**Regulation of cell differentiation in mycobacteria**

   Bacteria are found in different environments and during evolution they have adapted to handle exposure to various growth conditions. *Mycobacterium* spp. belongs to the phylum Actinomycetes and among these *M. tuberculosis* is the causative agent of tuberculosis. The mycobacterial cell shape varies and it can change dependent on environmental conditions and as other bacteria they form biofilms and some have been shown to form spores. Like other bacteria mycobacteria are equipped with an arsenal of proteins/ factors that ensure survival under different growth and stress conditions. The sigma factor (σ) is required for promoter recognition and transcription initiation and mycobacteria has several σ-factors. Dependent on growth conditions and exposure to various stressors different σ-factors are activated/ expressed in order to ensure that proteins/ factors are produced that enables the bacteria to survive. The σ-factors have also been demonstrated to play important roles during cell differentiation in a number of different bacteria such as *Bacillus subtilis* and *Streptomyces coelicolor*.
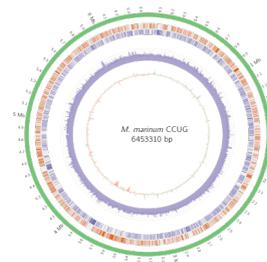
   Small non-coding RNAs (sRNAs) is another class of regulators of gene expression in bacteria. For example, in *Escherichia coli* several sRNAs have been shown to be involved in the regulation of the expression of the stationary phase σ-factor, σ^S (RpoS) while 6S RNA binds to the house keeping σ-factor and interferes with its activity. Several sRNAs including an sRNA that binds to RNA polymerase have been identified in mycobacteria however our understanding of their function is limited. We are interested in to identify and to understand sRNA function and role in mycobacteria with specific focus on the interconnection between sRNAs, σ-factors and cell differentiation. The aim of this project is to identify sRNAs with a role in cell differentiation in the *M. tuberculosis* model system *Mycobacterium marinum*.

   We have access to the *M. marinum* complete genome and complete/ draft genome sequences for a number of different mycobacteria and mycobacterial strains. In addition, our database include transcriptome data for several mycobacteria grown under different conditions, including various stress conditions, enabling us to extract information about the expression profiles of candidate sRNAs and to make comprehensive and evolutionary comparisons. The project will include both an experimental and a bioinformatics part and build on collaborations within the research team.

   The project will include participation in: i) the outline of *in silico* and wet experiments and choice of methods, ii) cloning and generation of DNA libraries, iii) microbiological techniques in connection working with *M. marinum*, iv) analysis of data and design of new experiments on the basis of the results, iii) discussion of the data in the format of research group discussion, as well as daily discussions, iv) presentation of the project and results in a group seminar setting and vi) writing a research report. In addition, it will be compulsory to participate in group-meetings where other currently running projects in the Molecular Biology program will be discussed.
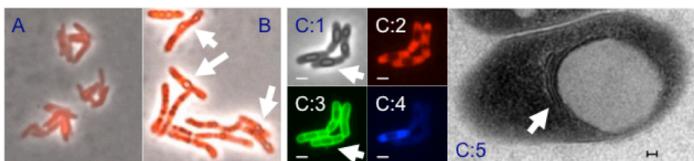
Changes in cell morphology – *M. marinum* CCUG^T

The *M. marinum* CCUG^T genome