Modeling in the cold: genome-scale prediction of metabolic fluxes in the Antarctic bacterium *Pseudoalteromonas haloplanktis* TAC125

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Understanding how the genetic potential of a microbe translates into its phenotype is a fundamental challenge in biology. Genome sequence information alone falls short in providing a dynamic and functional perspective on the real working scheme of a cell. Computational methods, such as constraint-based metabolic modeling (CBMM), are often used to bridge this knowledge gap. CBMM consists in the use of a mathematical representation of metabolism to perform genome-scale simulations and predict metabolic features at the cell level. This approach is rapidly expanding, as it combines reliable predictive abilities with conceptually simple frameworks. Among the possible outcomes of CBMM, the capability to i) guide a focused planning of metabolic engineering experiments and ii) provide a systems level understanding of (single or community-level) microbial metabolic circuits also represent primary aims in present-day microbiology. We will briefly introduce the theoretical formulation behind CBMM and then review the most recent and effective study-cases in microbes and microbial communities and, in particular, in the Antarctic bacterium *Pseudoalteromonas haloplanktis* TAC125. These will include the use of CBMM for simulating growth in a nutritionally complex environment and the integration of gene expression data for generating of context-specific metabolic reconstruction. Also, emerging challenges and possibilities in the use of such methodologies in microbiology/biotechnology will be discussed.