

Bacteria inhabit all ecological niches on Earth, including extreme environments. Their extensive metabolic variability is the result of acquisition of new genetic information by horizontal gene transfer (HGT). The main part in HGT is played by mobile genetic elements (MGE) – they are capable of mobilization of even large segments of DNA, whose transfer may change metabolic ability of the new host. Acquisition of such genetic information can considerably influence physiological properties of the new hosts, including creation of new pathogenic bacteria.

Comparative sequence analyses of bacterial genomes enable to identify mobile genetic elements as well as exogenous DNA integrated into host genome. It defines the directions of evolution of individual groups of microorganisms, including pathogenic species. This is especially important considering the increasing number of highly virulent, multiresistant strains, as well as new emerging pathogens. Analysis of the "new" pathogens is a very important research task, since the collected data may contribute to understand the mechanisms of the transition from saprophytic to pathogenic lifestyle and the development of effective prophylactic and therapeutic methods.

Strains of the genus *Paracoccus* (*Alphaproteobacteria*) make an interesting model organism for studying the acquisition of virulence genes and emergence of new pathogenic bacteria. This genus comprises several hundred strains, classified in over 50 species, isolated from diverse, often very contaminated niches. Interestingly, the only species associated with opportunistic infections in humans is *P. yeei*, which is a feature unique within the genus. We have collected a pool of *P. yeei* strains, comprising six clinical and two environmental isolates, which significantly vary in their physiological properties.

The main goal of this project is to conduct complex comparative analyses of the genomic nucleotide sequences of clinical isolates and their comparison with the genomes of the same species isolated from natural environment. The results of a genomic analysis will recognize the genes unique to the pathogenic strains, including virulence modules and define the influence of the MGEs on the transition from saprophytic to pathogenic lifecycle of the host. As an additional value of the project, complex functional analyses of the unique genetic modules identified in clinical isolates will be conducted. The results obtained in the project will provide data on genetic mechanisms of the generation of pathogenic strains among analyzed group of bacteria.