

Super model of the world – *Enterococcus faecalis*

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Enterococcus faecalis is a Gram-positive bacterium from the lactic acid group (figure 1). This natural inhabitant of the mammalian gastrointestinal tract is also an opportunist pathogen responsible for urinary tract infections, nosocomial infections, bacteremia and infective endocarditis [1]. *E. faecalis* normally grows as a commensal organism in the human gut, but it possesses very subtle virulence traits that are not easily identified. Additionally, its intrinsic physiological properties such as inherent antibiotic resistance and exceptional ability to adapt to harsh conditions, provides this organism with an enormous advantage in the infection processes.

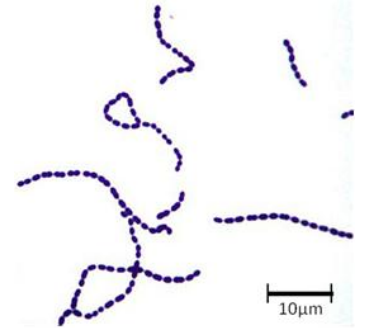


Figure 1: Gram stain of *Enterococcus faecalis*.

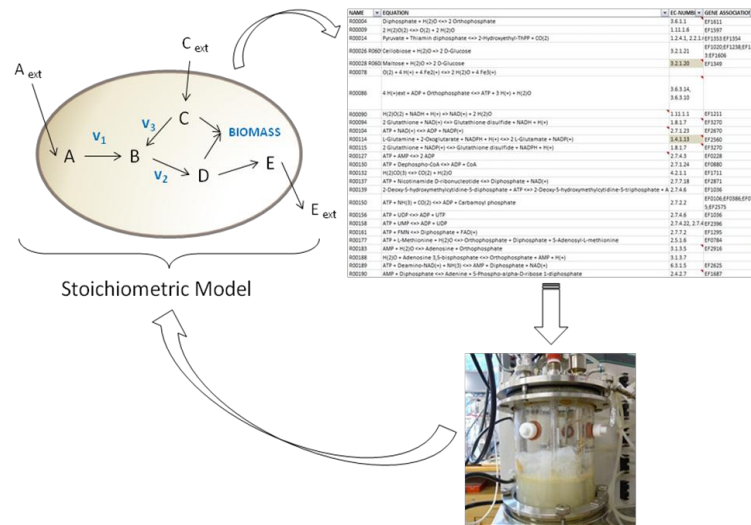


Figure 2: Genome scale metabolic reconstruction of *Enterococcus faecalis*.

(genomics, proteomics, fluxomics, metabolomics and transcriptomics) provided data to validate, test and sustain the robustness of the model. The first metabolic model generated for this bacterium allows correlating metabolite levels and fluxes and better understanding the 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 of the microbe under various genetic and environmental conditions. With so many capabilities and strengths, *Enterococcus faecalis* is a good candidate to be the next super model of the bacterial world?

[1] Paulsen, I. T., Banerjee, L., Myers, G. S. A., et al. Role of Mobile DNA in the Evolution of Vancomycin-Resistant *Enterococcus faecalis*. s.l. : American Association for the Advancement of Science, 12 de February de 2003, Science.

[2] Palsson, Bernhard O., and Edwards, Jeremy S. Systems Properties of the Haemophilus influenzae Rd. 18 June 1999.

[3] Rocha, I., Förster, J., and Nielsen, J. Design and Application of Genome-Scale Reconstructed: Protocols and Bioinformatics (A.L. Osterman, Gerdes, S., Eds.). In series: Methods in Molecular Biology, Vol. 416, Ch. 29, 409-431, Humana Press 2008 .

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