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Uncovering the metabolic capacities of *H. pylori* 26695 using ^{13}C labeling experiments

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The determination of nutritional requirements of pathogenic organisms is of great significance for understanding host-pathogen interactions. Despite the knowledge obtained so far concerning amino acid requirements in *H. pylori*, it is still unclear which are the metabolic pathways used for biosynthesis and catabolism. Thus, information on the carbon flow in this organism is required. Glutamate is a very important metabolite in bacterial metabolism that can be used as a carbon and nitrogen source. ^{13}C flux analysis has been largely applied to characterize phenotypes by quantifying *in vivo* the carbon fluxes. One of the most important applications of this approach is the identification of active pathways in less-studied organisms. Thus, in order to clarify the metabolic pathways used by *H. pylori* 26695, ^{13}C labeling experiments with ^{13}C-glutamate were conducted and labeled amino acids in biomass hydrolysates were analyzed by GC-MS. The obtained results confirmed L-glutamate as a potential sole and effective carbon source for *H. pylori*. Overall, all non-essential amino acids, except proline, presented a ^{13}C labeling pattern. We hypothesized that L-proline is produced from L-arginine, while L-alanine is probably produced from pyruvate by alanine dehydrogenase. Additionally, the full usage of complete TCA cycle, under the conditions used, was also demonstrated.