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Brevibacillus laterosporus supplementation diet modulates honey bee microbiome

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Abstract

Honey bees (*Apis mellifera*) are facing multiple stressors affecting their lifespan, health and productivity. Among them, bacterial and fungal pathogens *Paenibacillus larvae*, *Melissococcus pluton*, *Ascosphera apis* and *Nosema ceranae* play a major impact on honey bees colonies. Thus, developing alternative prophylactic and curative strategies are urgently needed. The use of probiotic bacteria in honey bee supplemental feeding is therefore promising to treat or prevent diseases. *Brevibacillus laterosporus*, Gram-positive endospore forming bacilli, is recognised as one of the promising antibacterial and antifungal agents producer.

The aim of this study was to examine the short-therm effects of *B. laterosporus* supplemented diet on worker honey bee microbiome.

Dry spores of *B. laterosporus* strain BGSP11 have been administrated through a sugar syrup diet to ten colonies and a representative specimen of worker honey bees was taken before the start of the treatment and immediately after the syrup was consumed. The microbial diversity was assessed before and after the treatment using Illumina MiSeq sequencing platforms (ID Genomics service, Seattle, WA, USA). 16s rRNA sequencing for bacterial community profiling and fungal Internally Transcribes Spacer for mycological taxa profiling were used. The next-generation microbiome bioinformatics platform QIIME2 v 2021.4 was used for filtering and denoising obtained sequences, calculation of diversity metrics and taxonomy assignment. The feature classifier was trained using the Greengenes v 13_8 for bacterial taxa and fungal UNITE database v 8.3. The results obtained in this study indicated statisticaly significant alfa diversity between control and experimental group honey bee microbiota composition. The diversity abundance was higher in control comparing to the group treated with *B. laterosporus* strain BGSP11 spores. There was no significant diference in Bray-Curtis distance among two groups of analysed samples. Regarding to mycological abundance, composition was completely different between two groups; control group had *Claviceps* as predominant genus, while in treated group of honey bee microbiome *Metschnikowia* genus was prevalent, indicating that the presence of fungal pathogens in treated group is highly diminished.

Keywords:

Brevibacillus laterosporus, honeybee microbiome, metagenomics, 16S rRNA sequencing, Internally Transcribes Spacer sequencing

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