

Whole genome, transcriptome, smallRNAome and methylome profiling during tomato-geminivirus interaction

Beatriz Romero-Rodríguez, Marko Petek, Maja Kriznik, Chen Jiao, Ian Morilla, Ana P. Luna, Zhangjun Fei, Kristina Gruden, Eduardo R. Bejarano and Araceli G. Castillo

BRR, IM, APL, ERB, ACG: Instituto de Hortofruticultura Subtropical y Mediterránea “La Mayora”, Universidad de Málaga-CSIC (IHSM-UMA-CSIC), Málaga, Spain. MP, MK, KG: Department of Biotechnology and Systems Biology, National Institute of Biology, Vecna pot 111, 1000 Ljubljana, Slovenia. CJ, KG: Boyce Thompson Institute for Plant Research, Cornell University, Ithaca, New York, USA

Tomato Yellow Leaf Curl Virus (TYLCV) belongs to the Begomovirus genus and is transmitted by the whitefly *Bemisia tabaci*. With only seven viral proteins, TYLCV must create a proper environment for viral replication, transcription, and propagation. Behind the apparent simplicity of geminiviruses lies a complex network of molecular interactions with their host and their natural vector, which induces a wide variety of transcriptional, post-transcriptional and chromatin changes in the host. To understand this virus-host interaction at a genetic and epigenetic level, we carried out a global approach to generate the transcriptome, smallRNAome and methylome of the TYLCV-tomato interaction. Total RNA and DNA was extracted from tomato-infected plants (three biological replicates) and analysed at 2, 7, 14 and 21-day postinfection (dpi). Analysis of the changes in host transcription during the infection and its correlation with changes in sRNA profiles (microRNA and phasiRNA) and DNA methylation patterns will be presented and discussed.