

Antonio Hernandez Lopez (EBM-LATP)

To tree or not to tree : quantifying horizontal gene transfer in Rickettsia bacteria

Résumé

There is broad general agreement now that horizontal gene transfer (HGT) is a major force in the evolution of prokaryotes. Within-species genome comparisons show 5-30% variation in gene content that is attributable to this process. During the adaptation of a bacterial population to a new ecological niche, and particularly for intra-cellular bacteria, selective pressures are shifted, resulting in a lower rate of genetic connectivity. Recombination and positive selection are therefore two important evolutionary forces in microbial pathogens that drive adaptation to new hosts or resistance to the action of antibiotics. Within the Rickettsiales, some species have highly stable genomes with virtually no repeats or mobile elements, while others have an extraordinarily high proportion of repeated sequences and conjugative elements. In this study, we investigate to what extent HGT has occurred in the intracellular Rickettsia bacteria, the effect of the use of different genomic regions in estimating reticulate evolution and potential HGT events, and the link of these to ecological adaptation (host specialization). We found that different genomic regions have different impact on both tree and non-tree based estimations of HGT through recombination, with information being lost when only core proteome is used. There is however a correspondence on the species for the different genomic regions used, with more generalist species having more HGT-recombination events. Finally, factors other than specialization must influence the amount of HGT, as not all species found to have large HGT-recombination events are generalists.