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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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MATERNAL ORIGIN OF HONEYBEE (APIS MELLIFERA) COLONIES FROM ACROSS EUROPE

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Abstract

Worldwide commercial beekeeping poses a threat to the native origin of the honeybee (*Apis mellifera*), with beekeepers favouring subspecies of Eastern European C-lineage ancestry, due to their docile behaviour and high honey production traits. In many parts of western and northern Europe, queens of Western European M-lineage ancestry have been massively replaced by queens of C-lineage ancestry, and this has led to the development of conservation programs aiming at recovering native lines. The maternally-inherited mitochondrial DNA (mtDNA), particularly the intergenic region $tRNA^{leu}$-cox2, has been the marker of choice for assessing honey bee variation at large geographical scales. Herein, we will show the results of the mtDNA analysis of over 850 colonies collected across 28 European countries. These samples were subjected to DNA extraction, followed by PCR, and Sanger sequencing. The analysis of the sequences was conducted in Mega 11. The results indicated that, apart from Portugal, Spain, and the conservation centres in France and Denmark, where the colonies exhibited African or M haplotypes, the remaining countries are dominated by colonies of C-lineage maternal ancestry. In conclusion, this unprecedented mtDNA analysis conducted across Europe underscores the worrying dominance of C-lineage genetic variation, highlighting the urgent need for strategic conservation efforts to preserve the native genetic diversity of *Apis mellifera*.

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