Bringing to light the dialogue between bacteria and prophages: AppY, a phage-encoded protein central to the bacterial regulatory network?

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Résumé

Bacterial genomes are extremely diverse. Part of this diversity is due to temperate bacterial viruses that can integrate into and maintain themselves in the host genome; once integrated, they become prophages. In bacteria, although most of the prophage genes are silent, some of them are expressed and give new properties to bacteria such as stress adaptation and virulence factors.
Recently, it has been shown in a genetic screen that the overproduction of AppY, a poorly studied transcriptional regulator encoded by the DLP12 prophage in *Escherichia coli* K12, leads to RpoS increase in the cell (Bougdour *et al.*, 2008). RpoS is the major sigma factor during stationary phase and under many stress conditions in γ-proteobacteria. This factor controls the expression of more than 500 genes in *E. coli* and is itself highly regulated, in particular *via* changes in protein stability. Indeed, once produced, RpoS is actively degraded by the ClpXP protease. To be recognized as a protease substrate, RpoS interacts with an adaptor protein called RssB, which brings RpoS to the degradation machinery. My recent results suggest that AppY stabilize RpoS through a direct interaction with the RssB adaptor protein, an interaction that I intent to characterize precisely.

Moreover, it has been suggested that AppY could regulate around 30 genes in the cell (Atlung *et al.*, 1989). In order to identify these potential AppY targets, we have performed RNA-seq experiments. Our results suggest a broader role for AppY in the bacterial physiology than previously anticipated. Overall, the objective of my research is to bring to light the regulatory pathways existing between genes from bacterial and phage origins and determine how these regulations contribute to bacterial physiology and adaptation to different stress conditions.

- Bougdour et al., 2008. *Mol. Microbiol.* 68(2):298-313.
- Atlung *et al.*, 1989. *J. Bacteriol.* 171(3) : 1683-1691

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