

Recherche avancée

Affichage des résultats 61 à 80 sur 7049 au total

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Pertinence:  100%

The Molecular Transformation of Evolutionary Biology.

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06/11/2020

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"Microevolution in Island Birds: Insights from white-eye colonisations of southwest Pacific islands »

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Apports de l'écotoxicologie dans la gestion de la qualité des eaux et des milieux aquatiques

Evaluer le bon état des masses d'eau, évaluer les impacts des activités humaines, détecter les polluants émergents à de très faibles doses, et évaluer leurs risques sur le long terme, etc., pour faire face à ces défis, de nouvelles connaissances et des technologies innovantes sont nécessaires. La gestion durable de la ressource en eau et des milieux aquatiques impose de s'appuyer sur des recherches finalisées de haut niveau. La loi sur l'eau et les milieux aquatiques (LEMA) a confié à l'Onema une mission explicite afin de renforcer l'utilisation des connaissances scientifiques et techniques pour éclairer la conception, la mise en œuvre et le suivi des politiques publiques dans le domaine de l'eau par une expertise de haut niveau. L'Onema conduit cette mission avec ses moyens propres et en construisant des partenariats avec les organismes nationaux de recherche. A travers plusieurs exemples de projets de recherche ou d'études menés dans le cadre des conventions partenariales de l'Onema, nous verrons dans quelle mesure les résultats de la recherche appliquée le domaine de l'écotoxicologie peuvent aider à la mise en œuvre de la directive cadre sur l'eau, notamment par le soutien à des travaux permettant de mieux comprendre les phénomènes de transfert des contaminants organiques hydrophobes dans les réseaux trophiques, le soutien à des travaux sur les effets des substances chimiques sur les écosystèmes soumis à des expositions chroniques et multiples pour en tirer des marqueurs d'effets utilisables sur le terrain, etc.

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Dynamic modelling of HPV transmission and cervical cancer natural history : implications for public health interventions

In the last three decades, the appreciation of the role of infections in cancer aetiology has greatly expanded. Among the 13 million new cancer cases that occurred worldwide in 2008, around 2 million (16%) were attributable to infections. Cervical cancer is a major example of infection-related cancer. The uncovering of a causal relationship between carcinogenic HPV infections and cervical cancer is shifting public health intervention from cancer control to infection control paradigm. Worldwide, vaccination and detection of infected individuals play an increasingly crucial role in cervical cancer control. In support of this paradigm shift, the use of infection transmission models has entered the field of infection-related cancer epidemiology. These models are useful to understand the infection transmission processes, to estimate the key parameters that govern the spread of infection, and to project the potential impact of different preventive measures. This presentation, focused on HPV transmission and cervical cancer natural history, aims to concisely illustrate the main principles of transmission dynamics, the basic structure of infection transmission models, and their use in combination with empirical data

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De la délimitation moléculaire des espèces à l'étude de leur génome : l'hétérozygotie dans tous ses états

La co-occurrence dans un même individu de deux demi-génomes semblables mais différents (hétérozygotie) est une caractéristique générale des organismes diploïdes qui pose de gros problèmes techniques lors du séquençage : double pics, échec de l'assemblage des données,... En dépit de ces difficultés apparentes, les séquences d'organismes hétérozygotes apportent une mine d'informations très utiles à la délimitation des espèces et à l'analyse de leurs génomes. Après avoir montré comment reconstruire les allèles d'individus hétérozygotes par séquençage direct, sans cloner, j'introduirai une approche nouvelle pour la délimitation moléculaire des espèces basée sur l'analyse de l'hétérozygotie : cette approche, appelée "haplowebs", ne repose pas sur le critère de monophylie et surpasse pour cette raison les méthodes actuellement utilisées en barcoding (GMYC, ABGD,...). Dans la deuxième partie de mon exposé, je montrerai comment l'analyse récente de l'hétérozygotie d'un rotifère bdelloïde a permis de prouver son asexualité et de mettre en évidence l'importance des conversions géniques et des transferts horizontaux dans l'évolution de son génome.

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GENOMIC APPROACHES TO UNDERSTANDING STRUCTURAL COLOUR IN PLANTS

While we often think of colour as synonymous with pigment, many of the most spectacular colours in nature are caused by differential interference of different wavelengths of light as they are scattered by nano structured surface features. There are many famous examples of such structural colour in animals, such as the iridescent scales on morpho butterflies and peacock feathers, but structural colour is also common throughout the plant kingdom, from algae to numerous groups of flowering plants. Structural colour in flowers is thought to aid in pollinator attraction, but it is also common in leaves, where its functional significance is not well understood. We are investigating the genetic basis and functional significance of structural colour in a variety of plant species with a range of approaches including genomics. We are working with genome-wide transcription data for two distinct lineages of iridescent plants: the living fossil *Selaginella*, which produces blue iridescence in the leaves and the flowering plant *Spiloxene* which has iridescent flowers. We have obtained RNAseq data for four different tissues for each of four *Selaginella* species exhibiting a range of iridescence intensities and for *Spiloxene capensis*. For each species, de novo transcriptome assemblies were produced and used for differential gene expression analysis. Between 14,000 and 26,000 gene families were found for each species, with between 150 and 250 gene families exhibiting significant differences in gene expression across the four tissues examined. We have identified several genes that code for cell wall modifying enzymes that are differentially expressed only in iridescent species as candidates for the generation of cell wall layering responsible for iridescence in *Selaginella*. We are also investigating differentially expressed photosynthesis genes to test the hypotheses that iridescence may play a role in increasing photosynthetic efficiency or in photoprotection. We hope that the use of functional genomics, coupled with detailed anatomical and developmental studies and optical modelling that are ongoing in our lab, will help to unravel the evolutionary origins and ecological roles of plant structural colour.

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Pitfalls and uses of lab studies in predicting ecological effects of chemicals in the field - my research career as a backflip artist

It has long been argued that single species laboratory tests do not necessarily predict the ecological effects of chemicals in the field. By ecological effects is used to mean effects on populations, communities and ecosystems. However ecotoxicologists have continued to use single species laboratory tests. My short research career has involved a number of change in direction - or backflips - in my attitude to these tests and I will illustrate this with examples of the effect of increased salinity on stream invertebrates, insecticides and fungicides on stream invertebrates and herbicides on benthic diatoms. I will discuss how such simple test systems combined with more complicated test systems can potentially serve as models to test hypotheses as to how chemical stressors effect ecological systems.

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Wolf Re-Introduction in the Northern Rockies, USA: From Population and Predation Trends to Policy and Economics

Conflicts between wolves and livestock have continued to escalate since wolf re-introduction in the Northern Rockies, USA. We will provide an overview wolf re-introduction, including trends in populations and predation rates. We will also review how wolves have (or have not) affected livestock management practices and ranch profitability. We will then review the legal framework for wolf control in Wyoming, including predation compensation policies. Compensation policies have attempted to reduce the impact of wolf-livestock conflicts by compensating producers for lost livestock. Compensation schemes, however, focus only on direct predation (i.e., confirmed losses) despite a growing body of evidence that predation pressure also have indirect effects on prey, particularly domesticated livestock (e.g., slower weight gain, higher disease rates, or lower reproduction rates). We will then discuss our research, which uses an economic model of livestock production to estimate the economic impact of both direct and indirect effects of wolf predation. Our results suggest that short-run (i.e., year-to-year) financial impacts of wolf indirect effects may be as large as or larger than the direct effects. Including indirect effects implies that the compensation ratio (i.e., number of calves compensated per confirmed depredation) necessary to fully offset the financial impacts of wolves would need to be two to three times larger than current 7:1 compensation ratio used in Wyoming.

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Le système immunitaire des invertébrés est-il "spécifique" ou "non-spécifique"?

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Modelling competition and dispersal in a statistical phylogeographic framework

Competition between organisms influences the processes governing the colonization of new habitats. As a consequence, species or populations arriving first at a suitable location may prevent secondary colonization. While adaptation to environmental variables (e.g., temperature, altitude, etc.) is essential, the presence or absence of certain species at a particular location often depends on whether or not competing species co-occur. For example, competition is thought to play an important role in structuring mammalian communities assembly. It can also explain spatial patterns of low genetic diversity following rapid colonization events or the "progression rule" displayed by phylogenies of species found on archipelagos. Despite the potential of competition to maintain populations in isolation, past quantitative analyses have largely ignored it because of the difficulty in designing adequate methods for assessing its impact. We present here a new model that integrates competition and dispersal into a Bayesian phylogeographic framework. Extensive simulations and analysis of real data show that our approach clearly outperforms the traditional Mantel test for detecting correlation between genetic and geographic distances. But most importantly, we demonstrate that competition can be detected with high sensitivity and specificity from the phylogenetic analysis of genetic variation in space. Joint work with L. Ranjard, D. Welch and M. Paturel.

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A quantitative genetic signature of senescence in plants

The evolution of senescence (the physiological decline of organisms with age) poses an apparent paradox because it represents a failure of natural selection to increase the survival and reproductive performance of organisms. The paradox can be resolved if natural selection becomes less effective with age, because the death of postreproductive individuals should have diminished effects on Darwinian fitness. A substantial body of empirical work is consistent with this prediction for animals. However, such evidence is still scarce in plants. I will discuss the plausible reasons why the genetic basis of senescence in plants was not studied from an evolutionary perspective in the past. I will also present our experimental results on the quantitative genetic basis of senescence in the short-lived perennial plant *Silene latifolia* and their contribution to our understanding of the evolution of senescence in plants.

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Heredity in evolution & evolution of heredity

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The genomics of adaptation in threespine sticklebacks

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Importance des microbiotes intestinaux dans les interactions socio-sexuelles

Les interactions qu'elles soient sociales ou sexuelles régissent un grand nombre de comportements et stratégies développés par les animaux pour maximiser leur valeur adaptative. Qu'elles soient conflictuelles ou symbiotiques, elles sont un puissant générateur d'évolution. Je suis une biologiste évolutive intéressée par les conflits sociaux et sexuels et comment ceux-ci sont résolus. Mes travaux de thèse et de premier post-doctorat ont porté sur l'étude phénotypique, génétique et chimique de la reconnaissance de parentèle chez les insectes parasitoïdes. Lors d'un second post-doctorat, je me suis intéressée à l'évolution des systèmes de reproduction (monoandrie et polyandrie) chez les drosophiles : conflits mâles/femelles, reconnaissance du partenaire sexuel et investissement reproducteur. A l'heure actuelle, j'ai intégré un troisième niveau dans mes recherches : les microbiotes intestinaux et comment les variations des communautés de microbiotes influencent les systèmes de reconnaissance et les interactions sexuelles chez les drosophiles

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Utilisation de phylogénies d'haplotypes pour l'identification de facteurs génétiques de risque

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A Tale of Two Insect Sterilizing Viruses

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Finding new partners in signaling pathways with message-passing algorithms

After a brief introduction to algorithmic complexity and some examples of graph problems in biology, I will present the formalism and algorithm we developed for the large-scale reconstruction of a signalling network, based on protein-protein interaction and transcriptomics data. The model we developed in consisted in modeling this reconstruction as a combinatorial optimization problem called the "Prize-collecting Steiner tree problem", and our algorithm, was applied to the reconstruction of the pheromone pathway in *S. cerevisiae*, with results that we were able to verify experimentally.

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Endosymbiosis in trypanosomatid protozoa: an eternal love affair

Some trypanosomatids harbor a symbiotic bacterium, which maintains a close association with the host, constituting an excellent model to study organelle origin and cellular evolution. Molecular data show that all endosymbiont containing trypanosomatids are grouped together in a single phylogenetic branch. Endosymbionts of different species are similar, being classified in the beta division of Proteobacteria, thus suggesting that a single evolutionary event gave rise to the symbiosis in the Trypanosomatidae family. The bacterium is enclosed by two unit membranes and presents a reduced peptidoglycan layer, which is essential for cell division and morphological maintenance. Regarding the protein composition, the number of intramembrane particles in the endosymbiont envelope is similar to that described for Gram-negative bacteria. Lipid analyses of purified endosymbionts show absence of sterols and indicate phosphatidylcholine as a major component of the envelope, as described in other intracellular bacteria. The endosymbiont promotes ultrastructural and physico-chemical alterations in the trypanosomatid and its presence influences the protozoan interaction with the insect host and mammalian cells. Symbiont-containing trypanosomatids are able to infect and to replicate inside fibroblasts and macrophages, whose microbicidal activity was deactivated by HIV-1 infection. The symbiosis in trypanosomatids is characterized by intensive metabolic exchanges; the bacterium contains enzymes and metabolic precursors that complete essential biosynthetic pathways of the protozoan. Conversely, the symbiont is capable of obtaining part of the required energetic molecules from the host glycosomes. Taken together, data suggest that the endosymbiont in trypanosomatids represents an intermediate evolutionary step between bacteria and eukaryotic cell organelles..

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Coûts et bénéfices dans les modèles mutualistes : le problème des marchés biologiques

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Modélisation de l'effet du dépistage du cancer du sein sur la mortalité à partir de données françaises: retour d'expérience

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