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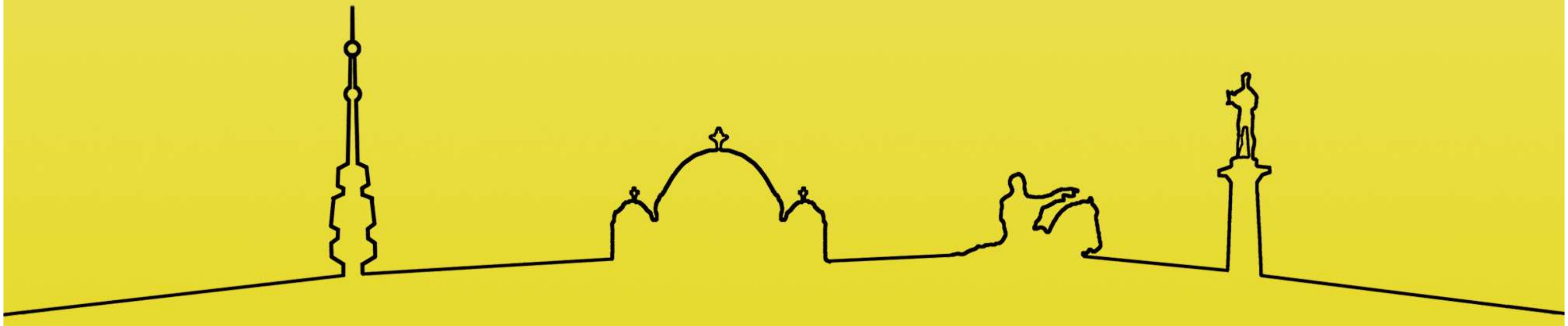
Abstract Book



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VIRAL GENETIC LANDSCAPE IN THE HONEY BEE POPULATIONS OF THE AZORES ARCHIPELAGO

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Honey bee decline can be attributed to many stressors, including pathogens and parasites, such as varroa and its vectored viruses. The global honey bee trade poses an important risk of pathogen dissemination. The arrival of varroa in the Azores because of (illegal) queen importations is clear evidence of that. Varroa was first detected on Pico in 2000, on Flores in 2001, and on Faial in 2008. The other six islands of the archipelago remain mite-free. Therefore, the Azores provide an interesting setting to study the impact of varroa in the viral landscapes, adding to previous studies. In July/August of 2014/2015 we sampled 402 colonies distributed across 8 islands. These were screened for DWV, BQCV and LSV by RT-qPCR and the positive samples were further examined by high-throughput sequencing (HTS) to uncover whether varroa has altered the viral genetic composition. Of the 8 islands, São Jorge and Terceira had no DWV-positive colonies and Pico and Flores showed the highest DWV prevalence. BQCV and LVS were detected on all the islands. The HST data indicated that DWV-A, -B, and -C variants were all present in the Azores, although with varying prevalences (DWV-A: 56%; DWV-C: 31.2%; DWV-B: 12.2%). The phylogenetic tree revealed a geographic pattern, in which most of the DWV variants from São Miguel and Santa Maria formed a clade with the DWV-C reference, whereas Pico, Faial, Flores, and Graciosa clustered with the DWV-A reference. Interestingly, the DWV-A sequences from Pico were more closely related with those from Faial than with those from Flores. If the DWV-A variant was introduced with varroa, then the illegal queen imports on Pico and Flores had independent origins, whereas the DWV-A variants on Faial might have originated from Pico. DWV-A and B have acquired a world-wide distribution in the wake of varroa, while variants DWV-C and DWV-D have become extremely rare, one plausible scenario is that DWV-C was one of the original genotypes in the Azores predating varroa and has been replaced by the variants A and B, due to their superior adaptation to varroa-mediated transmission. Also of interest is the distinct clade formed by the BQCV and LSV sequences of São Miguel and Santa Maria, as well as the independent cluster formed by Flores sequences supporting the previous scenario. All these findings will be discussed in this communication.

Keywords: Deformed Wing Virus, High-throughput sequencing, honey bee