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Drought stress-mediated transcriptome profile reveals *NCED* as a key player modulating drought tolerance in different cultivars of *P. davidiana* (Korean Aspen)

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Forest trees, including poplar, have evolved to overcome harsh environmental conditions including drought stress. *Populus trichocarpa* has been studied as a model poplar species through biomolecular approaches and is the first tree species to be genome sequenced. In contrast, the genome of *P. davidiana*, the Korean aspen, has not been sequenced and is considered highly tolerant to drought stress. In this study, we used high throughput RNA-Seq mediated leaf transcriptome analysis to investigate the response of 4 different *P. davidiana* cultivars to drought stress. Based upon preliminary studies including H_2O_2 measurements and histological staining, the cultivars were divided into two major groups "drought-tolerant (Seogwang9, Palgong2)" and "drought-susceptible (Palgong1, Junguk6-2)". *P. davidiana* plants grown on MS (Murashige and Skoog) media for 8 weeks were air-dried for 10 minutes and leaves were harvested for transcriptome analysis along with untreated control samples. Following RNA-Seq, we compared the transcriptome profiles between the two groups for DEGs (Differentially Expressed Gene), GO (Gene Ontology) enrichment analysis, and identified common drought stress marker genes. Further analysis identified two distinct DEGs with contrasting expression patterns in the drought-sensitive and tolerant groups i.e. up-regulated in the drought-tolerant group while down-regulated in the sensitive group. BLAST analysis showed that both these genes encode *9-cis-epoxycarotenoid dioxygenase (NCED)*, a key enzyme required for ABA biosynthesis. This suggests a significant role of these two genes in conferring drought tolerance to *P. davidiana* cultivars in the drought-tolerant group. This study presents the first evidence of a significant role of *NCED* genes in regulating ABA-dependent drought stress responses in *P. davidiana* as it has already been shown that *NCED* regulate ABA-dependent drought adaptation via mRNA de-capping machinery in certain varieties of some plant species. We therefore, suggest the utility of these genes as genetic markers for differentiating drought tolerant and sensitive poplar cultivars.

Biography

Byung-Wook Yun has completed his PhD jointly at Kyungpook National University (KNU) and Korea Research Institute of Bioscience & Biotechnology (KRIBB) in 1998, investigating the function of plant peroxidases. He completed his Post-doctoral and senior research fellowship at the University of Edinburgh (UK), studying Nitric Oxide (NO) signaling in plant immune system, mentored by Professor Gary Loake. Currently he is working as an Associate Professor of the School of Applied Biosciences at KNU. His Plant Functional Genomics Lab is focusing on NO-mediated plant defense system toward both biotic and abiotic stresses using transcriptomics approaches.

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