

Metagenomic studies of the honey bee gut microbiome: prospects for the development of pharmabiotics

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The honey bee *Apis mellifera* is a social insect species with a unique complex of adaptations to adverse environmental conditions. The unique characteristics of the honey bee colony are the result of the symbiotic relationship of the honey bee organism with the gut microbiome through chemical signals. The gut microbiome is an additional organ of the honey bee, which consists of a unique small anaerobic community of gram-negative (genera *Apibacter*, *Bartonella*, *Commensalibacter*, *Gilliamella*, *Parasaccharibacter*, *Saccharibacter*, *Serratia*, *Snodgrassella*, *Frischella*) and gram-positive (genera *Lactococcus*, *Lactobacillus*, *Bifidobacterium*) species of bacteria. These types of intestinal bacteria have undergone a long co-evolution with bees and have accumulated unique genes in their genomes that provide immunity, adaptation, and detoxification of xenobiotics and pesticides. The gut microbiome of honey bees contributes to the acceleration of growth, an increase in longevity, an increase in the absorption of food and an increase in the body weight of individuals. The microbiome is involved in the growth, development and reproduction of honey bees and contributes significantly to their metabolism. The microorganisms in the gut of honey bees synthesize biologically active substances, increase the efficiency of digestion and help to assimilate nutrients. The microbiome modulates the behavior of honey bees, sensing, memory and learning by influencing the brain and nervous system. The genome of the honey bee and the metagenome of the gut microbiome are combined into a single, functionally related complex genome, which should not be considered separately. Some strains of lactobacilli from the honey bee gut microbiome may be potential pharmabiotics for humans. Lactobacilli of the honey bee microbiome are believed to be the host's basic line of defense against pathogens using antimicrobial peptides and inhibitors [1, 2].

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References

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