EurBee 10

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Abstract book

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Estonian University of Life Sciences
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Table of Contents

Welcome

It is our sincere pleasure to welcome you on the EurBee 10 Congress in Tallinn, Estonia! The Congress is organized by the Estonian University of Life Sciences with assistance by Publicon OÜ.

EurBee is the event, where old and new friends get together to exchange the knowledge of novel scientific findings, associated with honeybees and other pollinators.
We encourage young researchers to meet the leading scientists on their field. Establishing networking and creating new connections is extremely important for sustainable bee research.

The City of Tallinn is the capital of Estonia. Tallinn's Hanseatic old town and nowadays modern architecture is a great mixture for every taste. We recommend you to discover the great Estonian flavors and the interesting culture that Tallinn offers you in abundance on every corner.

Looking further, Estonian nature with its forests, bogs and swamps is unique in the world – all the EurBee guests have the opportunity to experience its magic!

Experience magic – experience Estonia!

Sincerely Yours,

Risto Raimets
President of EurBee 10

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VARROA DESTRUCTOR AND NOSEMA CERANAE SHAPE THE HONEY BEE GUT MICROBIOTA

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Abstract

The Azores archipelago consists of nine islands with endemic bee populations belonging to the African lineage, although there is also genetic evidence of the introduction of European bees. These introductions have in all likelihood introduced pathogens like *Varroa destructor* (V) and *Nosema ceranae* (N). However, the restricted movement of bee colonies between islands has limited their spread throughout the archipelago, so that we can find islands with different combinations of these pathogens, i.e. positive (+) or negative (-) to *V. destructor* and/or to *N. ceranae*. In this work, we studied the microbiota of bees belonging to 4 islands with this different pathogen scenario to determine whether the presence of any of them has influenced the presence and/or abundance of any of the main bacterial taxa that make up the intestinal microbiota of bees. Therefore, 15 bees from 10 colonies of Pico (V+, N+), Flores (V+, N-), Terceira (V-, N+) and Santa Maria (V-, N-) were selected and pooled and the complete bacterial 16S rRNA gene was sequenced using PacBio Sequel II sequencing (HiFi/CCS mode). Preliminary results showed that bacterial taxa characteristic of the honey bee gut were found in almost all samples, with *Lactobacillus*, *Bartonella*, *Bifidobacterium*, and *Snodgrassella* being the most abundant. In the samples from Terceira, *Bifidobacterium* and *Bartonella* were less abundant than in the other islands, while *Arsenophonus* was more abundant. *Arsenophonus* was also found, although at lower abundance, on Flores and Pico and was virtually absent on Santa Maria, which interestingly is the island free of *V. destructor* and *N. ceranae*. These results provide a first characterisation of the gut microbiota of bees in geographically isolated areas such as the Azores and how pathogens such as *V. destructor* and *N. ceranae* may have influenced the gut microbiota of honey bees.

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