Genetic tool for identification proteins regulating supercoiling- sensitive promoter of gene encoding topoisomerase I from *Streptomyces coelicolor.*

In most bacteria species chromosome consists of the single DNA molecule. Its length is relatively large: in *Escherichia coli* it is 1 cm long, whereas cell size is 1000 times smaller. For that reason DNA molecule needs to be highly condensed to fit the small cell volume. The most important in the DNA compaction is DNA supercoiling, which is additional twisting of double-stranded DNA around itself. Bacteria possess special enzymes, called topoisomerases, which control DNA supercoiling in the cell. Among them there are enzymes which relax DNA and the ones which condense DNA by adding extra supercoils. DNA supercoiling is also changed in response to environmental factors such as elevated temperature, pH changes and nutrient depletion. Interestingly, chromosome supercoiling affects global gene expression.

We investigate bacteria from the genus *Streptomyces*. These organisms produce broad range of industrially useful compounds, including most of currently used antibiotics. As DNA topology can be considered as a global gene expression regulator, it is pivotal to understand how chromosome supercoiling changes can regulate expression of many genes, including those engaged in secondary metabolism.

Proposed project concerns TopA- the topoisomerase from *Streptomyces coelicolor*, model species for *Streptomyces* studies. TopA mediated chromosome relaxation affects the activity of the number of genes. Our aim is to understand the mechanisms which regulate TopA level in this bacteria. We hypothesise that there are many proteins, referred as transcriptional regulators, which influence *topA* gene activity. Thanks to application of random transposon mutagenesis we will construct *Streptomyces* mutants library. Using reporter genes (whose product may be detected due to light emission) we will be able to identify the genes which inactivation lower TopA production. This will allow us to find out which proteins regulate *topA* transcription and, thus, indirectly control DNA condensation and global gene expression regulation.