ABSTRACT (English)

This thesis is based on three published research papers studying bacterial REP (**r**epetitive **e**xtragenic **p**alindrome) elements. REP elements are one of the best-characterized groups of bacterial DNA repeats, distributed mostly in gammaproteobacteria, including enterobacteria. They are present in noncoding parts of host genomes, usually occurring in hundreds of copies. REPs are typically aggregated in higher order repeats. In the Gram-negative model *Escherichia coli*, interactions of several proteins important for cell's physiology with REPs were described, indicating significant role for these elements for host cells.

The first work (Nunvar et al. 2010) presents the discovery of a protein class, related to IS*200*/IS*605* transposases. These proteins, termed RAYTs (**R**EP-**a**ssociated t**y**rosine **t**ransposases), contain characteristic motifs in their amino acid sequences, which are absent in canonical IS*200*/IS*605* transposases. Another attribute of RAYTs is the arrangement of their encoding genes. These are single copy genes, always flanked at both termini by at least two REPs in inverted orientation. Based on the similarity between the REP-*rayt*-REP unit and insertion sequences of the IS*200*/IS*605* family, between RAYTs and tyrosine transposases and between REPs and subterminal sequences of the IS*200*/IS*605* family, the hypothesis about RAYTs being the mobilizers of REP elements was proposed.

The second work (Nunvar et al. 2013) explores the variability of REP copy numbers with respect to evolution of host bacteria. The analysis covers large dataset of genomic sequences from two bacterial lineages – fluorescent pseudomonads (63 strains) and stenotrophomonads (10 strains). Tens of unique classes of REP sequences and their cognate RAYTs were identified. The copy numbers of particular REP classes varied significantly among phylogenetic clades, as well as within the clades. High REP copy numbers were typically conditioned by the presence of

cognate RAYT genes. The results imply that long term presence of RAYTs is likely to lead to the proliferation of cognate REP elements.

The third work (Nunvar et al. 2012) examines the usefulness of species-specific REP sequences and their dynamics for easy genotyping of *Stenotrophomonas maltophilia* isolates. The developed method, termed SmrepPCR, employs polymerase chain reaction that uses single primer, complementary to the most abundant REP class in *S. maltophilia*. The grouping of 34 isolates, based on the similarity of their SmrepPCR profiles (banding patterns), correlated well with the branching of phylogram constructed from sequences of an essential gene (*gyrB*). The novel SmrepPCR is therefore suitable for estimation of clonal or phylogenetic relationships of environmental and clinical strains of *S. maltophilia*.

Keywords

Pseudomonas fluorescens, Stenotrophomonas maltophilia, REP element, IS*200*/IS*605*, RAYT, SmrepPCR, *gyrB,* molecular phylogenetics, comparative genomics