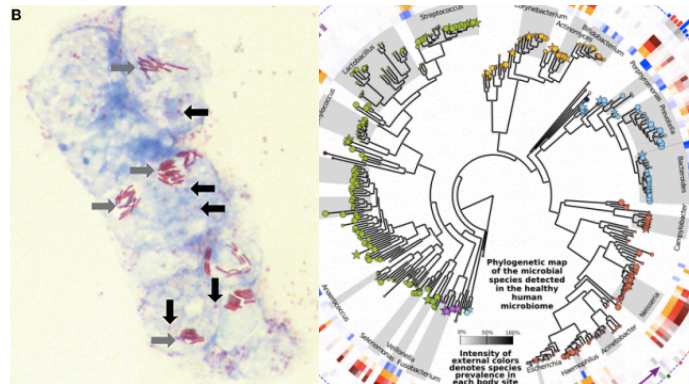


Unveiling the hidden diversity of *Legionellales* insect symbionts by metagenome mining



The gammaproteobacterial order *Legionellales* is an outstanding model to study host-adaptation. It harbors a quite wide ecological diversity, including *Legionella* and *Coxiella*, two human pathogens, but also independent lineages of endosymbionts: for example, *Rickettsiella* include an endosymbiont of pea aphids that can modify insect color. However, we know (almost) only what we can grow, and since host-adapted, intracellular bacteria are by definition hard to grow, the vast majority of the order is very probably yet to be discovered. To discover new forms of host-bacterium interaction, cutting-edge metagenomics and binning methods will be used to identify and reconstruct novel organisms from new and published metagenomes. In particular, insect symbionts are of interest, because they appear to have evolved several times, with fast tempo.

Goal

- Embrace and analyze the diversity of *Legionellales* species, with a special focus on insect symbionts.
- Identify hot spots where *Legionellales* diversity and abundance is high.
- Reconstruct novel, full genomes from existing metagenomes.
- Include the newly identified insect symbionts in the analysis of the order.

Data provided

New metagenomes from current sampling campaigns. Data published on major databases, with a specific focus on JGI (IMG/MER).

Methods

Next-generation sequencing, database mining, phylogenetics, metagenomics, metagenomic binning, phylogenomics.

Requirements

Curiosity, and wits indispensable. Skills in **bioinformatics and programming** necessary. Knowledge of **molecular evolution** highly desired.

Useful information

- Start date: as soon as agreed upon.
- Contact: Lionel Guy, IMBIM, lionel.guy@imbim.uu.se, 018-471 4366.