

Impact of Silica Supplementation on Cucumber Transcriptome

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Deposited Si protects plants from (I) abiotic and biotic stresses, (II) leads to improved physical stability, (III) disease resistance and/or (III) higher yield, showing its importance in plant protection. Up to now, Si is not seen as an essential but beneficial element for plants. The soluble form, silicic acid [Si(OH)₄], is taken up by plants via roots and is transported through the shoot and finally to the leaves. Silica gel is deposited in the space beneath the cuticle layer. Low silicon (Lsi) transporters are located in the roots and nodes. They are characterized from rice, wheat, corn and pumpkin. Fertilizers containing Si are routinely applied for rice, sugarcane and cucumber. The impact of Si is not limited on the improvement of mechanical barriers against fungal phytopathogens. In soluble form, it also plays a key role in plant disease or Silicon induced resistance (SiIR). These beneficial effects of Si are often visible in stressed plants. Little data is available from non-stressed, low Si accumulating plants. Our studies focus on the cucumber transcriptome under silicon treatment, and thereby providing candidate genes important for plant viral infections.

Cucumis sativus line B10 clones and draft genome of B10 were chosen to reveal differentially expressed genes (DEGs) due to Si supplementation and analyze SiIR. Direct regeneration of cucumber clones was performed derived from leaf microexplants. The plants were cultivated on Murashige and Skoog medium, non-supplemented and Si-supplemented (Na₂(SiO₂)_x·xH₂O), respectively. mRNA was enriched from pooled leaf and stem material from control and Si supplemented plants. RNA-Seq (Illumina) was performed.

Transcripts of 18,957 (control experiment) and 18,882 (Si supplementation) referring to 19,896 genes were determined. 1,136 DEGs were identified according to *P* values <0,01 and fold change of >1.5, functionally categorized and assigned to biological processes such as defence against abiotic and biotic stresses, primary and secondary metabolism and photosynthesis. Results support recent studies on the beneficial roles of Si. Some transcripts determined from Si treated plants were assigned to NaCl due to the used form of Si. Gene expression was validated by performing quantitative reverse transcription polymerase chain reaction (qRT-PCR) on selected genes. This transcriptome study provides first insights into the putative SiIR in cucumber.