

were contrasted. The evaluated responses were the displacement of the aphid in a gap of 300 seconds and the permanence in one of the chosen arms for 30 seconds (residential time). Repetitions with 20 aphids by bioassay were performed. The results were submitted to chi-squared test through the "R" software, at a significance level of 5%. In the first bioassay no significant differences were observed: 68% of the aphids choose passion fruit plants and 32% choose the control. These results confirm that *A. gossypii* not colonize neither is attracted by passion fruit plants. In the second bioassay, 89% of the aphids choosed the CABMV infected plants in detriment of the non-infected ones, confirming the preference of the *A. gossypii* for diseased plants. *A. gossypii* could have a chemical perception of volatiles compounds issued by infected passion fruit plants. New researches need to be performed to discover which volatiles issued by CABMV infected passion fruit plants affect the behaviour of the aphids.

Palavras-chaves: Aphid, virus, woodiness disease

VARIABILITY OF THE MOVEMENT PROTEIN GENES OF APPLE CHLOROTIC LEAF SPOT VIRUS ISOLATES FROM APPLE AND PLUM

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Resumo

Infections by *Apple chlorotic leaf spot virus* (ACLSV) occur, generally, latently in the majority of commercial apple and plum cultivars. In some cvs. the virus causes severe symptoms with substantial economic losses. ACLSV is a single stranded positive sense RNA virus in the genus *Trichovirus*, family *Betaflexiviridae*. Movement proteins (MP) exert an important role in cell-to-cell spread of viruses away from initial infection sites. Genetic variability and diversity in plant RNA viruses are determined by many viral and host factors, including the error-prone characteristic of polymerases, the absence of 3'-proof-reading capacity of polymerases of plant RNA viruses, and as result of a viral adaptation strategy. Sequence comparisons reveal high variability between ACLSV isolates. A comprehensive molecular knowledge of regional virus isolates of ACLSV is a fundamental support to improve virus detection and characterization. Total RNA was extracted by adsorption to SiO₂ from leaf samples of apple cvs. Cripps Pink, Golden Delicious, Red Delicious, and plum cv. Polli Rosa. Primers CL 5717s 5'-GAT GGC GAT GAT GAT AAG GGG TCA C-3' and CL 7103as 5'-GCC TCA CAC ACC TGG CGG-3' (NC_001409) were based on *in silico* analysis of GenBank data using CLC Sequence Viewer. Multiple alignment

MPs display the highest sequence conservation. Financial support: Embrapa Uva e Vinho, Project nr. 03.13.05.007; CNPq Process nr. 153694/2017-3.

Palavras-chaves: ACLSV, Movement protein gene, genetic variability, selection analysis, recombination

The tomato DnaJ protein SIDj1 co-localizes with potyvirus replication vesicles in plants infected by Turnip mosaic virus

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Resumo

Potyvirus is a large and important genus of plant viruses. Together, its members infect a great number of crops and wild plants around the world, causing serious economic losses. Potyviruses have a positive sense ssRNA genome that expresses eleven proteins which interact with host factors to manipulate the plant cell in favor of virus establishment and multiplication. Virus infection induces the remodeling of cellular membranes resulting in the formation of vesicles and other structures related to virus replication and cell-to-cell movement. The viral membrane-associated protein 6K2 is implicated in vesicle formation and can be used as a marker to visualize virus induced structures by microscopy. Many proteins containing the DnaJ domain, also known as Hsp40 proteins, are present in plant genomes. They act as Hsp70 co-chaperones and as chaperones themselves. The involvement of proteins from both families in infection by different viruses was described, acting in processes as viral encapsidation, movement and replication. A tomato (*Solanum lycopersicum*) DnaJ protein (SIDj1) was previously identified as induced during the infection by the potyvirus *Pepper yellow mosaic virus* (PepYMV). The downregulation of nine homologs to SIDj1 in *Nicotiana benthamiana*, results in phenotypic alterations that resemble PepYMV symptoms. The infection is reduced in silenced plants, suggesting that these proteins are involved in virus infection. Aiming to understand the role of SIDj1 in potyvirus infection, SIDj1 was fused to the fluorescent protein GFP and its subcellular localization was analyzed by confocal microscopy in *N. benthamiana* plants infected by an infectious clone of the potyvirus *Turnip mosaic virus* (TuMV) expressing the 6K2 protein fused to mCherry. SIDj1 co-localizes with 6K2 induced vesicles and with a perinuclear globular structure typically observed in TuMV infected