Abstract no.: P08.01

Comparison of *H. pylori in silico* metabolic model predictions with experimental data

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The Systems Biology approach has been replacing the reductionist view that dominated biology research in the last decades. Present biochemical knowledge and genomic databases allowed the development of metabolic models for several organisms, which, however, are still incomplete. The availability of the genome sequence of *H. pylori* has allowed the construction of a genome-scale metabolic model for this organism. The purposes of this work were to study the growth of *H. pylori* in a chemically defined medium, to compare the experimental data obtained with the simulated data supplied by the model and analyse the composition of the *in silico* media used.

Cultures were grown at 37ºC under microaerophilic conditions in Ham´s F-12 medium supplemented with fetal bovine serum. Optical density and the counting of CFU/mL were performed for assessing the growth. OptFlux, a software platform for metabolic engineering, which includes several tools such as flux balance analysis (FBA) was employed for simulate the behavior of wild type *H. pylori* under the conditions used *in vivo*.

The simultaneous use of both approaches allows to correct the *in silico* model, and on the other hand, to rationally adjust the medium components present in F-12. For instance pimelate, that has been considered to be essential in the latest metabolic model, is lacking in F-12 and is likely to be redundant in the model.

Our future work is not only to improve the genome-scale metabolic model, but also, identify potential targets for design more effective drugs for the inactivation of *H. pylori.*