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Abstract book

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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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ITS2 DNA-METABARCODING AS A TOOL FOR THE BOTANICAL AUTHENTICATION OF HONEY: COMPARISON WITH PALYNOLOGY ANALYSIS USING MOCK MIXTURES

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Abstract

Honey is appreciated globally for its nutritional and sensory attributes. However, it faces significant challenges due to widespread adulteration, with mislabeling of botanical origin being one of the most frequent frauds. Determining the botanical origin of honey traditionally relies on melissopalynology, a laborious method requiring expertise, and often providing only family-level identification. DNA-based pollen identification would allow a simpler and more accurate determination, and DNA-metabarcoding is emerging as one of the most promising approaches. However, the accuracy of the qualitative results as compared to melissopalynology and the reliability of using the number of sequences to estimate pollen percentages in honey still needs further evaluation.

Herein, 13 individual pollen samples representing different species were used to prepare mock mixtures for methods comparison. First, each pollen was analysed by microscopy to determine the number of pollen grains per milligram. Then, four pollen mock mixtures were created, two containing only 5 species and two 13 species. In each case, one of the mock mixtures was prepared with an equal mass of each pollen (corresponding to varying amounts of grains), and the other was prepared to contain a similar percentage of each pollen. Additionally, each of these mock mixtures was individually mixed with agave syrup (naturally pollen-free) to mimic the honey matrix. The pollen and agave mock mixtures were subjected to ITS2-metabarcoding and palynology analysis in a specialized laboratory.

The metabarcoding results align well between the pollen and agave mock mixtures, although certain species showed overrepresentation while others were underrepresented. In contrast,

palynology results closely matched the expected composition of the pollen mixtures, whereas significant discrepancies were observed in the agave samples.

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