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PROGRAM & ABSTRACTS

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pose a major threat to sustainable agriculture and food security globally. Investigating the molecular mechanisms underlying pathogenicity and spread of geminiviruses is a crucial step towards the design of effective strategies for agriculture protection. We are using *Tomato yellow leaf curl virus* (TYLCV), the main virus affecting tomato production, as a model to investigate the interaction between the virus genes and the host plant. TYLCV is mainly transmitted by an insect vector, the whitefly *Bemisia tabaci*, and only has one single-stranded circular DNA genome encoding six proteins from six open reading frames (ORF): two in the virion sense orientation, CP and V2, and four in the complementary orientation, C1 (also known as replication-associated protein or Rep), C2 ,C3 and C4. The Rep/C1 protein is the only viral protein essential for virus replication. We have observed that transient expression of Rep/C1 in *Nicotiana benthamiana* can induce the perinuclear localization of chloroplasts. Expression of TYLCV can also induce this effect, which seems to require production of reactive oxygen species. Treatment with the defensive hormones salicylic acid also results in perinuclear localization of chloroplasts. We hypothesize that this phenotype is caused by activation of the plant defence responses upon perception of Rep/C1 or its activity.

Uncovering the global plant gene expression and the role of the viral proteins during citrus leprosis virus C infection

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Citrus leprosis virus C (CiLV-C) is the prevalent virus causing a disease that affects the citrus industry in Latin America. Differently from other plant viruses, CiLV-C is unable to accomplish the systemic movement in any of its known hosts, being restricted to the feeding sites of its mite vector. A previous study suggests that this atypical locally-restricted infection is a consequence of a hypersensitive-like response (HR). To better understand the molecular mechanisms behind the plant-virus interaction, we used RNA-seq to assess the global

response of Arabidopsis along the course of the CiLV-C infection. At the earliest stage (6 h after infestation with viruliferous mites), the plant response to CiLV-C infection is undetectable. Plant transcriptome is progressively reprogrammed and high number of genes is differentially expressed at the pre-symptomatic stage (6 days after infestation). Gene set enrichment analysis revealed the modulation of plant immune pathways. Genes involved in the salicylic acid (SA) pathway and hypersensitive response (HR) were over-represented, and mainly up-regulated. To clarify the role of the CiLV-C proteins in triggering such responses, we expressed them individually in *Nicotiana benthamiana*. Agrobacterium-mediated transient expression of none of the CiLV-C proteins produces a visible altered phenotype but that using the p61 ORF. Expression of this protein consistently leads to a burst of reactive oxygen species, increased expression of SA- and HR-related genes and cell death. Mimicry of responses typically observed during CiLV-C-plant interaction put forward elements, indicating p61 as the putative viral effector to be neutralized by plant defenses.

Transcriptome analysis of *Phalaenopsis* orchid with synergistic infection of *Cymbidium mosaic virus* and *Odontoglossum ringspot virus*

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Synergistic viral interaction is commonly hallmarked with reinforced virus colonization and hindered host growth in mixed infected plants [1]. Here we characterized viral synergism between the two major orchid viruses, *Cymbidium mosaic virus* (CymMV) and *Odontoglossum ringspot virus* (ORSV), in *Phalaenopsis amabilis*, with signs of chlorotic ringspots, enhanced viral titer and spreading of CymMV at 10 days post inoculation (dpi). Based on symptom formation and progression of virus infection, we further designated the inoculated and adjacent non-inoculated tissues representing late and early stages of infection,