

Affichage des résultats 141 à 160 sur 7062 au total

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Pertinence:  100%

Regulatory potential of the U12-dependent spliceosome: Intron retention and beyond

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Ecologie et Evolution des Populations / Biostatistiques Santé

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Detecting adaptation in protein-coding genes using mechanistic codon models.

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Genome-scale problems in metazoan phylogeny: from comb jellies to purple socks

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The role of the host microbiome in Daphnia-food stress interactions

In aquatic ecosystems, food stress (more in particular cyanoHABS, cyanobacterial harmful blooms) has a strong negative impact on zooplankton grazers, and through the food web, disrupt the whole freshwater community. Deciphering the mechanisms underlying resistance to cyanoHABS in these grazers is thus essential to predict how cyanoHABS can be prevented or controlled. In the freshwater crustacean *Daphnia*, resistance is influenced by prior exposure to cyanobacteria and genotype, but the underlying mechanisms remain unclear. Through gut microbiota transplants, we here show that the gut microbiota plays a crucial role, and might mediate both genetic adaptation and acclimatization to cyanoHABS. Microbiota from resistant genotypes conferred a higher resistance to recipient *Daphnia* than microbiota from susceptible genotypes. Resistance to cyanobacteria in recipient *Daphnia* was not affected by the recipient genotype, but was strongly impacted by the donor genotype. This suggests that the *Daphnia* genotype acts indirectly on resistance to cyanobacteria, by shaping the gut microbiota. In addition, resistance was higher when donors were previously fed cyanobacteria, suggesting that gut microbiota responded to become more efficient in dealing with cyanobacteria after prior exposure. Next generation sequencing of 16S rDNA shows that resistance is associated with changes in microbiota structure. Our results provide evidence that resistance to toxic cyanobacteria in *Daphnia* is driven by the gut microbiota, which might thus be an important mediator of the genetic mosaic of coevolution between toxic cyanobacteria and their grazers, and a key determinant of how freshwater ecosystems respond to climate warming.

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Integrative modelling of gene and genome evolution roots the archaeal tree of life

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Pourquoi modéliser la trajectoire des patients en Insuffisance Rénale Chronique Terminale ?

L'enjeu du système de soins est d'offrir une réponse adéquate aux besoins des patients en IRCT. A l'échelon individuel, il s'agit de proposer une stratégie de soin efficace et adaptée aux besoins et aux choix du patient garantissant la meilleure espérance de vie possible tout en préservant la qualité de vie, l'autonomie et la proximité avec le lieu de résidence. A l'échelon collectif, il s'agit de proposer une organisation de l'offre garantissant des soins de qualité, adaptée à l'hétérogénéité des besoins et économiquement assumée. Or, dans un contexte de forte hétérogénéité des pratiques et de l'offre de soins et de forte hétérogénéité des patients, comment évaluer les pratiques ? Comment organiser, évaluer et anticiper l'offre de soins ? Comment bien informer les patients ? Nous pensons que la modélisation de la trajectoire des patients en IRCT nous permet et nous permettra : 1/ de mieux comprendre et mesurer l'impact de différents facteurs sur la dynamique du système, 2/ de mieux décrire le processus pour aboutir à une vision simplifiée et opérationnelle de cette prise en charge et 3/ de prédire à partir des données observées ou des changements simulés le devenir des patients avec une IRCT. Dans ma présentation, je montrerai rapidement les différentes outils qui ont déjà été développés et les développements à venir. L'objectif final de ces travaux est de mettre ainsi à disposition des néphrologues et des tutelles des outils d'aide à la décision afin d'améliorer la prise en charge des patients en IRCT.

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Analyzing the genomic landscape of liquid tumors

When a patient contract cancer, the diagnosis and the treatment options are decided based on phenotypic factor such as the primary organ and the pathology of the tumors. However, recent discoveries have shown that the molecular pathogenesis of the tumor may be a better indicator of the prognosis and the adequate therapeutical targets, underlining the need for a better understanding of the genomic characteristics of the disease. In order to solve this issue, initiatives such as TCGA have sequenced large groups of disease samples and used the size of the cohort to distinguish between driver and passenger events. We propose to adopt the same approach to analyze liquid tumors, where widespread heterogeneity within the tumor as well as between patients adds even more noise to the measurements. We will show the software infrastructure we built in order to track and analyze the samples as well as two examples of such studies. The first cohort we will discuss is a cohort of 53 patients with acute myeloid leukemia (AML). AML is the most common type of leukemia in adult, and the is still poorly understood. All these patients achieved complete remissions after standard chemotherapy and later suffered from relapse. We performed whole exome sequencing of germline tissue, primary sample as well as relapsed sample for each of these patients and will show analysis of this data compared to the knowledge that we have of the disease. The second cohort we will discuss is a cohort of 189 adult patients with B-cell acute lymphoblastic leukemia (B-ALL). B-ALL is the most common leukemic malignancy in the pediatric population but most of the knowledge that we have from the adult form of the disease is actually deduced from the childhood form. We will present here a integrated and targeted DNA/RNA sequencing solution that allowed us to extract short events (point substitutions and short insertions and deletions) as well as copy number aberrations, rearrangements and fusion events. We will use these two cases to discuss common problems that arise when analyzing genomic data as well as potential solutions."

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Two mitochondrial genomes for one bivalve, a major dilemma for the long-lived clam *Arctica islandica*

Mitochondrial genomes (mtDNA) are normally maternally inherited and encode for subunits of respiratory chain complexes and ATP synthase among others. The integrity of mtDNA is crucial for cellular energetic and redox homeostasis, and mtDNA mutations are associated with modifications of individual fitness and longevity. Bivalves are the only zoological group in which Doubly Uniparental Inheritance (DUI), characterized by the presence of two divergent mitochondrial genomes within different tissues of male individuals, is frequently observed. The F-genome, maternally inherited, is found in somatic tissue and female gonads whereas the M-mtDNA is found in male gonadic tissue only. The clam *Arctica islandica* is widely distributed throughout the North Atlantic shelf regions. Due to different environmental regimes (salinity, temperature, oxygen), the maximum lifespan of its populations varies between >500 years around Iceland and 35 years in the Baltic Sea. I will present our recent investigations that describe for the first time the existence of the DUI system in *Arctica islandica*. Based on 16S and cytochrome b markers, we highlight the presence of an M-genome in male gonads in individuals belonging to Baltic and North Sea populations. The two genomes show a low level of sequence divergence compared to other DUI species, around 6-8% at the nucleotide level. Whilst the analysis of mitochondrial markers generally indicated genetically homogeneity of all North Atlantic populations, they further reveal few clam individuals that carry a "divergent" mtDNA haplotype, resembling the M-genome. These individuals occurred however exclusively in the Icelandic population. Unlike the M-genome, which is confined to male gonadic tissue in DUI species, this "divergent" mtDNA occurs in somatic tissues from 20% of individuals of both sexes. In association with transcriptomic and biochemical data, we will discuss the possible impacts of this uncommon mitochondrial genome on *Arctica islandica* biology and cellular physiology. This study will enhance the understanding of the role of DUI and mtDNA in general for fitness, aging and adaptation of bivalves.

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Quantifying the nearly neutral theory of molecular evolution

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A positive psychology study and intervention on the well-being of PhD students in biology at Univ. Lyon 1

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The impact of size-selective harvest regimes depend on the horn growth rate

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The reconstructed ancestral flower and its subsequent diversification

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Demography of aging across the tree of life

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Equipe ETEP et Pôle info

- Équipe Éléments transposables, Évolution, Populations - Pôle informatique (présentation des travaux réalisés avec Sonia Kéfi (ISEM) et des collaborateurs chiliens/états-uniens, publiés dans le numéro d'août de PLoS Biology. Il s'agit de la première étude d'un réseau écologique "multiplexe", i.e. qui recense toutes les relations connues (trophiques et non-trophiques [facilitation, compétition]) entre les espèces d'une communauté écologique. Notre jeu de données concerne toutes les espèces présentes sur la côte du centre du Chili).

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Tissue-specific functional effect prediction of genetic variation and applications to complex trait genetics

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Bacterial endosymbionts and the evolution of host sex determination mechanisms

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Phylogeography of invasive species

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- Bioinformatique, Phylogénie et Génomique Evolutive : LifeMap: exploring the entire tree of life (Damien de Vienne)n- Epigénétique et Formation du Zygote

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Mathématique et Médecine

Merci de me confirmer votre présence par mail à mariethe.chaumeil@chu-lyon.fr

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