

Biology and systematics of Antarctic polar lactic acid bacteria strains of the genus *Carnobacterium* in the light of phenotypic and genetic analyses.

Territorial polar environments are mainly represented by ice deserts and areas covered with permafrost, characterized by the occurrence of very severe climatic conditions and resulting in a significant simplification of soil structures. A similar characteristic applies to post-glacial territories that are formed as a result of retreating glacier foreheads. The ice-free area of the glacier are characterized as a reservoir of many ecosystems with low biodiversity and simplified trophic structures. Antarctic soil is poorly documented as a source of terrestrial microbial communities, what is confirmed by a little number of available detailed studies. Certain taxa, that dominate in most of Antarctic soil habitats are species from the *Actinobacteria*, metabolically diverse *Proteobacteria* and *Actinomycetes*, which are very attractive from a biotechnological perspective of application as source of antibiotics. Several reports indicate that extremely harsh Antarctic soil environment can be a source of bacteria species that normally occur in a rich nutrition. The one of the example are species from the Lactic Acid Bacteria of the genus *Carnobacterium*.

Presently, the genus of *Carnobacterium* consists of thirteen species, which can be isolated from a wide variety of sources, like: food, fish, humans, glacial permafrost and anoxic waters. In polar environments, *Carnobacterium* spp. strains were isolated from the deep-water waters of glacial lakes and from the gastrointestinal tracts of the Arctic fish. The characteristics of these environments are primarily anaerobic conditions and a relatively large amount of nutrients. So far, in the scientific literature, there is no information on the isolation of *Carnobacterium* spp. strains from polar soil environments. In addition, the available articles contain characteristics of the basic geno- and phenotypic features that are to a small extent trying to explain what mechanisms are involved in adapting the LAB group to living in polar environments.

For this reason, the main goal of the proposed project is to perform a detailed genotypic and phenotypic characteristics of nine strains of LAB strains isolated from the unreported so far in the scientific literature- ornithogenic soil structures of post-glacial Arctic and Antarctic areas. For all isolated LAB strains, planned tasks will include taxonomy assignation and detailed phenotypic characterization in order to gain better knowledge of so far barely known group of bacteria. Taxonomy identification will be prepared with the use of wide spectrum of genetic analysis, including: isolation and sequencing of genomic and plasmidic DNA, detailed bioinformatics analyses of identified genes, phylogenetic analysis of housekeeping genes as well as 16S–23S rDNA intergenic spacers (ITS) restriction analysis (ITS-RFLP). In the whole process of phenotypic characterization of isolated strains, particular focus will be given on searching of unique phenotype properties, that could result in adaptation to oligotrophic polar environmental conditions of post-glacial soils. The use of high-throughput technique of Phenotype MicroArrays will allow us to simultaneously identify a wide range of phenotypes, including: catabolism of carbon, nitrogen, sulfur and phosphorus as well as others cellular properties such as resistance to osmolytes and antimicrobial compounds. Enzymatic activity, osmotolerance, resistance to acidification and environmental stress factors as well as antimicrobial compounds production will be investigated by the use of standard culture-based methods.

Taxonomy identification approach will be crucial to provide an indispensable basis for understanding the evolutionary relationships and phylogenetic similarities of isolates across all known *Carnobacterium* strains. It will also led us to identify whether polar post-glacial environments could be a source on novel LAB species isolation. Identification of metabolic features and phenotype properties of bacterial strains would be important for understanding of mechanisms that enable adaptation to harsh polar-specific environmental conditions. All of mentioned research task would give an significant insight to the community of microorganisms present in the very harsh and highly selective polar ecosystems and will led to identification of mechanism enabling occurrence in extremely harsh conditions of polar environments.