79th CRC Seminar

Dr. Gloria Muday

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Dr. Gloria Muday of Wake Forest University is the speaker of 79th CRC seminar. Dr. Muday is a leading scientist in the field of hormonal growth and regulation with an extensive expertise in auxin and ethylene. Recently her group has taken a transcriptional profiling approach in understanding the molecular bases of auxin-ethylene crosstalk. Dr. Muday will introduce the data and discuss on yet unidentified potential pathways that regulate root developmental processes through modulating auxin-ethylene interaction.

“Transcriptional events that mediate the synergistic and antagonistic actions of auxin and ethylene on root growth and development”

時間：2013 年 07 月 3 日（水）16:30～18:00

場所：総合教育研究棟（生命系）1 階 遠隔講義室

Ethylene regulates root elongation and lateral root development by modulating auxin signaling, synthesis, and transport. Auxin and ethylene synergistically inhibit root elongation while ethylene antagonizes the positive effect of auxin on lateral root formation. These effects of ethylene on root growth and development are mediated through canonical ethylene signaling pathways identified in regulation of hypocotyl elongation. We utilized genetic and molecular approaches to identify mechanisms by which ethylene reduces lateral root formation and enhances the polar transport of the hormone auxin. Plants with mutations in a subset of auxin influx and efflux proteins are insensitive to the inhibition of lateral root initiation and the enhancement of auxin transport. The abundance of transcripts encoding the transport proteins, AUX1, PIN3, and PIN7, are increased by ACC and IAA in an ETR1 and EIN2 (ethylene signaling) dependent and TIR1 (auxin receptor) dependent fashion, respectively. Using fluorescent protein fusions to these proteins, we observed that ACC treatment increased PIN3 and PIN7 expression resulting in elevated auxin transport, which prevented localized accumulation of auxin needed to drive lateral root formation. We have extended this work to identify the genome wide transcriptional changes in response to these two hormones, to better understand the molecular mechanism for crosstalk between these two hormones. We examined the transcript accumulation profiles in root samples isolated from seedlings treated with auxin (IAA) or an ethylene precursor (ACC) over an extended time course (from 0.5 to 24 hrs), to identify primary response genes, including transcription factors and signaling proteins, and the more slowly accumulated transcripts encoding proteins that control growth and development. We filtered for genes that had a consistent magnitude and pattern of expression across 3 biological replicates. We identified 1,246 and 449 genes that changed consistently in response to IAA or ACC, respectively, with an overlap of 139 genes. This analysis provided insight into the time course of gene expression changes for genes previously identified as primary auxin- or ethylene-responsive genes, and identified novel genes with informative patterns of induction or repression. Late genes whose expression is temporally linked to changing growth and developmental patterns after hormone treatment were also identified, along with genes whose expression suggests a role in either the synergistic or antagonistic actions of IAA and ACC. The combination of highly reliable kinetic transcript data and the timeline of the response to these hormones allowed development of hypotheses for transcript/protein function that are being tested by mutant analysis.

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