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

Beatriz Romero-Rodríguez[1], Ian Morilla1, Marko Petek[2], Maja Kriznik[2], Chen Jiao[3], Zhangjun Fei[3], Kristina Gruden[2], Eduardo R. Bejarano[1] and **Araceli G. Castillo**[1].

1 Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora", Universidad de Málaga-CSIC (IHSM-UMA-CSIC), Málaga, Spain.

2 Department of Biotechnology and Systems Biology, National Institute of Biology, Vecna pot 111, 1000 Ljubljana, Slovenia.

3 Boyce Thompson Institute for Plant Research, Cornell University, Ithaca, New York, USA

Geminiviruses constitute the largest family of plant-infecting viruses with small, single- stranded DNA genomes that replicate through double-stranded DNA intermediates. Because of their limited coding capacity, geminiviruses use plant nuclear machinery to amplify their genomes, which are packaged into nucleosomes forming chromatin as multiple circular minichromosomes. Thus, viral minichromosomes must encounter the nuclear pathways that regulate host gene expression and chromatin states. DNA methylation and post-transcriptional gene silencing play critical roles in controlling infection of geminiviruses and this pathogen can counteract these host defense mechanisms and promote its infectivity. 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 better understand this virus-host interaction at a genetic and epigenetic level we carried out a global approach of the TYLCV-tomato interaction to generate integrated single-base resolution maps by Next-Generation Sequencing of the transcriptome, smallRNAome and methylome of the pathogen and the host. Total RNA and DNA was extracted from tomato–infected plants (three biological replicates) and analysed at 2, 7, 14 and 21-day post-infection (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.