

Complex interaction among virus-plant-vector in the Tomato yellow leaf curl disease (TYLCD)

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RESUMEN

Geminiviruses constitute the largest plant family of DNA viruses that cause diseases in crops worldwide. Among them, Tomato yellow leaf curl disease (TYLCD) is one of the most devastating viral diseases affecting tomato crops in tropical, subtropical and temperate areas worldwide. Tomato yellow leaf curl virus (TYLCV), the first known causal agent of TYLCD is a monopartite Begomovirus transmitted by the whitefly *Bemisia tabaci*. In the recent years, several works have revealed a complex scenario in the interaction among the players that participate in the disease, the virus, the whitefly and the host plant, that may produce a different outcome depending on the interaction of each of the organism involved. To get insight to these three-way interaction, we have analysed the changes in the transcriptome, the smallRNA profile and the methylome of tomato plants infected with TYLCV either by agroinoculation or by *B. tabaci*. DNA and RNA samples were extracted from infected apical tomato leaves at 7, 14, 14 and 21 dpi (days post infection) and RNAseq, smallRNAseq and WGBS (Whole Genome Bisulfite Sequencing) was performed. Comparative analysis of the infection mediated by *Agrobacterium* and the whitefly lighted-up genes and DNA methylated regions, that were deregulated and in plants TYLCV-infected by *B. tabaci* and not by agroinoculation, suggesting a partially different plants response to TYLCV depending on the infection method used.

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