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'Dialogues' between squid and luminous bacteria during the establishment of the interaction and the building of the extended phenotype.

Symbiotic associations are widespread in nature, and constitute a driving force in the evolution of organisms. However, the interactions between partners that lead to the establishment, the specificity and the evolution of the association are oftentimes difficult to study. We used the binary mutualistic association between the squid Euprymna scolopes and the luminescent bacterium Vibrio fischeri as a natural model to study the dialogue between partners that facilitates the selection and colonization of the symbiont into host tissues, but also its maintenance over a strong diel rhythm. We coupled comparative transcriptomics analyses and functional characterizations to better understand how the initial molecular conversation between the two partners plays a role in determining the specificity of the association. We also studied the influence of the presence of a persistent luminous bacterium on the gene expression and physiology of its host. These studies reveal that a very limited number of symbionts is sufficient to reprogram host gene expression, leading to the specific establishment of the interaction and the building of its extended phenotype.

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EVENTS
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Bacterial species that are defined by genes but not by ecology

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Analysis of genomic structural diversity in wolf-like canids.

Structural variation in general, and copy number variants (CNV) in particular, has emerged as an important source of genetic variation. The genetic history and the extraordinary morphological, physiological and behavioral variation of dogs, make them an ideal mammal in which to study the effects of CNV on biology and disease. The dog genome revealed the existence of more than one thousand of CNV that overlap ≈ 400 genes, which are enriched for defense/immunity, oxidoreductase, protease, receptor, signaling molecule and transporter genes. Furthermore, CNV can have significant impacts on a wide range of phenotypes including breed-definiting traits and showed to be appropriate markers to analyze genetic relationships between dog populations. This finding implies that most of the surveyed CNVs were present in the pool of canine breed founders. In order to understand the ancestral dog genome organization, we designed a high density custom 720K probes NimbleGen aCGH chip based on all known dog CNV and segmental duplication and genotyped 15 wolves from 11 populations, with a wide distribution (including Europe, Asia and America), 5 dogs (Dingo, Basenji, Beagle, Boxer and Dachshund) and three outgroups (red wolf, coyote and golden jackal). The dataset analyzed in this study allow us to identify selected CNV during early dog domestication.

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Organization of genes along genome during evolution.

The organization of genes along a genome is not random. There exists various proofs of specific rearrangements such that operon for procaryote organisms.In the goal to better understand how this organization can explain the correlation between chromosomic mutation in cancer, we studied the organization of co-functional genes on the human genome (pathways, protein complexes, RNAt, etc). Using statistics, we observed significant concentrations (or dispersions) for sets of co-functioning genes. We evaluated the organization of these sets of genes through three aspects: number of chromosomes involved, genomic distance, spatial intra-chromosomic distance. This organization seems to depend on the functional category (FunCat) of each set of genes. From this results, we start to work on the evolution of these concentrations and dispersions among various species.Moreover, in order to observe some (dis)similarities between genomes, it is necessary to define realistic models and measures. We have implemented models (based of graph theory and mathematic programming) to compute in particular common adjacencies between genomes. These models take into account increasingly biologic information despite the complexity of the studied problems.

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Cancer: a missing link in ecosystem functioning?

Cancer is a disease that affects the majority of metazoan species and prior to directly causing host death, is likely to influence the competitive abilities of individuals, their susceptibility to pathogens, their vulnerability to predators and their ability to disperse. Despite the potential importance of these ecological impacts, cancer is rarely incorporated into model ecosystems. In this talk, I will describe the diversity of ways in which oncogenic phenomena, from precancerous lesions to generalized metastatic cancers, may affect ecological processes that govern biotic interactions. I will argue that oncogenic phenomena, despite their complexity, have predictable ecological consequences. Our aim is to provide a new perspective on the ecological and evolutionary significance of cancer in wildlife, and to stimulate research on this topic.

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Stratégies de recherche actuelles en génomique cardiovasculaire

La révolution technologique que vit depuis ces 10 dernières années la recherche biomédicale permet de mettre à disposition de la communauté scientifique et médicale des outils très puissants pour appréhender de manière agnostique l'ensemble des mécanismes génétiques et épigénétiques associées aux maladies humaines, qu'elles soient fréquentes ou rares. Les premières technologies de puces à ADN ou à ARN ("micro-array") ont tout d'abord permis la réalisation des études d'association génome-entier ("GWAS") et des études transcriptomiques dont les succès sont désormais légions. Depuis 3 ans, la technologie des puces fait petit à petit place aux outils de séquençage haut-débit ("Next Generation Sequencing" ou "NGS") permettant non seulement de déterminer de manière exhaustive la variabilité génétique de l'ADN mais également, à partir d'un type cellulaire donné ou un échantillon de fluides (plasma, sérum, urine), de quantifier précisément l'ensemble des isoformes d'un gène exprimé, de détecter et de quantifier l'ensemble des ARNs non codants, mais également de mesurer le degré de méthylation de l'ADN.L'objectif de cette présentation est de présenter les grandes stratégies de recherches actuelles basées sur les différentes technologies haut-débit dans le domaine des maladies cardiovasculaires. Une attention toute particulière sera portée aux besoins en biostatistique et en bioinformatique que requièrent l'application de ces nouvelles technologies à la recherche en génétique et épigénétique.

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The evolution of sexual dimorphism: Linking inter- and intra-sexual phenotypic and transcriptional variation

Males and females of most species share nearly the entire genome, and yet they use many of their shared genes in radically different ways. Differential expression between males and females is thought to be product of conflicting male- and female-specific selection over optimal transcription, and to form the underlying basis of sexual dimorphism in many species. If the relationship between sex-biased gene expression and sexually dimorphic phenotypes is true, then several simple predictions can be made. First, altering sex-specific selection should elicit a response in sex-biased gene expression, and this response should be more pronounced for genes linked to sex chromosomes. Second, although sexual dimorphism is often envisaged as a dichotomous comparison between female and male forms, many species show more of a continuum, with some individuals occupying intermediate points along an axis of dimorphism. In these cases, the magnitude of sex-biased expression should reflect the degree of sexual dimorphism. Third, the degree of sex-biased expression should accumulate over time in response to continuous sex-specific selection. Case studies using both comparative and experimental evolutionary frameworks will be presented to address these predictions.

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Génomique des tumeurs de la corticosurrénale

La génomique est un champ nouveau de la biologie, dont les techniques évoluent rapidement. Appliquées aux tumeurs de la surrénale, bénignes et malignes, ces approches permettent d'appréhender des aspects nouveaux de la physiopathologie de ces tumeurs, et de dériver des marqueurs diagnostiques et pronostiques.

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Evolution of evolvability under fluctuating selection

Empirical evidence suggests that fluctuating selection is a major evolutionary mechanism. The most straightforward consequence of rapid changes of the fitness function is the induced response of the mean phenotype in the population. Yet, repeated back-and-forth evolutionary trajectories are also suspected to affect the genetic architecture underlying the phenotypic characters subject to continuous adaptation. In order to better understand the long-term consequences of fluctuating selection, we modeled the response of complex, multilocus genetic architectures to various natural selection regimes — stabilizing, directional, and fluctuating. This model accounts for gene-gene interactions (through multilinear epistasis), and thus allows to investigate the dynamics of evolutionary potential at two distinct levels: (i) the standing genetic variation, i.e. the capacity for the population to respond immediately to directional selection, and (ii) the level of canalization (measured as the average effect of new mutations),which reflects the capacity for the population to replenish genetic variation. Both analytical results and individual-based simulations show that fast fluctuations (white noise change in the phenotypic optimum every generation) are essentially similar to stabilizing selection, promoting a degree of genetic canalization and low evolvability. In contrast, when large fluctuations of the phenotypic optimum (beyond the phenotypic range of the population) occur every 10 to 100 generations, equilibrium mutational effects and genetic variance are higher and the population is more evolvable. However, there was no evidence that decanalization and increased evolvability were adaptive, and fluctuating selection remains intrinsically more constraining than genetic drift.

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Identification of long non-coding RNAs (lncRNAs) in dogs using RNASeq

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Estimation of macroevolutionary rates from the fossil record

Understanding the processes of speciation and extinction is a major challenge in evolutionary biology and methodological advances have been improving our ability to infer the dynamics of species diversification from dated phylogenies of extant taxa and from the fossil record. The interpretation of diversity trajectories through time, however, goes beyond the estimation of rates of speciation and extinction, and may involve complex processes of niche filling, correlated trait evolution, and biotic interactions. Here I present a new Bayesian framework to analyze fossil occurrence data and jointly estimate times of origin and disappearance of taxa and rates of speciation and extinction. Speciation and extinction rates can vary through time and their temporal dynamics can be decoupled. Simulations show that model selection and parameter estimation are robust in the presence of incomplete taxon sampling. The statistical framework is extended to allow hypothesis testing with a particular focus on exploring the effect of diversity dependent processes, trait-correlated diversification, and competition among clades. The method is tested on fossil data sets of three mammal clades (the Rhinocerotidae, Ursidae, and Canidae) investigating different aspects of their Cenozoic diversification.

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Probabilistic approaches for detecting and locating whole genome duplications.

Whole Genome Duplications (WGDs) can be difficult to detect when they are old and when synteny has been disrupted by genome rearrangements. To test the presence of WGDs on a species phylogeny, I will present two methods which do not require synteny information and build strength from the phylogenetic framework. They rely on a probability model for the evolution of gene families on a species tree with WGDs. Both methods use multiple gene families across multiple species. One method relies on aligned molecular sequences and the other simply uses information on gene counts. We assessed their performance with simulations and on a benchmark yeast dataset, where we recover strong evidence for a well-established WGD and a low retention rate of duplicated genes after this WGD.

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Negotiation for resources in sibling barn owls: a model of animal communication dynamics

Animal conflict is usually seen as static, where each competitor has a definite underlying quality (i.e. condition, good genes) that determines its signal level. However, although many morphological signals are fixed during early development, some signals remain flexible through life (e.g. vocalisation, most behavioural traits). The level of signals of an individual can thus often fluctuate to avoid interferences, to adapt to both the presence of an audience or the resource holding potential and motivation of opponents. These fluctuations raise the question of how individuals decide at each moment their level of investment in signalling to claim a resource. Animals are indeed expected to constantly modulate their investment in a contest according to the payoff. Because of the inherent difficulty to study the temporal dynamics of communication between several individuals, how animals decide to enter or leave the contest and to what level invest in signalling has received mainly theoretical developments. Using the barn owl (Tyto alba) as a model species, I will present recent advances in the understanding of the role of cognition (individual recognition, memory) and social interactions in the dynamics of a communication process.

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The evolution of genetic architectures underlying quantitative traits (and its consequences)

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Evidence de sélection dans le génome humain: adaptation polygénique et fardeau d'expansion

Les populations humaines ont connu une expansion hors d'Afrique dans les 50,000 dernières années qui a certainement nécessité des adaptations au niveau génétiques, mais qui ont aussi pu avoir des conséquences sur leur fitness. Dans cette conférence, je présenterai nos travaux récents sur l'identification de sélection polygénique au niveau de voies métaboliques chez l'homme, ainsi que sur l'accumulation potentielle de mutations délétères lors d'expansions spatiales.

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Reconciliation-based detection of co-evolving gene families

Genes located in the same chromosome region share common evolutionary events more often than other genes (e.g. a segmental duplication of this region). Their evolution may also be related if they are involved in the same protein complex or biological process. Identifying co-evolving genes can thus shed light on ancestral genome structures and functional gene interactions.We devised a simple, fast and accurate probability method based on species tree-gene tree reconciliations to detect when two gene families have co-evolved. Our method observes the number and location of predicted macro-evolutionary events, and estimates the probability of having the observed number of common events by chance. Simulation studies confirm that our method effectively identifies co-evolving families. This opens numerous perspectives on genome-scale analysis where this method could be used to pinpoint co-evolving gene families and thus help to unravel ancestral genome arrangements or undocumented gene interactions.(Work in collaboration with Vincent Ranwez et Yao-ban Chan.)————————————————————-FRENCH————————————————————————-
Detection de co-évolution basée sur la réconciliation d'arbres phylogénétiquesEn comparaison avec des gènes situés sur des chromosomes distincts, les gènes situés dans une même région chromosomique prennent part à des évènements évolutifs communs (par exemple dans le cas d'une duplication en tandem de cette région). Leur évolution peut également être liée s'ils sont impliqués dans le même complexe de protéines ou dans le même processus biologique. Identifier des gènes qui ont co-évolué peut donc aider à mieux comprendre les structures génomiques ancestrales et les interactions fonctionnelles des gènes étudiés. Dans cette presentation nous allons decrire une méthode probabiliste basée sur la réconciliation d'arbres phylogénétiques: les macro-évènements évolutifs sont estimés avec une méthode de réconciliation; ensuite nous estimons la probabilité d'avoir le nombre d'évènements communs observés par hasard, faisant l'hypothèse forte que tous les macro-évènements évolutifs sont indépendants les uns des autres. Les simulations réalisées montrent que cette approche est prometteuse. Ce projet est issu de la collaboration avec Vincent Ranwez et Yao-ban Chan.

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Genome wide quantification of RNA transcripts

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