

International Conference on **Transcriptomics**

July 27-29, 2015 Orlando, USA

Identification by deep sequencing and profiling of conserved and novel hickory microRNAs involved in the graft process

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MicroRNAs (miRNAs) play a vital role in plant development and growth through negative regulation of post-transcriptional gene expression. *Carya cathayensis* (hickory) is an important species for dried nuts and oil in China with high nutritional and economic value. The graft technique is an important strategy for hickory cultivation. To understand the role of miRNAs involved in the hickory graft process, we constructed three small ribonucleic acid (RNA) libraries from hickory rootstock (2 years old) and scion (1 year old) at 0, 7 and 14 days postgrafting. Sequence analysis of the three libraries identified 21 conserved miRNAs belonging to 13 families and 10 novel and 8 potentially novel miRNAs belonging to 15 families. Among these miRNAs, 12 miRNAs were differentially expressed during the graft process in hickory and two-thirds were downregulated. Quantitative real-time polymerase chain reaction (qRT-PCR) validated that 14 miRNAs and their expression trends were similar to the results obtained by Solexa sequencing. Further, a total of 89 target genes for conserved and 26 target genes for novel miRNAs were predicted. This study will help in understanding the roles and regulatory modes of miRNAs involvement in the hickory graft process.

Biography

Bingsong Zheng has completed his PhD in 2003 from Zhejiang University and Postdoctoral studies from INRA. He is the Vice-Dean of School of Forestry & Bio-technology, Zhejiang A & F University. He has published more than 30 papers in reputed journals and has been serving as an Editorial Board Member of reputed.

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