mobile genetic elements with their host genomes and identifying misassembled metagenomic contigs.

*Speaker

Tracking the genomic homeland of horse domestication

Ludovic Orlando*[1]

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Abstract

The horse is one of the most frequently represented species in the cave art record of Western Europe, where it was central to the subsistence economy of Pleistocene hunter-gatherer societies. Its domestication by the mid-Holocene represents one turning point in human history. It truly globalized the world for the first time as not only people but their genes, their culture and their diseases could then spread across the Old World at an unprecedented pace. Charriots launched at full speed against the enemy lines or charging cavalries also provided warfare revolutionary tactics, which often proved decisive to some of the most famous battles in history. The horse was in fact paramount to the world economy up until the early 20th century when societies became increasingly mechanized. The global needs for horse meat, speed and power thus deeply impacted human history. They did not changed the horse anyless. In this talk, I will show how my group made use of ancient genomics to unfold the 5,500 years-long history of horse domestication, revealing both the mysterious homeland of the modern domestic horse but also how human management, selection and admixture hav contributed to reshape the horse genome through space and time until the present day.

*Speaker

Thousands of years of human-dog relationships: uncovering adaptation to dietary changes of dogs, resulting from the transition to farming

Deborah Diquelou[1], Frédérique Barloy-Hubler[2], Régis Debruyne[3], Marie Balasse[4], Colline Brassard[5], Anthony Herrel[6], Christophe Hitte[7], Stephanie Brehard[8], Adrian Balasescu[9], and Morgane Ollivier*[1]

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Abstract

The dog experienced and has witnessed the gradual evolution of human lifestyle and is a unique model that allows studying the biological changes resulting from the adaptation to cultural changes. A change in diet was a major shift during the Neolithic transition that also impacted dogs. Here, we investigate the effect of dietary changes resulting from the transition to farming on the evolution of dogs at the genomic, morphological and functional levels. We targeted 86 dogs and 9 wild-canid ancient samples coming from Paleolithic to late chalcolithic Romanian sites. The morphological study of the mandibles suggests that archaeological dogs may have had a jaw system optimized for hard biting at shallow gape angles. Isotopic analysis suggesting that Chalcolithic dogs are at a lower trophic level compared to the Mesolithic canids. HTS of ancient DNA extracted from the dental pulp and the coprolites allowed us

*Speaker

to study modification in digestive microbiota composition. We detected oral pathogens and typical gut bacteria, and showed that ancient dental pulp is a valid source of DNA from microbes. Finally, mitochondrial genome and nuclear SNPs captures were performed that allowed to reconstruct population history and to detect genomic variations that may have been selected troughout the Neolithic transition.

Paleogenomics: reconstruction of plant evolutionary trajectories from modern and ancient DNA

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Abstract

How contemporary plant genomes originated and evolved is a fascinating question. One approach uses reference genomes from extant species to reconstruct the sequence and structure of their common ancestors over deep timescales. A second approach focuses on the direct identification of genomic changes at a shorter timescale by sequencing ancient DNA preserved in subfossil remains. Merged within the field of paleogenomics, these complementary approaches provide insights into the evolutionary forces that shaped the organization and regulation of modern genomes and open novel perspectives in fostering genetic gain in breeding programs and establishing tools to predict future population changes in response to anthropogenic pressure and global warming (Pont et al. 2019a). Case examples from wheat paleogenomics will be given aiming at tracing wheat ancestry as well as cultivation origin and expansion during 10,000 years of hybridization, domestication, adaptation and breeding that has shaped the genetic makeup of modern bread wheats (Pont et al 2019b).
References:

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*Speaker

Ancient Giant viruses discovered through permafrost metagenomics

Sofia Rigou*[1], Jean-Michel Claverie[1], Sebastien Santini[1], Eugène Christo-Foroux[1], Jens Strauss[2], Guido Grosse[2], Alexander Fedorov[3], Karine Labadie[4], Chantal Abergel[1], and Matthieu Legendre[1]

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Abstract

Two giant viruses, *Pithovirus sibericum* and *Mollivirus sibericum* had been previously reactivated from a 30 000 year old permafrost sample prooving that viruses can remain infectious for a long period of time. These are members of the family Nucleocytoviricota, eukaryotic DNA viruses known today to be major player of the marine environment. Phycodnaviridae and Mimiviridae have been shown to be active and very diverse in aquatic sytems by independent studies. Despite several giant viruses that have been isolated from cryosoils, no metagenomic work have yet looked specifically at the overall Nucleocytoviricota diversity in these environments. Here, we present a very different virome composition in the family Nuceocytoviricota coming from russian surface cryosoil samples from Kamchatka and deep permafrost samples that are up to 50 000 year old from central Yakutia. A method was developed to extract viral sequences from whole shotgun metagenomics with a high sensitivity and specificity.

The ancient samples presented a high abundance of Mimiviridae and Pithoviridae/Orpheoviridae. These last ones give us a better understanding of the evolution of Pithoviridae from the ancestor of Pimascovirales. An analysis of terrestrial metagenomes from the JGI helped to confirm that this diversity pattern is quite unique. Despite rejecting binning for smaller, assembled scaffolds for reducing chimeras, we manage to recover large genomes up to 1.5 Mb, a few of which are believed to be near complete.

The extensive annotation of the extracted permafrost viral sequences reinforced the idea of a high variability in gene functions in between the different viral families. The large portion of unannotated genes reveal an immense gene reservoir with unknown functions waiting to be understood with the future advances in functional biology.

*Speaker

Impacts of agro-pastoral societies on biodiversity: palaeogenomic, palaeoecological and archaeological approaches

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Abstract

Thanks to the development of high-throughput sequencing (HTS), studies of paleoenvironmental DNA, retrieved from sedimentary archives, has been proven to be an added value for retrieving past presence of taxa in various kind of environments.
One promising method to investigate PalenvDNA is targeted capture approach followed by HTS. Its use as complement to archeological and geological data has already delivered promising results on humans, mammals and plants. However, despite rapid advances in aDNA techniques, there are no standards or criteria for the bioinformatic analysis that are classically based on mapping. Here, we propose a capture design targeting chloroplastic loci and mitochondrial genomes of several plants and mamals species of interest. We track their presence in sediment coming from lake and other challenging environments such as peatbogs and estuarine-lagoon where archeological context is known. We explore different assignation strategies by comparing mapping and k-mers approaches, and investigate the effects of database design.

*Speaker

Our results show that we could successfully retrieved PalenvDNA from sediments from various environments thanks to capture approach. We assess that the complementary use of mapping and k-mers efficiently improve ecologically informative PalenvDNA detection and authentication and propose a pipeline that can be used as a standard.

Microbial sequencing for individual and population health

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Abstract

The SARS-CoV-2 pandemic has put genetic sequencing into the spotlight because many countries implemented massive sequencing along with rapid data analysis and sharing. This swift response of some countries illustrates how widespread sequencing has become in human health at multiple levels. I will first show how progress in the recent field of phylodynamics has improved our ability to gain epidemiological insights from phylogenies of infections, using some of our team's work on the SARS-CoV-2 epidemic as an illustration. Then, moving to the individual level, I will focus on results from the PAPCLEAR clinical study to discuss how simple microbiota community profiling represents an opportunity for better understanding vaginal dysbioses and improve women's health.

*Speaker

Wild bee's pollination in sunflower crops: Who, which and why.

Marina Querejeta Coma*[1], Lorene Marchal[1], Paul Pfeiffer , and Stephane Boyer[1]

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Abstract

In our overpopulated planet, agricultural practices must be adapted to avoid the harmful consequences of traditional intensive agriculture on ecosystems, such as the known declines in flying insect abundance in the last 30 years. However, at the same time, we must produce enough food for an expanding human population. One potential solution is to move to ecosystem-based solutions, such as ecological intensification, and, for instance, increase the number and diversity of pollinators in the crops. But, for this strategy to work, it is necessary to acquire knowledge about pollinators and their role within crop ecosystems. In this work, we aim to describe the pollination activity of wild bees, including their use of wild flowers (the pollinated plants) in sunflower crops in Chizé (France). Also, we aim to test whether ecological factors, such as the insects functional traits or agricultural practices, influence the choice of plants pollinated by wild bees. For this purpose, pollen DNA was extracted from 300 wild bees using a washing protocol, and a DNA metabarcoding library was prepared and sequenced using Illumina MiSeq. Using our approach, we were able to describe the plants visited by wild bees, with Asteraceae and Brassicaceae being the most common families. Generalized Linear Models (GLMs) on biodiversity metrics show significant differences between the plants chosen by the bees in relation to the species of bee and its sex, weeds coverage, average height of the sunflower plants, sampling period (flowering or post-flowering) and the type or crop (organic or conventional). This study demonstrates the efficiency of our genomic approaches to study pollination in wild bees and, also, provides valuable information about floral resources used by wild bees under different conditions. This information is essential to the conservation of these key species, which provide essential pollination services in crop ecosystems.

*Speaker

Revisiting monitoring of biodiversity of coral reefs using metabarcoding and eDNA

Serge Planes*[1]

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Abstract

The climate change together with the rapid increase of the demography are driving unprecedent change in biodiversity leading to transformation of ecosystem equilibrium and services. The number one challenge is to objectively document the change in biodiversity and therefore to provided unbiased estimates of exact losses to emphasize the need for adapted conservation strategy. The starting point is to be able to provide a description of the biodiversity that is precise enough to account for the complexity and to monitor time series and derive trends. The rise of the "eDNA" concept is transforming already the environmental monitoring strategies and principles as it offers, on paper, the objectivity together with the details that are needed for accurate monitoring programs. While this approach is certainly the future of monitoring programs, there are challenges still requiring works before to rely on this technology. Among the challenges, we can mention questions related to the unbalanced DNA representativity of the difference species, the specificity of primers, the representativity of in situ sampling, ... Coral reefs ecosystems are certainly among the most complex one with a third of the marine biodiversity concentrated in 0,1% of the surface of the ocean. This ecosystem remains a challenge to assess the biodiversity using traditional observation methods and only few areas can be investigated. The eDNA approach is the next-generation perspective as it will allow spreading more survey throughout space and repeat them more often.

*Speaker

DNA metabarcoding of passive trap collection media for forest insect biomonitoring

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Abstract

Insect decline has been increasingly reported in the past years due to global change. Large-scale biomonitoring has thus become necessary to better understand the dynamics of insect communities and to preserve their essential role in ecosystem functioning. In that sense, coupling high-throughput sequencing and DNA metabarcoding has exponentially increased our potentiality to monitor insect communities over wider geographic regions and time scales. However, biomonitoring of entomofauna using molecular tools often results in destructive DNA extraction through voucher grinding, impeding primordial morphological back-up. Here, we filter unprocessed collection medium to assess insect communities through environmental DNA metabarcoding. We demonstrate that recovered communities are different yet complementary and that insect response to environmental changes remains similar to homogenate bulk metabarcoding. We also show that insect orders-by their contrasting sclerotization ratio-, and collection medium type, are unequal in yielding metabarcoding results. Overall, we believe it as an efficient alternative for biomonitoring insect response to ecological changes while preserving insect vouchers for identification and description, especially in tropical regions were singletons or undescribed species can be very common in trap samples.

*Speaker

eDNAbyss: A DNA-based exploration of the largest biome on Earth

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Abstract

The largest biome on Earth is by far the deep sea floor, yet the biodiversity it encompasses and the way it contributes to large biogeochemical cycles remain largely unknown. Technical challenges associated to its remote access, to gather the amount of material needed to inventory, and to integrate inventories based on distinct sampling strategies and performed by different experts in distinct areas of the world prevent a comprehensive appraisal of benthic biodiversity in the deep sea floor. The relatively small amount of material required to perform metabarcoding and metagenomics assessments based on eDNA, and the level of standardization they allow offered new promises to advance toward complementary and interoperable biodiversity assessment and improve our understanding of the extent and drivers of deep sea biodiversity. In the framework of the project Pourquoi Pas les Abysses (2016-2019), launched by Ifremer in 2016 and of the following France Génomique project eDNAbyss (2018-ongoing), we developed a series of standard protocols from sampling to bioinformatics analysis, to assess benthic diversity of the deep sea floor across the tree of life, allowing to foresee the ability to gather concerted efforts across the international community, to gain a global holistic appraisal of the large reservoir of biodiversity in the deep ocean.

*Speaker

Restructuring of genomic provinces of surface ocean plankton under climate change

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Abstract

The impact of climate change on diversity, functioning and biogeography of marine plankton is a major unresolved issue. Here, niche theory is applied to plankton metagenomes of 6 size fractions, from viruses to meso-zooplankton, sampled during the *Tara* Oceans expedition. Niches are used to derive plankton size-dependent structuring of the oceans south of 60∘N in *climato-genomic* provinces characterized by signature genomes. By 2090, assuming the RCP8.5 high warming scenario, provinces would be reorganized over half of the considered oceans and quasi-systematically displaced poleward. Particularly, tropical provinces would expand at the expense of temperate ones. Compositional shifts among planktonic grazers and nitrogen-fixing bacteria suggest impacts on the nitrogen and carbon cycles. Sea surface temperature is identified as the main driver of the changes (_˜51%) followed by phosphate (11%) and salinity (10%). These results demonstrate the potential of integration of genomics with physico-chemical data for higher scale modeling and understanding of ocean ecosystem dynamics.

*Speaker

Tales from the unknown: expanding our idea of taxonomic protist diversity

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Abstract

Marine protists are major actors in the ocean that remain scarcely explored due to their important diversity. Subsequently, they are poorly represented in genomic reference databases and in culture collections. The exploration of the vast protist diversity in natural communities relies mostly on the study of metabarcodes. However, to the present day, still about $\frac{1}{4}$ of metabarcodes remain taxonomically unknown (*i.e.* unassigned). Recent studies revealed *known unknowns*, *i.e.,* unassigned sequences shared across ecosystems. We developed a computational workflow to unify the known and unknown sequence space while analysing datasets retrieved from 6 distinct metagenomic projects, in order to characterise the unexplored marine protist diversity. The distribution of *known unknown* sequences was studied through space and time. *Known unknowns* were revealed to be shared within distinct deep mesopelagic areas. The majority of the unknown diversity was detected at the lowest taxonomic ranks and belonged to 4 major protist groups: Dinoflagellata, Ochrophyta, Radiolaria and Ciliophora. Among these groups, the known and unknown diversity were supported by different environmental niches. Our study highlighted the extent of taxonomical novelty in metagenomic datasets and established an original and robust framework for detecting ubiquitous unknown sequences of potential interest for ecosystem processes.

*Speaker

The anti-phage defensome of TARA Oceans microbial metagenomes

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Abstract

The genomic invasion of bacterial cells by a variety of mobile genetic elements (MGEs) such as plasmids and phages, is a catalyst of evolution but may also lead to cell death. Faced with the rapid evolution and turnover of such parasites, bacteria have evolved various defense mechanisms to evade infection and killing leading to an evolutionary arms race. This prokaryotic immune system (or *defensome*) encompasses a growing variety of lines of defense that include well-studied innate and adaptive systems such as abortive infection, CRISPR-Cas and restriction-modification, but also newly found cryptic systems such as Gabija, Shedu, and Zorya. While the abundance and distribution of such systems is well-known in complete and culturable genomes1, there is a void in our understanding of their diversity and richness in complex environmental communities. Here we have performed a large-scale in-depth analysis of the defensomes of 885 high-quality non-redundant metagenome-assembled genomes from the TARA Oceans project2. We observed a wide variation in the frequency of immune systems among large phyla, which correlated with lifestyle and genome size. Immune system's co-occurrence was frequently observed within MGEs and defense islands. Interestingly, we found evidence of stochastic phase variation in the target recognition domains of multiple methyltransferases, supporting the possibility of novel epigenetic mechanisms for phenotypic diversification. Hence, our results provide the first detailed picture of the multiple immune barriers present in marine microbial communities, and bring to the fore novel and ingenious strategies of methylome (and thus defense) diversification.

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*Speaker

Exploring the lignocellulolytic potential of aerobic and anaerobic microbial consortia derived from termite gut microbiome

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Abstract

Nowadays, our societies are aware that fossil resources such as oil, natural gas or coal are limited and that their intensive use has a significant impact on the climate. This leads us to try to find new ways to provide the industry with energy and chemicals. In this context, the lignocellulosic biomass can be an important source. Not only is it an abundant non-food resource, it is also renewable. Lignocellulose can be used for energy and chemicals production, as a substitute for petrochemicals or for high value-added applications. This is where the world of bioeconomy and biorefinery begin.
Termites are known as the most efficient lignocellulose degraders in nature; they can feed on lignocellulose and transform it into energy and termite biomass. Nevertheless, the exact role of the termite gut microbiome in lignocellulose conversion has not been fully characterized. Therefore, we have implemented the termite microbiome to degrade lignocellulose in controlled bioreactors useful for biorefinery purposes.By combining shotgun metagenomics, and using advanced analytical technics, including 2D HSQC NMR and 13C-IS py-GC-MS, this work bring new information on how termite microbiomes degrade lignocellulose, including its lignin fraction.

Interestingly, termite gut microbiomes managed to remove lignin, although hemicellulose and cellulose were degraded more efficiently. Important structural differences, indicative of ligninolytic action, were discerned in the residual lignin. Whole metagenome sequencing, allowed characterization of the community dynamics along biomass degradation and reconstruction of the metagenomic species involved in biomass transformation. We analyzed the temporal succession of metagenomic species and genes coding for functions related to plant cell wall deconstruction and provide new information on the underlying cooperation between bacteria to achieve lignocellulose and lignin degradation.
In addition, our work provides microbial consortia capable of degrading lignocellulose so that they can be used to screen for new enzymes and potentially applied to a biorefinery.

*Speaker

Genoscope's SeqLab at 25: extending the genomic revolution to decode life

POSTER 1

Thibaut Audouy*[1], Odette Beluche[1], Laurie Bertrand[1], Isabelle Bordelais[1], Elodie Brun[1], Maria Dubois[1], Corinne Dumont[1], Barbara Estrada[1], Evelyne Ettedgui[1], Thomas Guerin[1], Zineb El Hajji[2], Chadia Hamon[1], Sandrine Lebled[1], Patricia Lenoble[1], Claudine Louesse[1], Ghislaine Magdelenat[1], Eric Mahieu[1], Sophie Mangenot[2], Nathalie Martins[2], Claire Milani[1], Jacqueline Muanga[1], Céline Orvain[2], Marine Paillard[1], Emilie Payen[1], Peggy Perroud[1], Emmanuelle Petit[1], Dominique Robert[1], Muriel Ronsin[1], Sophie Sanchez[2], Benoit Vacherie[1], Jean-Marc Barbance[1], Beraud Mélanie[1], Corinne Cruaud[1], Karine Labadie[1], Aude Perdereau[1], Julie Poulain[2], Patrick Wincker[2], and Pedro H. Oliveira[1]

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Abstract

The Sequencing Laboratory (SeqLab) at Genoscope-National Sequencing Center has led to remarkable transformations in genomics over its proud 25-year history. Since its creation, the SeqLab has provided the scientific community with all the (meta)-omics expertise and data production capacities necessary to leverage multiple collaborative projects with high scientific impact. In 2003, it contributed to the Human Genome Project, publishing the complete sequence of chromosome 141. Since then, an expanding number of large-scale sequencing projects have been carried out in the environmental and agronomic arenas, including those of numerous plants (*e.g.*: coffee, rapeseed, pea), animals (*e.g.*: Oikopleura, trout), fungi (e.g.: Hemiascomycetes), and of thousands of microbial communities (*e.g.*: from the Tara Oceans project2). The SeqLab houses an expanding portfolio of state-of-the-art sequencing equipment, including optical mapping devices, the Illumina NovaSeq 6000, the Oxford Nanopore Promethion, and the MGI DNBSEQ-400. We are also equipped with a suite of automated liquid-handling systems, which allow for improved process streamlining and parallelization. Researchers at SeqLab are at the forefront of testing and benchmarking new protocols, setting up *de-novo* sequencing pipelines, and implementing novel lines of research in environmental metagenomics and epigenomics3. From the complexity of new sequencing technologies, to the need for fine-tuned computational biological analyses, it becomes clear that multidisciplinarity and an ambitious forward-looking agenda will be key to moving the genomics field forward. In this regard, the SeqLab welcomes opportunities to initiate and foster interactions with researchers and stakeholders from different areas, to help tackling eminent biological and technological questions, and further revolutionize the sequencing field.

*Speaker

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Biogenouest: the network of life science and environment core facilities in Western France

POSTER 2

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Abstract

Major breakthroughs in sciences often result from combining interdisciplinary approaches and development of new technologies. Scientific research increasingly relies on new technologies, turning out to be more and more challenging to be implemented. Identifying expert scientists able to adapt novel technologies and up-to date core facilities is of increasing importance to conceive and implement innovative and competitive projects. For example, the emergence in the early 2000's of "next generation sequencing" technologies boosted the rise of technological core facilities and directly contributed to the development of genomics. In this context, Biogenouest was initiated in 2002 as a Scientific Interest Group, joining together 11 members: Universities and national research organizations established in Western France, *i.e.* Régions Bretagne and Pays de la Loire. Today, this network joins together 34 core facilities, organized in 6 technological areas: genomics, proteomics, bioinformatics, functional exploration, bioimaging, structural and metabolomic analysis. They cover 4 research fields: marine science, agriculture and food-processing, human health, and bioinformatics.
By joining together resources and relevant skills, Biogenouest aims to facilitate and promote access to cutting-edge technologies to a broad scientific community, delivering hands-on solutions and innovation to public and private research laboratories in life and environmental sciences. Biogenouest also contributes to optimize and coordinate financial supports allowing core facilities to provide cut-edging technology and facilitating innovative developments. These core facilities share knowledge, provide concerted and coordinated services, and propose training sessions to students and researchers. Most core facilities are part of national and European research infrastructures, reflecting their expertise and leading roles in their scientific domains.
Biogenouest is supported by its members, by the Régions Bretagne and Pays de la Loire, and by IBiSA.

*Speaker

High-density SNP development in black soldier fly (Hermetia illucens L.) via throughput DNA Pool Sequencing

POSTER 3

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Abstract

Use of genomic tools is now widespread in animal genetic breeding programs. In black soldier fly (BSF) breeding, which is a promising candidate for the development of the insect farming industry, these genomic tools are still non-existent, while they could accelerate and improve genetic gain of selection programs in increasing accuracy. The purpose of this study was to call SNPs from DNA pool sequencing to design high, medium and low-density SNPs chips. Pooled DNA library preparation was performed using several BSF populations from the breeding companies Innovafeed and Agronutris. Generated library pools were sequenced on Illumina platform in 2x150bp and the sequences were assigned to the samples based on their index sequence. Over 300 million of Paired-End reads and 43X of sequencing depth was obtained on average per pool. The last BSF genome with chromosome assembly level (≈1 Gb) was used as reference to call 52 million SNPs. Filters based on Quality, Minor Allele Frequence (MAF), genome coverage (depth) and non-informative sites were used to yield a final set of 9.7 million high quality SNPs that can be later used to develop the first genotyping chip for BSF. Beyond their use in genomic selection, these resources will be useful to address other questions in BSF: manage inbreeding with adapted panels for DNA chip, parentage and paternity assignment, improve selection or diffusion efficiency based on QTL detection after association genetic studies (GWAS).

*Speaker

Assembly and annotation of the yellow mealworm genome

POSTER 4

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Abstract

In the context of a global effort for more ecologically friendly nutrition resources, the yellow mealworm beetle, Tenebrio Molitor, is a good protein-rich alternative source for animal and human feeding while its farming has relatively low environmental impact compared to conventional agriculture. In order to optimize its production at an industrial scale through breeding, a good knowledge of its genome is needed.
For that purpose, we firstly combined different technologies such as long reads (Oxford Nanopore) and Illumina Hi-C data to build a high-quality assembly. Subsequently, we used RNA-seq data and other available coleoptera proteomes to predict genes.
The current genome assembly has a N50= 21.9 Mb with a gene completeness of 99.5% and about 21,435 predicted genes.
Moreover, we observed a quite conserved synteny between *T. molitor* and *Tribolium castaneum* (the red flour beetle).
The genome we provide, will be useful knowledge for the development of new mealworm lines to meet future human nutrition demands.

*Speaker

Research and development at the I2BC Next-generation Sequencing Facility: an overview

POSTER 5

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The multiplicity of newly developed methodologies and techniques pushes forward core facilities in their goal to support the needs and projects of their users. Since its creation in 2010, the mission of the I2BC next-generation sequencing facility (PSI2BC) is to provide the scientific community, whether academic or industrial, with services and support in the domain of high throughput sequencing and its applications in functional genomics and transcriptomics. We present an overview of recent research and development (R&D) projects carried out at our core facility and based on both Illumina and Oxford Nanopore Technologies (ONT). Firstly, we are developing expertise in the study of DNA and RNA modifications : (1) detection of 5-methylcytosine (5mC) modifications of DNA, a well-characterized mark associated with transcriptional repression using ONT sequencing. (2) detection of pseudo-uridine, the most widespread modification in RNA, present in all living organisms using ONT sequencing. (3) development of an improved small RNA Illumina library preparation method with less bias and better detection of 2'O-Methyl RNAs. Several types of RNA such as plant microRNAs (miRNAs) carry a 2'-OMe modification at their 3' terminal nucleotide. This modification complicates library preparation as it inhibits 3' adapter ligation. Our protocol has less overall bias and is less affected by the modification than standard methods. We also present our advances in ONT long read sequencing : (4) generation of ultra-long ONT reads. We have used the recently released ONT kit for a first test and we have obtained a large proportion of reads of tens to hundreds of kilobases in length. (5) targeted ONT sequencing of specific genomic regions using a Cas9 directed approach. We have tested a novel ONT kit based on a recently published method (nCATS), which has allowed us to strongly enrich for a specific region of the mouse genome.

Whole genome metagenomics and the benefits of pacbio HiFi long reads, an ongoing study within the framework of axis 3 of the SeqOccIn project.

POSTER 6

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Abstract

The SeqOccIn (Sequencing Occitanie Innovation) project, supported by Get-PlaGe and Genotoul Bioinfo platforms, was selected by the Occitanie Region as part of the call for projects "Regional Research and Innovation Platforms".
One of the objectives is to acquire expertise in metagenomic to better characterize complex microbial environments.

Questions that we addressed in the SeqOccIn project are :

· What is the best extraction protocol to produce high quality DNA for long read sequencing ?

· What are the main benefits of HiFi long reads compared to short reads in metagenomics analysis ?

· What is the best strategie to take the maximum of the long reads benefits ?

· What would be the associated sequencing costs ?

· What would be the best balance between cost and quality of results?

To answer those questions, we analysed data from ZymoBIOMICS' mock (8 bacterial species and 2 fungi) and from feces microbiome from pigs. Both types of data were obtained from Illumina short reads technologie (NovaSeq) and from Pacbio Sequel2 HiFi technologie.

Main steps of the molecular biology analysis are (i) to test different extraction protocols in order to produce high DNA quality samples to deliver a high taxonomic resolution, (ii)

*Speaker

to optimise the Pacbio metagenomics shotgun protocol for the libraries preparation on pig feces samples and mock to allow the production of Hifi reads.

Main steps of the bioinformatics analysis are (i) assembly, (ii) taxonomic profiling and (iii) function profiling. We are interested in studying the information we can get from the data both directly from the reads and from the assemblies on several sequencing depths.

POSTER 7

Metatranscriptomic and metabarcoding approaches unravelling functional and taxonomic diversities of a coastal aquatic ecosystem and their reaction to hypoxia

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*Speaker

Abstract

Two previous integrative research programs: PREDHYPO (AMIDEX Foundation 2015-2016) and PREDHYP-O2 (EC2CO 2016-2017, CNRS-INSU) have enabled the coupling between physics and biogeochemical processes of the Berre lagoon sediment during a laboratory experiment under controlled oxygenation conditions. We followed the biological and chemical dynamics of sediment core samples during a three weeks incubation period. Because microorganisms are key actors of biogeochemical processes and organic matter turnover, we dedicated an important part of these research programs to the characterization of taxonomic and functional responses of the sediment microbiome to hypoxia events. We thus combined metabarcoding and metatranscriptomic approaches based on next generation sequencing and Illumina technologies. Following data submission to the European Nucleotide Archives (ENA) and functional annotation by the Mgnify support team, we present preliminary analysis of taxonomic and functional diversities of the sediment microbiome and how they respond to differential oxygenation conditions.

Growth using dichloromethane (methylene chloride): Genome-wide identification of essential genes in Methylorubrum extorquens DM4

POSTER 8

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Abstract

Dichloromethane (DCM; CH2Cl2) is one of the most industrially produced halogenated solvent and a potential carcinogen, and thus a widespread contaminant of various environments (air, soil, aquifers). To rehabilitate contaminated sites, a few DCM-degrading bacteria that grow using this pollutant as their sole source of carbon and energy have been used. Among them, *Methylorubrum extorquens* DM4 is the reference DCM-degrading strain in which it has been demonstrated that growth with DCM generates many stresses (e.g. solvent effect, genotoxicity, and intracellular production of acid and Cl- ions). During my PhD, one of my objective is to identify other essential genes for coping with DCM utilization in strain DM4 using **transposon-sequencing (TnSeq)** approach. This high-throughput method is based on random saturated mutagenesis by insertion of a mini-transposon combined with Illumina sequencing of PCR-amplified insertion sites. The genes for which no insertion is detected by bioinformatic analysis will be ranked as essential for growth with DCM. During my master's degree, I initiated TnSeq under growth conditions with DCM or with methanol, a compound assimilated by the same metabolic pathways, but not generating the same stresses. In total, _˜ 1 million mutants per condition were generated and their genome extracted. Among the identified essential genes, some will be studied experimentally to explore their roles in the mechanisms of adaptation to DCM and possibly serve as biomarkers of microbial exposure to DCM in the environment.

*Speaker

Biosurveillance for invasive xylophagous beetles using a DNA metabarcoding approach

POSTER 9

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Abstract

Invasive xylophagous beetles represent a threat to forests worldwide. There is an urgent need to develop a biosurveillance system for early detection of invasive species. We have used multi-component blends for mass trapping both native and exotic longhorn beetles at several European ports of entry. With this biological material at our disposal, we are developing reference databases of Cerambycides in order to improve the number of species detectable in metabarcoding analyses. We are also working on the design of new primers to improve the detectability rate of these species. Finally, we are developing a non-destructive DNA extraction method for multiple insects at the same time allowing the conservation of all extracted samples.

*Speaker

Reconstructing past vegetation communities of a glacial lake in northern Norway

POSTER 10

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Abstract

Multiple studies have used sedaDNA metabarcoding to reconstruct the past vegetation communities of arctic and alpine lakes, however none of these previously studied lakes have been located in the catchments of a currently active glacier. Here, we reconstruct the changes in vegetation occurring over the holocene at Jøkelvatnet, a lake located directly downstream from Langfjordjøkelen glacier in northern Norway. We metabarcoded 35 samples from a lake sediment core spanning 10,300 years using primers targeting the trlL P6 loop region. A total of 203 plant taxa were identified and show a pattern of continually increasing richness over the span of the core. Vegetation surveys conducted around Jøkelvatnet show a high concordance with the taxa identified through sedaDNA metabarcoding. The two major shifts in vegetation communities at ca. 4,370 and 9,600 cal. BP mirrored the climatic shifts recorded by the Langfjordjøkelen glacier. This study highlights the utility of examining glacial activity when reconstructing holocene vegetation communities through sedaDNA.

*Speaker

sedaDNA Insights into Marine Biodiversity During the Transitions of the Last Interglacial

POSTER 11

Danielle Grant*[1,2], Kristine Steinsland[1,2], Tristan Cordier[1,3], Dag Inge Blindheim[1], Ulysses Ninneman[2,4], Jessica Louise Ray[1], and Stijn De Schepper[1,2]

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Abstract

There is an urgent need for new knowledge about natural climate variability in order to understand the potential consequences of global warming for biodiversity. Climate proxy reconstructions indicate that the climate transition to the Last Interglacial (LIG) period was relatively rapid and resulted in warmer than present conditions, making it an interesting analog for future global warming (as predicted by RCP8.5 projections). In this study, we used metabarcoding analysis of sedimentary ancient DNA, *sed*aDNA, to investigate the transition into and out of the LIG. We are specifically focused on the transition from MIS 6, the penultimate Glacial period ($>$ 128 kybp) through the LIG (MIS 5e; ¯128-116 kybp) and into the cooler stage of the LIG known as MIS 5d ($<$ 116 kybp), to understand the link between a warming climate and shifts in biodiversity. We investigated relevant sections of a giant piston sediment core collected on the Eirik Drift in the Labrador Sea, which is an important paleoceanography location. The Eirik Drift is a site suited for monitoring changes in deep water formation and Arctic freshwater export from the East Greenland Current. Here we present the first high-resolution *sed*aDNA metabarcoding record for the LIG detailing eukaryote biodiversity shifts relative to major climate transitions recorded at the Eirik Drift. We successfully amplified the V7 hypervariable region of the small subunit ribosomal RNA gene from 85 of 100 downcore sediments, representing 22, 46, and 17 time points from MIS 6, MIS5e, and MIS 5d, respectively. Multivariate statistical analysis of metabarcoding results reveals significant shifts in alpha and beta diversity metrics between the three climate stages. Biodiversity shifts indicated by *sed*aDNA metabarcoding analysis mirror diversity shifts in depth-matched Dinocyst microfossil assemblages. We are currently performing an in-depth taxonomic analysis of this exciting *sed*aDNA record to reveal past biodiversity and identify taxa associated with specific climate stages. Furthermore, linking specific taxa or *sed*aDNA signatures to environmental variables may provide a more nuanced understanding of biodiversity shifts during the LIG.

*Speaker

Nudivirus endogenization event in Campopleginae wasps, from the characterization of a new endogenous virus to the functional analysis of domestication.

POSTER 12

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Abstract

Nudiviruses are large double-stranded DNA viruses that are pathogens of insects and crustaceans. These viruses have been involved in three events of virus domestication, after their integration in the genomes of parasitoid wasps. "Virus domestication" means the integrated virus is no longer a pathogen but has evolved to become beneficial for the wasp. The endogenous nudiviruses play a key role in wasp parasitism success. Indeed, particles are produced in the ovaries of the wasp together with the eggs before being injected during oviposition. In the case of the parasitoid wasp *Venturia canescens,* viral particles devoid of DNA called "VLPs" for "Virus-Like-Particles" confer a local protection to wasp eggs from the encapsulation immune response of parasitized caterpillars. These VLPs were thought to be unique to the species *Venturia canescens*. Recently, we have characterized an endogenous nudivirus in *Campoplex capitator*, an ichneumonid wasp, which is closely related to *Venturia canescens*. This wasp is an interesting model for the biological control of the vineyard pest *Lobesia botrana*. PacBio Genome sequencing, transcriptomic and electron microscopic analyses revealed that nudivirus sequences were integrated in the genome, expressed in wasp ovaries and produce VLPs. The comparison between the viruses domesticated in *Venturia* and *Campoplex* shows that these elements originated from the same viral integration event in the genome of a common ancestor of these wasps. Comparison of the nudiviruses integrated in these two wasps enable us to study the mechanisms involved in viral domestication. In addition, RNA interference approaches have been developed in *Venturia canescens* allowing us to assess the function of nudiviral genes. This work sheds light onto genomic and functional evolution of wasp-virus associations, opening a promising avenue for future research on the evolution of endogenous viruses beneficial to their hosts.

[*]Speaker

How many bacteria does it take to keep a hemipteran alive?

POSTER 13

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Abstract

Most hemipterans feed on plant sap and rely on intracellular microorganisms to supply essential nutrients (i.e., vitamins, essential amino acids). The Auchenorrhynchia (cicadas, planthoppers, spittlebugs) have long been known to require at least two co-endosymbionts to provide all essential nutrients, one of which is always '*Ca.* Sulcia muelleri'. Recent studies showed that within the Fulgoromorpha clade, the picture is even more complex and three bacterial endosymbionts co-exist within the same bacteriome. Using whole-genome sequencing of the planthopper *Cixius wagneri* (Fulgoromorpha, Cixiidae), we discovered a new triple-endosymbiosis, involving '*Ca.* Sulcia muelleri' and two undescribed bacteria. The first co-endosymbiont is a Gammaproteobacterium which is phylogenetically close to other enterobacteria exhibiting an intracellular lifestyle. The second bacterium is a close relative of '*Ca.* Vidania fulgoroideae' (Betaproteobacteria), another nutritional endosymbiont of Fulgoromorpha. A phylogenomic analysis further refined the two endosymbionts' taxonomic assignment, indicating that they belong to two new genera. Metabolic reconstruction of the symbiotic system shows that the *Vidania*-like endosymbiont provides seven out of the ten essential amino acids (i.e., Trp, Thr, Met, Lys, Arg, His, Phe), while the Gammaproteobacterium supplements biotin and riboflavin, leaving '*Ca.* Sulcia muelleri' with the biosynthesis of leucine, isoleucine and valine, three amino acids with similar biosynthetic pathways. Our work contributes to the increasing knowledge of host-endosymbiont co-evolutionary histories in this diverse insect group.

*Speaker

Gut content analysis of preserved carabid specimens reveals past trophic interactions

POSTER 14

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Abstract

Significant carabids collections have been built in many research institutes as part of studies focusing on biodiversity assessments or biological control in agricultural landscapes. Often, these specimens are preserved in ethanol. A metabarcoding analysis of these carabids' gut contents would allow the determination of past trophic interactions and their evolution through time. The Zone Atelier Plaine & Val de Sèvre (ZA-PVS) in Western France has carabid specimens collected yearly since 1995, although, sample collection and specimen preservation were not conducted specifically for molecular analyses. This collection constitutes a repository of information about prey communities in agricultural landscapes in the past decades.

We analysed 250 specimens from two generalist predatory species (*Nebria salina* and *Poecilus cupreus*) collected between 2013 and 2019. Specimens were dissected and prey DNA was amplified from the insects' crop using generalist PCR primers. The diet of carabid was then analysed using a metabarcoding approach,

By using existing collections of ethanol preserved carabids, our method has the potential to inform on the biocontrol services provided by carabids and its evolution through time. When focusing on generalist predators, this method can be used to detect potential shifts in arthropod communities that may be related to global changes, agricultural practices, land management or any other event.

*Speaker

POSTER 15

Role of bracovirus and transposable elements in a parasitoid wasp ongoing speciation.

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Abstract

A recent study documented that two parasitoid wasp populations of *Cotesia Congregata* have different ecological niches and present an inability to produce viable offspring in some crossings. Specific courtship songs and genetic differentiation have also been reported that suggests that a speciation is in progress in these parasitoid wasp populations, that would already represent nascent species. *Cotesia* development which occurs at the larval stage within the body of parasitized caterpillars relies on highly regulated molecular host-parasite interactions involving an endogenous virus (bracovirus) used to circumvent host immune response, thus ensuring wasp reproductive success. As parasitism rate is high in populations of Lepidoptera and as the issue of parasitism is the death of the host or the parasite, a strong selection pressure is imposed leading to a constant adaptation of both protagonists to survive. The bracovirus is thus tightly adapted to the specific wasp lepidopteran host and likely contributes to the divergence of the two wasp populations. In addition, an hybrid fertility asymmetry in *Cotesia congregata* was described, which resembles the one described in *Drosophila* (hybrid dysgenesis) involving transposable elements (TE) and their piRNA repression system. We hypothesize that a TE could contribute to speciation by limiting genetic exchanges between the two wasp populations.

The project aims to evaluate the contributions of the bracovirus and TEs to the speciation in progress, using comparative genomics and resequencing of genomes to check for transposition of an active TE. Preliminary results, obtained by piRNA sequencing, sustain the hypothesis that an active TE is invading wasp populations. If confirmed, this will allow to monitor for the first time the invasion of a genome by a TE in the field and to identify transmission routes at the level of the ecological network. Indeed, it should be noted that TEs such as P and I elements have been studied in *Drosophila* long after their genomes had been invaded worldwide.

*Speaker

POSTER 16

What factors shape host-associated microbiota? The neglected role of biological invasions.

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Abstract

The composition of host-associated microbial communities is driven by many biotic and abiotic factors, primarily the host genotype and many environmental conditions. In this context, invasive species represent good model systems to disentangle the respective contribution of host genotype and host habitat. Indeed, in such models, both factors can importantly vary between the native and the introduced (*i.e.*, invasive) ranges of the hosts.
Using the xylophagous termite *Reticulitermes flavipes* as a model, we studied the microbiota of the host in its native (Louisiana, USA) and invasive (Charente-Maritime, France, 280 years after its direct introduction from Louisiana) ranges. In the latter area, we also sampled colonies of the sympatric species *R. grassei*. For each sample, we used a metabarcoding approach targeting SSU rRNA amplicon sequences to investigate the diversity of the main microorganisms colonizing *Reticulitermes* guts, namely Bacteria, Oxymonadida and Parabasalia.
Our study aims at: (*i*) testing how the gut microbiota of *R. flavipes* evolved from its native to invasive ranges, (*ii*) testing the hypothesis of a microbiota exchange between the two French sympatric species. We hypothesized that (*i*) the overall diversity of the gut microbiota of *R. flavipes* will decrease in the invasive species compared to the native one, mainly due to the lower diversity of wood species present in France; (*ii*) microbial exchanges can be detected between the French sympatric species since they share the same niche and can interact physically. Our analyses revealed (*i*) distinct trends of *alpha* and *beta* diversity patterns for both the bacteria and protists associated with the two allopatric populations of *R. flavipes*; (*ii*) the existence of shared bacteria and protists between the sympatric species but absent from the American *R. flavipes*, supporting our second hypothesis. Altogether, our data highlight the role of biological invasion as a driver of the evolution of gut microbiota.

*Speaker

What did 3 generations of genome sequencing technologies allow to learn about the biology and evolution of root-knot nematodes?

POSTER 17

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Abstract

In 2008, in a collaborative effort with Genoscope, we sequenced the first genome for a plant-parasitic animal, the root-knot nematode *Meloidogyne incognita*. This was also the first for an animal reproducing exclusively without sex. Genome analysis revealed different idiosyncrasies possibly linked both to adaptation to a plant-parasitic lifestyle and to evolution in the absence of sexual reproduction. This included a peculiar duplicated yet diverged genome structure and genes specific to this genus. Aided by progresses in sequencing technologies genome assembly completeness and annotation improved while comparative and population genomics allowed gaining information about the mechanisms of genome plasticity possibly underlying adaptive evolution in this species. More recently, as part of the France Génomique project 'ALPAGA', we used long-read sequencing and Hi-C technologies to improve further the contiguity and resolution of the genome of *M. incognita* as well as other root-knot nematodes. The progresses obtained in disentangling the complex polyploid genomes of these species now paves the way towards study of genome compartmentalization and organization. In this poster, I will highlight the main progresses achieved in our understanding of the biology and evolution of root-knot nematodes, enabled by these genome data obtained by three successive genome sequencing technologies.

*Speaker

Characterising and Harnessing the Haematococcus algal Microbiome - towards Biocontrol of the fungal Pathogen Paraphysoderma sedebokerense

POSTER 18

Caroline Kunz[1,2], Jeanne Miebach*[1], and Claire Gachon*[1]

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Abstract

The single-celled fresh water green alga *Haematococcus pluvialis* is cultivated industrially to produce astaxanthin, a highly sought-after carotenoid. Its production is compromised by the fungal pathogen *Paraphysoderma sedebokerense* (Blastocladiomycota). The bacterial microbiota of *H. pluvialis* might, as for plants, constitute a barrier against infection by pathogens. In order to identify potential biocontrol strategies against this fungus, we are exploring the tripartite " alga-microbiota-pathogen " consortium, using algal strains stemming from central Europe and the Parisian region. We propose to barcode algal strains, test them for their susceptibility to *P. sedebokerense* and characterise their microbiome through shotgun sequencing. Their cultivable microbiota will be also isolated and barcoded. Our project is an asset to address fundamental questions such as microbiota domestication in algae, cross-kingdom chemical signaling as well as the development of biocontrol tools for the industry.

*Speaker

Impact of rising temperature and inputs of terrestrial organic matter on bacterial-fungal interactions in aquatic ecosystems

POSTER 19

Emile Laymand*[1,2], Lucas Tisserand[1], Lucie Bittner[2], and Fabien Joux[1]

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Abstract

Lakes are very productive systems because of the terrigenous Dissolved Organic Matter (tDOM) they receive, and constitute an important economic resource for human societies. Climate change threatens these ecosystems: rising temperatures could alter the mixing and the oxygenation of waters, and an increase in the frequency of intense rainfall events could promote soil leaching, leading to increased inputs of tDOM that may brownify surface waters and reduce primary production.

The TOMATO project (response of aquatic microbes to inputs of Terrestrial Organic MATter from different Origins at different temperatures) aims to understand the effects of an increase in temperature and/or tDOM inputs on bacterial and fungal communities in lakes. 18 mesocosms were set up and monitored for 20 days, and climate change was simulated by adding two types of amendments from peat or manure, and/or by increasing the temperature by +5∘C compared to current mean temperature. Illumina sequencing was carried out to produce ASV abundance matrices for three time points.
We demonstrated using multivariate statistics that the quantity and the nature of tDOM, as well as an increased temperature have a significant effect on the composition of communities. Moreover, cooccurrence networks showed that particle-attached bacteria always constitute the majority of the central nodes while Fungi – mostly of unknown phyla – emerge as key players as tDOM becomes increasingly different from control. At last, using an iterative deletion protocol of the most central nodes, we also demonstrated that contrary to previous results obtained for human microbiota, bacterial-fungal interactions do not appear to increase the robustness of microbial networks, and thus do not allow to predict an ecosystem benefit in lakes.

*Speaker

Transcriptional and functional analyses of Symbiodiniaceae across the Pacific Ocean.

POSTER 20

Julie Lê-Hoang*[1,2], Eric Armstrong[1,2], Quentin Carradec[1,2], and Patrick Wincker[1,2]

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Abstract

Coral reefs are important and complex biological ecosystems, essential for the life of many marine species. In turn, the heath of corals relies on the establishment and maintenance of a symbiotic partnership with a micro-algae of the Symbiodiniaceae family, which lives in obligatory endosymbiosis within their coral host. Symbiodiniaceae supply photosynthetic products to their host, while corals provide shelter and inorganic nutrients to the micro-algae. This symbiosis has been extensively studied in the context of coral bleaching, which results from a breakdown of the normal symbiotic relationship between the Symbiodiniaceae algae and the coral host, leading to Symbiodiniaceae expulsion and the loss of coral coloration. Coral bleaching increases coral mortality in almost all reefs and is linked to exposure of corals to stress, including rising temperature, ocean acidification or local pollutants. In order to study this symbiosis *in situ* and at ocean scale, the *Tara* Pacific expedition realized a vast sampling campaign to study healthy corals in their environmental context. The main objective is to better understand the adaptation of these organisms to environmental changes. We analyzed metatranscriptomic data sequenced from 3 corals genera (*Millepora, Pocillopora* and *Porites*) sampled around 11 islands during the *Tara* Pacific expedition in the Pacific Ocean. With these data and several bioinformatic methods we were able to (i) identify the different Symbiodiniaceae species present in each coral (ii) examine genes differentially expressed between islands and coral hosts, and (iii) realize functional analyses in order to observe the transcriptional adaptation of Symbiodiniaceae to different environmental conditions. We observed differences in Symbiodiniaceae gene expression profiles which correlated with the geographic location and/or physico-chemical environmental parameters. Overall, biological functions of differentially expressed genes reveal the capacity of adaptation of the coral micro-algae across the Pacific Ocean.

*Speaker

Exploring parasitic life-style in marine ecosystems

POSTER 21

Betina Porcel*[1]

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Abstract

Parasitism is a very common lifestyle in nature and a major source of evolutionary pressure both for the hosts and the parasites. The emergence of parasitism has occurred repeatedly across the tree of life, furthermore following several parallel pathways in some Phyla, often leading to reductions in genome size and sometimes even in the number of genes initially present as a common ancestral genetic repertoire. The interdependence of a parasite and its host (and the associated environmental pressure) has progressively shaped parasite genomes, leading them to evolve into increasingly specialized and host-dependent forms. The effectors involved in this host-parasite interaction have been studied in apicomplexans and kinetoplastids for many decades. Their best-known representatives are intracellular vertebrate parasites responsible for human and veterinary diseases such as malaria, toxoplasmosis, sleeping sickness and others, which are now major references for these phyla. These groups are outstanding targets for studying how environmental constraints have shaped parasite genomes during evolution. Nevertheless, an important part of the drivers of genetic diversity, allowing a better understanding of the transition from a free-living stage to parasitic life, remains to be discovered in ecological niches such as the planktonic community. Many questions remain unsolved: which are the evolutionary constraints orienting a protist towards parasitism? Are there as many different effectors as there are pathogenic species? (i.e.: are they species-restricted markers? are they environment-restricted?") Has this process evolved independently in each lineage or, conversely, is it possible to identify "parasite state markers"? Some examples of host-parasite "effectors" of certain branches of the tree of life, identified through bioinformatics analyses of the Tara Oceans Eukaryote Gene Catalog, will be presented.

*Speaker

Genomic mechanisms driving evolution of the Coxiella genus along the parasitism-mutualism continuum

POSTER 22

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Abstract

Background

Coxiella burnetii is a parasitic intracellular bacterium initially isolated from a tick. It causes Q fever, a zoonotic disease in humans, and represents a notable problem for livestock production. *C. burnetii* presents a biphasic cycle with both active and resistance forms. The latter can persist for long periods in the environment and is the primary infective form. Contrary to other intracellular pathogens, *C. burnetii* replicates inside the host cells pahogolysosomes, which presents an acidic pH. Interestingly, several *Coxiella*-like endosymbionts (*Coxiella*-LEs) phylogenetically related to *C. burnetii* have been recently described as nutritional mutualists of ticks, leading to the question of the evolutionary origin of *C. burnetii:* Did it evolved from a mutualistic symbiont by gaining different virulence factors or was the ancestor a parasite?

Methods

To answer this question, we conducted a comparative genomic and phylogenetic analysis

*Speaker

using two newly obtained *Coxiella*-LE from ticks and 40 additional Coxiellaceae genomes.

Results

All *Coxiella* representatives were found to be able to produce B vitamins and co-factors, while this was rarely possible in the other examined Coxiellaceae. The Dot/Imc T4 Secretion System (Dot/Imc SS) is essential for *C. burnetii* pathogenicity since it is used to hijack the host's phagolysosome to allow its replication. This secretion system is generally present among all Coxiellaceae.
In *C. burnetii,* the Dot/Imc SS seems part of a pathogenic island that has been lost or inactivated in Coxiella-LEs. Hence, the ancestor of *C. burnetii* and *Coxiella*-LE probably was a parasitic organism able to produce vitamins and cofactors. Interestingly, *C. burnetii* lineage has acquired laterally a Na+/H+ Mrp (Multiple resistance and pH) antiporter which is involved in alkali resistance and sporulation in other bacteria. We propose that this Mrp antiporter may have a role during the environmental phase of *C. burnetii* (resistance form).

Functional complementarity of saprotrophic and mycorrhizal fungi in forest soils highlighted by metatranscriptomics

POSTER 23

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Abstract

These authors contributed equally: Lucas Auer, Marc Buée.

In forest soils, fungi impact tree health and productivity, and they are undoubtedly major players in carbon sequestration and biogeochemical cycles. Fungi play a key role in the two major life-supporting processes in forest ecosystems: plant growth and plant decomposition. Indeed, they belong to large ecological guilds, such as saprotrophs, parasites (or pathogens) and mycorrhizal symbionts. The comparison of the genomes from soil decomposers, wood decayers and ectomycorrhizal (ECM) symbionts has revealed several independent lifestyle transitions from saprotrophism to mutualism in fungal lineages. No study has yet investigated the contrasted functional divergences/complementarities of ECM and saprophytic fungi in different forest soils, through the actual expression of genes related to the decomposition of soil organic matter. Here, we used a metatranscriptomic approach to characterize the environmental RNA extracted from four contrasted forest soils (boreal, temperate and Mediterranean biomes) in Europe and Canada. Using a dedicated fungal mRNA annotation pipeline and the JGI MycoCosm database (1000 Fungal Genomes Project), we compared the expressed functional activities of the main ecological guilds of soil fungi. We focused our analysis on transcripts coding for fungal N-foraging and N-mobilization pathways and the different families of transcripts related to the degradation of SOM: plant cell wall (PCW) degrading enzymes and microbial cell wall (MCW) degrading enzymes (DE). Confirming the

*Speaker

genome analyses, our results demonstrated that genes encoding PCW Carbohydrate-Active Enzymes (CAZymes) were significantly more expressed by saprotrophic fungi than by ECM and pathogenic fungi at the fungal community level. For pathogenic fungi, the expression of PCW CAZymes was significantly the lowest. The genes coding for secreted FCW CAZymes were also lowly expressed by pathogenic fungi in these forest soils. On the other hand, saprotrophic and symbiotic guilds expressed in a similar way and at a high level genes related to FCWDE families. While the expression of genes encoding secreted proteases were similar between these three guilds, the transcripts for N-related transporters and inorganic ion transporters were strongly expressed in ECM fungi compared to the other two groups of fungi. Metatranscriptomics provides new insights in the functioning and ecological interactions of different groups of fungi both at community and the species (or genus) scales.

ERA-BIO-IT: a Bioinformatics Platform for Applied Research in Plant Breeding

POSTER 24

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Abstract

1. Introduction

ERA-Bio-IT was created in 2020 by three partners, two French seeds companies (Lidea [1] –ex Euralis Semences and Caussades Semences- and RAGT 2n [2]) and a technical Institute (Arvalis [3]) wishing to share bioinformatics resources for crops breeding and cultivars evaluation.

2. Infrastructure

The computing infrastructure is managed by Portalliance Engineering [4]. It is composed of a virtualization server, hosting various virtual machines (JBrowse, Galaxy...), a High-Performance Computing (HPC) server managed with SLURM and data storage Qumulo solution. Those computing resources are scalable to answer quickly to each partner needs.

3. Objectives

Firstly, the aim of ERA-Bio-IT is to set up basics tools (such as JBrowse or Galaxy) for each partners bioanalysts, oriented toward the genetic and genomic study of major crops (maize, wheat, barley...).

Once the platform fully functional, more advanced genomic analyses and bioinformatics developments are expected as support for each partner. The platform will be open for multi-partnership projects, including with new private and public partners.

Finally, the ERA-Bio-IT platform aims to support the omics technology and methodology watch for its partners in order to provide a cutting-edge expertise in these fast-evolving fields.

4. Current Challenge: Plant Pangenomics

Facing the constant increase in newly sequenced genomes for crop species, ERA-Bio-IT wishes to help the transition from the traditional reference genome approach in genomics for plant breeding to a complementary pangenomic approach. Working with *Zea mays* as

*Speaker

our model specie, we are studying methods to construct, visualize and explore pangenomes for crop improvment and evaluation. We are looking forward to exchange with public and private teams interested in this matter.

Acknowledgements

ERA-Bio-IT is financed by Lidea, RAGT and Arvalis.

References

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ARVALIS - www.arvalisinstitutduvegetal.fr.

Portalliance Engineering - www.portalliance.fr.

Organophosphorus pesticide affects the gut microbiota of two endogeic earthworm species, Aporrectodea caliginosa and Allolobophora chlorotica and the turnover of the soil microbiota they achieve during digestion

POSTER 25

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Abstract

As they drill galleries and feed on soil, earthworms are key soil ecosystem engineer that contribute to soil aeration and organic matter turnover. The earthworms' activities involve numerous interactions with the soil microbiome, most particularly during soil transit in the earthworm gut, which likely constitute a biological filter ending with modified microbiota in dejected casts. In the context of growing usage of xenobiotics in agriculture, questions arise on unintentional deleterious effects they produce on non-target organisms such as earthworms. Besides toxicity assessments on earthworms' behaviour, mortality, reproduction, enzymatic and cellular processes, few studies have considered the earthworm's digestive filter and associated gut microbiota should respond to chemical inputs. Here, we investigated the effects of the organophosphate insecticide ethyl-parathion on digestive abilities of two endogeic earthworm species, *Aporrectodea caliginosa* and *Allolobophora chlorotica*. We used an amplicon-sequencing approach to decipher bacterial and micro-eukaryotic communities present in the ingested soil, the intestine and dejected casts. For each compartment, we measured changes of microbial abundance and composition according to the worm species and to the pesticide treatment. Also, because ethyl-parathion damage the enzyme acetylcholinesterase that enhance intestinal contraction, we focus a particular attention to fractions of the soil microbial diversity that were upheld or suppressed during digestive transit of the soil in the earthworms' gut.

*Speaker

Population structure of French honey bees from sequencing a large panel of haploid drones

POSTER 26

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Abstract

The honey bee *Apis mellifera* comprises numerous subspecies originating mainly from Africa, Europe and the Middle East, each of which corresponds to a specific geographical area. However, due to the interest of beekeepers for various phenotypic characteristics related to honey production or behaviour, several subspecies have been imported into France and have been hybridised voluntarily or naturally with the local populations. In order to study the impact of these exotic imports on the genetic structure of the French population, originally composed of the subspecies *Apis mellifera mellifera* only, we sequenced the whole genome of 870 haploid drones, each representing a colony. The sample is representative of imported subspecies and French queen producer populations. We identified nine genetic backgrounds, of which five correspond to described subspecies, two relate to isolated populations on islands and two can be attributed to human management of populations selected for specific phenotypic characteristics. Apart from the reference populations for the subspecies, the majority of the bees analysed are a mixture of the different backgrounds identified, with the exception of those selected for royal jelly production. Our analyses also revealed long haplotype blocks, some of which could coincide with the position of the centromeres. The largest of these is 3.6 Mb long on chromosome 11, representing 1.6% of the genome.

*Speaker

Make visible the invisible: Optimised development of an environmental DNA metabarcoding tool to characterise trematode parasitic communities

POSTER 27

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Abstract

The world's parasitic and mutualistic biodiversity is undergoing major upheavals related to changes in host community structures, changes in interactions between species, shifts in species distributions, and through co-extinction events. Trematodes are an important component of this invisible biodiversity, not only in terms of species richness, but also because of their role in the functioning of ecosystems and in the emergence of associated diseases. Together, these elements point to the need for a better assessment and understanding of the structure and dynamics of trematode diversity. Through a poster, we present our study which aims to develop an optimized eDNA-based metabarcoding approach to detect and characterize the trematode communities from environmental, and more specifically water-sediment interface samples. The efficiency of this new tool was first assessed by an exhaustive in silico and in vitro validation step. We next compared our eDNA-based approach to a classical trematode monitoring method in natura over four different ecosystems from Occitanie Region (Southern France). Our eDNA-based monitoring tool has displayed a high amplification enrichment of trematode DNA compared to all other organisms tested, a 100% detection score for tracking back an in vitro mock community composed of 28 trematode species, and high genetic resolution which makes it relevant to discriminate between even phylogenetically close trematode species. Over the four natural ecosystems screened in natura, we detected 11 species while only 5 were detected using the classical trematode monitoring method. We believe that this new eDNA-based metabarcoding tool will open new perspectives for fundamental and applied studies in conservation, sanitary survey, and field ecology.

*Speaker

From the environment to the communities and vice-versa: towards predicting functions from environmental data in the planktonic ecosystem

POSTER 28

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Abstract

As metagenomics now generate huge amounts of data, there is a genuine need for innovative data-driven methodologies to quantify and predict microbial ecosystemic functions in their environment. As a proof of concept, we focused on marine microbes, which play a crucial role in climate regulation, biogeochemical cycles, and trophic networks. We reanalyzed 885 marine metagenome-assembled genomes through a network-based approach and detected 233,756 protein functional clusters, from which 15% are functionally unannotated. We investigated all clusters' distributions across the global ocean through machine learning, and identified biogeographical provinces as the best predictors of protein functional clusters' abundance. The abundances of 14,585 clusters were predictable from the environmental context, including 1347 functionally unannotated clusters. We analyzed the biogeography of these 14,585 clusters, identifying the Mediterranean Sea as an outlier in terms of protein functional clusters composition. Applicable to any set of sequences, our approach constitutes a step towards quantitative predictions of functional composition from the environmental context.

*Speaker

Genomic adaptation of Pelagomonas calceolata to temperate iron-poor oceans revealed by a chromosome-scale assembled genome

POSTER 29

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Abstract

Marine phytoplankton are abundant in all oceans, are key actors in CO2 sequestration and account for 45% of net primary production on earth. Climatic models predict an increase of oligotrophic areas in the next decades that could affect the abundance and ecological role of the photosynthetic picoeukaryotes (PPE). Among them, the micro-algae *Pelagomonas calceolata* (Stramenopile/Pelagophyceae) is present in all oceans but despite being quite abundant, its ecological impact is unknown.
To study this species, *P. calceolata* genome was sequenced, assembled and annotated. We used this genome to study its genetic content compared to other PPEs and describe its ecological niche using Tara *Oceans* metagenomic datasets.

Comparative genomic analysis between *P. calceolata* and 8 other PPEs show that *P. calceolata* has iron-free metabolic pathways, potentially allowing to grow in low-iron conditions. Iron uptake and storage doesn't seem to be more efficient in *P. calceolata* than in other PPE however, some uncommon proteins such as phytotransferrins and ferroportins could play a role in iron transport.

In addition, *P. calceolata* present a large collection of genes encoding, nitrate, nitrite and urea transporters but only a few ammonium transporters suggesting that the major source of nitrogen could be nitrite or nitrate. An interesting feature is the presence of potential intracellular and extracellular nitrite/nitrate sensing proteins, carrying a protein-kinase domain and a transmembrane domain respectively.

Finally, we measured a high relative abundance of *P.calceolata* in temperate and iron-poor oceanic regions supporting genomic observations.
Temperature, iron concentration and nitrogen source and quantity could be essential drivers of *P. calceolata* ecological success. The next step is to identify the differentially expressed genes under variable environmental conditions by analysing 1) Tara *Oceans* and *Pacific* metatranscriptomic datasets, and 2) RNA-seq data gathered during growth under defined parameters of temperature, iron concentration and nitrogen source and concentration.

*Speaker

Genomic diversity in the bloom-forming cyanobacterium Aphanizomenon gracile and its phycosphere

POSTER 30

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Abstract

Huge genotypic diversity and helper bacteria are considered as key factors of adaptative success in marine cyanobacteria. While marker heterogeneity surveys showed that harmful cyanobacteria blooms in freshwater lakes were not clonal, the real extent of genetic and functional diversity within such population and the associated phycosphere remain unclear. Here, comparative omics of four monoclonal *Aphanizomenon gracile* strains, a toxinogen filamentous cyanobacteria blooming worldwide in fresh and brackish environments, isolated from a single drop of water reveals extensive heterogeneity of chemotypes and gene contents, despite similar genome size and high similarity indices. These variations are notably associated with horizontal gene transfers (HGT) and biosynthetic gene clusters (BCG) - some of them producing secondary metabolites thought to be involved in cyanobacterial fitness. A novel siphophage infecting *A. gracile* displaying characteristics of temperate phages has been characterized and is suspected to participate to this genotypic diversification. In spite of high variability in heterotrophic taxa relative abundances, *A. gracile* phycospheres displayed functional redundancy implying biosynthesis of public goods. Altogether, these results suggest that a bloom could be a highly heterogenous population of *A. gracile* genotypes, where losses and gains of BCGs would compel cyanobacteria individuals to cooperate together and with heterotrophic bacteria.

*Speaker

A metagenomic approach for monitoring new and re-emergent pathogen viruses in ecosystems

POSTER 32

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Abstract

The field of viral ecology has had a massive improvement from the advances made in metagenomics (i.e. viromics), however, the detection of new and re-emergent viruses involved in human health is still difficult since they are often found at low abundances in the environment. We therefore propose an alternate sequencing method to target a specific single-stranded RNA virus group, while the original microbial diversity is unimpaired. This enrichment is performed at the stage of the cDNA library preparation by using specific oligonucleotides targeting the viral genomes of interest designed with viroExplorer pipeline, in addition to random hexamer traditionally used in target-independent metagenomic sequencing. This pipeline wraps multiple tools/softwares and scripts in one command for designing a set of specific oligonucleotides of a collection of single-stranded RNA virus genomes (e.g. *Enterovirus*, SARS-Cov2). It identifies oligonucleotides candidates by applying k-mer counting algorithm instead of multiple sequence alignment in order to optimize the pipeline performance for large input. All oligonucleotide candidates' stability is evaluated by physical-chemical properties conventionally used for PCR primer, and their specificity is ensured by the removal of oligonucleotides aligned to non-target genomes. After the oligonucleotide candidates' stability and specificity have been checked, viroExplorer allows to select a final set of oligonucleotides covering the whole virus genomes at a defined threshold. In this work, we assessed the efficiency of this method on *Enterovirus* with wastewater samples collected from urban sewage.

*Speaker

Partial overlap between inversions and genomic islands of divergence during early stages of ecological speciation.

POSTER 33

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Abstract

The role of inversions in speciation events is still questioned. The modification of the genomic architecture generated by chromosomal inversions can impact the genome in several ways (decrease in chromosomal recombination, protection of advantageous allelic combinations ...).
Drosophila yakuba mayottensis, discovered in 2016, is a species of fruit flies specializing in a poisonous plant called Morinda citrifolia. During our population genomics study, a nanopore sequencing of D. y. mayottensis was performed and compared to the reference genome of Drosophila yakuba thus highlighting the presence of multiple inversions in our population of interest. Some of the inversions observed in the genome of D. y. mayottensis seem to correspond to genomic islands of speciation (GIS) - the first regions of the genome evolving during speciation - identified during the measurement of the Population Branch Excess (PBE).

When inversions are closely related to the evolutionary traces observed on the genome, we can ask ourselves whether their impact on the speciation event is due only to the suppression of recombination thus generating a divergence between the two sister species or to a protective role of inversions on their genetic combinations and/or "key" genes of adaptation.
Inversions identified in D. y. mayottensis are non-existent in Drosophila sechellia, the first species described as a specialist in M. citrifolia. They are therefore not essential for adaptation on the host plant. Nevertheless, the abundance of inversions in D. y. mayottensis and their correlation with several GIS has led us to question the role of inversions in this particular speciation event.

*Speaker

Improving biodiversity inventories of the deep sea using Capture by Hybridisation

POSTER 34

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Abstract

The metabarcoding of environmental DNA (eDNA) opened large prospects for the future biomonitoring of marine environments. Yet, Metabarcoding still relies on Polymerase chain reaction (PCR) of relatively short fragments, mostly through the use of "universal" primers. Small fragment size limits both the accuracy of taxonomic assignment and the reconstruction of robust phylogenies. Direct sequencing (such as shotgun sequencing) may solve these limitations through the reconstruction of longer fragments, yet metagenomes are usually dominated by DNA from microorganisms and do not allow a good coverage of metazoans genomes. Here we present an intermediate, less expensive option using capture by hybridization (CBH) for inventorying biodiversity in deep-sea sediment samples. First studies revealed a broader spectrum of prokaryotic, eukaryotic, and particularly metazoan communities than metabarcoding using "universal" primers, and allowed reconstructing full-length barcode regions (up to 1900bp). We built on this first steps and designed new probes to still improve the detection of a broader range of metazoans, and test them on mock communities. In the current work, we also add the mitochondrial COI barcode region and increase the sequencing depth to improve taxonomic identification. The aim is to better describe unknown taxa (and possibly) phyla, to overcome major gaps of the reference system through better phylogenetic reconstruction and enhanced taxonomic resolution. This works show the promise of CBH in environments still largely underrepresented in public databases and is a valuable addition to current eDNA based marine biomonitoring approaches.

*Speaker

Mito-nuclear coadaptation in bivalves with doubly uniparental inheritance of mitochondria may rely on alternative splicing

POSTER 35

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Abstract

Mito-nuclear incompatibilities (MNIs) can lead to a desynchronization of the machinery required for efficient cellular energy production (oxydative phosporylation OXPHOS). Therefore, coevolution and coadaption of mitochondrial and nuclear genes involved in this mechanism are primordial. In species with doubly uniparental inheritance (DUI) of mitochondria such as *Limecola balthica*, both males and females are able to transmit their mitochondria, the former to all their progeny and the latter to their male offspring, where the male mitogenomes (mt) are quartered in gametes. Two highly divergent mt-genome coexist within males, likely to disrupt mito-nuclear coadaptation. RNA-seq data from somatic tissues and purified gametes from 2 males and 2 females were produced to test if mitotype-specific nuclear alleles, paralogous nuclear genes, or alternative splicing could play a role in mito-nuclear coadaptation. Differential expression profiles showed oocyte specificity but also high variability between replicates. The *atp5c1* gene coding for the gamma subunit of the ATP-synthase FO/F1 complex, presented 9 isoforms which contained overall 32 different exons. These isoforms were composed of 10 to 21 exons and were differentially expressed between sexes. Sex-specific exons were genetically very close (89.3 to 92.9 % of identity). Inferring the tertiary structure of these isoforms revealed that sex-specific exons are likely in direct interaction with a mt-encoded subunit of the ATP-synthase. These results suggest the existence of a mutually exclusive alternative splicing mechanism in the expression of *atp5c1* between males and females. Additional analyses will be performed on additional samples and the other genes involved in the OXPHOS chain to test for the presence of alternative splicing.

*Speaker

Development of molecular markers to determine the genotype of individuals carrying a feminizing genetic element.

POSTER 36

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Abstract

The common pillbug (*Armadillidium vulgare*) has various sex determinants. One of these, called the *f*-element, represents the insertion of the genome of a feminizing bacterium (*Wolbachia*) into the host genome. The *f*-element has the feminizing ability of *Wolbachia*, i.e., individuals carrying it typically become females. However, some may carry 2 copies of the *f*-element per cell if they inherit it from both parents. Quantifying the number of copies carries by individuals is essential to assess the frequency of the *f*-element in natural populations. To determine that number, we use quantitative PCR (qPCR) and droplet digital PCR (ddPCR). With these methods, the amplification of the target sequence is compared to a reference sequence whose number of copies per cell is known. If the reference gene is present as two copies in the host diploid genome, individuals carrying two copies of *f*-element (homozygotes) will have relative value of 1, individuals carrying one copy (heterozygotes) will have relative value of 0.5. These assays require establishing primers amplifying a non-duplicated target in the *f*-element. However, the *f*-element has many unresolved duplications of *Wolbachia* sequences. To avoid these duplications, we took advantage of Illumina sequencing runs performed on two pillbug lines which carry the *f*-element. Sequencing reads were aligned to the reference genome of *Wolbachia* to identify regions with low sequencing depth. These regions were selected to design primers. Primers were tested in ddPCR and qPCR, together with fluorescent probes to enable genotyping tests in duplex experiments (amplifying both the target and the reference gene at once). We aim to apply this approach to natural populations.

*Speaker

Metabarcoding body remains sieved from tree hollow wood mould to characterize forest insects

POSTER 37

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Abstract

Tree hollows are key microhabitats providing food, refuge and breeding site to a rich insect diversity including keystone or endangered species. The survey of hard-to-access hollows is essential for conservation and biodiversity monitoring. Within-hollow sampling often implies destructive protocols and results in excavating the wood mould to identify morphologically insect specimens (current presence) or body remains (past occurrence). The morphological analysis of biotic samples often overlooks their hyperdiverse community and requires high taxonomic expertise, making it difficult to apply on a large scale.

In the present study, we apply metabarcoding techniques on insect body remains sieved from tree hollow wood mould to characterize insect communities. We highlight the complexity of the sample generally typified with low DNA concentration and the important presence of PCR inhibitors deriving from cuticular pigments and traces of humic acid. We describe a protocol overcoming these molecular limitations on the way to a scalable, reproducible and cost-efficient method for biomonitoring of hollow-associated insect past communities.

*Speaker

Tracking genomic footprints of environmental stressors in Haemonchus contortus, a parasitic nematode of veterinary interest.

POSTER 38

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Abstract

Haemonchus contortus is a hematophagous parasitic nematode of veterinary interest. Building on the recent release of its reference genome, we have performed a survey of H. contortus genome-wide diversity using a panel of 223 individual worms from 19 isolates. Comparison of genetic diversity between population revealed evidence of past migrations associated with slave trade and colonization of Australia. Analyses of genome-wide diversity also revealed evidence of selection acting on genes associated with anthelmintic drugs used for worm control, and genetic signatures compatible with climate-driven adaptation, implicating a gene acting as an epigenetic regulator associated with desiccation stress resistance. In parallel of these efforts, we have applied a back-cross design and a pool-seq framework to map quantitative trait loci (QTL) associated with resistance to levamisole, an anthelmintic drug. This approach highlighted previously known functional candidate genes such as the cholinergic receptor subunit genes (acr-8, unc-63 and unc-29), as well as QTL encompassing genes encoding proteins with calcium ion binding capacities. Taken together, these results expand our current understanding of the underpinnings of levamisole resistance.

Relying on one of the best parasite nematode genome assemblies to date, our results have revealed new perspectives on the biology of this globally important parasite. Current efforts are dedicated to delineate its ability to establish and survive in hosts with enhanced resistance to parasite infection.

*Speaker

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