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Transcriptome analysis of Arabidopsis light and brassinosteroid mutants

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Light plays critical roles in plant development. Depending on the light conditions, plants flexibly elongate or shorten their hypocotyls and leaves. Plant hormones including auxins, gibberellins, and brassinosteroids (BRs) regulate these processes acting alone or in concert. To understand the molecular signature of gene expression under the control of both light and BRs, we performed an Affymetrix genome-wide transcriptome analysis using total RNAs prepared from the four genotypes of *Arabidopsis* seedlings, Ws-2 wild type, phyB-77, bri1-5, and phyB-77 bri1-5 double. Using the list of genes filtered through the criteria of p<0.01 and fold change >1.5, we made three comparisons: phyB-77 vs. Ws-2; bri1-5vs.Ws-2; and phyB-77 bri1-5vs. Ws-2. Comparisons enabled us to find list of genes under epistatic interactions; bri1-5was epistatic to phyB-77. The genes were further validated through quantitative RT-PCR and transgenic analysis. When At5g53870 was over expressed in the bri1-5 mutant, the dwarf phenotype of bri1-5 was suppressed. Furthermore, we expressed two Peroxidases (PRX2 and PRX73) that were down regulated in phyB-77 but were up regulated in bri1-5 in the antisense orientation; both PRX2 RNAi and PRX73RNAi transgenic plants exhibited elongated hypocotyls and the expression of the target genes was greatly reduced. Our transcriptome analysis followed by qRT-PCR and transgenic expression identified the genes that are critical in light-dependent growth of Arabidopsis.

Biography

Sunghwa Choe has earned his PhD from University of Arizona and Postdoctoral studies from Ceres, Inc., a California-based plant biotech company. He is a Professor at Seoul National University, a premier University in South Korea. He has published more than 50 papers in reputed journals and has been serving as an Editorial Board Member of repute journals including Molecules and Cells.

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