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**Comparative metabolomic analysis of the cambium tissue of non-transgenic and multi-gene transgenic poplar (*Populus × euramericana* 'Guariento')**Xiaohua Su<sup>1,2</sup>, Kun Ning<sup>1</sup>, Changjun Ding<sup>1</sup>, Wenxu Zhu<sup>3</sup>, Weixi Zhang<sup>1</sup>, Yufeng Dong<sup>4</sup> and Yingbai Shen<sup>5</sup><sup>1</sup>Chinese Academy of Forestry, China<sup>2</sup>Nanjing Forestry University, China<sup>3</sup>Shenyang Agricultural University, China<sup>4</sup>Shandong Academy of Forestry, China<sup>5</sup>Beijing Forestry University, China

Poplar, a model for woody plant research, is the most widely distributed tree species in the world. Metabolites are the basis of phenotype of organisms, enabling a more intuitive and effective understanding of biological processes and their mechanisms. However, metabolomic analysis of non-transgenic and multi-gene transgenic poplar remains poorly characterized, especially the influences on species and relative abundance of metabolites after introduction multi stress-related genes in plants. In this study, we investigated the cambium metabolomes of one non-transgenic (D5-0) and two multi-gene (*vgb*, *SacB*, *JERF36*, *BtCry3A* and *OC-I*) transgenic lines (D5-20 and D5-21) of hybrid poplar using both Gas Chromatography-Mass Spectrometry (GC-MS) and Ultra-Performance Liquid Chromatography-Tandem Mass Spectrometry (UPLC-MS/MS) with an aim to explore the effects of the transferred multi-exogenous genes on the metabolites and screen out metabolites with important biological function. Finally, 239 named metabolites were identified and the relative abundance of them were determined. Among the 239 detected metabolites, of 197 metabolites were significantly different across the three tested lines. They occupied 9 primary and 43 secondary metabolism pathways. Arginine and glutamate as substrates and intermediates in nitrogen metabolism may play important roles in growth and stress-related processes, sucrose and UDP-glucose and their derivatives are major carbon precursors for cell wall pathways and catechol is relevant to insect resistance, all of which differed greatly between the genetically modified and non-transgenic poplar. These findings may provide a basis for further study of cambium metabolism, and fully excavate metabolites related to poplar quality and yield or associated with stress response.

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