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Analysis of *Salmonella typhimurium* pathways and metabolic model improvement

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Live attenuated strains of *Salmonella typhimurium* have been extensively investigated as vaccines for several infectious diseases. However, a better knowledge of *S. typhimurium* metabolism is required to develop protocols to improve bioprocesses for the production of biotechnological products in large scale. Currently, genome scale metabolic models are important tools for better understanding the phenotypic behavior of many microorganisms. In this work, a genome-scale metabolic model reconstructed for *S. typhimurium* (STMv1.0 model) was used to determine the *in silico* fluxes distributions of end-products and to compare with *in vivo* data. Experimental data from glucose-limited chemostat at different dilution rates (0.1 to 0.67 h^{-1}) with *S. typhiumurium* LT2 were compared with *in silico* simulations performed with Optflux 3.2.4 software, using the same environmental conditions (glucose and O2 experimental uptake fluxes). *Salmonella* cultures showed deviation of carbon towards acetate formation, starting at dilution rate above 0.1 h^{-1}, with flux of 4.16 mmol acetate/(gDCW . h) at the higher dilution rate. Nevertheless, this model, which was based on *E. coli* model, overestimates the biomass production and, consequently, minimizes the fluxes of acetate. Thus, changes in metabolic model are required to improve its accuracy to predict the fermentation patterns observed experimentally, including changes in model equations related to P/O ratio and ATP yield. ^{13}C Fluxomic analysis are being carried out to better understand the *S. typhimurium* central carbon metabolism and to improve the model predictions.

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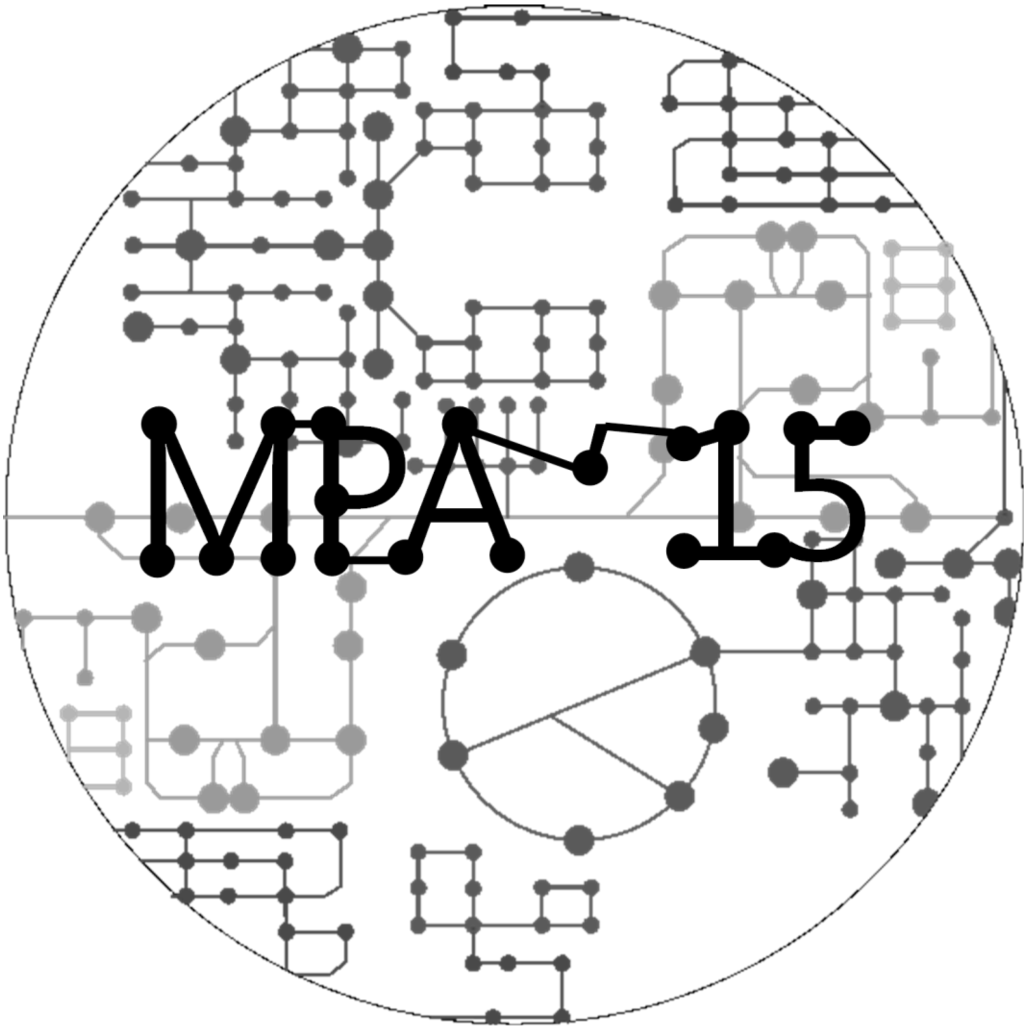

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