

A virus on the move: Molecular methods for Citrus Leprosis Virus and its vector, *Brevipalpus* mites

Danny Vasquez¹, Laura Torres², Roxanne Farris¹, and Evan Braswell¹

¹ CPHST Mission Laboratory, Edinburg, Texas; ² The University of Texas-Pan American, Edinburg, Texas

Citrus Leprosis Virus (CiLV) causes devastating economic losses to the citrus industry. Its northward trend of movement from South America to Mexico suggests an impending invasion of the U.S. Moreover, the widespread distribution of the disease vector, flat mites in the genus *Brevipalpus*, threatens rapid spread should invasion occur. Recent work has highlighted our poor understanding of the diversity of both disease agent and vector. At one third of a millimeter, these extremely small mites are difficult to identify morphologically. Therefore, the development of molecular methods for identification of these mites is of great value. Previous methods allowed isolation of DNA from a minimum of ten mites. Here, we reduce this to a single mite while extracting DNA and RNA simultaneously. Polymerase chain reaction (PCR) and sequencing of the DNA from these mites is providing valuable data that will be aligned with morphological data to bring forth accurate identifications of the mite species currently found in South Texas. Real-time PCR methods have been applied to test the mite RNA for the presence of CiLV, an RNA-based virus. In conclusion, we have developed the necessary molecular methods to identify an individual mite while also determining whether or not that same mite carries the virus. This work will impact not only our understanding of distribution of virus and vector but the associations between virus and vector as well. Further, this work has application in staving off invasion of the U.S. by CiLV through improved detection at ports of entry.