



Managing microbial communities for sequentially reconstruct genomes from complex metagenomes

Tom O. Delmont, Timothy M. Vogel, and Pascal Simonet

Equipe «Génomique Microbienne Environnementale» (Environ. Microb. Genom. Group) UMR CNRS 5005, Laboratoire Ampère, Ecole Centrale de Lyon, 36 avenue Guy de Collongue, 69134 Ecully Cedex, France

Global understanding on environmental microbial communities is currently limited by the bottleneck of genome reconstruction. Soil is a typical example where individual cells are currently mostly uncultured and metagenomic datasets unassembled. In this study, the microbial community composition of a natural grassland soil was managed under several controlled selective pressures to experiment a “multi-evenness” stratagem for sequentially attempt to reconstruct genomes from a complex metagenome. While lowly represented in the natural community, several newly dominant genomes (an enrichment attaining 105 in some cases) were successfully reconstructed under various “harsh” tested conditions. These genomes belong to several genera including (but not restricted to) *Leifsonia*, *Rhodanobacter*, *Bacillus*, *Ktedonobacter*, *Xanthomonas*, *Streptomyces* and *Burkholderia*. So far, from 10 to 78% of generated metagenomic datasets were reconstructed, so providing access to more than 88 000 genes of known or unknown functions and to their genetic environment. Adaptative genes directly related to selective pressures were found, mostly in large plasmids. Functions of potential industrial interest (e.g., novel polyketide synthase modules in *Streptomyces*) were also discovered. Furthermore, an important phage infection snapshot (>1500X of coverage for the most represented phage) was observed among the *Streptomyces* population (three distinct genomes reconstructed) of a particular enrichment (mercury, 0.02g/kg) during the fourth month of incubation. This “divide and conquer” strategy could be applied to other environments and using auxiliary sequencing approaches like single cell to detect, connect and mine taxa and functions of interest while creating an extensive set of reference genomes from across the planet. Next limit could turn out to become our imagination defining novel selective pressures to sequentially make dominant the 1030 cells of the biosphere.