A PROTEÍNA DE MOVIMENTO E NUCLEOPROTEÍNA DOS DICHORHAVIRUS FORMAM UM COMPLEXO PROTEICO QUE PODE SER NECESSÁRIO PARA A DISSEMINAÇÃO DO VÍRUS E INTERAGE *IN VIVO* COM AS PROTEÍNAS DOS CILEVIRUS RELACIONADAS AO MOVIMENTO VIRAL

DICHORHAVIRUSES MOVEMENT PROTEIN AND NUCLEOPROTEIN FORM A PROTEIN COMPLEX THAT MAY BE REQUIRED FOR VIRUS SPREAD AND INTERACTS *in vivo* WITH VIRAL MOVEMENT-RELATED CILEVIRUS PROTEINS

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Resumo:

Introduction. *Brevipalpus*-transmitted viruses (BTVs) belong to the genera *Dichorhavirus* and *Cilevirus* and are the main causal agents of the citrus leprosis (CL) disease. **Objective**. In this report, we explored aspects related to the movement mechanism mediated by dichorhaviruses movement proteins (MPs) and the homologous and heterologous interactions among viral proteins related to the movement of citrus leprosis-associated viruses. **Methodology and Results**. The membrane-spanning property and topology analysis of the nucleocapsid (N) and MP proteins from two dichorhaviruses revealed that the MPs are proteins peripherally associated with cell membrane, exposing their N- and C-termini to the cytoplasm and the inner part of the nucleus, whereas the N proteins are not membrane-associated. Subcellular localization analysis revealed the presence of dichorhavirus MPs at the cell surface and in the nucleus, while the phosphoproteins (P) were located exclusively in the nucleus and the N proteins in both the cytoplasm and the nucleus. Co-expression analysis with the MP, P and N proteins showed an interaction network formed between them. We highlight the MP capability to partially redistribute the previously reported N-P core complex, redirecting a portion of the N from the nucleus to the plasmodesmata at the cell periphery, which indicates that the MP might guide the intracellular trafficking of the viral infective complex, but also that the N protein may be associated with the cell-to-cell movement mechanism of dichorhaviruses. The movement functionality of these MPs was analyzed by using three movement defective infectious systems. Also, the MP capacity to generate tubular structures on protoplast surface by ectopic expression, was analyzed. Finally, we evaluated the *in vivo* protein-protein interaction networks between the dichorhavirus MP and/or N proteins with the heterologous cilevirus movement components, which suggest a broad spectrum of interactions, highlighting those among capsid proteins (CP), MPs and Ns from citrus leprosis-associated viruses. **Conclusion**. This data may aid to understand the mixed infection process naturally observed in the field caused by distinct BTVs.

Palavras-chave: Dichorhaviruses; Citrus leprosis pathosystem; Virus movement; *In vivo* protein-protein interaction; Protein membrane association and topology

Apoio

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