

## Genome-scale regulation of protein levels and microbial physiology

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An in-depth understanding of proteome regulation during microorganism adaptation to changing environment can be achieved via a vertical integrative approach of genome-scale (experimentally acquired and mathematically determined) biological data. Here, I will present systemic regulation of protein levels in connection with the bacterial physiology.

First I will focus on the comparison of proteomic and transcriptomic data and their statistical integration through normalization and correlation studies. Protein concentrations correlated weakly to transcript concentrations, several other factors were thus assumed to be involved in protein determination. By statistical modeling of *Lactococcus lactis*, the model lactic acid bacterium, both intrinsic and environmental-specific determinants of protein concentrations were identified. Furthermore, the influence of systemic translation regulation on proteome was explored. For the first time in a bacterium, the profound translational status (translatome) of all mRNAs present in the cell was determined. A high diversity of translational states allowing individual gene differentiation was experimentally demonstrated highlighting the importance of translation-level regulations in protein concentration. Lastly I will introduce the idea that degradation of both mRNA and protein can vary as a function of environmental constraints and can thus also be involved in the control of protein concentrations in bacterial cells.

In light of the results presented here, it will be clear that a full picture of protein level control in bacteria will only be obtained through a multiple-level analysis of the cell response.

### Biography

Laurence Girbal received a Ph.D. in Microbiology in 1994 in Toulouse, France. Following a post-doctorate at the University of Groningen, The Netherlands, she joined in 1998 the French National Centre for Scientific Research. Her research field is the study of Bacterial Physiology and Metabolism. During ten years, she studied electron and carbon flow regulation in bacteria to optimize biofuel productions. In 2008, she joined the group of Muriel Cocaign-Bousquet to study genome-scale regulation of bacterial physiology. In this context, Dr Girbal focused her work on the analysis of translation regulation and its integration in the multi-stage regulation of protein expression.

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