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Metabolism and evolution: A comparative study of reconstructed genome-level metabolic networks[1]

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The availability of high-quality annotations of sequenced genomes has made it possible to generate organism-specific comprehensive maps of cellular metabolism. Currently, more than twenty such metabolic reconstructions are publicly available, with the majority focused on bacteria. A typical metabolic reconstruction for a bacterium results in a complex network containing hundreds of metabolites (nodes) and reactions (links), while some even contain more than a thousand. The constrain-based optimization approach of flux-balance analysis (FBA) is used to investigate the functional characteristics of such large-scale metabolic networks, making it possible to estimate an organism's growth behavior in a wide variety of nutrient environments, as well as its robustness to gene loss. We have recently completed the genome-level metabolic reconstruction of *Yersinia pseudotuberculosis*, as well as the three *Yersinia pestis* biovars *Antiqua*, *Mediaevalis*, and *Orientalis*. While *Y. pseudotuberculosis* typically only causes fever and abdominal pain that can mimic appendicitis, the evolutionary closely related *Y. pestis* strains are the aetiological agents of the bubonic plague. In this presentation, I will discuss our results and conclusions from a comparative study on the evolution of metabolic function in the four *Yersiniae* networks using FBA and related techniques, and I will give particular focus to the interplay between metabolic network topology and evolutionary flexibility.

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