



Category: Plant Genomics

Response of *Populus deltoides* Bartr. ex Marsh genes under elevated CO₂ through Next-Generation Sequencing (NGS)

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Abstract

The impact of climate change has attracted considerable attention globally. Atmospheric Carbon Dioxide (CO₂) is expected to increase to 900 $\mu\text{mol mol}^{-1}$ from present level of 400 $\mu\text{mol mol}^{-1}$ by the end of 21st century. CO₂ is a greenhouse gas that leads climate change have significantly affected structure and function of the terrestrial ecosystem, global carbon, water balance, and also crop productivity. These responses of the plant appear by altering gene expression pattern of different genes involved in anabolic and catabolic processes.

We have conducted a study to see the response of genes to elevated CO₂ inside open top chambers on *Populus deltoides*. One-month-old ramets were exposed for 180 days to treatment (CO₂ 800 $\mu\text{mol mol}^{-1}$) and control (CO₂ 400 $\mu\text{mol mol}^{-1}$). After completion of treatment, leaf tissues were outsourced to Sci-genome for transcriptome sequencing.

This study demonstrated, higher (1754) number of transcript expression in treatment (119,306) compared to control (121,060). Differential gene expression analysis shown 1951 transcripts were down regulated while 2603 transcripts up regulated and 159,982 transcripts have no significance in treatment.

Our results show that plants growing in an environment where atmospheric CO₂ is higher may alter plant adaptation, productivity, vegetation and ecosystem health by changing; the first, number of genes and second, altering gene expression patterns. Such behavior may be a good indicator of developing adaptation strategies of the plant.

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