

## IN BRIEF

# Dynamic Histone Modifications in Light-Regulated Gene Expression

Chromatin can be modified via DNA methylation and/or histone marks, and these chemical modifications can affect transcription levels. However, evidence is mounting that specific modifications act not as simple positive or negative regulators, but rather in complex combinations whose effects depend upon context (reviewed in Berger, 2007). New work from **Charron et al. (pages ■■■)** examines dynamic changes in histone modification at the genome level to ask whether it could play a role in light-regulated gene expression. Seedlings undergo photomorphogenesis upon exposure to light, and the authors postulate that the concomitant change in the transcriptome (reviewed in Jiao et al., 2007) is a good candidate for involving chromatin regulation of global transcription patterns.

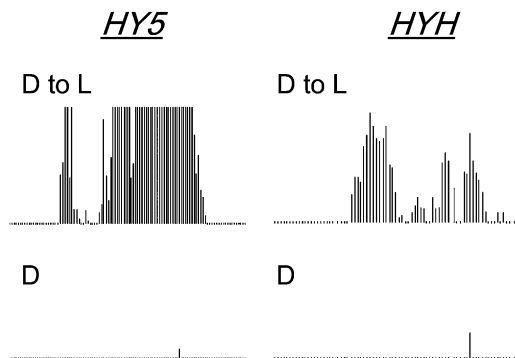
Charron et al. compared *Arabidopsis thaliana* seedlings that had been grown entirely in the dark (etiolated) to those that had been exposed to the light for 6 h (deetiolated). In agreement with previous reports, they found that 15% of the genes that were expressed in

seedlings were either induced or repressed by exposure to light. They then mapped global patterns of four histone marks by immunoprecipitating regions of the genome associated with those modifications and hybridizing the resulting DNA to microarrays. This analysis showed that all four modifications were enriched in regions of the genome where genes are found. In addition, there were differences between etiolated and deetiolated plants in modification levels, providing evidence that histone modification could play a role in regulating the large-scale changes in gene expression seen in these plants.

Charron et al. found that although there was a fair amount of overlap between the two growth conditions in the specific genes that were targeted by each modification, there were also many genes that were targeted differentially. These data point to the complexity of the histone modification code; the same modifications appear to be light regulated on some genes and not on others. The authors then examined their expression data for correlations with histone modification. In

this analysis too, there were differences between etiolated and deetiolated plants. Intriguingly, light exposure changed the degree to which a specific acetylation mark was correlated with gene expression, suggesting that in the two treatments there are different factors reading the histone modification code.

The authors went on to examine modifications in genes encoding two transcription factors involved in photomorphogenesis. Both had high levels of a particular acetylation mark in the light but not in the dark (see figure). Furthermore, the same mark also affected putative downstream targets of at least one of these transcription factors. This ability to mark multiple levels of a transcription cascade is consistent with chromatin modification playing a role in changing global gene expression patterns. Overall, Charron et al. provide a dynamic view of histone modification patterns throughout the genome. Although the field is at the early stages of understanding these patterns, these data emphasize the complexity of the system as well as its potential to regulate gene expression at the genome level.



The genes for *ELONGATED HYPOCOTYL 5* (*HY5*) and *HY5-HOMOLOG* (*HYH*) are marked by acetylation on lysine 9 of histone 3 in seedlings exposed to light (D to L, top panels) but not those kept in the dark (D, bottom panels). Positions of acetylations along the genes are indicated by vertical lines. (Adapted from Figure 5 in Charron et al. [2009].)

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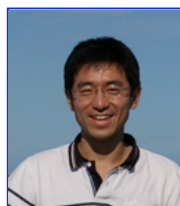
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**Dynamic Landscapes of Four Histone Modifications during Deetiolation in *Arabidopsis***

Plant Cell Charron et al. 10.1105/tpc.109.066845

*This Article*▶ [Abstract](#)*Services*▶ [Email this article to a friend](#)▶ [Alert me to new issues of the journal](#)▶ [© Get Permissions](#)*Citing Articles*▶ [Citing Articles via CrossRef](#)**Author Profile****Jean-Benoit F. Charron and Hang He****Jean-Benoit F. Charron****Current Position:** Assistant Professor, Department of Plant Science, McGill University**Education:** Ph.D. (2007) and M.Sc. (2001) in Molecular Biology, Département des Sciences Biologiques, Université du Québec à Montréal; B.Sc. in Biochemistry (1998). Université de Montréal, Canada**Non-scientific Interests:** Gardening, golfing, cooking.

Growing up in a remote mining town of Northern Canada (with snow six months of the year and temperatures frequently dropping below -35°C), I was amazed by the capacity of various plants to survive harsh winter conditions. Thus, I became determined to learn more about the capacity of plants to adapt to their environment. With that thought in mind I joined the team of Prof. Fathey Sarhan at Université du Québec à Montréal where I worked on understanding the cellular and molecular bases of low temperature tolerance in cereals. After finishing my Ph.D. I was given a once in a lifetime opportunity to join the team of Prof. Xing Wang Deng as a postdoc. During my stay at Yale University, I had the chance of using cutting edge technologies to study the dynamics of the epigenome in response to the plant's changing light environment. The plasticity of the epigenome revealed by the present work is fascinating but inevitably raises a critical question: How does this all work? This simple question is the focus of my research program at McGill University (Montréal, Canada) which aims at characterizing the chromatin regulatory mechanisms that control stress tolerance in cereals.

**Hang He****Current Position:** Postdoctoral researcher, Xing Wang Deng Lab, School of Life Sciences, Peking University, China**Education:** Ph.D. in Bioinformatics at Institute of Biophysics, Chinese Academy of Sciences, China**Non-scientific Interests:** Reading, Soccer and music, my favorite singer is the cranberries.

After graduating with a B.S. in mathematics from Peking University, I began my graduate research on Bioinformatics in Runsheng Chen's lab at Institute of Biophysics in China. Then I was fortunate to be given the opportunity to go to the US, to work on plant genomics with Dr. Xing Wang Deng (Yale University). During the two years in Yale University, I was interested in genome transcriptomic and epigenetic analysis in plants, and directed by Dr. Xing Wang Deng, I was able to apply bioinformatics studies on transcriptions and histone modifications using microarray and sequencing methods. In this project, four histone modifications and their regulations during light-dark treatment in *Arabidopsis* were studied by Dr. Jean-Benoit Charron and me. Beside this, I continue to enjoy discovering more about epigenetic regulation in plant heterosis.