Reconstruction and validation of a genome-scale metabolic model for *Helicobacter pylori* 26695

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Helicobacter pylori 26695, a highly pathogenic bacterium, is a human gastric epithelia colonizer, correlated with the development of duodenal and gastric ulcers, and gastric cancer worldwide. Its genome has been previously sequenced and annotated, and two genome-scale metabolic models have been developed; however, since their publication, vast amounts of data and new methodologies have been developed. In order to maintain accurate and relevant the information on this bacterium, and to generate new information and new approaches for its analysis, the assignment of new functions to *H. pylori* 26695's genes was performed and a new genome-scale metabolic model was reconstructed.

This work originated the *i*TR383 metabolic model, a compartmentalized model containing 383 genes and composed by 640 different reactions and 412 metabolites.

Gene essentiality analysis and growth simulations were performed using experimental data and nutrient uptake rates to assess the predictive capabilities of the model. Metabolite and flux distribution in the central carbon metabolism pathway using different carbon sources were analyzed, as

well as pathways for non-essential amino acids biosynthesis, the nitric oxide influx effect, and electron transport and respiratory chain.

This model accurately predicts *H. pylori*'s phenotypic response to different carbon sources and is in agreement with experimental results obtained in minimal and complex media. We believe that this work represents a significant advance in understanding *H. pylori* 26695's metabolism and will provide relevant biological information to the scientific community working on new approaches for enhanced treatments.