DESCRIPTION FOR THE GENERAL PUBLIC

The aim of each living organism is to protect, duplicate and transfer its genetic material to next generation. In bacteria, due to absence of nuclear envelope typical for eukaryotes, the duplication of genetic material (replication) occurs in cytoplasm and is spatiotemporally coupled with its segregation to daughter cell. With some exceptions, in bacteria the chromosome segregation is supported by the activity of dedicated proteins ParA and ParB as well as centromere-like sequences named *parS*. Whereas ParB binds *parS* sequences and forms a large nucleoprotein complex - segrosome, ParA, due to hydrolysis of ATP actively moves segrosomes towards opposite cell poles. Due to direct interaction between molecules ParB can spread along DNA double helix and subsequently bridge its distant regions. Recent studies have shown that ParB binding to *parS* sites affects spatial structure (topology) of the chromosome. Although the chromosome segregation in bacteria occurs according to a common model, details of the process can differ remarkably meeting the challenges of cell shape and genome organization.

Streptomyces, are a soil, sporulating, multigenomic bacteria, known as producers of secondary metabolites used commonly as antibiotics and immunosuppressants. They resemble simple fungi in their grow mode involving formation of branched multigenomic hyphae and sporulation. Their large chromosome (8-11 Mb) is a single and linear DNA molecule. The segregation of *Streptomyces* chromosomes to spores is supported by the activity of *parABS* system. However, in *Streptomyces* the number of identified *parS* sequences is higher than in other bacteria (24 in *Streptomyces coelicolor* in contrast to 10 in *Bacillus subtilis*, 3 in *Mycobacterium smegmatis*), thus the architecture of segrosome seems to be more complex in comparison to other species. In *Streptomyces* the partitioning of segregation complex is supported by topoisomerase I (TopA). Through transient breaking and rejoining of DNA strand, the enzyme removes DNA loops and knots that generate topological problems that may disturb chromosome separation. The cooperation of segregation proteins (including ParB) with TopA protein as well as the exact architecture of the segrosome remain still unclear.

The major purpose of our project is a detailed analysis of the architecture of *Streptomyces* segregation complex focusing mostly on DNA topology. We will verify the model, in which ParB binding to *parS* sequences leads to cohesion of distant chromosomal regions and we will determine the global structure of the chromosome in a living cell. Moreover, using a set of biochemical and microscopic methods we will study the role of TopA protein during chromosome segregation to spores. Our work will combine biochemical studies on single molecule level with global chromosome architecture capturing.