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Zhanyuan J Zhang

University of Missouri, USA

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

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.

Biography

Zhanyuan J Zhang has expertise in Plant Genetic Transformation and Gene Regulation. He got his PhD in the area of plant genetic engineering at University of Nebraska-Lincoln, NE, USA. He has been the Director of Plant Transformation Core Facility at University of Missouri, Columbia, Mo, USA since 2000. The mission of his core facility is to enhance both basic and applied plant biology studies by providing plant transformation services and to advance transgenic technologies. He has contributed to the transformation system improvements in soybean, maize, sorghum, wheat, and switchgrass. His interest in gene regulation has led to the validation and revealing of effective RNAi in soybean and novel approach for plant gene silencing employing artificial *trans*-acting siRNA. His research efforts in basic study of *Agrobacterium*-mediated transformation have discovered the role of the heat shock protein 90.1 in this T-DNA transfer process.

zhangzh@missouri.edu

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