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OP-061 [Bee Biology]

Mitochondrial DNA Variability in the Honey bee Apis mellifera L., Implications for Conservation

Cristina Vella[1], Sandro Lanfranco[1], Raquel Martín Hernández[3], Mariano Higes[3], Antonio Nanetti[4], M. Alice Pinto[5], Carlos Yadró[5], Dora Henriques[5], Giovanni Cilia[4], Soledad Sagastume De Andrés[3], Noureddine Adjlane[6], Banan Al Shagour[7], Ahmad Al Daour[8], Mustafa Necati Muz[9], Dilek Muz[9], Chadi Hosri[10], Marion Zammit Mangion[2], Thomas Galea[11]
[1]Department of Biology, University of Malta, Malta
[2]Department of Physiology and Biochemistry, University of Malta, Malta
[3]IRIAF- Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal de Castilla-La Mancha, Centro de Investigación apícola y agroambiental (CIAPA), Marchamalo, Spain
[4]Research Centre for Agriculture and Environment (CREA-AA), Bologna, Italy
[5]Cimo, La SusTec, Instituto Politécnico de Bragança, Portugal
[6]Department of Agronomy, University of Boumerdes, Algeria
[7]Bee Research Directorate, National Agricultural Research Center (NARC), Jordan
[8]Jordanian Beekeeping Association, Jordan
[9]UNK- University of Namik Kemal, Faculty of Veterinary Medicine, Tekirdag, Turkey
[10]Lebanese University, Faculty of Agriculture, Lebanon
[11]Breeds of Origin, 63, Nerik Sant street, Zebbug, Malta

The Western honey bee (Apis mellifera L.) is a keystone species that plays a vital role in maintaining environmental health and agricultural productivity. However, it faces significant threats, including indiscriminate pesticide use, parasite ecosystem expansion, climate change, and the uncontrolled importation of non-native subspecies. The PRIMA project MEDIBEES (Monitoring the Mediterranean Honey Bee Subspecies and Their Resilience to Climate Change for Sustainable Agro-Ecosystems) aims to identify the current genetic structure of native honey bee populations across the Mediterranean and neighbouring regions to help support breeding programmes and conservation efforts.

A. mellifera subspecies may be classified into four major mitochondrial DNA lineages: A (Africa), M (Western and Northern Europe), C (Eastern and Central Europe) and O (Western and Central Asia), each of which is sub-divided into a number of haplotypes. The occurrence of non-native lineages is a strong indicator of introduction of foreign subspecies.

In this study, the mtDNA tRNA-COII region of over 1,344 DNA samples was amplified using standard PCR methods, sequenced and then analysed using Geneious Prime 2024 software. These samples were collected from the Mediterranean and neighbouring regions including A.m. ligustica (Italy), A.m. siciliana (Italy, Sicily), A.m. cypria (Cyprus), A.m. syriaca (Jordan and Lebanon), A.m. ruttneri (Malta), A.m. meda (Iran), A.m. anatoliaca and A.m. caucasica (Turkey), A.m. jemenitica (UAE and Oman), A.m. sahariensis (Morocco and Algeria), A.m. macedonica (Greece) and A.m. intermissa (Algeria).

Results indicate that lineage C, typical of A.m. ligustica and A.m. carnica, was present in a number of studied samples, suggesting the introduction of non-native C lineage subspecies through the importation of commercially managed colonies. This presentation will focus on describing the current distribution of mtDNA haplotypes within these subspecies as well as evidence of non-native lineages, indicating the possible introduction of other subspecies into these regions. The implications of the data including insights into the movement and transfer of subspecies in these areas and potential impact on local beekeeping practices will be discussed.