

Microdiversification in genome-streamlined ubiquitous freshwater Actinobacteria

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Actinobacteria of the *acl* lineage are the most abundant microbes in freshwater systems, but there are so far no pure cultures of these organisms, possibly due to metabolic dependencies on other microbes. This, in turn, has hampered an in-depth assessment of the genomic basis for their success in the environment. In my talk, I will present genomes from the first 16 axenic cultures of *acl* Actinobacteria. The isolates were not only of minute cell size, but also amongst the most streamlined free-living microbes, with extremely small genome sizes (1.2-1.4 Mbp) and low genomic GC content. Genome reduction in these bacteria has led to auxotrophy for various vitamins, amino acids, and reduced sulphur sources, thus lending support to the predictions of the 'Black Queen' hypothesis. Genome analysis, moreover, revealed a surprising degree of inter- and intraspecific diversity in metabolic pathways, especially of carbohydrate transport and metabolism, and mainly encoded in genomic islands. The striking genotype microdiversification of *acl* Actinobacteria might explain their global success in highly dynamic freshwater environments with complex seasonal patterns of allochthonous and autochthonous carbon sources. We propose a new order within Actinobacteria ('*Candidatus* Nanopelagiales') with two new genera ('*Candidatus* Nanopelagicus' and '*Candidatus* Planktophila') and nine new species.