Theme 6
Oral presentation

Insights into molecular impact of silica on virus infected cucumber cultures

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The cell wall with incorporated SiO_2 is important as a strengthened mechanical barrier for plant defence. Also, silicic acid in a soluble form is reported to be important for defence. Up to now, the role of Si in relation to viral pathogens is not clarified. To address this topic, an *in vitro* approach using the model plant *Cucumis sativus* and Cucumber mosaic virus (CMV) was chosen for transcriptome analysis. In addition, molecular information obtained by Raman microspectroscopy was used for the overall biochemical characterization of the plant material under varying growth conditions. In the first step, this study aims to analyse the impact of silicic acid on the transcriptome of cucumber plants.

Therefore, *in vitro*-grown *Cucumis sativus* line B10 clones were generated derived from leaf microexplants and cultivated on Murashige & Skoog medium. The medium was supplemented with and without silicic acid. Control plants were cultivated on non-modified M & S medium, respectively. Per treatment, 6 clones were obtained. Half of the clones were experimentally inoculated with CMV. RNA isolation including DNase treatment was carried out on leaf and stem samples. Absence or presence of CMV-infection was confirmed by reverse transcription (RT)-PCR. mRNA enrichment was conducted by polyT-oligonucleotide hybridization. Initial RNA-Seq (Illumina) was performed on control and Si treated mRNA. CLC Genomics Workbench V7 was used for the mapping on the genomic draft of *C. sativus* line B10.

Clonal tissue cultures were established successful and subsequently cultivated on regeneration medium. Furthermore, infection experiments using CMV were successfully applied in micropropagation experiments for follow-up experiments and mRNA of control, Si and NaCl treated plants were obtained.

RNA-Seq analysis of the Cucumber transcriptome derived from mRNA samples of control and of Si treated plants indicated a shift in gene expression caused by Si

supplementation. Transcripts of 18,000 cucumber genes were identified. A 2-fold change in expression was obtained for 1,180 genes. The confirmation by quantitative (q) reverse transcription (RT)-PCR is in progress. Subsequent analyses will focus on the role of Si on CMV infection in cucumber.