Fifth Journée Darwin

Institut Henri Poincaré

November 15, 2013

Amphithéâtre Hermite

Program

10:00 Welcome

10:15 **Eduardo Rocha**
Génomique évolutive des microbes - Institut Pasteur / CNRS

Horizontal transfer in genomes: massively parallel innovation impacting microbial social evolution.

11:15 *Coffee break*

11:30 **Christine Dillmann**
UMR Quantitative Genetics and Evolution - Le Moulon

The genotype-phenotype map and the response to selection: Insights from empirical biology

12:30 *Lunch break*

14:00 **Hélène Morlon**
CMAP, Ecole Polytechnique, Paris

Understanding biodiversity patterns using the Tree of Life

15:00 *Coffee break*

15:15 **Félix A. Rey**
Institut Pasteur / CNRS, Paris, France

Cell-cell fusion events in multicellular organisms and relations with enveloped viruses.

Abstracts

Horizontal transfer in genomes: massively parallel innovation impacting microbial social evolution.

Eduardo Rocha
Génomique évolutive des microbes - Institut Pasteur / CNRS

Evolutionary processes are typically described as the result of mutation, descent and selection. Many microbes lack sexual reproduction but have the ability to acquire genetic information from very distantly related organisms. Horizontal gene transfer allows the instantaneous acquisition of new complex adaptive traits and their transmission to subsequent generations. This speeds up evolutionary processes as exemplified by the acquisition of virulence traits in emerging infectious agents and by antibiotic resistance in most human bacterial pathogens. In bacteria, horizontal gene transfer is much more frequent than gene duplication and affects different types of functions. This shapes the population genetics of bacteria and blurs species' definitions. Rapid spread of genes encoding social traits also has the potential to drive social interactions in bacterial communities. Hence, horizontal gene transfer drives the evolution of bacterial cells and bacterial communities in many ways.

The genotype-phenotype map and the response to selection: Insights from empirical biology

Christine DIllmann, Delphine Sicard
team Fundamental Quantitative Genetics UMR Quantitative Genetics and Evolution - Le Moulon

Our research aim at modelling the link between genetic polymorphism and phenotypic diversity to better understant how populations can adapt to environmental changes. Adaptation defined as the increase of the average fitness of the population in response to environmental changes is accompanied by phenotypic changes on life-history traits that can be either plastic, genetic or epigenetic. Two examples of experimental evolution conducted in the lab will be presented to illustrate our approaches. In nature, the yeast S. cerevisiae show a variety of life-history strategies. Using an experimental evolution experiment starting from different strains evolved under different selection regimes, we show examples of phenotypic convergence, and the maintenance of trade-offs between life-history traits that can be interpreted as adaptive constraints. In maize, a divergent selection experiment for flowering time is conducted for 16 generation in field conditions. Starting from an inbred line, Late and Early populations have diverged, with a range of variation that now covers the range of variation of cultivated maize under temperate climate. Despite a constant response to selection, only a handfull of polymorphisms have been identified. Results can be interpreted as a case of missing heritability.

Understanding biodiversity patterns using the Tree of Life

Hélène Morlon
CMAP, Ecole Polytechnique, Paris

Species richness results from past and current speciation, extinction and dispersal events, themselves influenced by various ecological and evolutionary processes. Estimating rates of diversification, and understanding how and why they vary over evolutionary time, geographical space, and species groups, is thus key to understanding how ecological and evolutionary processes generate biological diversity. Phylogenetic approaches are critical for making such inferences, especially in groups or regions lacking fossil data. I will illustrate how phylogenies, coupled with models of cladogenesis, can be used to test the role of ecological limits, boom-then-bust diversity dynamics, the paleoenvironment, and population dynamics on the biodiversity patterns that we observe today.

Cell-cell fusion events in multicellular organisms and relations with enveloped viruses.

Félix A. Rey
Institut Pasteur / CNRS, Paris, France

Enveloped viruses can be classified in two main categories, regular and irregular. The regular viruses are such that each virus particle has the same number of surface glycoproteins arranged with icosahedral symmetry. In contrast, iirregular viruses have different number of glycoproteins, with no symmetric organization of the particle surface. In both cases, the envelope glycoproteins are responsible for interaction with the target cell for entry, via a glycoprotein-catalyzed membrane fusion reaction. This process results in the viral genome deposited into the cytoplasm of the target cell, which becomes infected. The fusion proteins of regular viruses such as flaviviruses, alphaviruses and phleboviruses – which all happen to be arthropod-borne - have been shown to have homologous envelope proteins, displaying the same fold in spite of the lack of sequence conservation. We have recently identified that the rubella virus fusion protein is also related, displaying the same fold but with important variations, although the virus particles appear pleomorphic and lack icosahedral symmetry. This indicates that in this case, the protein has undergone divergent evolution from a distal, ancestral gene, which may have evolved from a putative symmetric virus. Strikingly, we have now discovered that the cellular fusion protein EFF-1, involved in syncytium formation during the genesis of the skin in nematodes (C. elegans) and in other multicellular organisms, also displays the same 3D fold, thereby indicating common ancestry, highlighting an unprecedented amount of exchange of genetic information between viruses and cells. My talk will discuss the implications of this finding, which highlights the intricate exchange of genetic information that has taken place between viruses and cells during evolution. This analysis also suggests a mechanism for the homotypic cell-cell fusion process