10th CONGRESS OF APIDOLOGY

16.-19.09.2024 Tallinn, ESTONIA

Abstract book

eurbee10.ee

www.emu.ee
Eesti Maaülikool
Estonian University of Life Sciences
Põllumajandus- ja keskkonnainstituut
Institute of Agricultural and Environmental Sciences
Chair of Plant Health

visit estonia

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

The host committee

Risto Raimets (PhD), Congress chair
Prof. Marika Mänd (PhD)
Reet Karise (PhD)
Sigmar Naudi (MSc)
Margret Jürison (MSc)
Kaarel Pent (MSc)
Egle Liiskmann (MSc)

The scientific committee

Dalial Freitak, University of Graz, Austria (Chair)
Reet Karise, Estonian University of Life Sciences, Estonia
Tiit Teder, University of Tartu, Estonia
Helena Wirta, Umeå University, Sweden
Jens Pistorius, Julius Kühn-Institut, Germany
Fabio Manfredini, University of Aberdeen, United Kingdom

Congress organiser

www.emu.ee
Eesti Maaülikool
Estonian University of Life Sciences
Põllumajandus- ja keskkonnainstituut
Institute of Agricultural and Environmental Sciences
Chair of Plant Health

Congress secretariat

PUBLICON

PCO Publicon
eurbee10@publicon.ee
+372 5919 2019
www.publicon.ee/

Acknowledgements

The organisers of EurBee 10 wish to wholeheartedly thank all our generous sponsors, supporters and exhibitors for participating in the congress!

Bronze sponsor

ALVEIS
By Chemicals Laif

Best student talk and best student poster award sponsor

IBRA
INTERNATIONAL BEE RESEARCH ASSOCIATION

Exhibitors

VITA beehealth

since 1968 ANEL anel.gr

Dalan ANIMAL HEALTH

The congress is supported by

Eva Crane Trust

Eurbee 10 is co-funded by

Co-funded by the European Union

Investing in your future

Kindly supported by

Tallinn

EXPLOITING THE MITOGENOMES OF APIS MELLIFERA SUBSPECIES TO DEVELOP AN AUTHENTICATION TOOL TO VERIFY THE ENTOMOLOGICAL ORIGIN OF MEDITERRANEAN HONEYS

Mónica Honrado[1,2,3], Dora Henriques[1,2], Joana Santos[1,2], Carlos Yadro[1,2,4,5,6], Raquel Martín-Hernández[7], Antonio Nanetti[8], Amelia Virginia González[7], Banan Al_Shagour[9], Chadi Hosri[10], Dylan Farrugia[11], Giovanni Cilia[8], Marion Zammit-Mangion[11], Mustafa Necati Muz[12], Nizar Haddad[9], Thomas Galea[13], Yamina Haider[14], Wisam Obeidat[15], Abdessamad Aglagane[16], Alireza Arab[17], Andri Varnava[18], Asmaa A. Eissa[19], Dilek Muz[20], Fani Hatjina[19], Fouad Lamghari[21], James Arruda[21], Leonidas Caristos Caristos[22], M. Alice Pinto[1,2], Joana Amaral[1,2]

[1]Centro de Investigação de Montanha (CIMO), Instituto Politécnico de Bragança, Bragança, Portugal
[2]SusTEC, Instituto Politécnico de Bragança, Bragança, Portugal
[3]LAQV-REQUIMTE & Department of Chemistry, University of Aveiro, Aveiro, Portugal
[4]Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Porto, Portugal
[5]CIBIO, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal
[6]BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal
[7]Centro de Investigación Apícola y Agroambiental (CIAPA). IRIAF. Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal, 19180 Marchamalo, Spain
[8]CREA-AA Centro di Ricerca Agricoltura e Ambiente, Consiglio per la Ricerca in Agricoltura e l'Analisi dell'Economia Agraria, Bologna, Italy
[9]Bee Research Directorate, National Agricultural Research Center (NARC), Jordan
[10]UL Lebanese University, Faculty of Agriculture, Beirut, Lebanon
[11]Department of Physiology and Biochemistry, University of Malta, Msida, Malta
[12]Department of Parasitology, Faculty of Veterinary Medicine, University of Namik Kemal, Tekirdag, Turkey
[13]Breeds of Origin Conservancy, 63, Nerik Sant, Haz-Zebbug, Malta
[14]Department of Agronomy, Faculty of Science, M'hamed University Bougara of Boumerdes, Independence Avenue, Boumerdes 35000, Algeria. Laboratory of Bioinformatics, Applied Microbiology, and Biomolecules (BMAB), Algeria
[15]National Agricultural Research Center, Jordan
[16]Laboratory of Biodiversity and Ecosystem Functioning, Faculty of Science, Ibn Zohr University, Agadir, Morocco
[17]Department of Animal Science, College of Agriculture and Natural Resources, University of Tehran, Iran, Islamic Republic of
[18]Department of Agricultural Sciences, Cyprus University of Technology, Limassol, Cyprus
[19]Plant Protection Research Institute, Agricultural Research Center, Dokki, Giza, Egypt
[20]University of Namık Kemal. Faculty of Veterinary Medicine. Departman of Virology. Tekirdağ, Turkey

[21]Fujairah Research Centre, Fujairah, UAE
[22]Institute of Animal Science & Department of Apiculture, Greece

Abstract

Honey is highly susceptible to adulteration. Currently, the assessment of its geographical origin remains one of the most difficult tasks, which is typically performed by melyssopalynology. Recently, the attention has shifted towards indirect approaches such as the entomological origin based on geographical distribution patterns of honey bee subspecies. Although queens' trade has impacted the natural subspecies distribution, honeys produced with autochthonous bees or bearing a Protected Designation of Origin specifying the producing honey bee subspecies, offer a unique avenue for authentication.

In the MEDIBEES project, we aim to develop a DNA-metabarcoding approach to authenticate honey's entomological origin focusing on mitochondrial lineages A, M, C, and O. To achieve this goal, the DNA from 1251 honey bees representing 16 subspecies (*A.m. sahariensis, A.m. intermissa, A.m. siciliana, A.m. ruttneri, A.m. iberiensis, A.m. ligustica, A.m. macedonica, A.m. adami, A.m. cecropia, A.m. cypria, A.m. caucasia, A.m. meda, A.m. anatoliaca, A.m. syriaca, A.m. jemenitica, A.m. lamarcki*) was extracted and the whole genome sequenced. From those, 740 mitogenomes were assembled using the MitoZ software. The quality of the assembled mitogenome was assessed by aligning all the sequences using MEGA and 348 samples were deleted. Finally, a phylogenetic analysis was conducted to eliminate non-local subspecies, resulting in a total of 326 mitogenomes. This dataset was used for calculating the fixation index (FST) pairwise values, and a sliding window of 400bp was used to identify single nucleotide polymorphisms that effectively differentiate (FST>0.98) the four lineages, enabling the identification of promising regions for primer design. In this study, three regions were identified that discriminate the four maternal lineages while showing an appropriate length for metabarcoding, namely in the COI, ND1 gene, and CYTB genes.

This work was funded by PRIMA project "MEDIBEES" and national funds through FCT/MCTES (PIDDAC): UIDB/00690/2020|UIDP/00690/2020, LA/P/0007/2020. M.Honrado acknowledges the PhD scholarship (2021.08119.BD).