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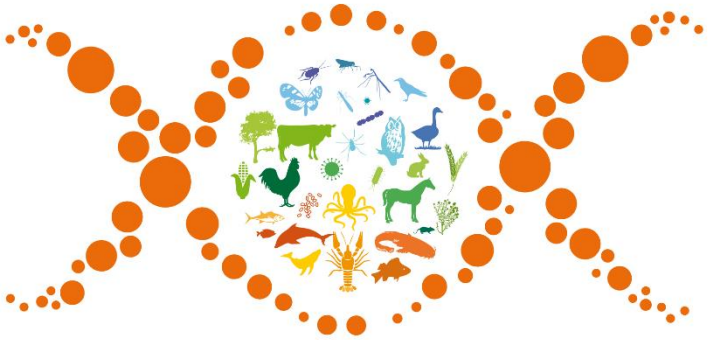

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BOOK OF ABSTRACTS

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Exposome-driven modulation of xenobiotic responses in the Asian tiger Mosquito *Aedes albopictus* through microbiota interactions

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Abstract

Over recent decades, the Asian tiger mosquito *Aedes albopictus* has colonized all inhabited continents, thriving especially in urban environments. Such settings expose the species to a wide range of anthropogenic compounds, including xenobiotics. Adaptation to these compounds involves not only the mosquito's detoxification pathways but also potential modulation by its microbiota. We investigated these interactions using a multifactorial approach encompassing various xenobiotics, concentrations, spatial scales and biological endpoints. Overall, this work highlights the pivotal role of the microbiota in shaping mosquito responses to urban pollutants and suggests that microbial interactions may constribute to the successful establishment of *Aedes albopictus* in anthropized environments.

Keywords:

Using environmental DNA to monitor gastrointestinal parasites in Northern Ireland sheep farms.

Emer MCCANN

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Abstract

Gastrointestinal nematode (GIN) infections pose a major challenge to UK and European sheep farming. The current situation is further complicated with key species such as Teladorsagia circumcincta, showing increasing resistance to various anthelmintics. While faecal egg counting remains the main diagnostic method, high costs often deters its use, leading to blanket anthelmintic treatments that accelerate resistance. This problem highlights the urgent need for alternative surveillance tools to support animal welfare and productivity. Environmental DNA (eDNA) analysis, while widely used in aquatic species monitoring, recent studies show potential for parasite detection. Since water samples present high turnover and contamination risks, grass and soil as more stable and representative matrices should be considered In a longitudinal study across four active sheep farms in Northern Ireland, grass samples from pastures and drainage areas were collected in parallel routine faecal egg counts. Bioinformatic and molecular diagnostic tools, including eDNA digital PCR assays, were used to track parasite distribution across seasons. This integrated approach, combined with abiotic data, enables precise identification of high-risk areas and species; Through informed pasture management, guiding livestock rotation, and supporting targeted anthelmintic use, we hope improvements in sustainable sheep farming can be achieved.

Keywords: eDNA, Agriculture, Parasites, Anthelmintics, ddPCR

Metabarcoding and metagenomics of bat guano uncovers ecological processes and ecosystem health

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Abstract

Traditional biodiversity assessments, though effective, often focus on single groups, lack scalability, and require intensive logistics. In this study, we used bats as natural, and wide-ranging samplers of biodiversity, capturing a snapshot of ecosystem complexity through trophic aggregation. Each insect a bat consumes carries not only its own DNA but also DNA of its own food source and associated microorganisms. Thus, using bat guano offers a unique and non-invasive approach for multi-taxon biodiversity monitoring and ecosystem health assessment. We collected guano from two bat species (Rhinolophus hipposideros and Eptesicus serotinus) in 18 colonies spanning three European bioclimatic zones (temperate oceanic, humid continental, and Mediterranean). Synchronous sampling occurred monthly from May to September over two consecutive years. Using multi-marker metabarcoding, we identified DNA from plants, arthropods, and fungi. This was complemented by metagenomic analyses of the associated viral communities. This yielded over 5 000 insect, 4 000 fungal, and 1 000 plant OTUs, including invasive and pest species, along with numerous viruses (mainly insect-associated), some impacting pollinators or crops. Together, these data enabled a comprehensive analyses of species diversity, community composition and the reconstruction of multilayer ecological networks, demonstrating that bat-based biomonitoring can offer a powerful lens into ecosystem health across space and time.

Keywords:

The conquest of the horse and the horse of conquest: tracking the genetic hoofprints of domestication and colonization

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Abstract

The domestication of the horse marked a turning point in human history, reshaping societies, economies, and empires. But who truly "conquered" whom? This keynote explores the dual narrative of the horse as both a subject of human domestication and a powerful agent of human expansion and domination. By tracing the genetic hoofprints left in ancient genomes, we uncover the origins of early horse domestication, the spread of key lineages, and their pivotal role in the colonization of new territories from the Eurasian steppes to the far reaches of modern colonial empires. Drawing on cutting-edge ancient DNA research, this talk will reveal how horses and humans co-evolved, how domestication unfolded across time and space, and how, by becoming indispensable partners in warfare, trade, and cultural exchange, these animals reshaped human history until the early 20th century.

Keywords:

Tracing tropical plankton evolution over half a million years using sedimentary ancient DNA

Sarah ROMAC

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Abstract

Ancient DNA preserved in marine sediments (sedaDNA) offers a powerful new window into the evolutionary history of plankton, especially where the fossil record is incomplete. In this study, we used shotgun metagenomics to explore the genomic dynamics of tropical plankton communities preserved in sediments spanning the past 500,000 years, and possibly extending to 1.2 million years. Sediments were collected from a tropical Indian Ocean core using an ultra-clean protocol to avoid contamination from modern and exogenous DNA. sedaDNA was extracted from five key stratigraphic layers and DNA libraries built from highly degraded fragments were sequenced on Illumina platforms. Characteristic cytosine deamination signatures confirmed the preservation of authentic tropical sedaDNA beyond 500,000 years. Taxonomic profiles were reconstructed using MALT and curated nuclear, plastidial, and mitochondrial genome databases as references. The recovered eukaryotic assemblages were dominated by haptophytes (notably the coccolithophore Gephyrocapsa.) alongside Rhizaria, Archaeplastida, and Opisthokonta sequences. These findings demonstrate that genomic information can be recovered from tropical sediments over orbital timescales, opening new perspectives for coupling paleogenomic and fossil evidence. Ongoing mapping of metagenomic reads to reference genomes enables exploration of intra-species diversity within key lineages such as Gephyrocapsa.

Keywords: sedimentary ancient DNA, tropical oceans, plankton evolution, metagenomic reconstruction

Ancyromonads provide a window into the early evolution of eukaryotic gene content

Jazmin BLAZ

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Abstract

Ancyromonads, a diverse and globally distributed group of heterotrophic flagellates, hold a pivotal deep position within the eukaryotic tree of life. Despite their evolutionary significance, their biology is still poorly understood. Here we sequenced the nuclear genomes of six diverse ancyromonad species unveiling their gene content. Through a large-scale evolutionary analysis, using state-of-the-art phylogenetic reconciliation methods, we explored the relative importance of gene family origination, duplication, transfer, and loss during the diversification of ancyromonads, and compared it with patterns observed in diverse representatives of the eukaryotic tree of life. We showed that a high amount of gene family originations predate the diversification of ancyromonads and important turnovers of gene families involved in signal transduction and cytoskeleton associated proteins further contributed to a great variation of the gene content among ancyromonad species. Moreover,ancyromonad genomes contain genes with prokaryotic origins, that could have been laterally acquired. Our study provides the first insights into the intriguing genome diversity of ancyromonads and offers a unique view of the early evolution of the eukaryotic domain.

Keywords: genome evolution, LGT, protists

From Bacteria to eukaryotes and nucleomorphs: the prominent evolutionary journey of the DNA polymerase III

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Abstract

Cryptophytes have acquired a plastid from red algae (secondary endosymbiosis) and a remnant of the engulfed red algae nucleus, the nucleomorph, persists in multiple lineages. Here, we completed the first genome-resolved metagenomic survey dedicated to nucleomorphs using the Tara Oceans 'omics legacy. We successfully resolved the triumvirate environmental genomes (nuclear, nucleomorph and plastid) of the genus Teleaulax, which is abundant and widespread in the sunlit oceans. Unexpectedly, Teleaulax nucleomorphs encode the first DNA polymerase III (DNApol-III) genes documented among eukaryotes. Phylogenetic analyses firmly connect the Teleaulax DNApol-III to Cyanobacteria, favoring a primary endosymbiosis origin for this prominent gene. This scenario implies that some red algae have maintained this gene at least up to the point of the Cryptista-related secondary endosymbiosis event. By leveraging eukaryotic genomic databases, we found that a few red algae and green algae also contain this DNApol-III, demonstrating its occurrence in distantly related eukaryotes and supporting a primary endosymbiosis origin. Finally, knowledge surrounding Teleaulax suggests that DNApol-III plays a critical ecological role. Indeed, the plastid and nucleomorph of Teleaulax are sequestrated together by the ciliate Mesodinium over relatively long periods of time. We hypothesize that DNApol-III is used for plastid genome replication in both Teleaulax and Mesodinium.

Keywords: Evolution, Ecology, Eukaryotic plankton, Tara Oceans, Teleaulax, nucleomorph, chloroplast, primary endosymbiosis, secondary endosymbiosis, DNA polymerase III, Mesodinium, kleptoplasty, lateral gene transfers, phylogeny, guided genome, resolved metagenomics

Unveiling the Evolutionary Dynamics of the X Chromosome in Aphids

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Abstract

Sex chromosomes often display distinct evolutionary dynamics compared to autosomes. In many species, the X chromosome evolves faster ("faster-X" effect) due to the exposure of recessive alleles in hemizygous males and differences in effective population size. Aphids, with their XX/X0 sex chromosome system and cyclical parthenogenesis, provide an exceptional model to investigate these processes. We hypothesize that the X chromosome in aphids undergoes accelerated sequence divergence and promotes the emergence of novel genes. To test this, we conducted a comparative genomic analysis across 51 aphids species, including four newly assembled high-quality genomes. Chromosome-level assemblies were used to assess macro-synteny conservation, and quantify sequence divergence between X chromosomes and autosomes. Our analyses reveal that the X chromosome maintains conserved macro-synteny across aphids yet exhibits significantly higher sequence divergence than autosomes, consistent with a genome-wide "faster-X" pattern. We identified over a thousand species-specific duplicate genes, many likely arising from transposon-mediated duplication events, that are enriched on the X chromosome. Transcriptomic analyses further show that these duplicates often display male-biased expression, suggesting functional differentiation following duplication. Collectively, our findings provide the evidence that the X chromosome in aphids evolves faster than autosomes and acts as a hotspot for transposon-driven genetic innovation. This study underscores the pivotal role of sex chromosome architecture in shaping genome evolution and generating new genetic diversity across the aphids.

Keywords: Aphids, X chromosome, faster X, transposons, sex biased expression

Ecological adaptation to life in extreme environments is linked to structural genome evolution in cryptobiotic Panagrolaimus nematodes

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Abstract

There is mounting evidence that genomic structure shapes evolution and adaptation to novel habitats. While morphological and genetic adaptations to environmental changes have been extensively studied, their impact on chromosome structure remains less explored. Advances in genome assembly enable detailed investigations of chromosome structure, revealing both conserved and highly rearranged patterns across animal phyla. In nematods, 7 linkage groups have been identified.Cryptobiotic species can withstand extreme conditions in a state of suspended life, and this process may disrupt chromosome structure conservation by inducing DNA breaks and repairs. Few animal species have this ability, yet it is found in several nematode genera, such as Panagrolaimus. Panagrolaimus species are desiccation and freezing tolerant, enabling them to populate harsh environments such as the Atacama desert or the Siberian permafrost. This genus offers a unique opportunity to study the influence of ecological pressures on genome evolution.We generated genome assemblies for cryptobiotic Panagrolaimus species to investigate the relationship between cryptobiosis and genome structure. We found extensive intra- and interchromosomal rearrangements, several events of blunt chromosome fusion, and at least two events of triploidization. Macrosyntenies of phased assemblies reveal that these rearrangements and fusions are haplotype exclusive. These rearrangements may stem from DNA breaks induced by cryptobiosis that were not repaired to the original chromosome structure, and suggest a lenient genome repair machinery in Panagrolaimus. Chromosome plasticity in Panagrolaimus is expected to be a driver of their ecological adaptation.

Keywords: Cryptobiosis, chromosome structure, genome plasticity

Sequence locally, Think globally: Biodiversity genomics at scale

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Abstract

Biodiversity is in crisis, with anthropogenic habitat loss and climate change threatening all of the planet's ecosystems. Biodiversity is also a potential solution to this crisis, as diverse species have already solved many of the problems we face. Biodiversity has value both in itself, and in what we can learn from it to improve the health of human societies and the natural world. One fundamental route to realisation of the value of biodiversity is through genomics. By generating high-quality genomes for large numbers - possibly all - of the species on earth we can have access to the blueprints for their diverse biologies, and use this information to conserve species and ecosystems, devise new drugs and biomaterials, and engineer our crops and farm animals to be more resilient to future challenges. At Tree of Life we are generating reference quality genomes at a scale never before achieved - releasing 8 genomes a day. We are sequencing across phylogeny, from single celled eukaryotes to plants, fungi and animals, and to date have released nearly 4,000 genome sequences. I will review how we have achieved this goal, discuss the setup of our “genome engine”, and illustrate the power of the new genomic data in understanding new biology.

Keywords:

Pangenomes Enhance the Characterization of Genetic Bases of Agronomic Traits in Cultivated Grapevine

Baptiste PIERRE

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Abstract

Pangenomes have been developed for several horticultural crops, but their exact contribution to adaptation and agronomic traits remains poorly understood, particularly the role of accessory genes and genome organisation. In this study, we constructed a pangenome for cultivated grapevine, Vitis vinifera L. subsp. vinifera, from 16 varieties representative of the three main known genetic groups. We identified that 59.7% of genes belong to the accessory genome, enriched in biological functions related to adaptation, and that transposable elements contribute significantly to genomic variability. Using this pangenome to genotype structural variants in a panel of 277 grape varieties, we performed genome-wide association analyses on three traits related to berry development and composition. Our results show that the pangenomic reference allows the identification of loci that escape approaches based on a single reference genome. These results highlight the value of pangenomes for characterising the genetic basis of agronomic traits and adaptation in grapevines.

Keywords: pangenome, cultivated grapevine, structural variation, agronomic traits, genome, wide association studies (GWAS)

Unravelling genomic drivers of speciation in Musa through comparison of wild banana ancestor genomes.

Guillaume MARTIN

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Abstract

Cultivated bananas are the result of hybridisation between wild species and subspecies of Musa that diverged in the region of Southeast Asia and New Guinea. These hybridisations produced diploid and triploid hybrids, some of which yielded parthenocarpic seedless fruit, which were selected and propagated by humans. As a result, banana genomes are complex mosaics of large blocks of sequences involving nine genetic groups including one unknown contributor. We generated continuous genome assemblies of these contributors including a hybrid that provided access to part of the unknown ancestor's genome. Comparative genomic and phylogenetic analyses between those genomes revealed chromosomal rearrangements and centromere diversification. The centromeric regions have incorporated different types of repeated sequences, notably tandem rDNA repeats that may reduce fertility in hybrids. Chromosome rearrangements are mainly reciprocal translocations, sometimes with complex structures, that reduce recombination in structural hybrids and were generally found preferentially transmitted to progenies. These factors could contribute to an ongoing speciation process within Musa by reinforcing reproductive isolation, which probably originated from past fluctuations in climatic conditions and land connections in the Southeast Asia/New Guinea region.

Keywords: Genome evolution, Musa, Comparative genomics, Speciation, Chromosomal rearrangements, Centromere

Evolutionary Dynamics of Fall Armyworm Global Invasion

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Abstract

Biological invasion poses a severe threat to global agriculture and biodiversity, with the recent global expansion of the Fall Armyworm (FAW, Spodoptera frugiperda: Lepidoptera: Insect) representing a critical example. Originally native to the Americas, this major pest, which exists as two host-differentiated strains (corn and rice), was first reported as an invader in 2016 and has since spread rapidly across Sub-Saharan Africa, Asia, and Europe, causing devastating maize yield losses (e.g., up to 23-53% in Sub-Saharan Africa). Our population genomics analysis, using globally collected 177 samples, revealed that the invasive population originated from a genetically admixed subset within the corn strain. Furthermore, the initial introduction was estimated to have occurred approximately 100 years ago, implying a prolonged lag phase before the pest became widely invasive. The successful invasion appears to have been driven by a combination of evolutionary forces, including adaptive evolution, highlighted by selective sweeps and bioassays demonstrating enhanced host-plant adaptation and insecticide resistance, and purifying selection, with population statistics and Loss-of-Function mutation analysis suggesting that the purging of recessive deleterious mutations during the lag phase played a key role. These findings underscore the combined contributions of both adaptive and purifying selection to the FAW's rapid global success, providing essential evolutionary context for urgent pest management efforts.

Keywords: Spodoptera frugiperda, fall armyworm, Invasion, lag phase, insecticide resistance, host plant adaption

The genomic footprints of wild Saccharum species trace domestication, diversification, and modern breeding of sugarcane

Angélique D'HONT

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Abstract

Sugarcane is a major crop accounting for 80% of the sugar production and increasingly used for bioethanol production. Its origin remained unclear due to its complex polyploid interspecific genome. To address this, we produced whole-genome sequence data from 390 wild and cultivated representative accessions and developed new approaches and analytical tools adapted to complex polyploids. We analyzed the distribution of repeated k-mers as a proxy for transposable elements and performed local admixture inference based on read-based haplotypes. Our results supported that Saccharum officinarum was domesticated in the New Guinea region from hybrids between wild S. robustum subgroups. We discovered a wild unknown Saccharum contributor to most modern cultivars, that could be traced back to the initial phases of modern sugarcane breeding. We highlighted two early centers of sugarcane diversification associated with human transport, one in continental Asia through hybridization with different wild S. spontaneum subgroups and one in the Melanesian and Polynesian islands via hybridization with the discovered ancestor and Miscanthus. This study reconstructed the complete domestication trajectory from wild progenitors to cultivated hybrids resolving long-standing taxonomic debates and providing a definitive evolutionary framework for the crop. It also revealed untapped wild Saccharum diversity as a source of alleles for breeding programs.

Keywords:

Uncovering recessive lethal and female infertility disorders in cattle using large-scale genomic and phenotypic data

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Abstract

Cattle breeds are genetically small populations prone to recurrent outbreaks of recessive genetic defects, threatening animal welfare and the profitability of the industry. The advent of next-generation sequencing and genomic evaluation has transformed our ability to detect and manage these disorders. Today, pedigree information, performance records for dozen of traits, and medium-density SNP genotypes are available for millions of animals. In parallel, international efforts have sequenced the genomes of the main ancestors of each breed, enabling reverse genetic strategies to identify defects previously overlooked by positional cloning. In this talk, I will present two complementary data-driven approaches: the search for homozygote depletion and the identification of homozygous enrichment or depletion in phenotypically contrasted animal groups, as compared with expectations based on their ancestors' genotypes, which are complemented by validation and functional characterization analyses. I will provide an overview of our achievements across 15 cattle breeds, focusing on loci affecting embryonic survival, juvenile mortality, and female fertility. Finally, I will illustrate how these discoveries not only advance livestock genetics but can also provide insights into the function of poorly studied genes in mammals, using cattle as an opportunistic model.

Keywords:

Pangenome graphs construction in sheep and goats provides new insights into their genetic diversity

Valentin SORIN

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Abstract

The current reference genome assemblies, based on a single individual, fails to capture the whole spectrum of genetic variations within a species. Structural variations (≥ 50 nucleotides) are difficult to detect using only standard approaches of either short or long-read sequence mapping to the current reference genome assembly. Meanwhile, recent advances in long-read sequencing technologies coupled with the development of appropriate bioinformatic tools make it possible to de novo genome assemblies a high number of animals across various sheep and goat breeds. Using these technologies, we have constructed both sheep and goat pangenome graphs that incorporate genetic diversity for these two species. The sheep pangenome integrates data from 9 de novo genomes and 6 haplotype-resolved assemblies representing 12 breeds, while the goat pangenome includes 8 de novo genome and 2 haplotype-resolved assemblies from 9 breeds. We combined complementary approaches to characterize the structural variations identified within the graphs and uncovered several additional megabases of novel sequences missing from the respective reference genome assemblies. These newly discovered sequences, referred to as Non-Reference Unique Insertions (NRUIs), were further characterized and investigated for potential associations with phenotypes of interest. This work was conducted in both the SeqOccIn project (funded by the Occitanie region, FEDER, and Apis-Gene) and in the H2020 Rumigen project

Keywords: Pangenome, Sheep, Goat, Structural variants, Non, reference unique insertions

Modelling genetic and epigenetic selection signatures from pool sequencing

Sonia EYNARD

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Abstract

Selection is known to drive genome evolution but what is its effect on epigenetic marks through time? In the context of animal breeding it appears crucial to be able to account for factors driven by the environment, under the current challenges such as adaptation to climate change, evolution of breeding conditions, animal health and welfare, reduced resource use and environmental impact. Livestock species, traced for many generations and of large census population size, offer a unique opportunity to describe the evolutionary trajectory of genetic and epigenetic patterns over time. We analysed pools of sperm, from reproducers, coming from 15 generations of selection for a sino-european pig breed. Genetics and epigenetics information were obtained through Oxford Nanopore Technology sequencing, providing about 8 millions genetic variants and about 20 millions CpGs sites. Genetic selection signatures were identified using Hidden Markov Models based on the evolution of allele frequencies. Epigenetic selection signatures were modelled on the one hand as differentially methylated regions across the 15 generations and on the other through a statistical framework combining poisson log normal, functional principal component analysis and Dirichlet process Gaussian process mixture modelling of the evolution patterns of CpGs islands. Finally, we inferred the local correlation between genetic and epigenetic selection signatures, allowing to disentangle between epigenetic changes driven by genetic or epigenetic inheritance associated with selection. In this study we contribute to a better understanding of the evolution of epigenetic marks throughout time and its relationship with genetics and selection decisions.

Keywords: selection signature, genetics, epigenetics, high throughput sequencing technology

A comprehensive genome-wide scan for parent-of-origin expressed genes in the pig clarifies the conservation landscape of genomic imprinting

Julie DEMARS

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Abstract

Genomic imprinting, a mechanism resulting in parent-of-origin expression of genes through epigenetic regulation, intersects with a broad range of biological fields including evolution, molecular genetics and epigenetics and determinism of complex traits. Although next generation sequencing technologies enable to detect imprinted genes in a genome-wide manner, a wide spectrum of this phenomena is evaluated only in humans and rodents. Here, we propose to map genes showing a parental expression bias in hypothalamus, muscle and placenta in piglets around birth using an extensive strategy that minimized biases. We detected 141 genes with strong to exclusive parental expression bias (ratio above 25:75). A large proportion (80%) of genes have never been shown to exhibit parent-of-origin expression and a small proportion (15%) are shared by at least two tissues. Interestingly, we identified novel parent-of-origin expressed genes involved in neurodevelopmental (PREPL) and fetal growth (FAM20B and POU6F2) functions. In-depth analyses of specific loci highlighted specific imprinted isoforms of COPG2 and confirmed livestock-specific imprinted genes such as ZNF300-like. Altogether, our results provide an atlas of parent-of-origin expressed genes in pig making it the most documented species for genomic imprinting after humans and rodents. Our findings indicate a weak conservation of this mechanism across species and tissues, suggesting a distinction between a small number of core imprinted genes shared across eutherians and others. These latter parent-of-origin expressed genes might be subjected to evolutionary forces that would determine their imprinting status either in a livestock-specific or tissue-specific manner.

Keywords: Parent, of, origin expression, allele, specific expression, transcriptomics, genomics, mammals specificity

Transmission of DNA methylation : genetic or epigenetic ? A transgenerational case study in quails

Stacy ROUSSE

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Abstract

Part of the environmental story of individuals lies within their DNA methylation (DNAm). Variations in the environment can trigger changes at the DNAm level and translate to phenotypic variability, even in the progeny of the individuals directly impacted. However, the amount of environmental information transmitted between generations via epigenetic phenomena is hardly quantifiable. The present study analyses DNAm from Reduced Representation Bisulfite Sequencing (RRBS) data for 1267 quails (Coturnix japonica) within 3 successive generations following an environmental modification. Among 111,168 dinucleotides CG (CpG) used, we estimated an average heritability of DNAm of 0.22. After a sub-selection of CpG sites showing high heritability and a significant difference in methylation between two epilines, we conducted methylation Quantitative Trait Loci (metQTL) analysis at those sites in order to shed light on the origin of the high heritability of those sites : genetic or epigenetic ?

Keywords: DNA methylation, metQTL, RRBS, transgenerational, epigenetic

Evolutionary consequences of unorthodox reproductive modes: Insights from stick insects

Tanja SCHWANDER

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Abstract

Reproduction is a defining feature of life, yet the strategies organisms use to reproduce are remarkably diverse. While sexual reproduction is widespread, many species deviate from this norm, ranging from parthenogenesis, in which populations consist entirely of females, to systems in which only the maternal or paternal genome is transmitted to offspring. Drawing on our recent research on stick insects, I will illustrate how the loss of recombination and outcrossing affects genome evolution, and how "unorthodox" reproductive modes provide unique opportunities to investigate the roles of genetic conflict and sex-specific selection in evolution.

Keywords:

Hidden diversity behind the deadliest mammalian wildlife disease: genomic and ecological evidence for two white-nose disease pathogens

Sébastien PUECHMAILLE

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Abstract

Emerging infectious diseases, particularly those caused by fungal pathogens, represent major threats to public health, biodiversity, and ecosystem stability. Although host–pathogen interactions and environmental factors have been intensively studied, the contribution of pathogen genetic variability often remains underexplored. This is especially true for white-nose disease in bats (caused by Pseudogymnoascus destructans), which has caused the most severe disease-induced mortality ever recorded in non-human mammals. Using a global reference dataset of 5,479 fungal isolates from 27 countries, collected through the coordinated efforts of hundreds of volunteers, we demonstrate that the pathogen traditionally regarded as a single species in fact comprises two sympatric cryptic species, each showing distinct host specialisation. Comparative genomic analyses reveal extensive recombination within, yet pronounced genetic divergence between, the two species, including differences in genome organisation. Both species exhibit clear geographic population structure, enabling identification of the lineage introduced to North America and tracing its origin to a region in Ukraine. By uncovering this previously unrecognised pathogen diversity, our study demonstrates that the evolutionary and genomic complexity of fungal pathogens can critically influence disease emergence and spread. These findings highlight the importance of incorporating pathogen genetic variability into frameworks for disease surveillance, risk assessment, and management. A more holistic understanding of pathogen evolution and host adaptation is essential to predict and mitigate the impacts of fungal diseases on wildlife and ecosystems.

Keywords: fungal pathogen, chiroptera, genomics, disease, host, specialisation, adaptation

Beyond nutrients: genomic diversity empowers cyanobacteria to bloom

Sébastien HALARY

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Abstract

Cyanobacteria, oxygen-producing photosynthetic bacteria, have colonized all photic ecosystems. A remarkable intraspecific diversity drives the adaptation of oceanic genera to spatiotemporal environmental variations, allowing them to thrive in time and across tropical to temperate regions, from surface waters to the base of the photic zone. However, this aspect remains largely unexplored in continental cyanobacteria, especially in blooming taxa that dominate eutrophic aquatic environments and increasingly threaten ecosystems and health. To investigate the links between diversity and adaptive capacity in blooming taxa, we combined sequencing and phenotyping of hundreds of strains from two distinct species sampled across different ecosystems, niches, and times. Each taxon displays extensive gene content diversity, conserved at a single population level. Horizontal gene transfers may decisively impact their physiology, notably through the acquisition of chromatic acclimation ability. Yet, phenotypic diversity appears more closely linked to specific alleles, associated with adaptation to salinity and photosynthetic capacity, including a potentially novel mechanism of far-red light adaptation that seems advantageous under very high cell density. Finally, our results indicate that diversification within a population is continuous and contributes to niche partitioning in the ecosystem. We propose that such diversity enables colonization of varied ecosystems and sustains populations' ability to bloom in, and actively reshape, changing environmental conditions.

Keywords: Cyanobacteria, Bloom, Intra, specific genomic diversity, Population genomics, Adaptation

Decoding low-light adaptation of the microalgae Pelagomonas calceolata

Chloé SEYMAN

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Abstract

Accounting for more than 45% of photosynthetic primary production on Earth, and at the basis of oceanic food webs, phytoplankton is of vital importance for marine ecosystems. Climate change is progressively warming ocean surfaces, reducing vertical mixing within the water column and strengthening stratification, which leads to oligotrophic conditions. Only phytoplankton species able to cope with oligotrophic conditions or accessing deeper nutrient-rich layers, where the light is scarce, are expected to persist. Among the most abundant picoalgae, the cosmopolitan pelagophyceae Pelagomonas calceolata (stramenopiles) is particularely abundant in oligotrophic oceans and at low light. This project aims at deciphering the mechanisms that allow P. calceolata to thrive in low-light environments by identifying the genes and pigments responsible for this adaptation. To achieve this, we combined the analysis of environmental data and controlled laboratory experiments. On one hand, we use environmental metatranscriptomes collected during the Tara expeditions to identify differentially expressed genes under varying light conditions, focusing on light-harvesting complexes (LHCs) and light-sensitive proteins. On the other hand, we cultivate P. calceolata under different light intensities and wavelengths in the laboratory, to conduct transcriptomics, fluorescence and pigments analyses. We observed that P. calceolata's genome carries a large number of genes coding for LHCs. Among them, the subfamily LHCq is particularly amplified and the genes coding for this family are overexpressed under low light conditions, showing a particular role of these proteins for the adaptation to low-light environments.

Keywords: Transcriptomics, Microalgae, Light Harvesting Complex (LHC)

Discovery of environmental yeast hybrids with pathogenic potential: evolutionary and clinical implications

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Abstract

Hybrids originate from the mating of two diverged organisms, resulting in novel lineages that have chimeric genomes. Hybrids may exhibit unique phenotypic traits that may enable them to thrive in new environments. Many hybrid lineages have been discovered among fungi, and growing evidence shows that they are more common than previously thought. Work from our group has unveiled that several emerging human pathogens have an origin through hybridisation. As compared to their parentals, they are more prevalent in the clinics and seem to display a higher potential to disperse and colonise humans. Here we discuss how hybridisation and its genomic and phenotypic outcomes may play a role in the emergence of new human pathogens.

Keywords:

A Global Perspective on Coral Holobiont Biocomplexity and Climate Resilience

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Abstract

The productivity and biodiversity of coral reef ecosystems depend on the health of reef-building corals—sessile anthozoans that form intimate symbioses with dinoflagellates of the family Symbiodiniaceae and diverse microbial partners including bacteria and archaea. These associations form the coral holobiont, a dynamic metaorganism whose structure and function are critical to reef resilience. Understanding this system requires examining the biocomplexity of the holobiont—specifically, the interactions between microbial diversity, ecological function, and emergent coral phenotypes. Despite advances, we still lack an integrative framework to assess how holobiont composition and function vary across environmental gradients and geographic scales, and how such variation shapes coral responses to climate stressors. In this talk, I present recent efforts toward establishing standardized approaches that link holobiont biodiversity, physiological performance, and environmental context. These frameworks aim to identify assemblages and traits that confer resilience, with the goal of advancing predictive models of coral holobiont responses in a rapidly changing ocean.

Keywords:

Integrative approaches to assess mitochondrial DNA copy number as a biomarker of coral health

Marine POULLET

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Abstract

Coral reefs, although covering less than 1% of the ocean surface, sustain nearly 25% of marine biodiversity. Their ecological success relies on symbiosis between reef-building corals and their dinoflagellate partners, an equilibrium sensitive to environmental change. Under disruptive stress, the metabolic activity of both partners can generate excessive reactive oxygen species, tipping the balance towards oxidative stress, a key driver of coral bleaching and mortality. Mitochondria are both a major source and a primary target of oxidative damage. In animals, variations in mitochondrial DNA (mtDNA) copy number have been recognised as a marker of metabolic state and resilience, yet its functional significance in corals remains largely unexplored. We propose to investigate mtDNA copy number as a potential biomarker of oxidative metabolism and stress response in corals, using an integrated multi-omics approach. Building on the Tara Pacific dataset, comprising ~300 Pocillopora spp. colonies, we quantified for each colony a mtDNA/nDNA ratio from whole-genome sequencing and integrated it with transcriptomic profiling and large-scale environmental metadata. Differential expression analyses were performed to identify modulations associated with metabolic activity, while variance partitioning analysis was applied to assess the relative contributions of genetic and environmental factors to gene expression variance. This approach investigates how mtDNA copy number correlates with mitochondrial activity, gene expression and environmental gradients. This work aims to assess the potential of mtDNA copy number as an adaptive biomarker and to advance data-driven strategies for monitoring coral health under global change.

Keywords: Coral reefs, Mitochondrial DNA copy number, Adaptive biomarkers

Dynamics of adaptation and genome evolution in fungal populations

Fabrice NTAKIRUTIMANA

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Abstract

The emergence of fungicide-resistant plant pathogens threatens global food security and ecosystem stability. Resistance management strategies typically rely on the assumption that resistance carries fitness costs in the absence of selection. Recent evidence shows that fungicide mixtures and alternation strategies can slow resistance evolution. However, their impact on pathogen genotypic landscapes and long-term evolutionary trajectories remains less understood. Understanding the link between fungicide strategies, mutation dynamics, and evolutionary trajectories is therefore key to developing sustainable resistance management. Our study leverages experimentally evolved populations of the globally distributed wheat pathogen Zymoseptoria tritici—the causal agent of Septoria tritici blotch disease. We performed whole-population sequencing to track genomic changes in response to diverse fungicide selection pressures across multiple time points. Our results demonstrate how fungicide regimes drive rapid fungal adaptation by directing mutation accumulation and reshaping allele frequency dynamics through standing genetic variation and genetic linkage. Furthermore, our comparative study on both experimental and natural Z. tritici populations pinpoints key adaptive genomic variations under both laboratory and field conditions. Our work provides a genomic framework for tailoring resistance management strategies and offers new insight into the evolutionary potential of fungal pathogens.

Keywords: Zymoseptoria tritici, fungicide resistance, experimental evolution, fungal genomics, genetic variations

piRNA pathway in the parasitoid wasp Cotesia congregata and impact on its endogenous bracovirus

Jean-Michel DREZEN

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Abstract

Tens of thousands of parasitoid wasp species of the braconid family are associated with bracoviruses integrated into their genome that produce virus particles injected into the parasitized host during wasp oviposition. The genes encoded by the DNAs packaged in the particles are expressed by host cells and produce virulence factors enabling successful development of wasp larvae by altering host immune defenses. Bracoviruses originate from the endogenization of a large double strand DNA virus 100 million years ago in a common ancestor of these braconid wasps. A previous study found no overexpression of immune genes during particle production, suggesting that the virus particles might be considered as self by the wasp after 100 million years of virus evolution within the wasp genome. Thus it seemed that no residual conflict remains between the wasp and the virus, unlike the situation described among partners of many symbiotic relationships. However, another way to control viruses relies on specialized small non-coding RNAs, the piRNAs (Piwi-interacting RNAs), as shown in mosquitoes. We have undertaken its characterization in C. congregata. Then we studied whether piRNAs could be involved in bracovirus regulation. We identified the genomic loci of piRNA production and discovered a -850 kb long- pericentromeric region on chromosome 8 short arm that concentrates over 40% of piRNA production in C. congregata ovaries. We also detected a significant piRNA response targeting bracovirus sequences of the “macrolocus”, a genomic region encoding 80% of the virulence genes. This response might induce virulence genes mRNA degradation thus limiting the production of proteins involved in parasitism success potentially harmfull for the wasp.

Keywords: Parasitoid wasps, bracovirus, piRNA response, genomic immunity

Evolution of structural variants in C. elegans

Héloïse MULLER

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Abstract

Structural variants (SVs) are alterations of the genome involving at least 50 bp. Although less numerous than SNP or indels, SVs can make up a larger portion of the genome given their large size, leading to significant contribution to genome evolution and phenotypes. Yet, SVs remain poorly characterized in natural populations of many species. Here, using Hifi sequencing, we firstly characterized SVs in 16 inbred founder strains of Caenorhabditis elegans; these strains were picked to represent the species natural diversity. Then, we performed experimental evolution in controlled laboratory settings with hybrid populations derived from the founder strains. Thanks to these hybrid populations, we were able to follow transposable element mobility and the outcome of the SVs identified in the founder strains. This ongoing analyze allows us to better understand SV evolution and dynamics in natural populations.

Keywords: Structural variants, genome evolution, experimental evolution, Caenorhabditis elegans, transposable elements

Wolbachia metapangenomics of individual Culex mosquitoes reveal shared phage rearrangements across large geographic distances

Maxime MAHOUT

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1 - Maladies infectieuses et vecteurs : écologie, génétique, évolution et contrôle (France)

Abstract

The widely distributed bacterium Wolbachia, influencing pathogen transmission and conferring manipulative reproduction phenotypes including cytoplasmic incompatibility through key prophage WO genes is of particular interest for mosquito vector control strategies. In addition to its phage WO, the Wolbachia mobilome of Culex species comprises a highly conserved and likely beneficial plasmid pWCP for the bacterium. However, despite its importance, little is known about the dynamics of the mobilome in Wolbachia of Culex populations across large geographic distances. Here, we used state-of-the-art assembly, binning and metapangenomic approaches to study the ecology and genetic diversity of Wolbachia from a hundred Culex quinquefasciatus, Culex pipiens pipiens and Culex pipiens molestus mosquito individuals collected in Mexico, New Caledonia, La Reunion, Corsica, Martinique, Guadeloupe, Thailand, Singapore, Tunisia, and French Polynesia. Metapangenomics, hereby defined as the conjoint study of the pangenomic information and the genomic environmental information, enabled a well-curated and refined analysis of the Wolbachia assembly results in comparison to reference genomes. This coupled analysis confirmed the widespread presence of pWCP plasmid worldwide, and allowed for the identification of genomic islands belonging to specific WO prophage regions differentially present among sampled localities. In addition, data allowed the classification of Wolbachia from these environmental samples into the standard phylogenic groups for Wolbachia of Culex pipiens complex species. Further bioinformatics and modelling analyses will be performed to confirm the nature of WO phage rearrangements at large scale.

Keywords: phage rearrangements, metagenomics, pangenomics, mosquito ecology

Pangenomics in cattle : from structural variant discovery to association studies on key phenotypes

Mekki BOUSSAHA

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Abstract

The current cattle reference genome assembly, based on a single Hereford cow fails to capture the whole spectrum of genetic variations within the species. Structural variations (> 50 nucleotides) are difficult to detect using only standard approaches of either short or long-read sequence mapping to the current bovine genome assembly. Meanwhile, recent advances in long-read sequencing technologies coupled with the development of appropriate bioinformatics tools make it possible to construct de novo genome assemblies for a high number of animals across various cattle breeds. Using these technologies, we have developed two extensive cattle pangenome graphs that incorporate genetic diversity from 64 high-quality de novo genomes and 16 haplotype-resolved assemblies, which represent 15 French dairy and beef cattle breeds along with their close relative, the Yak (Bos Grunniens). We employed a combination of complementary methods to characterize a broad range of insertions and deletions, and we report several additional megabases of genome sequences that are missing from the current Hereford reference genome assembly, known as NRUIs (Non-Reference Unique Insertions). Furthermore, we identified several SVs and NRUIs that are strongly associated with economic phenotypes in cattle. This work was conducted in both the SeqOccIn project (funded by the Occitanie region, FEDER, and Apis-Gene) and in the H2020 Rumigen project

Keywords: Cattle, de novo geneome assemblies, pangenome, SVs, Non, Reference Unique Insertions, Phenotypes

Tools and methods for microbial pangenomics

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Abstract

Prokaryotes are diverse, ubiquitous organisms with vast impacts on health, soil, and ocean ecosystems. Large-scale genome sequencing and pangenomics have revealed their molecular diversity, especially the role of Mobile Genetic Elements (MGEs). Pangenomics analyzes genetic variability across all genomes of a group, distinguishing between core genes (shared by all) and accessory genes (variable, linked to phenotypic traits). For several years now, the LABGeM team has been working on a model to represent genomic data as a pangenome graph at the gene family level, enabling the compression of information from thousands of genomes while preserving the chromosomal organization of genes. The PPanGGOLiN software suite [1] has been developed to reconstruct and analyze pangenome graphs at the species level. It encompasses methods for the identification of regions of genomic plasticity, including MGEs and Genomic islands, (panRGP method) [2] and their fine description in conserved modules (panModule method) [3], demonstrating their utility for identifying genomic islands and their MGEs. LABGeM is also developing PanGBank, a database of pangenomes reconstructed from public genomes from Genbank and RefSeq databases using the GTDB classification. It currently gathers pangenomes for over 4300 prokaryotic species. These developments address the challenge of big data in biology, advancing our understanding of microbial evolution in epidemiological and environmental contexts. [1] Gautreau G, et al. PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. PLoS Comput Biol. 2020;16: e1007732. doi:10.1371/journal.pcbi.1007732 [2] Bazin A, et al. panRGP: a pangenome-based method to predict genomic islands and explore their diversity. Bioinformatics. 2020;36: i651–i658. doi:10.1093/bioinformatics/btaa792 [3] Bazin A, et al. panModule: detecting conserved modules in the variable regions of a pangenome graph. bioRxiv. 2021. p. 2021.12.06.471380. doi:10.1101/2021.12.06.471380

Keywords:

"Le French Gut": mapping the intestinal microbiota on a large scale, issues and challenges

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Abstract

The gut microbiota, a complex collection of microorganisms including prokaryotes, eukaryotes, and viruses, plays a central role in many human physiological functions, such as digestion, immune development, and protection against pathogens. Gut dysbiosis has been linked to a wide range of diseases (obesity, irritable bowel syndrome, inflammatory bowel disease, ...), making the microbiota a major player in human health. Given its high inter-individual variability and the influence of multiple environmental factors, the study of the microbiota requires large-scale approaches in order to capture its diversity, identify robust associations with environmental factors, and better understand its links to health and disease. In this context, the French Gut project is a national initiative aimed at studying a large cohort of intestinal microbiota from French donors, combined with the analysis of clinical, demographic, and nutritional data. This project relies on citizen participation and the collaboration of major microbiota partners from public institutions, clinics, and industry. The objective of this presentation is to address the challenges associated with setting up and exploring such large-scale cohorts, in terms of logistics, methodology, and computation. In particular, we will address issues related to data standardization, quality assessment, and large-scale exploration.

Keywords:

Discovering Environmental Genomic Diversity at Unprecedented Scale: New Tools for the Logan Dataset

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Abstract

The Logan dataset represents the largest genomic resource ever assembled, comprising 27 million datasets totaling 50 petabases of sequence data, including nearly 5 million metagenomic datasets from all SRA submissions before December 2023. This unprecedented resource offers comprehensive coverage of global genomic diversity. The Logan-search tool enables search over the whole SRA using 31-mers. However, it has limited sensitivity to distant homologs, which constrains biological insights.We present two transformative tools that dramatically enhance Logan dataset accessibility and sensitivity. The first employs full-text indexing via LexicMap software, enabling querying of all metagenomic datasets in minutes while retrieving sequences with ≥90% similarity. This browser is being deployed on Galaxy for widespread researcher access. The second tool offers protein-space searches using 137 billion complete proteins called from Logan contigs via Prodigal. Powered by the gLM2 protein language model, this browser identifies homologs with sensitivity matching state-of-the-art aligners like DIAMOND, but at unprecedented scale and speed.As proof-of-concept, we queried 50 RuBisCO proteins representing known families. Within five minutes, our browser returned 84,114 distinct homologs, found in great part in environmental metagenomes. These tools unlock Logan's potential for environmental genomics, enabling researchers to explore biological diversity and gene distribution across ecosystems at previously impossible scales.

Keywords: Environmental genomics, Logan dataset, Large, scale metagenomics, Homology search

Country-scale study of antimicrobial resistance in French soils by metagenomics

Domitille JARRIGE

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Abstract

Antimicrobial resistance (AMR) increasing prevalence constitutes a major threat to global health. In 2014, bacterial AMR was responsible for at least 700 000 deaths globally and projections suggest that it could cause around 10 million deaths in 2050. As such, it is crucial to better understand the mechanisms of AMR transmission in natural and anthropized environments and to uncover new potential antibiotics to update the arsenal against infectious diseases. Soil is an understudied and astounding reservoir of microbial biodiversity, harbouring millions of taxonomic groups per gram, each with its own metabolic functions and its potential antibiotics and antibiotic resistance strategies. To study AMR diversity and its prevalence in soils at the French territory scale, 200 samples from the second campaign of the Soil Quality Monitoring Network (RMQS-2) were selected for shotgun metagenomic sequencing, based on their varied pedo-climatic properties and surrounding environmental characteristics (land use, geomorphology, slurry treatments...). After sequencing, around 11 billion read-pairs were obtained, representing 1.4 Tbytes of data. Taxonomic assignation of the reads was performed with Kaiju v1.9.2 and community structure reflected various soils properties (pH, land-use). Assemblies of the reads were conducted with SPADES v3.15.3. To search for AMR genes in the obtained contigs, we used Meta-MARC v1 and updated its models to exploit the MEGARes v3 curated AMR database. Study of AMR prevalence, types and spatial dispersion at the scale of France, in light of soil properties, geomorphology, climate and land use will help disentangle the emergence, transmission and dynamics of these critical pathways.

Keywords: soil, antimicrobial resistance, metagenomics, microorganisms

Metagenomics of soil aggregates: are microaggregates hotspots for bacterial diversity generation in soils?

Marie-Ange PALOMARES

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Abstract

Background. Soil is a dynamic and heterogenous environment shaped by geochemical properties, organic matter content and the metabolic activity of its microbiome, which drive key biogeochemical cycles, contributing to the stability of aggregates with size-dependent porosity. The aim is to characterize the microbiome across five soil water-stable aggregates size fractions (ASFs) in a calcareous silty-clay soil, to understand their roles in soil aggregation stability. Results. We analyzed taxonomic and functional profiles of the soil microbiome in ASFs using metagenomic approaches. Microaggregates were enriched in Acidobacteria and in rare taxa, and harbored hotspots of mobile genetic elements (MGEs). Conversely, macroaggregates hosted biodiversity hotspots dominated by exopolysaccharide (EPS)-producing taxa, particularly Bradyrhizobium, and are linked to motility and signalling pathways. Intermediate mesoaggregate ASFs were characterized by filamentous Actinomycetota and associated with stress adaptation and defense functions. All the ASFs showed distinct Actinomycetota signatures. Conclusions. Soil aggregate water-stability seems to be driven by its microbiota: (1) filamentous enmeshment by Actinomycetota, and (2) biofilm-mediated stabilization by EPS-producing taxa in micro- and macroaggregates, reinforcing aggregates cohesion. Microaggregates also hosts a reservoir of MGEs that might facilitate horizontal gene transfer and microbial genetic diversification.

Keywords: Soil aggregation, Microbiome, Metagenomics, Mobile genetic elements (MGE), Bradyrhizobium, Actinobateria, Acidobacteria

The impact of land-use change on groundwater communities in Switzerland using eDNA metabarcoding

Marjorie COUTON

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Abstract

Groundwater is Earth's largest freshwater ecosystem, home to unique biodiversity that provides vital ecosystem services. Despite its importance, groundwater is often poorly managed, and its communities face threats such as declining water levels and aquifer pollution. Understanding how human activities affect these ecosystems is essential for their protection. Groundwater organisms remain understudied due to sampling difficulties, limited taxonomic knowledge, and their low abundance. However, new molecular methods using environmental DNA (eDNA) now enable the simultaneous study of multiple taxonomic groups. In this study, we assessed how changes in surface land use impact groundwater biodiversity. These communities largely depend on nutrient inputs from the surface, so shifts in land use could alter community composition. We collected water samples from 30 Swiss springs used for drinking water and sequenced three genetic markers—COI for metazoans, 18S for micro-eukaryotes, and 16S for bacteria. Our results showed differences in community structure between forested and human-impacted sites, with a noticeable decline in eukaryotic diversity in areas influenced by human activities. We hope our findings represent a first step toward establishing protection zones to preserve groundwater communities.

Keywords: environmental DNA, metabarcoding, biodiversity, anthropogenic impact, groundwater, subterranean biology, community ecology

The viral counter-defensome

Pedro OLIVEIRA

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Abstract

Bacteria and phages have co-evolved tit-for-tat strategies to combat one another for survival. To overcome phage infection, bacteria have developed various defense systems (the defensome), and in response, phages have evolved a counter-defensome to inhibit or evade such defensive strategies. While significant progress has been achieved on mechanistic, structural and functional aspects of the defensome, the study of the phage counter-defensome is relatively new, with very limited information available on the diversity and distribution of these systems across complex environmental phageomes. Here we present a large-scale analysis of the counter-defensome of approximately 40,000 high-quality phage population genomes reconstructed from soil, marine, and human gut environments. We observed a wide variation in the frequency and nature of the counter-defensome across phage families, which correlated with host range, habitat, and geographic background. A substantial fraction of the counter-defensome clustered in islands, with some families significantly co-localizing. Moreover, multiple defense and counter-defense genes were also detected across multiple virophage genomes and nucleocytoplasmic large DNA viruses, suggesting frequent across-clade horizontal gene transfer. Hence, our results provide a detailed picture of the multiple counter defenses present in environmentally distinct viral communities and set the stage for subsequent identification of novel and ingenious strategies to mediate conflicts and alliances in bacteria-virus immunity networks.

Keywords: phage, bacteria, arms, race, horizontal gene transfer, giant viruses

Host ecology and phylogeny shape the temporal dynamics of social bee viromes

Vincent DOUBLET

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Abstract

Virome composition is often dependent on a combination of eco-evolutionary factors such as host trait and ecological niche. To identify the drivers shaping bee viromes, we sampled honeybee and co-foraging bumblebees, and sequenced their RNA across three time points during one year: in spring when colonies emerged, in early summer, at the peak of colony productivity, and in late summer, when colonies produce sexuals. We identified more than 100 viral species, one third being plant viruses. We used host genetic and ecological distances (measured from plant-pollinator networks) to explore the virus spatio-temporal dynamics. We found that insect viruses were mainly host specific, with honeybees showing a distinct and more diverse virome than bumblebees. Using small RNA sequencing, we also found a very small proportion of viruses that can infect both bumblebees and honeybees, whilst bumblebees share more viruses within the clade. In contrast, the presence of plant viruses in bee samples was defined by the bee's ecological niche and time of year, reflecting the dynamics of plant-pollinator interactions. This work demonstrates the respective role of host phylogeny and host ecology on the composition of pollinator viromes (Doublet et al. 2025 Nat. Commun). In addition, our results highlight the vectoring capacity of social bees for plant viral diseases, and illustrate further our concern of potential pathogen spill-over from commercial bumblebees into natural ecosystems.

Keywords: Virome, Bees, Transmission, Pollinators

Ecology and evolution of traits in natural populations: meta-omics as an opportunity to study trophic strategies in planktonic ecosytems

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Abstract

Marine unicellular eukaryotes exhibit a wide spectrum of trophic strategies from specialists (strict phototrophy or phagotrophy) to generalist (mixotrophy). Generalist strategies enable flexibility in nutrient sources, which impacts biogeochemical cycles, energy fluxes in planktonic food webs as well as species biogeography.Dinoflagellates exhibit all trophic strategies, making them a key group for studying the ecological success of trophic traits from a biogeographical perspective. Yet, our understanding of what drives their biogeography remains limited although they are a major component of planktonic communities. Combining environmental genomics databases with state-of-the-art species distribution modelling, we tested if trophic specialists exhibit distinct spatial distributions and abiotic drivers compared to generalists. Our models revealed differences in environmental niches at the trait level: mixotrophy is favoured in tropical oligotrophic regions whereas strict phagotrophy is favoured in the productive high-latitudes. At the species level, mixotrophs show similar responses across nutrient gradients, whereas responses to abiotic gradients are divergent within strict phagotrophs. The latter pattern is consistent with a trait scenario of multiple evolutionary convergences. Trophic classification thus successfully predicts generalist distributions but less effectively explains specialist patterns, which may depend on evolutionary history, species interactions, or cell size. This work paves the way for further studies on spatiotemporal mechanisms and patterns of mixotrophy in oceanic ecosystems, whether at the functional trait scale or at the level of the planktonic community.

Keywords: meta, omics, unicellular eukaryotes, dinoflagellates, traits, trophic strategy, SDM, biogeography, mixotrophy, phagotrophy, molecular ecology

Spatial metatranscriptomics on the brown alga Saccharina latissima

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Abstract

Algae live in association with a diverse microbiota that influences their growth, defence and health, forming a 'holobiont' that integrates the host and its microorganisms (viruses, bacteria, archaea, fungi). The complex interactions between algae and microbiota, but also between microorganisms themselves, are organised on a microscopic scale into spatial networks. The interactions between algae and their microbiota play a central role in the health of the host. New in vivo and in situ imaging techniques provide accurate information on the origin, distribution and concentration of molecules, shedding light on the role of each partner. However, current approaches do not yet allow for the simultaneous exploration of all spatial interactions on tissues. The adaptation of spatial metatranscriptomics could overcome these limitations. Global warming is causing a rise in temperature and an increase in atmospheric concentrations in the oceans, affecting the performance and survival of marine habitats such as algae. The direct or indirect effects of these changing environments on the associated microbiota remains enigmatic. This work proposes the adaptation of this method to marine algae to identify eukaryotes and prokaryotes, offering an innovative view of the roles and interactions of the members of the holobiont in times of changing environmental conditions.

Keywords: marine fungi, macroalgae, transcriptomics

More than just disorder - metabolite diversity of Microcystis strains shows tight correspondence to genotype and may contribute to ecotype specificities

Benjamin MARIE

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Abstract

Microcystis is one of the most common bloom-forming cyanobacteria in freshwater ecosystems worldwide. This species remarkably produces numerous bio-active accessory metabolites, which are believed to be potentially involved with different ecological and/or physiological processes. Their genuine contribution to the evolutive success of Microcystis blooms remains undetermined. To better depict the potential relation between the local genetic diversity of blooming Microcystis populations and the respective associated chemical diversity, we conducted a joined genomic and metabolomic analysis of 65 Microcystis strains collected from various lakes from France and European countries. Interestingly, both core- and noncore-gene phylogenetic analysis place 59 of these strains in 12 distinct genetic clades of at least 2 genomes, being widely distributed along the whole Microcystis phylogeny and presenting specific signatures of accessory metabolite biosynthesis. The chemical analysis of metabolite diversity produced by these strains, cultured under lab conditions, reveals the production of stable metabolite corteges, beyond little variations along replication, growth phases and culture conditions. Indeed, these strains belonging to 12 different genotypes correspond to 13 distinct metabotypes according to an accurate one-metabotype-for-one-genotype rule. This observation reveals that Microcystis collected from certain environments present a large set of genetic and subsequent corresponding metabotype diversity, whereas all strains originating from certain other lakes present a net genetic uniformity.

Keywords: Cyanobacteria, accessory metabolites, diversity, ecology, cultures.

POSTERS

Session: Agrogenomics and diversity

Poster #01 : Genome-wide association and genomic prediction for agronomic traits in the yellow mealworm (Tenebrio molitor)

Lucas ROCHA FERREIRA

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Abstract

To improve industrial production of the yellow mealworm (Tenebrio molitor), breeding programs require genomic tools to develop high-performing lines. However, the genetic basis of key agronomic traits remains unknown. Here, we developed new genomic resources and identified robust quantitative trait loci (QTLs) associated with growth and reproduction traits through a multi-model genome-wide association study (GWAS). We genotyped 3,575 individuals using a high-density array leading to 284,452 SNPs analyzed via a consensus across frequentist and Bayesian GWAS models with population-structure correction and LD-based clumping to define QTL. We identified 8 robust QTLs for pupa weight (PW), including a chromosome 3 region co-localized with an ecdysone receptor gene. To assess predictive value, we measured emergence weight (EW; a PW proxy) in 98 independent individuals and compared GBLUP models using genome-wide SNPs, QTL-window SNPs, and significant SNPs only. Prediction accuracies were moderate: r^2 = 0.21, 0.17, and 0.15, respectively, showing that reduced marker sets still retain most of the signal. We then analyzed 2,605 individuals phenotyped for egg-hatching rate (EHR), detecting 12 robust QTLs were detected, including a major locus on chromosome 5 co-localized with a nuclear hormone receptor. This multi-model GWAS identifies robust QTLs and supports the feasibility of targeted SNP panels for genomic prediction and selection in T. molitor breeding.

Keywords: Tenebrio molitor, yellow mealworm, GWAS, QTL, genomic prediction, GBLUP

Poster #02 : QTL mapping of key postharvest quality traits in diploid and triploid banana populations

Margot ARESI

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Abstract

Bananas (Musa spp.) are among the world's leading fruit crops, yet postharvest losses due to finger drop and bruising remain major challenges for breeders and producers. We investigated the genetic control of these traits using QTL mapping in two related populations differing in ploidy (diploid and triploid). Finger drop showed moderate heritability in both populations (H^2 = 0.47 and 0.38, respectively), with significant loci detected only in the diploid background on chromosomes 7 and 11, explaining nearly 30% of the phenotypic variance. One major region on chromosome 7 (M7_1@60.1) was associated with stronger peel rupture force in triploids, pointing to a conserved functional effect across ploidy levels. For bruising susceptibility, heritability was higher in triploids (H^2 = 0.57) and two genomic regions showed near-significant effects. Together, these results identify promising loci for improving postharvest quality through marker-assisted breeding and demonstrate the value of comparative genomics across banana ploidy levels.

Keywords: Banana (Musa spp.), QTL mapping, Postharvest quality, Finger drop, Bruising susceptibility, Marker assisted breeding

Poster #03 : Cracking the code in eggshells: ancient DNA recovery

Priyadarshini ROY

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Abstract

In the palaeogenomic context, eggshells have so far been a relatively underutilised sample type compared to other ancient materials, such as bones and teeth, for ancient DNA (aDNA) research. However, they are a high-potential substrate for aDNA recovery, due to a mineralised matrix that traps intracrystalline DNA, preserving better-quality DNA than extracrystalline surface or pore DNA, and a much lower microbial load than ancient bones. Building on previous research, this study evaluates the effectiveness of two lysis protocols, Oskam et al. (2010) and a slightly modified version of the Grealy et al. (2023) protocol, for the retrieval of endogenous DNA from archaeological chicken eggshells. We varied incubation time, sample weight, and collection sites and subsites across the two protocols to determine how these factors affect total and endogenous DNA yield. To further interpret these results, metagenomic profiling will be carried out to characterise microbial communities and identify potential contamination sources. Collectively, these data indicate that while LMUGrealy is marginally superior to the Oskam protocol, extraction efficiency depends not only on the protocol chemistry but also on preservation variability. Additionally, taxonomic identification of the recovered sequences confirmed that the eggshell samples were from Gallus gallus (chicken), thereby confirming the authenticity of the recovered ancient DNA. Optimising endogenous yield rather than total yield provides a more accurate measure of true recovery success for aDNA analysis of avian eggshells.

Keywords: aDNA, eggshells, ancient chicken, protocol optimisation

Poster #04 : A phylogenomic investigation of ancestral gene exchanges between Eukaryotes and Nucleocytoviricota

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Abstract

Nucleocytoviricota viruses represent a remarkably diverse and potentially ancient component of the eukaryotic virome. They infect wide range of eukaryotic clades, setting them as putative pathogens of the last common eukaryotic ancestor, LECA. With recent studies suggesting extensive gene transfers between Nucleocytoviricota and Eukaryotes, and a viral origin of critical proteins for the cellular functions, their long-lasting interactions may have played a significant role in the formation of the eukaryotic cell. Leveraging large databases of reference and environmental genomes of eukaryotes and their nucleocytoviruses covering their currently known diversity, we estimated the conservation and distribution of gene families at multiple taxonomic levels. This approach settles a phylogenomic context to the origin and early evolution of both the eukaryotic domain and the Nucleocytoviricota phylum, which we are now using to detect and characterize putative gene tranfers between the two at deep evolutionary scale, through sequence and structural similarity comparisons and phylogenetic inferences. We expect this project to provide a comprehensive assessment of ancestral gene fluxes between Eukaryotes and giant viruses, and to better understand the deep co-evolution between them.

Keywords: eukaryogenesis, eukaryotes, giant viruses, orthologs, phylogeny, coevolution

Poster #05 : Alpha-solenoid proteins involved in organellar gene expression

Ingrid LAFONTAINE

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Abstract

In photosynthetic eukaryotes of the green lineage, the expression of the chloroplast genome is mainly regulated post-transcriptionally, by RNA-binding proteins encoded in the nuclear genome (OTAF for organelle trans-acting factor). Most of those identified to date belong to two families of alpha-solenoid proteins (PPR and OPR) and interact with specific sequences on their target mRNAs, allowing their maturation, splicing, editing, stabilization and translation activation. I will present novel machine learning approaches that we developed to complete the catalogue of OPR and PPR and to propose the first catalogue of alpha-solenoid candidate regulators of organellar genomes from other protein families, some of which are currently being characterized in the laboratory. Importantly, we propose for the first time such candidates in red algae and in glaucophytes, in which everything remains to be discovered, opening the way to explore the plastid regulation of photosynthetic eukaryotes derived from secondary endosymbiosis. I will also present the results of molecular dynamics simulations that we carried out on PPR proteins that revealed structural properties instrumental to understand the co-evolution required between OTAF encoded in the nuclear genome and their RNA target encoded in the organellar genomes.

Keywords: endosymbiosis, chloroplast, mitochondria, regulation of gene expression, evolution

Poster #06 : Analysis of de novo gene in diatoms

Alix BOUTHEROUE-DESMARAIS

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Abstract

Diatoms, the most diverse group of algae with over 100,000 species, generate about 20% of Earth's oxygen and account for nearly half of oceanic algal biomass. They have acquired their plastids through secondary endosymbiosis with a red alga, which itself originated from a primary endosymbiosis event between a prokaryotic cell and a photosynthetic bacterium. Endosymbiosis triggers a series of cell adaptations, including significant gene loss in the plastid genome, with many genes either disappearing or being transferred to the host nucleus. Diatoms have evolved innovations to cope with secondary endosymbiosis. We will present our in-depth analysis of those diatom-specific proteins among which are genes that could have arose de novo from non-coding sequences, that may have driven diatom specific innovations. To this end, we performed a phylostratigraphy analysis of protein-coding genes among 58 high-quality annotated diatom genomes and took advantage of diatom transcriptomic datasets (public ones and those generated in the lab). 97 % of the genes are grouped into 30.886 families. 185 287 proteins are found only in diatoms, and on average, a diatom proteome contains 16.6% of diatom-specific proteins. Preliminary analysis of transcriptomic datasets in Phaeodactylum tricornutum identified 61 expressed diatom-specific de novo gene candidates.

Keywords: diatoms, phylostratigraphy, de novo, endosymbiosis

Poster #07 : Comparative plastome analysis reveals evolutionary patterns in the parietal clade of Malpighiales

Astrid DE MESTIER

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Abstract

Salicaceae is a plant family distributed in both temperate and tropical regions. It contains taxa that play crucial roles in both ecosystems and economies, such as Populus and Salix. Nevertheless, its circumscription remains debated, particularly concerning the taxonomic status of its subfamilies, and its next relatives are still unclear. Salicaceae is also part of the parietal clade of the Malpighiales, whose phylogenetic relationships remain to be solved. Phylogenomics analysis based on the plastome is a method of choice to resolve relationships within plant clades. Nevertheless, studies often focus on either the coding regions or the whole plastome, ignoring potentially divergent signals of the introns and spacers. In this study, we employed a whole plastome approach to resolve phylogenetic relationships within the parietal clade, analyzing the phylogenetic signal of each partition. We aimed at comparing the structure of the plastid within Salicaceae and the parietal clade, to unravel structural mutations and potential synapomorphies, exploring the phylogenetic signal of exons, introns, and spacers. We found that the Salicaceae plastome has a conserved structure, representing the ancestral state of the Malpighiales. All three partitions present congruent topologies for the family, but differ at the level of the parietal clade, with codons and introns partitions recovering different relationships than the spacers partitions. Our results underscore the need for carefully curated genomes and the potential of the whole plastome in unravelling evolutionary diversification within the Malpighiales.(Based on: de Mestier et al., 2025. https://doi.org/10.1093/aob/mcaf148)

Keywords: comparative plastome analysis, phylogenomics, Salicaceae, Malpighiales

Poster #08 : Differential dynamics of Wolbachia and its pWCP plasmid in Culex mosquitoes

Alice BRUNNER

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Abstract

Mosquitoes are major vectors of pathogens such as arboviruses and parasites, causing significant health impacts each year. Wolbachia, an intracellular bacterium widely distributed among arthropods, represents a promising vector control solution. This bacterium can indeed reduce the transmission of arboviruses and manipulate the reproduction of its host through its WO phage. Although research on the Wolbachia mobilome primarily focuses on WO phage and the phenotypes it induces, the function of Wolbachia plasmid pWCP, reported to be strikingly conserved worldwide, remains unknown. In this study, we analyzed the presence and abundance of pWCP as well as Wolbachia in two different species of Culex mosquitoes, one of the most widespread genera in the world and a vector of numerous diseases. We compared relative densities of the bacterium and its mobile genetic element in two species of Culex, a facultatively autogenous and an anautogenous species, throughout their development from larval stage L1 to adult individual specimen using quantitative PCR. Our results indicate that both Wolbachia and pWCP exhibit distinct dynamics throughout the mosquito's life cycle in each species, with each element showing increased levels at specific development stage. Nonetheless, data revealed an overall correlation between pWCP and bacterial density within individual mosquitoes. These findings suggest potentially distinct roles and behaviors of the plasmid in the bacterium's biology in different mosquito species as well as complex interaction dynamics between Wolbachia and its host during its life cycle. We are now generating both long- and short-read genomic datasets for Culex to characterize the Wolbachia mobilome at higher resolution.

Keywords: Wolbachia, Plasmid, Culex

Poster #09 : Rooting Biases and Underlying Premises in Wood-Ljungdahl Pathway Phylogeny

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Abstract

The Wood–Ljungdahl Pathway (WLP) is an ancient and versatile metabolic route crucial for carbon cycling in methylotrophic and methanogenic organisms, as well as in others with distinct metabolisms. The evolutionary origin of the WLP's H4MPT branch remains contentious, as phylogenetic rooting profoundly influences interpretations of early metabolic evolution. Different rooting hypotheses lead to contrasting conclusions regarding the precedence of methanogenesis or methylotrophy. One of the latest analyses (2016) suggested an archaeal origin of the branch, followed by lateral gene transfer (LGT) to bacteria, giving rise to methylotrophy. Given the large number of novel genomes now available, we aimed to re-evaluate the origin of the H4MPT methyl branch. We constructed a high-quality phylogeny and developed custom software for synteny analysis and gene profiling to shed new light on the evolutionary history of this pathway. Typically, the origin of a metabolic pathway is associated with the colocalization of its genes in the genome. The widespread distribution of these genes across diverse bacteria and non-methanogenic archaea, together with the conserved bacterial gene order, strongly supports vertical inheritance—or even an ancestral LUCA origin—over multiple independent LGT events. In this context, the observed degradation of synteny in bacteria further illustrates the complexity of these ancient evolutionary processes.

Keywords: evolution, Wood Ljundahl Pathway, WLP, methanogenesis, methylotrophy, phylogeny, phylogenetic tree

Poster #10 : KmerCity and AdmixKmer: repeated K-mers-based tools for analyzing ancestry in complex admixed genomes

Olivier GARSMEUR

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Abstract

We developed an approach based on the distribution of repeated k-mers derived from whole-genome sequencing data to analyze genome ancestry in complex admixed and/or polyploid genomes. This approach is based on the premise that highly repeated k-mers predominantly correspond to transposable elements (TEs), which, due to their lineage-specific activity, generate traceable genomic signatures that can serve as markers of hybridization events. Two computational tools, KmerCity and AdmixKmer were developed: KmerCity extracts and selects repeated k-mers from whole-genome sequencing data (WGS) and builds a repeated k-mers count matrix that enables the comparative analysis of k-mers distribution among accessions. The shared k-mer profiles are visualized using a graph-based approach, which allow the identification of genus-, species-, or subgroup-specific k-mer signatures. These signatures can then be used to detect admixed accessions. AdmixKmer is a method adapted from classic admixture models (like STRUCTURE and ADMIXTURE). It exploits the repeated k-mers count matrix generated by KmerCity to estimate proportions of ancestral contributions in the panels of analyzed accessions. Both tools do not require reference genome assembly and are alignment-free methods making them broadly applicable to species with limited genomic resources. Because they rely on repetitive k-mers, they require limited sequencing depth, which is of particular interest for polyploid species. They allowed the detection of small ancestral contributions even in the absence of pure representatives of the contributor. KmerCity and AdmixKmer should be particularly useful for characterizing genomes and populations combining admixture and polyploidy.

Keywords: Genome ancestry, admixture, repeated k, mers, transposable elements, polyploid, bioinfomatique tools

Poster #11 : Identification and Functional Characterization of Genetic Module Associated with Trichome Development in Cotton

Heng WANG

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Abstract

Introduction: The trichomes with different structures are involved in various functions, particularly in response to abiotic and biotic stress. Cotton leaf and stem surface trichomes are similar to cotton fiber in structure, and the development process is regulated by genes related to fiber development. In all wild Gossypium species, the phenotype of long trichome can be only observed in A genome species. As the doner of A genome of tetraploid cultivars, wild species and cultivated species of A genome are important materials for studying the molecular regulation mechanism related to trichome elongation. Through these approaches, we aim to clarify the environmental adaptive evolution and molecular regulatory mechanisms of cotton trichomes, thereby providing genetic and germplasm resources for the breeding of cotton with enhanced insect resistance, and UV radiation resistance. Results and Expectation: (1) Environmental Adaptive Evolution of Cotton Trichomes (2) Identification and Function Analysis of Candidate Genes for Trichome Elongation (3) Molecular Mechanisms Regulating Cotton Trichomes The function of GaCPR5 was identified based on transgenetic cotton lines.Transcriptomes of GaCPR5 knockout lines, overexpression lines, and wild-type plants was sequenced and comparatively analyzed to identify differentially expressed genes. The genetic regulation module will be constructed. Through the elucidation of molecular regulatory mechanisms, and the study of environmental adaptive evolution, this research aims to provide genetic and germplasm resources for the breeding of cotton varieties with combined resistance to insects, drought, and UV radiation, tailored to the major cotton- producing regions in the world.

Keywords: Cotton, Regulatomics, Trichomes, Gossypium genus diversity

Poster #12 : Application of adaptive sampling for selective long-read sequencing in marine dietary metabarcoding: a case study.

Carolina DE OLIVEIRA MAGALHÃES

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Abstract

Understanding trophic interactions and biodiversity patterns in marine ecosystems largely depends on the ability to recover taxonomically informative DNA fragments from complex samples. In this study, we evaluated the potential of Oxford Nanopore's adaptive sampling as an innovative selective sequencing strategy applied to dietary metabarcoding, through the analysis of stomach contents from benthic shrimps (active consumers) and sponge tissues (passive filter feeders). Nuclear and mitochondrial markers were selected to be sufficiently long for accurate sequencing while also informative for taxonomic identification. Reference genomes of shrimp and sponge were generated and used as exclusion references during adaptive sampling runs, allowing the active rejection of host DNA and the enrichment of prey-derived sequences. Preliminary results indicate that this approach is applicable for metagenomic analyses, enabling improved recovery of dietary and environmental diversity while reducing the proportion of non-informative reads. Our findings highlight the potential of adaptive sampling to enhance future eDNA-based and environmental monitoring studies, offering a real-time, targeted strategy to increase taxonomic resolution in complex marine samples.

Keywords: Adaptive sampling, eDNA, stomach contents, metagenomic, metabarcoding, Oxford Nanopore

Poster #13 : Comparison of taxonomic assignment tools to species and strain-level and application to piglets gut microbiota with different diet (human milk vs infant formula)

Lune ANGEVIN

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Abstract

Several studies have shown that some bacterial species, such as E. coli, can have both beneficial and pathogenic strains. Therefore, it is necessary to identify bacteria down to the strain level in order to understand the functional diversity of a microbiota. Often cited as state-of-the-art, Kraken2 uses k-mers, which saves considerable time in the taxonomic assignment. However, it was not originally developed for long reads, even though it now works on them. The recently designed tool Sylph, based on average nucleotide identity with k-mers, was made for long reads. It has shown better accuracy than Kraken2 for low-abundance species. But both are limited to the species level. New tools are being developed for taxonomic identification at the strain level. ORI is based on spaced seed models. It has to be used after a species-level identification tool to perform an initial sorting. It is accurate but was developed for a simple environment. MADRe is a metagenomic classification pipeline for long reads, allowing direct identification at the strain level. MORA also allows long reads to be assigned at strain-level. I evaluated the performance of these tools on the ZymoBIOMICS GUT mock community (18 bacterial strains, with 5 E. coli strains, 2 yeasts and 1 archaea). I will also present the initial results of a study of the gut microbiota of piglets fed breast milk or infant formula, the first step of which is the precise composition and comparison of these different microbiotas. Later, the next step will be to reconstruct the metabolic networks of these strains and predict their metabolites production. The long-term goal is to improve infant formula by adding missing bacteria or metabolites.

Keywords: bacteria, strain, gut, taxonomic assignment, mock community

Poster #14 : Omics-Based Exploration of the Microbiome and PHA-Producing Halophiles from Tunisian Hypersaline Environments.

Fatma KARRAY

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Abstract

Background and Aim : The extensive use of non-degradable plastics poses a serious threat to human health, wildlife, and ecosystems. Polyhydroxyalkanoates (PHAs) are biodegradable, biocompatible polymers emerging as sustainable alternatives to petroleum-based plastics. Halophilic microorganisms represent promising natural cell factories for PHA production, with potential applications in health, agriculture, and packaging. This study explored the microbiome of Tunisian hypersaline ecosystems to prospect for PHA-producing halophiles using metagenomic and genomic approaches. Methods : Brine samples from hypersaline environments (solar salt marshes and chotts) were collected, and environmental DNA was extracted. Enrichment cultures were performed to isolate PHA-producing strains. Hypersaline genomes and metagenomes were sequenced, and bioinformatics tools were developed and applied to detect key biosynthetic genes involved in PHA production. Results: In silico screening of hypersaline metagenomes enabled the characterization of microbial biodiversity and the identification of several promising candidate genes (including phaC) associated with PHA biosynthesis pathways. Furthermore, whole-genome sequencing and analysis of halophilic strains revealed the presence of genes involved in PHA biosynthesis and degradation. Genetic engineering approaches will be applied to validate their roles in the PHA production process. Conclusion : Bioinformatics analyses demonstrated the high biosynthetic potential of halophilic microorganisms, highlighting their promise as sustainable producers of bioplastics.

Keywords: Polyhydroxyalkanoate, Hypersaline Lake, Whole Genome, Metagenome

Poster #15 : Paleogenomic analysis of a ~7,300-year-old Iberian goat skin and 16th-century Italian parchments and papers

Zoé ROBINET-GUYET

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Abstract

Advances in paleogenomics and metagenomics have expanded our ability to study ancient organisms and the microbial communities associated with archaeological materials. In this study, we apply these tools to a ~7,300-year-old animal skin from the Neolithic site of Cueva de los Murciélagos (Córdoba, Spain), and twelve 16th-century Italian manuscripts. The first objective was to authenticate and genetically characterize the Neolithic skin. The second aimed to characterize the microbiomes of both the skin and the Italian manuscripts to investigate how material type, human handling, and preservation context shape microbial communities. We extracted DNA and prepared sequencing libraries in a dedicated ancient DNA cleanroom, following authentication protocols, and subsequently analyzed the skin using population genomics approaches. We characterized the microbiomes of the historical documents by removing host DNA and performing metagenomic profiling using KrakenUniq v1.0.4 (Breitwieser et al., 2018). Our results identify the Neolithic skin as belonging to a domestic goat from the Iberian Peninsula, with highly fragmented DNA and a fungal-dominated skin microbiome. Italian papers showed predominantly environmental and human-skin-associated bacteria, while parchments displayed more microbial signatures from the animal source material and cellulose-degrading bacteria. To our knowledge, the Murciélagos goat skin represents the oldest endogenous DNA recovered from a well-preserved skin in a non-periglacial environment. Microbiome analysis of ancient materials offers new insights into their degradation and authentication.

Keywords: caprine, parchment, ancient DNA, Neolithic, domestication

Session: Exploring ecosystems using metagenomics, Ancient DNA and paleo-environments, Genomics of plants and animals and their microbiota, Agrogenomics and diversity, Genomics of biological interactions: holobionts, pathogens, symbionts

Poster #16 : The HerbaSoil project: unravelling two centuries of soil microbiome evolution using herbarium collections

Gianluca GRASSO

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Abstract

Soil and plant-associated microbial communities are key components of agroecosystems, contributing to plant health, nutrient cycling, and ecosystem stability. However, little is known about their long-term evolutionary responses to agricultural intensification. The HerbaSoil Project investigates herbarium soils associated with two crop species (wheat and barley) collected between 1820 and 1970 to reconstruct the evolution of soil microbial communities over the past two centuries and to assess the historical impacts of intensive farming practices. By comparing 60 historical and 40 modern soil samples linked to the same crop species, this museomic study aims to quantify changes in soil microbial diversity across time. Indeed, herbarium soil samples contain highly fragmented DNA (50-100 bp). Using a metagenomic approach, the study characterizes microbial communities from both taxonomic and functional perspectives. Deep sequencing efforts are being conducted to enable de novo assembly of historical soil metagenome-assembled genomes (MAGs). Through the integration of paleogenomics and metagenomics, HerbaSoil provides new insights into the long-term evolution and resilience of soil microbiomes throughout the Anthropocene, a period profoundly shaped by agricultural intensification and global environmental change.

Keywords: soil microbiome, herbaria, metagenomics, agricultural intensification, historical DNA, aDNA

Poster #17 : A metagenomic and transcriptomic study of RNA virus-diatom interactions

Florian THIRIOT

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Abstract

Diatoms represent a major component of oceanic biomass and play a central role in sustaining marine food webs. Viruses, the most abundant biological entities in the ocean, influence these trophic networks by converting living biomass into dissolved organic matter through cell lysis, thereby fueling the microbial loop. While DNA viruses were long considered the principal actors in this process, recent studies suggest that RNA viruses may account for half of marine viral assemblages. The BONUS project seeks to explore the largely underlooked interactions between diatoms and their RNA viruses. My work within this project focuses on investigating host–virus molecular interactions during the infection of the model diatom Mediolabrus sp., using transcriptomics. To achieve this, I will generate a high-quality, annotated reference genome of Mediolabrus sp. through hybrid de novo assembly of short- and long-read sequencing data. This annotated assembly will support the analysis of RNA-Seq datasets collected during a controlled time-course infection experiment, enabling the quantification of gene expression and the identification of transcriptional changes throughout the infection cycle. In addition to this transcriptomic analysis, the project also integrates an ecological dimension. Using metagenomics, I will characterize viral communities from samples collected over a year at the SOMLIT-Astan station in the English Channel, where Mediolabrus sp. is a dominant taxon. The diversity and dynamics of diatom-specific RNA viruses will be assessed using RNA-dependent RNA polymerase markers. This approach will provide new insights into how fluctuations in viral communities influence diatom populations in natural ecosystems.

Keywords: RNA virus, diatoms, metagenomics, transcriptomics

Poster #18 : Identification of microeukaryote genes associated to corals holobionts with a metatranscriptomics approach

Mathieu ZALLIO

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Abstract

Coral reefs, vital ecosystems for marine biodiversity, are declining due to global stressors such as ocean warming and acidification[1]. While the symbiotic relationship between coral hosts and Symbiodiniaceae is well known, the diversity and ecological roles of other microeukaryotes associated with corals remain underexplored[2]. Using genomic and transcriptomic data from the Tara Pacific expedition (2016–2018), we identified and characterized microeukaryotic genes associated with Millepora platyphylla and Pocillopora meandrina across 32 Pacific islands. A bioinformatics workflow combining RNA assembly (rnaSPAdes), clustering (CD-HIT), annotation (DIAMOND, InterProScan), and binning (CONCOCT, Canopy)[4] enabled the identification of hundreds of putative transcriptomes. Distinct community structures were observed between coral genera. Millepora holobionts showed higher abundances of Ulvophyceae, notably Ostreobium quekettii[3], whereas Pocillopora displayed an enrichment in Conoidasida, a class of parasitic eukaryotes related to corallicolids[5]. These patterns suggest coral-specific associations and divergent ecological roles within the holobiont. Several bins remain to be analyzed, revealing hidden diversity among coral-associated eukaryotes. Future analyses focusing on Conoidasida-related transcriptomes may uncover their roles in coral health and resilience. [1] Hughes et al. https://doi.org/10.1038/s41586-018-0041-2 [2] Bonacolta et al. https://doi.org/10.1007/s00338-023-02352-0 [3] Iha et al. https://doi.org/10.1016/j.cub.2021.01.018 [4] Yue et al. https://doi.org/10.1186/s12859-020-03667-3 [5] Kwong et al. https://www.nature.com/articles/s41586-019-1072-z

Keywords: Corals holobionts, Microeukaryotes, Tara Pacific, Genomics, Transcriptomics

Poster #19 : Partial draft genome of amoebic gill disease causative agent, Neoparamoeba perurans, Young et al. 2007 and associated bacterial microbiota

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Abstract

Amoebic gill disease (AGD), caused by the free-living, ubiquitous ectoparasite Amoebozoa Neoparamoeba perurans Young et al. 2007, is one of the most prevalent gill diseases affecting cultured Atlantic salmon Salmo salar. Over recent years, an increased incidence has been reported in the majority of Atlantic salmon farming countries, including Norway, Scotland and Ireland, making it one of the most significant health threats in Atlantic salmon farming. No prophylactic treatments currently exist against AGD, with only recurrent freshwater treatments as an effective method for reducing mortality - which can reach up to 80% if left unchecked, with a high recurrence rate. Much remains to be learnt about the pathogen life cycle, virulence factors, interaction mechanisms with both its host, S. salar, and eukaryotic endosymbiont, Perkinsela sp. and genome information of the ectoparasite would help understand the disease development and establish mitigation strategies such as vaccines. Here we present preliminary results of genomic assemblies based on PacBio sequencing of N. perurans DNA from cell cultures isolated from infected Atlantic salmon farmed in Ireland. We assemble scaffolds and contigs (N50: 2.12 Mb, longest fragment: 0.44 Mb, BUSCO C score (Eukaryota): 39.2%) as well as its mitogenome that shares most of the gene repertoire with its closest relative, N. pemaquidensis, if not its gene order. From the assembly, circularised sequences were identified as complete bacterial genomes (BUSCO C score (Bacteria): 100%). These do not match genetic data from either the host gill microbiota or co-occurring organisms present during AGD infection and may correspond to the yet uncharacterised intracellular bacteria of Neoparamoeba perurans.

Keywords: Neoparamoeba perurans, amoebic gill disease, de novo assembly, PacBio sequencing, intracellular bacteria

Poster #20 : Effect of DNA Extraction Protocols on Pig Tonsil Microbiota Profiling

Katell HERCOUET

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Abstract

The palatine tonsils, located at the intersection of oral and respiratory systems, host a protective commensal bacterial barrier. However, in case of dysbiosis, tonsils can become a reservoir for pathogens able to infect deeper tissues. Metagenomic approaches –including metabarcoding or whole-genome shotgun sequencing– enable a comprehensive analysis of this bacterial microbiota. However, a major limitation is the low bacterial DNA yield from tonsillar swabs. This study aims to optimize bacterial DNA recovery from these low-concentration samples. Tonsil swabs collected from sows and piglets, were processed using three commercial DNA extraction kits: PowerSoil DNAeasy (Qiagen), NucleoMag Microbiome and NucleoMag Veterinary (Macherey–Nagel). A mock community (Zymo) and DNA-free water were included as control. Total bacterial and host DNA were quantified by qPCR, targeting the 16S rRNA and β-actin genes, respectively. The V3–V4 region of the 16S rRNA gene (for metabarcoding) and the shotgun metagenomic libraries were sequenced on Illumina platform. Reads related to the16S rRNA gene were processed using QIIME2, and taxonomy was assigned using the SILVA database. For shotgun analysis, Kraken2 and Sylph were used to generate taxonomic profiles and relative species abundance tables. The taxonomic profiles of a single sample varied depending on the extraction kit used; however, one extraction method produced results that more accurately reflected the mock community composition. Tonsil swabs were found to contain very high levels of host DNA, which can interfere with accurate taxonomic assignment, especially at low sequencing depths. This issue may be mitigated by employing host DNA depletion techniques.

Keywords: Tonsil microbiota, Pig, Metabarcoding, Shotgun

Poster #21 : When Viruses Meet the Gut: Trophic and Microbial Correlates of Coronavirus Infection in Bats

Pauline VAN LEEUWEN

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Abstract

Sarbecoviruses, a subgenus of Betacoronavirus, are known for their respiratory and gastrointestinal tropisms, suggesting that infection could alter gut microbial communities. Yet, the ecological and physiological signatures of infection in wild bats remain largely unexplored. We investigated the interplay between Sarbecovirus infection, bacterial microbiota, and diet in Rhinolophus shameli roosting in northeastern Cambodia. Fecal samples collected across dry and wet seasons (2023–2024) underwent full-length 16S rRNA sequencing and insect DNA metabarcoding. We compared alpha/beta diversity, screened for microbial biomarkers of infection, and tested bacterial–diet co-occurrence while controlling for seasonality variation. Sarbecovirus-positive bats displayed gut dysbiosis, marked by a significant enrichment of Shigella and Escherichia species alongside a depletion of Enterobacter spp, that are both typical signs of epithelial inflammation, oxidative stress, and intestinal barrier disruption in bats. These shifts indicate a pro-inflammatory microbial state potentially reflecting active gastrointestinal pathology. In contrast, dietary composition showed little variation between infection groups, reinforcing the independence of viral effects on microbiomes from trophic ecology. Our findings suggest that Sarbecovirus infection in wild bats may induce gastrointestinal imbalance and inflammatory-type dysbiosis, providing rare ecological evidence of subclinical symptoms in a natural reservoir host. Integrating viral, microbial, and dietary data uncovers early physiological footprints of infection and opens perspectives for non-lethal monitoring of disease processes in wildlife.

Keywords: microbiome, wildlife, epidemiology

Poster #22 : Commercial soil amendments trigger soil dysbiosis and impair Douglas fir reforestation

Romain DARRIAUT

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Abstract

Reforestation of agricultural soils faces challenges from altered physicochemical and microbiological soil properties and herbaceous competition. Consequently, forest managers increasingly adopt soil microbiome interventions using commercial probiotics and prebiotics. However, their ecological impacts remain poorly understood. We investigated effects of commercial prebiotic and probiotic amendments on Douglas fir across three former agricultural land types in Brittany: grassland, heathland, and cereal fields. Over one year, we monitored 90 trees, assessing plant physiology, soil chemistry, and bacterial and fungal communities through amplicon sequencing. Contrary to expectations, treatments triggered a cascade of negative effects. Treated seedlings rapidly exhibited severe stress with reduced photosynthetic pigments and increased mortality. Amendments caused ammonium accumulation and pH fluctuations. Within one month, microbial analyses revealed severe dysbiosis characterized by declining symbiotic fungi coinciding with pathogen enrichment. Enzymatic activities in carbon, nitrogen, and phosphorus cycles were substantially disrupted. Despite partial microbial recovery after six months, plant stress persisted for one year, indicating limited ecosystem resilience. Grassland soils showed greatest vulnerability, highlighting land-use history influence. These findings challenge assumptions about universal benefits of commercial microbial amendments. Results underscore the need for site and plant-specific evaluation and suggest that native microbiome restoration may be more sustainable than commercial products for successful reforestation of agricultural lands.

Keywords: microbial dysregulation, microbiome engineering, ecosystem resilience, land, use history, pathogen enrichment

Poster #23 : From Vision to Impact: NGS4ECOPROD – A Horizon Europe Twinning Project Advancing Genomic Innovation for Sustainable Bioproduction – A Case Study on Sporeless Biopesticides

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Abstract

The Horizon Europe NGS4ECOPROD Twinning project aims to strengthen research capacity in the field of sustainable bioproduction by harnessing the potential of Next-Generation Sequencing (NGS) technologies. Its primary objective is to advance genomic tools that support the development of safe, efficient, and eco-friendly microbial bioproducts. This keynote will present the project's scope, methodology, and emerging results, with an emphasis on its scientific and societal impacts across biotechnology, agriculture, and regulatory frameworks. As a concrete example from WP1, we highlight the development of a sporeless Bacillus thuringiensis biopesticide targeting vector-borne diseases and agricultural pests. The task combines classical mutagenesis with second- and third-generation Whole Genome Sequencing (WGS) to generate and screen microbial mutants. Using advanced genomic platforms, we performed high-resolution analyses of selected mutant genomes and evaluated their biosafety in accordance with regulatory and environmental requirements. Results demonstrate successful isolation of sporeless bacterial strains with confirmed biopesticidal activity. The integration of WGS significantly accelerated the design–validation cycle, offering a robust model for future microbial product pipelines. This approach not only addresses urgent needs for sustainable pest control but also sets a precedent for safe bio-innovation based on genomic precision. In conclusion, NGS4ECOPROD illustrates how NGS-enabled workflows can translate scientific research into scalable, environmentally responsible solutions, supporting the broader green transition in Europe and beyond.

Keywords: NGS4ECOPROD, Genome structural variants, Bacillus thuringiensis, Eco, friendly Biopesticides, Genomic data analysis Random Mutagenesis

Poster #24 : The sea urchin serves as a new toxicological model to elucidate the effects of chlordecone cocktail pesticides

Calli PAUL

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Abstract

In the Anthropocene, organisms face increased exposure to synthetic chemicals. Particularly endocrine disrupting chemicals (EDCs), which even at low chronic doses, have marked biological effects. Chlordecone (CLD), an EDC, was heavily utilized in the French West Indies (FWIs) from 1973-1993 as a banana crop insecticide. CLD is a persistent organic pollutant, lipophilic, and a primary pollutant in the FWIs despite being banned for over 30 years. CLD exposure is associated with higher risks of cancers, developmental and gestational impairments, and endocrine disorders. However, the cocktail effects of CLD and other pollutants present in the FWIs are unknown. Current regulation addresses chemicals individually, which does not reflect the actual extent of pollution, as chemicals pollute simultaneously. The sea urchin, Paracentrotus lividus, complies with EU directive 2010/63/EC as an alternative model to vertebrate toxicology testing. With a sequenced genome and human orthologs, P.lividus serves as a tool to investigate how cocktail pesticide exposure affects gene expression. P. lividus individuals were exposed to environmentally relevant concentrations of a CLD, Aminomethylphosphonic acid, and Azoxystrobin for 7 days. Post subacute exposure, RNA was extracted for RNA-Seq processing to assess differential gene expression. This is the first study assessing chlordecone cocktail effects, while introducing the sea urchin as a new model for toxicology testing. Future perspectives of this study include testing the cocktail effects of CLD and its metabolites, and the use of sea urchins as ecosystem health indicators in the presence of EDC cocktails. Increasing cocktail pesticide exposure warrants further studies.

Keywords: Chlordecone, Cocktail pesticides, RNAseq, Sea urchin, Endocrine disrupting chemicals

Poster #25 : Isolation and identification of antibiotic resistant bacteria and genes from soil. The effect of animal manure use as a fertiliser on antimicrobial resistance in an Irish beef and sheep farm.

Brian JOYCE

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Abstract

Introduction: Antimicrobial resistance (AMR) is a public health issue affecting many areas including agriculture. In farms, animal manure can contain antibiotic resistant genes, antibiotic resistant bacteria and undegraded antibiotics. Due to the use of animal manure as a fertiliser and its deposition on soil, there are fears that AMR could spread through the food chain from animals to the environment. Therefore, the impact of animal manure spreading on AMR needs to be investigated. This study aims to; take soil and animal manure samples before and after animal manure spreading; extract DNA and characterise the taxonomic and AMR gene profile using shotgun sequencing and isolate resistant bacteria to investigate multidrug resistance (MDR) and resistance mechanisms. Methods: Animal manure samples were taken before spreading and soil samples taken before, 2 weeks, 1, 2 and 3 months after manure spreading. Bacterial DNA was extracted from soil and manure and sent for shotgun sequencing. Antibiotic resistant bacteria were isolated by diluting soil samples in phosphate buffered saline solution and inoculating directly onto antibiotic media. Results: 36 colonies resistant to ampicillin, ertapenem, ciprofloxacin, colistin, chloramphenicol, trimethoprim, amikacin and tetracycline were isolated so far and are being tested for multidrug resistance. These results highlight the presence and dissemination of MDR on farms. Conclusion: This work investigates the effects of animal manure use as a fertiliser on the spread of AMR on farms. Shotgun sequencing data will reveal the impact of animal manure spreading on the microbial taxonomic and AMR gene profile of soil in agricultural fields.

Keywords: AMR, Antibiotic resistance, Agriculture, Shotgun sequencing, animal manure

Session: Other

Poster #26 : Microbial diversity in Parisian urban soils: the impact of tree species and soil characteristics

Amandine HECQUET

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Abstract

Soil is a key component of terrestrial ecosystems, providing many essential ecosystem services. It provides vital nutrients for plants and is usually home to a rich diversity of microorganisms. Soil microorganisms interact with plants directly influencing their growth and development. While the impact and feedbacks of plant and soil types on the structure of microbial communities has been widely studied in crops and natural systems, this relationship remains poorly understood in urban environments. The aim of this study is to characterise the overall microbial diversity in urban soils and to identify specific patterns relating to tree species and soil functioning, in order to improve our understanding of their interactions. We sampled 48 urban soils in Paris (France), representing four distinct conditions: soil beneath linden, plane and pagoda trees (the most commonly planted species in Paris) of the same age category and bare soil where no trees have been grown. Samples were collected at a depth of 10-20 cm in triplicate. Total microbial diversity was quantified and sequenced (archaea, bacteria and fungi) and physicochemical properties of these soils were analysed. The results suggest that microbial diversity is influenced by the interactions with trees, and that soil properties in urban environments may also play a role in these patterns. Some of these microorganisms have likely adapted to urban conditions and could help newly planted trees in cities withstand climate change and harsh environmental conditions (pollution, soil compaction...). This highlights the need for a better understanding of microbial diversity in this context, which could inform the practices of green space managers in tree planting and urban soil management.

Keywords: urban soils, trees, microbiota, biodiversity

Session: Other

Poster #27 : Tracking Antibiotic Resistance on Slurry-Exposed Soil for Monitoring of Antimicrobial Resistome Changes

Stephen RYDER

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Abstract

Background. The rise of antimicrobial resistance (AMR) is a significant threat to human society. Many AMR genes originate and reside in soil environments. The interactions of these environments with farmers and agricultural products creates the possibility for AMR transmission into society. Slurry spreading is a common agricultural practice with high potential to transmit resistant microorganisms from farm animals to both farmers and the soil. This work aims to evaluate the effect of slurry spreading on the soil antimicrobial resistome. Methods. Isolates were collected at three different time points: before and two and four weeks after slurry spreading. Isolates were screened for resistance to Amikacin, Ampicillin, Aztreonam, Cefepime, Chloramphenicol, Ciprofloxacin, Colistin, Ertapenem, Tetracycline, and Trimethoprim, by plating onto media with antibiotics. The isolates' antibiotic resistance profile was characterised via antibiotic disc diffusion. DNA isolation was prepared for 16S identification as well as metagenomic shotgun sequencing (bulk soil samples). Results. Resistance to all antibiotics was obtained at all timepoints. Number of resistant isolates recovered after slurry spreading was double that recovered prior to spreading. At four weeks, the number decreased slightly but was still higher than prior to spreading. Beta-lactam resistance, including Aztreonam, Ampicillin, and Cefepime were common at all time points, with some Ertapenem resistance obtained. Conclusion. This study is part of the multidisciplinary Resist AMR group, and it highlights how AMR in the soil and certain agricultural practices, such as slurry spreading, can impact the overall dissemination of AMR in the farm environment.

Keywords: Antimicrobial Resistance, One Health, AMR, Soil Microbiome, Agriculture, 16S Sequencing, Whole Genome Shotgun

Poster #28 : Annotation transfer in pangenome graphs

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Abstract

The increasing availability of genome sequences has highlighted the limitations of using a single reference genome to represent the diversity within a species. Pangenomes, encompassing the genomic information from multiple genomes, thus offer a more comprehensive representation of intraspecific diversity. However, pangenomes in form of a variation graph often lack annotation information, which limits their utility for downstream analyses. We developped GrAnnoT, a tool designed for efficient and reliable integration of annotation information in such graphs. It projects existing annotations from a source genome to the graph and subsequently to other embedded genomes.GrAnnoT was benchmarked against state-of-the-art tools on pangenome graphs and linear genomes from rice, and tested on human and E. coli data. The results demonstrate that GrAnnoT is consensual, conservative, and fast. It provides informative outputs, such as presence-absence matrices for genes, and alignments of transferred features between source and target genomes, aiding in the study of genomic variations and evolution.GrAnnoT's robustness and replicability across different species make it a valuable tool for enhancing pangenome analyses. GrAnnoT is available under the GNU GPLv3 licence at https://forge.ird.fr/diade/dynadiv/grannot. The preprint of the paper presenting GrAnnoT is available at https://doi.org/10.1101/2025.02.26.640337.

Keywords: Pangenome, Graph, Pangenome graph, Annotation transfer, Annotation

Poster #29 : Individually assembled genomes from field-collected Spodoptera frugiperda reveal that intact gene copy number variants from retrotransposition are retained under relaxed selection

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Abstract

Copy number variations (CNVs) are a major source of genetic variation, affecting large portions of genomes. Typical CNVs are well known to have short evolutionary half-lives due to deleterious effects, with anecdotal events of adaptive evolution. However, it is not known whether the same trends apply to CNVs with intact open reading frames (iORF-CNVs), which can encode functional proteins. Here, we investigate the mechanistic origins and evolutionary dynamics of iORF-CNVs in Spodoptera frugiperda, a globally distributed pest species where CNV-mediated adaptive evolution has been reported. Using PacBio HiFi reads, we generated high-quality, individually assembled genomes for 36 field-collected individuals and identified over 349 polymorphic iORF-CNVs. These elements are short, intronless, and display molecular signatures of LINE-mediated retrotransposition, including cis- and trans-acting effects. iORF-CNVs showed reduced divergence at the first and second codon positions and elevated nonsynonymous-to-synonymous polymorphism ratios, consistent with evolutionary constraint imposed by purifying selection. Orthology analyses indicated that these CNVs originate from genes under weak evolutionary constraint, while transcriptomic and promoter motif analyses revealed that many are transcribed and retain regulatory features. Together, we conclude that observed iORF-CNVs are generated through retrotransposition from weakly constrained genes and that the duplicates are selectively maintained for coding potential, albeit under reduced purifying selection. These results imply that pseudogenization is not an inevitable evolutionary fate of retrotransposed gene copies when the open reading frame is preserved.

Keywords: Copy number variation, Individually assembled genome, Intact ORF, Long Lnterspersed Nuclear Element, Retrotransposition, Spodoptera frugiperda

Poster #30 : PanGBank: a Database of Pangenome Graphs for Comparative Microbial Genomics

Jean MAINGUY

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Abstract

Pangenome analysis provides crucial insights into microbial diversity, evolution, and adaptation. However, publicly available downloadable pangenome resources to support such studies are currently lacking. In this context, we present PanGBank, a comprehensive database compiling pangenome collections constructed with the PPanGGOLiN software suite (1). PanGBank currently provides pangenomes for 3,873 prokaryotic species represented by ≥15 genomes, built through a reproducible NextFlow pipeline. The resource includes a RESTful API for programmatic access and a user-friendly web interface (https://pangbank.genoscope.cns.fr) for intuitive exploration by non-developer researchers. As of today, PanGBank comprises two pangenome collections built from genomes (originating from RefSeq and GenBank) of the GTDB taxonomic database (release R10-RS220) (2) ensuring broad coverage of microbial diversity. PanGBank provides a scalable and updatable platform for pangenome exploration across microbial clades. By offering multiple curated pangenome collections, it fills a critical gap in the field and paves the way for broader, collaborative, and data-driven microbial genomics research. As a use case, PanGBank and the new features introduced in PPanGGOLiN version 2 are being applied to explore antibiotic resistance in Acinetobacter baumannii from a pangenome perspective. References 1. Gautreau G, et al. PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. PLoS Comput Biol. 2020 2. Parks DH, et al. GTDB: an ongoing census of bacterial and archaeal diversity through a phylogenetically consistent, rank normalized and complete genome-based taxonomy. Nucleic Acids Res. 2022

Keywords: microbial genomics, pangenome graph, pangenome database

Poster #31 : Savanache : Interactive Visualization of Pangenomic Diversity

Mourdas MOHAMED

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Abstract

Savanache is an interactive visualization tool dedicated to exploring pangenomic diversity, whether through comparisons between individuals across multiple pangenomes or through the analysis of structural variations (SVs) within a single pangenome. It enables intuitive navigation through genomic rearrangements insertions, deletions, and inversions while providing a continuous zoom from the chromosomal to the nucleotide scale. Originally developed as a prototype within the framework of a doctoral thesis (Durant, 2022), Savanache has since been fully implemented and extended. Combining a high-performance indexing engine with a responsive web interface, it dynamically highlights affected regions and their genomic context. Compatible with the GFA graph format, it now supports both population-level and individual-level analyses, bridging large-scale pangenome graph data with biological interpretation in an efficient and scalable way.

Keywords: Graphical, Visualization, Pangenomics

Poster #32 : Using pangenome graph to perform association studies

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Abstract

Association studies aim to link genomic regions to phenotypes. The statistical power required for this implies growth, phenotyping and sequencing of hundreds of individuals. Such studies often produce results in the form of large regions,sometimes with annotations of candidate genes. However, limitations such as linkage disequilibrium mean that these analyses are not always satisfactory. A new way of representing genomes and in particular variation between individual could be a great support to improve such analysis. The use of reference genomes introduces a bias to all genomic studies that rely on them, since a single individual from a population is not representative of the full genetic diversity. Pangenomes, accessible thanks to lower sequencing costs, bring together several complete genomes in a single data structure. A compact way to represent this complex data is the pangenome graph,which groups similar or divergent regions of the graph into nodes that may or may not be traversed by their individuals genomes. The hypothesis is that combining the pangenome graph topology with phenotypes could highlight specific patterns (such as a certain node/phenotype configuration only found in resistant individuals, for example) and enable the development of a reference-free method from scratch. Some methods are being developed using clustering methods or even graph neural network modelsto recognise such patterns. Augmenting the graph with additional data is also under development and could improve the precision of these methods. Investigating phenotypes using the graph could allow us to use far fewer individuals in association studies and direct functional research towards specific variations rather than positions on a reference.

Keywords: Pangenome, GWAS, graph, association studies.

Poster #33 : Wolbachia population genomics across mosquito organs in single Culex pipiens individuals

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Abstract

The maternally inherited intracellular bacterium Wolbachia is largely used in biocontrol strategies due to its capacity to modulate arthropod reproduction and limit pathogen transmission. While Wolbachia infections are generally assumed to be monoclonal in Culex mosquitoes, a comprehensive insight into the extent of homogeneity within Wolbachia populations at the whole genome-scale is lacking. Here, we investigated patterns of intra- and inter-individual variations across mosquito organs following the reconstruction of Wolbachia genomes from separated ovaries and midgut metagenomes of single Culex pipiens mosquitoes from Southern France. Our study showed a highly conserved core pangenome both at the level of gene presence-absence signal and single-nucleotide polymorphisms (SNPs) within single individuals, confirming the presence of a dominant Wolbachia that is maintained under strong purifying evolutionary forces. However, we identified several punctual mutations between individuals, in some cases non-synonymous, in the same core pangenome, demonstrating the presence of some level of genomic heterogeneity among Wolbachia that infect the same Culex pipiens field populations. We are investigating these questions further, including in the accessory genome, using long read sequencing that may enable a better reconstruction of genomic data loaded with repeated and mobile genetic elements.

Keywords: Mosquitoes, Wolbachia, pangenomics, polymorphism

Poster #34 : Are your organisms functionally hyper-diversified? Dinoflagellates as a case study, and LAGOON-MCL as a user-friendly tool designed to study them

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Abstract

With the massive sequencing of genomes, transcriptomes and environmental samples, the quantity of sequences is increasing exponentially, forcing us to develop new, faster and more efficient methods. We propose here a method to address these two problems. LAGOON-MCL is a Nextflow pipeline for annotating and comparing protein sequences. First, sequences are annotated using Pfam and user-supplied data (e.g. taxonomy) and compared to AlphaFold Protein Structure Database (AlphaFold DB) to obtain structural information. Next, a sequence similarity network is built from pairwise alignments, and a graph clustering algorithm is applied, enabling sequences to be compared and putative protein families to be constructed labeled with the annotations. The pipeline was tested on 101 dinoflagellate transcriptomes (6.1 million sequences). 25% of sequences are annotated with Pfam and 58% have a similarity in AlphaFold DB. They are clustered into 368,286 protein families. Of these, 16% contain at least one sequence annotated with Pfam, the addition of AlphaFold DB enables 20% more families to be annotated. In the end, 82% of sequences are in annotated families and 65% of unannotated clusters have less than 3 sequences. The pipeline is adaptable to other organisms and data (e.g., metagenomic), providing a versatile solution for sequence annotation and comparison. Tool reference: https://github.com/jroussea/lagoon-mcl

Keywords: Comparative genomics, Functional annotation, Sequence Similarity Network, Markov Clustering algorithm

Poster #35 : Development of a blood-based transcriptional biosignature for the detection of cattle infected with Mycobacterium bovis, which causes bovine tuberculosis

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Abstract

Mycobacterium bovis is the chief causative agent of bovine tuberculosis (bTB), an economically damaging infectious disease to global agriculture. In Ireland, bTB control is underpinned by two diagnostic tests: the in vivo field-based single intradermal comparative tuberculin test (SICTT) and an ancillary laboratory-based in vitro interferon-γ release assay (IGRA). The sensitivities of SICTT and IGRA are estimated at 75% and 90%, respectively, for confirmed bTB cases. The suboptimal sensitivity of both tests impedes bTB control and eradication. Efforts have been made to identify blood-based transcriptional biosignatures of M. bovis infection, and we now apply machine learning (ML) techniques to such data. We analysed ex vivo blood-based transcriptomics data from cattle naturally or experimentally infected with M. bovis (n = 139) and control non-infected cattle (n = 115). Splitting the integrated data set into a 70% training (n = 183) and 30% testing set (n = 71), we identified 1,115 significantly DEGs (FDR Padj. < 0.05) between M. bovis-infected and control non-infected cattle in the training set. Using these DEGs, we trained eight ML algorithms and assessed their performance via 5-fold cross-validation before evaluating their generalisability on the test set. We observed that a 41-gene signature identified by lasso logistic regression performed well, achieving average area under the receiver operating characteristic curve (AUROC) values of 0.947 in the training set and 0.924 in the test set. Overall, our results indicate that accurate discrimination of control, non-infected, and M. bovis-infected cattle can be achieved using blood-based transcriptomics data.

Keywords: tuberculosis, cattle, Mycobacterium bovis, transcriptomics, machine learning, biomarker, diagnostics

Poster #36 : Neural network-based cross-species chromatin annotation goes beyond sequence conservation

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Abstract

Analogous to the Encyclopedia of DNA Elements (ENCODE) project, the Functional Annotation of ANimal Genomes (FAANG) consortium has produced chromatin annotations for domesticated animals, albeit in smaller amounts. Classical methods based on sequence conservation can be used to infer missing annotations, but are inappropriate for non-conserved sequences. Here, we demonstrate the ability of neural networks trained with human data to infer the missing chromatin annotations in livestock species. For this purpose, we comprehensively assessed predictions of transcription factors, chromatin accessibility, and histone marks in several species. Our results showed good predictions for various annotations in mammalian genomes, and surprisingly, also for bird genomes, despite the large phylogenetic distance from the human genome. Moreover, predictions were accurate even for non-conserved sequences, unlike conservation-based methods. Our results advocate the widespread use of neural networks in cross-species genome annotation, a key step in understanding the genetic architecture of complex traits.

Keywords: annotation, livestock species, chromation regulation