EurBee 10

10th CONGRESS OF APIDOLOGY

16.-19.09.2024 Tallinn, ESTONIA

Abstract book

eurbee10.ee

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

visit estonia

1-2 Bee immunity and diseases. Poster presentations

LAKE SINAI VIRUS IN AZOREAN HONEY BEES: UNDERSTANDING THE IMPACT OF *VARROA DESTRUCTOR* ON PREVALENCE, LOADS, AND STRAIN DISTRIBUTION

Ana R. Lopes[1,2], Matthew Low[3], Raquel Martín-Hernández[4], Joachim R. de Miranda[3], M. Alice Pinto[1,2]

[1]Centro de Investigação de Montanha (CIMO), Instituto Politécnico de Bragança, Bragança, Portugal
[2]Laboratório Associado para a Sustentabilidade e Tecnologia em Regiões de Montanha (SusTEC), Instituto Politécnico de Bragança, Bragança, Portugal
[3]Department of Ecology, Swedish University of Agricultural Sciences, Sweden
[4]Centro de Investigación Apícola y Agroambiental (CIAPA). IRIAF. Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal, Spain

Abstract

Lake Sinai virus (LSV) is a pathogen affecting honey bees worldwide. It was first discovered in 2009 in Lake Sinai, USA, and manifests as a multi-strain virus. The Azores archipelago comprises islands with and without *Varroa destructor*, offering a unique setting for studying viral epidemiology. Building upon insights from the heterogeneous distribution of Deformed wing virus (DWV) strains, which was modulated by varroa's invasion, this study sought to evaluate prevalence, load, and diversity of LSV in the Azores, and explore potential changes in the viral landscape attributable to the mite's presence. In July/August of 2014/15 and 2020, 494 colonies were sampled across the archipelago. These were screened for LSV using RT-qPCR with a primer pair that allowed detection of at least four strains (LSV-1,-2,-3, and -4). Positive samples were further examined by high-throughput sequencing (HTS). The impact of varroa on prevalence and loads was evaluated using general linear mixed models in the framework of Bayesian analysis. LSV was detected on all islands (prevalence range: 7.7%–89.9%), with varroa's presence significantly increasing prevalence (mean increase: 19.5±9.5, Probability of increase=97.6%). HTS identified two known strains (LSV-2, LSV-3) and one novel strain (LSV-9). Phylogenetic reconstruction revealed a strong geographic structure in which LSV-2 was found dominating all varroa-infested islands (Flores, Faial, and Pico) and one varroa-free island (São Jorge). LSV-3 and LSV-9 dominated varroa-free islands, Graciosa and Terceira, and São Miguel and Santa Maria, respectively. Viral loads varied greatly among islands, from 4.77 log10 copies/bee to 8.71 log10 copies/bee. Varroa's presence affected LSV-2 loads, with a mean increase of 2.5±0.7 log10 copies/bee (Pr=100%). Our findings highlight mite-driven evolutionary changes in LSV in the Azores and identify a novel strain dominating the easternmost islands, coinciding with the unique refuge of DWV-C existing in this part of the archipelago.