

DESCRIPTION FOR THE GENERAL PUBLIC

Bacteria inhabit almost all environments on our planet, including those that are too harsh for other organisms, i.a. due to the low availability of nutrients, high levels of pollution or extreme physical and chemical conditions. They are also ideally adapted to living inside other organisms, and their presence is sometimes profitable for the host (in the case of symbiotic bacteria), but more often cause diseases, which are sometimes fatal (in the case of pathogenic bacteria). Such high adaptability often comes from the introduction of varied genetic information, derived from other microorganisms, into the bacterial cells, as a result of a phenomenon known as the horizontal gene transfer (HGT). It is commonly known that HGT is the driving force of evolution of prokaryotes. It compensates for the lack of possibility of sexual reproduction, which determines the genetic variability in higher organisms. As a result of HGT, any fragment of a bacterial genome can in theory be transferred to other, unrelated microorganisms. The genetic information introduced may provide bacteria an immediate emergence of new traits, i.a. enabling them to spread to new environments. Plasmids, which are self-replicating, circular DNA molecules that can be passed between the cells of different species of bacteria play a key role in the cycle of mobile DNA.

The existence of HGT has been known for a long time, but only by learning the genetic information of the complete genomes of many bacteria and conducting a comparative analysis of genomes of related strains, the immense extent of this phenomenon was discovered. Identification and analysis of the pool of mobile DNA involved in the HGT is an important research task, providing valuable information about the variability and evolution of bacterial genomes. As a result of this type of research we also obtain valuable data on the direction of flow of genetic information between different groups of microorganisms, as well as the role of foreign DNA in determining the characteristics and properties of the new hosts.

More comprehensive genomic analyses allow to define the pangenomes of particular species of bacteria (i.e. the total number of genes present in all strains of the species) and the grouping of genetic information, indicating the preserved genome core (genes present in all strains of the species) and the pool of genes specific only for single strains, which were introduced as a result of a number of HGT events. Another path of research involves identification and general analysis of plasmids occurring in a given group of bacteria (i.e. plasmidome) and defining the pool of mobile DNA transferred by them.

This project combines the two streams of research, as it involves characterization of both plasmidome and pangenome of a group of related microorganisms. Bacteria of the genus *Listeria*, which are commonly found in the environment (in soil, water, plants, sewage), and in digestive tracts of many mammals were chosen as the research model. Some of these strains are considered to be pathogenic to humans and animals.

The current knowledge about the plasmids of these bacteria is very limited. In the project, we intend to explore and characterize the complete genetic information of a large pool of plasmids from large collection of bacterial strains (isolated from different environments and different geographical regions) representing several *Listeria* species. A database comprising the genes of all plasmids of these bacteria will be created. It will be used to conduct comparative analyses with *Listeria* spp. pangenome and plasmidomes of other taxonomic groups of bacteria. These analyses will provide much valuable data on the direction of the flow of genetic information in the analyzed group of bacteria, and the role of plasmids, and the genetic information they contain, in the shaping of the structure of genomes and the pangenome of *Listeria* spp. We also plan to extend the study to include mobile genetic elements other than plasmids, transposons, to obtain a more comprehensive image of *Listeria* mobilome.