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Genes that respond to H₂O₂ are also evoked under light in *Arabidopsis*

Dianjing Guo Chinese University of Hong Kong

 $\mathbf{T}_{2}O_{2}$ has been recognized as a signal molecule involved in gene expression regulation. Arabidopsis microarray data analysis $\mathbf{1}$ revealed that about 1–2% of the transcriptome and one-third of the transcription factor mRNA are altered after exposure to H_aO_a). In the green plant, H_aO_a is mainly produced during the process of photosynthesis, respiration, photorespiration, and wound/pathogen-triggered ROS burst. Apart from the ROS burst mediated by membrane-associated NADPH oxidases (rboh A~F family) under wounding and/or pathogen invasion, the photorespiration and electro transfer during photosynthesis constitute more than 90% of the H₂O₂ production in healthy mesophyll cells. Both photorespiration and electro transfer during photosynthesis require light, which indicates major H₂O₂ production is light-dependent. Therefore, a high background level of H₂O, may exist in the light-grown plant, which may interfere with the observation of the H₂O, effects in planta. The high background level of endogenous H_2O_1 in the light-grown seedlings may suggest that the oxidative effect has taken place and interfered with the observation of the H₂O₂ effects in planta, especially when investigating gene expression. In this study, the light-induced oxidative response was elucidated at the transcriptome level. The transcriptome profiles of plants grown under dark, light, and 5-mM H,O, treatment under dark were investigated and compared. Each condition contained two biological replicates and total RNA extracted from 7-day-old seedlings were used for microarray analysis (Affymetrix Arabidopsis ATH1 Genome Array Microarray). In total, 2050 and 8540 genes showed altered expression under H_aO_a and light treatment, respectively (p < 0.01), accounting for about 10% and 37.5% of the Arabidopsis transcriptome, respectively. Interestingly, out of the 2050 H₂O₂ -responsive genes, 1595 (77.8%) were also co-regulated by light. Among the 1595 genes, 1027 were up-regulated and 486 were down-regulated by both H2O2 and light, accounting for ~95% of the co-regulated genes and 73.8% of H2O2-regulated genes. Co-expression was measured as Pearson's correlation coefficient, which is ~0.79 between the log2 transferred fold change in expressions, indicating a high correlation between these two transcriptome profiles. The fact that a high percentage of H_2O_2 -responsive genes are also regulated by light suggests the existence of H_2O_2 signaling under normal light conditions in Arabidopsis. The H₂O₂ - and light-co-regulated genes were analyzed using the gene ontology (GO) enrichment plugin tool BiNGO. Over-represented GO categories were found enriched. Both the co-up- and downregulated gene sets were analyzed for over-represented functions. It was found that co-up-regulated genes are highly related to plastid/nucleus functions and gene regulation function, such as nucleotide binding, protein binding, DNA binding, chromatin binding, transcription regulator activity, transcription process, and DNA metabolism. Other functions such as stress responserelated, organelle organization, embryonic, and post-embryonic development were also enriched. Surprisingly, when the 486 co-down-regulated genes were analyzed, only the GO term of 'response to biotic stress' was enriched. The GO enrichment analysis indicated the genes co-up-regulated by light and H₂O₂ are involved in divergent biological processes and molecular functions, especially in gene expression regulation, but not restricted to stress-related. H₂O₂ is highly abundant in light-grown plants, indicating the active ROS signal pathways. Previous studies have implied the crosstalk between the light and H₂O₂ signal pathways. For example, Early Light Inducible Protein 2 (ELIP2) and Ascorbate Peroxidase 2 (APX2) genes were activated by both high light and H₂O₂ treatment, suggesting a H₂O₂ -dependent pathway was involved in light stress signaling. Genomewide expression study revealed that H₂O₂ plays a key role in the transcriptional up-regulation of small heat shock proteins during high-light stress. In addition, H₂O₂ was involved in high blue-light-induced chloroplast avoidance movements in Arabidopsis. These studies have revealed the ROS signal profiles in the high-light situation.

Biography

Dianjing Guo is an Associate Professor at the Chinese University of Hong Kong. Prior to joining CUHK, she was a senior researcher at the Virginia Bioinformatics Institute. Dianjing received her Ph.D from the Chinese Academy of Science.Her primary research interests are in the field of genomics and computational biology. She has published many research articles in peer reviewed academic journals over the past 10 years.