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RNA-seq analysis reveals host plant transcriptomes in response to *Agrobacterium*-mediated transformation

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Agrobacterium-mediated plant transformation has become a predominant tool for many basic studies and biotechnological applications. Discoveries in molecular mechanisms governing this transformation process have significant implications in both basic and applied plant biotechnological applications. To date, however, knowledge about plant genes and associated pathways involved in the Agrobacterium-mediated T-DNA transfer has been very limited. Here, we employed RNA-seq to exploit *Arabidopsis thaliana* transcriptomes in responses to Agrobacterium transformation process. We used two contrasting Agrobacterium strains to infect *Arabidopsis* young seedlings using AGROBEST assay protocol. The two strains included a non-oncogenic disarmed Agrobacterium strain, A136, and At804 which is a derivative of EHA105 and contains a disarmed super virulent Ti-plasmid and a binary vector pBISN1. The strain A136 lacks Ti-plasmid and therefore is unable to deliver T-DNA and effector (Vir) proteins to plant cells. This is in contrast to At804 which is capable of transferring both T-DNA and effector proteins into plant cells. *Arabidopsis* tissue samples for RNA-Seq were from three different treatment conditions, i.e., mock, A136 and At804, at 6 different time points (0, 3, 6, 12, 24, and 48 hours), respectively, during the Agrobacterium infection. Total RNA samples at each time point were then subject to NGS analysis. The transcriptomic analysis results showed that many plant genes responded to Agrobacterium infection. GO (gene ontology) analysis revealed that many plant biological processes are involved during Agrobacterium-plant interactions. These processes include hormone signaling, defense response, cellular biosynthesis, and nucleic acid metabolism and so on. Key genes displaying substantial changes in their transcripts were further validated by qRT-PCR and mutant screen. More details will be presented.

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