

Dynamic epigenome changes in response to light in *Brachypodium distachyon*

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Abstract

Light plays an important role in many plant biological processes such as photosynthesis and photomorphogenesis. In this study, we applied RNA-seq, ATAC-seq and ChIP-seq to study transcriptional regulation at multiple levels in *Brachypodium distachyon* (B. *distachyon*) under controlled light and extended darkness conditions. We have identified 8,400 differentially expressed genes (DEGs), and they are enriched in photosynthesis Gene Ontology terms. ATAC-seq signal decreased after extended darkness, indicating that light has a genome-wide impact on chromatin accessibility. We also found that differential H3K4me3 and H3K9ac modifications are enriched in gene loci associated with photosynthesis and other light-dependent reactions. Finally, ChIP-seq revealed that a HY5-Like transcription factor could directly bind to the promoter open chromatin regions of these light reaction genes. Taken together, our results indicated the dynamic transcriptional reprogramming associated with light-dark changes in *Brachypodium* could be resulted from the combinatorial action of multiple epigenetic features.

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