

Global analysis of the geminivirus Tomato yellow leaf curl virus (TYLCV) genome expression and DNA methylation during infection in tomato plants

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Geminiviruses are the plant largest family of DNA viruses that cause devastating diseases in crops worldwide. Upon the infection, viral genomes and transcripts are targeted by the plant gene silencing machinery, that processes the viral transcripts into viral small interfering RNAs (vsRNAs) and directs viral DNA methylation. To counteract these plant responses, geminiviruses encode proteins that are able to suppress both, post-transcriptional and transcriptional gene silencing.

To get an insight into geminiviral infection, the transcriptional and DNA methylation landscape of the geminivirus TYLCV (Tomato yellow leaf curl virus) from tomato-infected leaves, was characterized for the first time at high coverage by Illumina high-throughput sequencing during a time course infection. Three week-old tomato plants (*Solanum lycopersicum* cv. MoneyMaker) were infected with TYLCV by agroinoculation or using its natural vector, the whitefly *Bemisia tabaci*. RNA and DNA were extracted from samples collected at 2, 7, 14 and 21 dpi (days post infection) and RNAseq, smallRNAseq and WGBS (Whole Genome Bisulfite Sequencing) was performed.

We will present the RNA and vsRNA expression profiles along the infection and the complete DNA methylation landscape of a geminivirus by both inoculation methods, discussing the correlation with viral transcripts, vsRNA and viral DNA accumulation.