

Research field:

Biochemistry / Life Sciences

Genomics, proteomics / Life Sciences

Title:

Exploration of sulfur métabolism in Acinetobacter baylyi ADP1

Abstract:

Sulfur, one of life's essential atoms, is crucial in cell chemistry. It is found in two amino acids -methionine and cysteine- and in several metabolites and cofactors. Methionine biosynthesis is carried out from aspartate through the formation of homoserine and homocysteine, the immediate methionine precursor. From homoserine, two routes can lead to the biosynthesis of methionine: (1) the ?transsulfuration pathway? where inorganic sulfur, first incorporated into cysteine is afterwards found in cystathionine and homocysteine, and (2) the ?direct sulfhydrylation pathway? where inorganic sulfur is directly incorporated into homocysteine. Both routes can be found together in fungi and higher plants but rarely coexist in bacteria.

The soil bacterium Acinetobacter baylyi ADP1 is used as a ?model? organism in our laboratory to investigate and revisit metabolic knowledge (de Berardinis et al., Curr Opin Microbiol. 12:568-76 (2009)). We have sequenced and annotated its genome with particular attention to genes involved in metabolism (Barbe et al., Nucleic Acids Res. 32:5766-79 (2004)). To extend our knowledge of metabolism in this organism we have constructed a pangenomic collection of 2600 deletion mutants (de Berardinis, et al., Molecular Systems Biology 4:174 (2008)).

According to its genome annotation, both methionine biosynthetic pathways exist within this organism. Nevertheless, the phenotyping on various carbon and sulfur sources of our collection of mutants revealed unexpected results which may contest the validity of annotation-based knowledge of sulfur metabolism, and in particular an unpredicted pathway for the recycling of methionine. First, the function of the annotated genes will be biochemically validated since most of the genes involved in this pathway have similar sequences that may lead to improper annotation. Moreover, the genes involved in the recycling of methionine will have to be identified and their function experimentally established.

Our projects are based on a multidisciplinary combination of different methodologies including comparative genomics, high-throughput growth phenotyping, molecular biology and biochemistry (enzymology and high resolution mass spectrometry).

Location:

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Genoscope - Centre national de séquençage

Laboratoire de génomique et biochimie du métabolisme

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