Postdoctoral position – mRNA decay in *Bacillus subtilis* and *Synechocystis*

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RNA sequence features that govern initiation of mRNA decay in *B. subtilis* and *Synechocystis*

The instability of mRNA is crucial to the control of bacterial gene expression. Initiation of mRNA decay in prokaryotes is predominantly mediated by endoribonucleolytic cleavage in the body of the mRNA. Probably the major parameter that determines when and where the initial cleavage takes place is the efficiency of translation of a given mRNA. This quality control thus links the life span of an mRNA to its usefulness. we want to determine with high precision the position of endonucleolytic cleavages within mRNA molecules on a global scale, in the firmicute *B. subtilis* and the cyanobacteria *Synechocystis.* In a second step, we want to analyse a possible link that likely exists between cleavage at a certain position in the mRNA and the translation efficiency immediately upstream of the cleavage site. The experimental approach is based on a genome-wide identification of RNA 5' ends using the EMOTE technique (Exact Mapping Of Transcriptome Ends; Redder, 2015; Kirkpatrick et al. 2016). Variations of this method that is based on the conditional ligation of an oligonucleotide to RNA 5' ends allow to identify 5' tri-, mono- or non-phosphorylated 5' ends. This is necessary to distinguish native 5' ends (5'-PPP) from cleavage products (5'-P or 5'- OH).

The transcriptomic data providing the genome-wide cleavage positions will then be analyzed with respect to their localization within an open reading frame. Statistical analyses will look at codon overrepresentation in the vicinity of the cleavage site. A second analysis will take into account the local folding energy of the mRNA. Recently, analyses of a protein expression dataset using multi-parameter logistic-regression modeling made it possible to predict with high accuracy the influence of codon identity on the translation efficiency in *E. coli* (Boël *et al*., 2016). New developments of this method have shown that codon influence can be predicted also from transcriptomic or proteomic data that are available for both *B. subtilis* and *Synechocystis.* The bioinformatic analysis as well as the work on *Synechocystis* will be carried out in close collaboration with the group of Grégory Boël (UMR8261) who has already begun to apply the new algorithms to *B. subtilis* and the cyanobacterial analysis will follow. By the time the transcriptomic data have been obtained, we will thus be able to make meaningful comparisons between the two organisms.

General predictions will then be validated by the study of individual examples through the introduction of mutations that take into account the codon context and RNA secondary structure.

We believe that in order to understand the fundamental aspects of bacterial mRNA metabolism that might be evolutionarily conserved, it will be important to start working with organisms like cyanobacteria that are distant to both *E. coli* and *B. subtilis* but at the same time amenable to basic genetic manipulation.

The postdoc position is for **2 years** fulltime (one year followed by one year renewal) with salary according to standard CNRS remuneration. The salary includes pension benefits and health insurance.

The **start date is May-November 2017**.

Desired skills and experience

The ideal candidate should be familiar with bacterial genetic and molecular biology. Expertise in RNA biochemistry and bioinformatics analyses is a plus.

How to apply:

To apply, send a **CV** with a statement of **research interests** and **contact details** for at least **2 references** directly to Harald PUTZER (putzer@ibpc.fr).

International candidates are encouraged to apply.

Deadline for application is the **27th of February 2017**.