CHARACTERIZATION OF THE TRANSLATIONAL LANDSCAPE OF THE PLANT-VIRUS INTERACTION

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Tomato yellow leaf curl virus (TYLCV) is responsible for a disease that causes massive damage to tomato crops around the world (Prasad *et al.*, 2020). Due to its viral nature, it requires the host's cellular machinery to be able to infect, which implies complex interactions between the virus and the plant. Most studies about this association are based on transcriptomics and interactomics, while translatomics analyses have, so far, been scarce. Understanding the translational machinery that is responsible for the production of viral proteins and, consequently, its propagation will allow to shed some light on these interactions and gain knowledge about the changes at the translational level that tomato plants experience upon infection.

To that end, we are characterizing the translational landscape of the plant-virus interaction using the emerging technique Ribo-Seq. And to deepen our knowledge on the regulatory mechanisms involved in the translational response, two isogenic tomato lines, one resistant (the *ty-5* mutant) and one susceptible (Santa Clara) to TYLCV are being employed. *Ty-5* is a recessive mutation located on the *Pelota* gene, which is involved in the recycling phase of the translation cycle (Lapidot *et al.*, 2015), so the study of this mutant will inform about the role of the translational machinery in the viral infection. In addition, and using RIP+MS, we are attempting to uncover the translational machinery associated to viral transcripts to determine if certain riboproteins or translation factors are preferred for the translation of viral transcripts.

We will present the advances we have made regarding these objectives.

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