

Summary

In addition to such benefits as honey and bee products (wax, propolis, etc.), honeybee farming exerts an impact on the yields of entomophilous plants that are naturally pollinated by bees. The decline in the number of these insects observed in recent years and caused by e.g. environmental pollution, climate change, reduced food diversity, and diseases, with varroosis, nosemosis, and American foulbrood (AFB) as the major threats, may reduce food production worldwide. Given the multifactorial threats to honeybee colonies and the prohibition of the use of antibiotics in many developed countries, alternative methods for treatment and enhancement of honeybee health are being searched, and the use of probiotics is gaining in importance. The dissertation focuses on the evaluation of the probiotic potential of 14 strains of lactic bacteria (LAB) isolated from healthy honeybees and their potential to be used for the production of probiotics.

Based on the sequence analysis of the 16S rRNA encoding gene and the *recA* gene, the 14 strains of lactic bacteria analysed in the study were classified as *Lactobacillus kunkeei* (12 strains) and *Fructobacillus fructosus* (2 strains) species, and the classification to the species was verified via a comparative analysis of their phenotypic characteristics with reference *L. kunkeei* and *F. fructosus* strains. The analysed lactic acid bacteria belong to a special group of LAB, i.e. fructophilic lactic acid bacteria (FLAB), which have adapted to living in a D-fructose-rich environment and are found naturally in honeybee guts. These bacteria exhibit the characteristics of probiotics, i.e. sensitivity to antibiotics, which ensures safety of their use in the honeybee diet, production of organic acids e.g. antibacterial lactic and acetic acids (100% mortality of vegetative forms of *P. larvae* bacteria, i.e. the etiological agent of AFB), high hydrophobicity of the cell surface, the ability to aggregate and produce biofilm, which proves the bacterial ability to adhere and interact with the surface of honeybee alimentary tract cells, and the ability to live in the alimentary tract of honeybees, as confirmed by *in vitro* and *in vivo* tests. Therefore, it can be concluded that the *L. kunkeei* and *F. fructosus* bacteria analysed during the dissertation study are good candidates for the production of a probiotic dedicated to honeybees.

Keywords: fructophilic lactic acid bacteria, 16S rDNA sequence analysis, *recA* gene analysis, honeybees, probiotics

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