

The *Lactobacillus* genus microorganisms belong to a very large heterogeneous group of lactic acid bacteria that are commonly applied in the food and pharmaceutical industries and in agriculture. These bacteria include among others *Lactobacillus casei*, *Lactobacillus paracasei* and *Lactobacillus rhamnosus* species that are collectively treated as a *Lactobacillus casei* group. Many studies have proved that some strains belonging to this group may induce positive effects on the bodies of men and livestock. It is commonly believed that the *Lactobacillus casei* group bacteria stabilize gut microflora, inhibit the development of pathogenic microorganisms, eliminate or minimize symptoms of lactose intolerance, prevent or alleviate the course of bacterial, viral and post-antibiotic diarrheas as well as normalize disorders of gut peristalsis. Furthermore, it has been demonstrated that man's diet supplementation with probiotic bacteria may stimulate the immune system and may positively affect regulation of cholesterol blood level. Owing to the imposed ban on the use of antibiotic growth stimulants in animal feeding, increasing importance is ascribed to studies on other additives permitted for use in feeding. The use of probiotics in animal feeding enables increasing the effectiveness of agricultural production – as it results in increased digestibility of feedstuffs and synthesis of some vitamins, thereby increasing body weight gains, as well as allows improving health status of animals, increasing their resistance to stress conditions, and ensuring faster recovery of the body after disease.

The isolation of novel strains and their throughout characteristics in terms of health-promoting traits allows introducing innovative, competitive probiotic preparations onto the market with an ever increasing applicatory potential. During the isolation and selection of novel strains, highly significant is the issue of frequent occurrence of prophage sequences in genomes of bacteria from the genus *Lactobacillus*. In most cases, the presence of a sequence encoding bacteriophage proteins in a genome is perceived as a phenomenon linked with a high likelihood of induction and release of bacteriophages. This process usually proceeds as a result of cell lysis, which may in turn cause great losses from the viewpoint of the food and pharmaceutical industries wherein the *Lactobacillus* genus bacteria are increasingly often applied.

On the other hand, the presence of prophage sequences in bacterial genomes contributes to the introduction of genetic variability of bacteria, which may have a positive effect on a bacteria host. Apart from the common lytic cycle, described were also other forms of phages existence like lysogeny, pseudolysogeny or chronic infection, that do not lead directly to bacterial cell lysis. It has also been proved that the presence of prophages in genomes may allow the bacteria to reach the environmental preponderance in a given medium. It results, i.a., from the fact that prophage sequences may contain genes encoding enzymes, exotoxins or bacteriocins owing to which microorganisms are capable to more efficiently compete for their natural ecological niche including, e.g. the gastrointestinal tract of man.

Summing up, the planned studies will be aimed at analyzing the presence and biodiversity of phages occurring in genomes of *Lactobacillus casei* group bacteria. Based on results obtained, novel genetic markers of the phage origin will be selected to be used for specific identification of intestinal bacteria from the analyzed group at the species and strain level. The successive stage of the studies will include genetic, proteomic and physiological characteristics of the selected so far not described bacteriophages. Afterwards, bacteriophage gene expression will be analyzed at various stages of growth of the investigated strains. An attempt will also be undertaken to characterize various forms of co-existence of selected phages and their bacterial hosts, which may contribute to the extension of knowledge regarding interactions between phages and bacteria, which – excluding the classical lytic cycle – seems to be still insufficient.