

Exploring virome dynamics in *Varroa destructor* resistant and susceptible honey bee colonies

Arredondo, Daniela^{1,2}; Grecco, Sofia^{3,4}; Panzera, Yanina^{3,4}; Zunino, Pablo^{1,2}; Antúnez, Karina^{1,2}

1) Laboratorio de Microbiología y Salud de las Abejas, Departamento de Microbiología, IIBCE, MEC; 2) Centro de Investigación en Ciencias Ambientales (CICA), IIBCE, MEC; 3) Sección Genética Evolutiva, Departamento de Biología Animal, Facultad de Ciencias, UdelaR; 4) Plataforma Genómica, Facultad de Ciencias, UdelaR. Montevideo, Uruguay

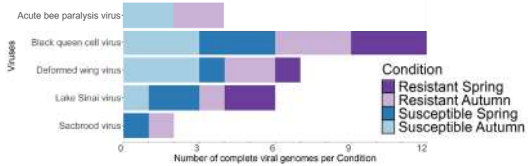
Introduction

Varroa destructor feeds primarily on the fat body and hemolymph of honey bee pupae and adults, impairing host immunity, reducing lifespan, and acting as a highly effective vector for several honey bee viruses¹. Honey bee colonies often host multiple RNA viruses including Acute Bee Paralysis Virus (ABPV), Black Queen Cell Virus (BQCV), Deformed Wing Virus (DWV), Lake Sinai Virus (LSV), and Sacbrood Virus (SBV) whose prevalence and viral loads can vary considerably across seasons². Some bee populations exhibit natural resistance to *V. destructor*, thanks to traits like hygienic behaviour, grooming, suppressed mite reproduction, and potentially enhanced antiviral responses³. In the northeast part of Uruguay, a population of Africanized honey bees has demonstrated resistance to *V. destructor* without the use of acaricides, due to a high hygienic behavior. In a previous study, we sequenced the virome (viral communities) from nurse honey bees collected from both *V. destructor* - resistant and susceptible colonies in nearby apiaries during spring and autumn.

This study aimed to characterize the diversity and phylogenetic relationships of honey bee viruses present in Uruguay using high-throughput sequencing

Materials and Methods

In a previous work, we obtained the complete genomes of ABPV (n=4), BQCV (n=12), DWV (n=7), LSV (n= 6) and SBV (n= 2) from resistant and susceptible colonies. Whole genomes of each virus were aligned using Clustal Omega 1.2.2 with those available at NCBI⁵, and maximum-likelihood phylogenetic trees were built with 1000-replicate bootstraps using MAFFT and FastTree plugins with default settings in Geneious Prime 2024.0.5 software.



Results and discussion

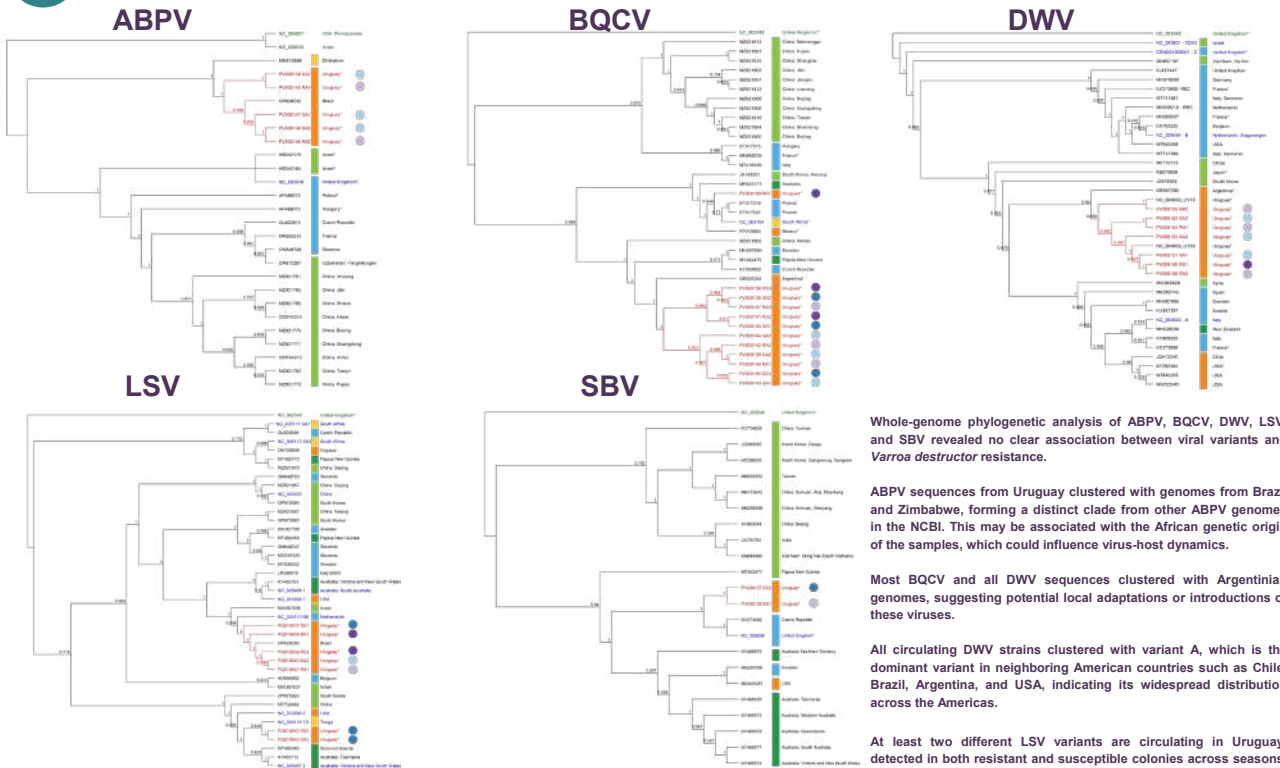


Figure 1- Phylogenetic dendrograms of complete genomes. Uruguayan genomes (red), outlier group (green), reference genome (blue), and the rest of the sequences (black). All sequences used for comparison were obtained from the NCBI database (accession numbers are indicated). The continents are rectangles marked with colours: Africa, America, Asia, Europe and Oceania.

Whole-genome phylogenetic analysis of ABPV, BQCV, DWV, LSV, and SBV revealed no clear association between viral variants and *Varroa destructor* resistance.

ABPV sequences from Uruguay clustered with genomes from Brazil and Zimbabwe, forming a distinct clade from other ABPV genomes in the NCBI. This may be associated with the African genetic origin of the samples, which could influence virus-host dynamics.

Most BQCV and all DWV sequences clustered with Argentinian genomes, suggesting potential local adaptations or introductions of these viruses.

All circulating DWV strains clustered with variant A, which is the dominant variant in neighboring American countries such as Chile, Brazil, Argentina, and USA, indicating its widespread distribution across the Americas.

At least two different LSV variants are circulating in Uruguay, detected in both resistant and susceptible colonies across seasons, though their pathogenic role remains unclear.

Conclusions and Perspectives

We report the complete genomes of ABPV and SBV for the first time in South America.

We successfully reconstructed the phylogenetic relationships of the studied viruses.

High-throughput sequencing proved to be a powerful approach for characterizing the honey bee virome.

Distinct viral variants were found circulating in Uruguay

Future research will focus on detecting novel viruses beyond reference-based mapping.

This study provides key insights into the complex interactions among viruses, varroa mites, and honey bees in resistant and susceptible colonies, contributing to a better understanding that supports sustainable beekeeping.

Acknowledgments

The authors thank the Ministerio de Educación y Cultura (MEC-DICYT) (FVF_2023_421) and Programa de Desarrollo de las Ciencias Básicas, PEDECIBA-MEC-UdelaR (Despegue científico 2023) for their financial support.

References

- Warner, et al., (2024). A scoping review on the effects of Varroa mite (*Varroa destructor*) on global honey bee decline. STOTEN, (906)
- Beaurepaire, et al., (2020). Diversity and global distribution of viruses of the western honey bee, *Apis mellifera*. Insects, 11(4).
- Locke, (2016). Natural Varroa mite-surviving *Apis mellifera* honeybee populations. Apidologie, 47(3).
- Mendoza, et al., (2020). Unravelling honey bee–Varroa destructor interaction: Multiple factors involved in differential resistance between two Uruguayan populations. Veterinary sciences, 7(3).
- National Center for Biotechnology Information (NCBI) Available from: <https://www.ncbi.nlm.nih.gov/>.



Daniela Arredondo¹, Sofia Grecco², Yanina Panzera², Pablo Zunino¹, Karina Antúnez¹

¹Laboratorio de Microbiología y Salud de las Abejas, Departamento de Microbiología and Centro de Investigación en Ciencias Ambientales (CICA), Instituto de Investigaciones Biológicas Clemente Estable, Ministerio de Educación y Cultura, Montevideo, Uruguay

²Sección Genética Evolutiva, Departamento de Biología Animal, and Plataforma Genómica Facultad de Ciencias, UdelaR, Montevideo, Uruguay

Honey bees are native to Africa, Europe, and the Middle East. They have been introduced to Oceania, Asia, and America in several waves, mainly due to honey production and their importance in pollination. With the spread of honey bees, the mite *Varroa destructor* and several viruses have also been distributed worldwide. Most beekeepers rely on acaricides to control mite populations. However, the emergence of acaricide-resistant *V. destructor* populations has been reported, limiting their long-term efficacy. One promising strategy to cope with the mite is the identification of *Varroa*-resistant honey bee populations that survive infestations naturally. In the northeast part of Uruguay, a population of africanized honey bees has demonstrated resistance to *V. destructor* without acaricides due to a highly hygienic behaviour. In a previous study, we sequenced the virome (viral communities) from nurse samples collected from *V. destructor*-resistant and susceptible colonies in apiaries nearby in spring and autumn. In this study, we continued studying the viral profiles of these populations and aimed to characterize and compare their viromes and the whole genomes obtained. Our results revealed that virome composition varied significantly with season rather than *V. destructor* - resistance or susceptibility. The whole-genome phylogenetic analysis of the Acute Bee Paralysis Virus (ABPV), Black Queen Cell Virus (BQCV), Deformed Wing Virus (DWV), Lake Sinai Virus (LSV), and Sacbrood Virus (SBV) did not indicate any clear association between viral variants and *V. destructor* resistance. Interestingly, phylogenetic reconstruction and bootstrapping analysis of ABPV clustered Uruguayan genomes with sequences from Brazil and Zimbabwe and separately from the rest of ABPV complete genomes available at the NCBI. Most of the BQCV and all DWV genomes clustered with a genome from Argentina. We also observed that there are two variants of LSV circulating in our country. Future research will focus on detecting new viruses in both *V. destructor*-resistant and susceptible colonies to enhance our understanding of the complex interactions among viruses, *Varroa* mites, and honey bees to promote sustainable beekeeping.