

Due to their unusual adaptive skills, bacteria are still looking for new possibilities of colonizing unused ecological environments and acquiring new carbon and energy sources. Therefore, it is understandable that a group of bacteria, mainly called lactic acid bacteria (LAB), have evolved by living in nutrient-rich human intestines or milk. By adapting to the conditions of the digestive tract, these bacteria have lost certain genes due to the easy access to sources of carbon, nitrogen, or vitamins, but have also developed appropriate mechanisms allowing them to compete for this rich environment with pathogenic bacteria. Thanks to their high specialization and plasticity, lactic acid bacteria are extremely common and inhabit areas of plants and animals that permeate each other.

Recent research has led to identification of group of bacteria among LAB that have specialized in living in environments rich in sugars and in particular in fructose. They are fructophilic lactic acid bacteria called FLAB occurring in flower nectar, fruit, and gastrointestinal tracts of insects feeding on food rich in fructose, such as bees and bumblebees. It is already known that they are a beneficial microflora for pollinators. Due to the ongoing dangerous extinction of bee colonies, scientists are increasingly focusing on methods of restoring their health or extending the viability of these insects by the use of microorganisms associated with this ecological niche.

The aim of this project is to study the metabolism of fructophilic lactic acid bacteria, and more specifically their fructose preferences as a main source of energy. The cause of this atypical metabolism of these bacteria is not fully understood, and stands as a major gap in knowledge about this group of microorganisms. It has been suggested that this is due to the loss of genes and in particular the *adhe* gene. Since this group is heterogeneous and contains species from the genus *Fructobacillus* and *Lactobacillus*, this information does not apply to the whole group. Additionally, phenotypic studies of different fructophilic bacteria indicate that they are capable of simultaneous efficient utilization of glucose from their environment, which contradicts with the definition of these bacteria which are the preferences of fructose.

We want to study the mechanism of metabolism of simple sugars in these bacteria and properly define the FLAB group. We have isolated new Polish strains of bacterial species belonging to FLAB from various ecological niches; they will constitute the research material in this project. We have chosen only those species that exhibit different types of fructophilicity. We want to sequence genomes of 5 species that will be submitted to the GeneBank NCBI as a bioproject. Based on the results, we will design an experiment on gene expression. By growing the bacteria in different conditions, for example on a medium with glucose and on a medium with fructose, we will know the expression of genes in real time which are directly involved in this metabolism. We will check their capacity of metabolism of various sugars and compare growth on different media and the amount of sugar consumed during cultivation. We will be able to compare the data with the species isolated from mead that we have sequenced. The results will be subjected to statistical analysis mainly using the PYTHON algorithms. The methods used guarantee publication in high-scoring magazines from the JCR list.

The proposed combined studies at the genetic, transcriptome, and phenotypic level, will give a full picture of the fructophilicity of this group of bacteria. The results of this project will contribute to broadening the knowledge in microbiology as well as the ecology of the bee microbiome.