Abstract:

Metabolic network reconstruction of the pathogen *Enterococcus faecalis*.

Enterococcus faecalis is a Gram-positive bacterium with a low G_C content in its genomic DNA. This natural inhabitant of the gastrointestinal mammalian tract is also an opportunist pathogen responsible for urinary tract infections, nosocomial infections, bacteremia and infective endocarditis. *E. faecalis* normally grows as a commensal organism in the gut, but it possesses very subtle virulence traits that are not easily identified. Besides, its intrinsic physiologic properties such as inherent antibiotic resistance and exceptional ability to adapt to harsh conditions provide this organism with an enormous advantage in the infection processes. Recognizing the medical importance of this bacterium, The Institute for Genomic Research has undertaken the genome sequencing of *E. faecalis* strain V583 and based on that, the first genome-scale metabolic model of *E.faecalis* will be reconstructed.

To support the reconstruction, high throughput techniques, generally referred to as "omics techniques" (genomics, proteomics, fluxomics, metabolomics and transcriptomics) will provide data of different levels to validate, test and sustain the robustness of the model. The different levels of data will comprise genome, metabolite, protein and flux profiles.

The first metabolic model generated for this bacterium will allow correlating metabolite levels and fluxes which enables identification of key control points in its metabolism.

As it has been previously shown for other organisms, the metabolic network reconstruction may serve as a valuable tool to predict the phenotypic behaviour under various genetic and environmental conditions.