

Intregrated transcriptome, methylome and smallRNA profile analysis of a geminivirus infection

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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.

To better understand this virus-host interaction at a genetic and epigenetic level we have analysed the transcriptome, sRNA profile and methylome of tomato plants infected with the geminivirus, TYLCV (*Tomato yellow leaf curl virus*). Total RNA and DNA was extracted from tomato-infected plants (three biological replicates) and analysed at 2, 7, 14 and 21 days post-infection (dpi). Analysis of the changes in host transcription during the infection and its correlation with changes in sRNA profiles and DNA methylation will be discussed/shown.

This work represents the first comprehensive study of the genetic and epigenetics interactions established during a geminivirus infection in its natural host.