

Research field:

Biochemistry / Life Sciences

Genomics, proteomics / Life Sciences

Title:Identification of gene function by high resolution mass spectrometry in the bacterium *Acinetobacter baylyi* ADP1**Abstract:**

We study metabolism using a "model" organism, the soil bacterium, *Acinetobacter baylyi* ADP1. We have sequenced and annotated its genome with particular attention to genes involved in metabolism (Barbe et al., *Nucleic Acids Research* 32, p 5766 (2004)). Of about 3300 genes annotated, more than 400 encode putative enzymes for which the function is unknown. 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)).

We now wish to develop metabolomics as a tool for functional genomics to elucidate gene functions. The term metabolome refers to the complete set of metabolites synthesized by the cell according to its metabolism, and can be considered as the final product of both gene expression and cellular regulation. To determine gene function, we aim to understand how the deletion of a given gene can impact the metabolite composition of the cell. The goal is to compare the metabolic profiles of mutants for genes encoding enzymes of unknown function (acquired through high resolution mass spectrometry), which will, in favourable cases, make it possible to link the deletion of a gene to changes in a small number of metabolites which will have to be identified. These correlations will be then combined with biochemical approaches to experimentally specify the function of these genes. This project will be developed within the metabolomics team of Genoscope.

Location:

Institut de Génomique

Genoscope - Centre national de séquençage

Laboratoire de génomique et biochimie du métabolisme

Starting date: 01/10/2010

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More about:<http://www.genoscope.cns.fr/spip/Thesaurus-metabolique.html>**University/Graduate School:**

Evry Val d'Essonne

Des Génomes aux Organismes - Evry -

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