

DOKTORSKÝ STUDIJNÍ PROGRAM

NÁVRH TÉMATU/PROPOSAL OF THEME

Studijní program/*Study Program*: **Animal Science**

Katedra/*Department of*: **Microbiology, Nutrition and Dietetics**

Školitel (včetně titulů), email/*Supervisor, email*: **doc. Ing. Věra Neužil Bunešová, Ph.D., bunesova@af.czu.cz**

Konzultant (včetně titulů)/*Co-supervisor*: **Assoc. Prof. Clarissa Schwab, Ph.D.**

Forma studia/*Form of Study*: **Full_time**

Typ tématu/*Type of Theme*: **Framework**

Téma/Theme: Interaction of bifidobacteria with other taxa of intestinal microbiota

Hypotéza/Hypothesis: Bifidobacterial pangenome contains a number of genes that allow interactions with other taxa and components of gut microbiota. In addition, mobile genetic elements can yield many strain-specific properties of bifidobacteria. We hypothesize that bifidobacteria and other genera of probiotic bacteria, occurring in environments which is rich of pathogenic microorganisms and dysbiotic conditions, may enrich their genome with genes encoding, for example, adhesins and invasins, which use pathogens for their virulence; which could enhance their competitive ability against pathogens. On the other hand, genes for antibiotic resistance and the production of undesirable metabolites and specific properties can be obtained as well.

The occurrence of pathogenic bacteria in food, feed and the digestive tract of humans and animals is influenced by a number of external and internal factors. These factors significantly affect both their further development in a given environment and the production of individual metabolites and the ability to virulence. One of the possibilities of elimination of pathogenic bacteria and their virulence is the presence and possible application of probiotic bacteria, such as bifidobacteria. The selection of a suitable probiotic strain that will be able to colonize the host's digestive tract for a long time or for a certain period of time and suppress the pathogens present is a prerequisite to reduce the use of antibiotics and eliminating their growing resistance. The occurrence of bacteria of the genus *Bifidobacterium* is detected in a variety of ecological niches, such as fresh fermented dairy products, wastewater and the digestive tract of insects living a social life. However, their main reservoir is the digestive tract of animals and humans. All these ecosystems represent extensive and complex niches in terms of the number and variability of microorganisms. Thus, it can be expected that there will be interactions between commensal bacteria with probiotic statuses such as the genus *Bifidobacterium* and any pathogenic microorganisms present. The aim of this work is the detection of genes encoding virulence factors, antibiotic resistance and the production of specific metabolites in the genome of bifidobacteria and other probiotic genera. This detection will be used to design primers for these genes and their subsequent detection at the molecular genetic level in bifidobacteria and other probiotic genera derived from a variety of hosts, environments and conditions. The obtained knowledge will be used for testing interactions with pathogens *in vitro*, testing adhesion on cell lines and possibly in animal models. The experiments will also include analysis of the microbiome of faecal samples, with the aim of monitoring selected probiotic, pathogenic, and other microbial groups. The aim will be to clarify the ability of bifidobacteria colonization and their benefits for the host.

Zdroj financování/Source of: The project will be financed from the internal resources of the department and partly from the NutRisk project. The issue of the topic is part of the submitted GACR project.

Datum/*Date*: 6.11.2020

Podpis/*Signature*: