IN BRIEF

Chromatin Remodeling ATPases and Plant Development

ATP-dependent chromatin remodeling is an important facet of the regulation of gene expression in eukaryotes. Assembly of DNA into nucleosomes, the basic unit of chromatin, restricts the accessibility of cis-regulatory elements in the core DNA for transcription factors that recognize and bind these sites. Chromatin remodeling ATPases use the energy derived from ATP hydrolysis to induce conformational changes in the histone octamer/DNA interaction or transiently displace the histone octamer, altering the accessibility of the core DNA. The SWI/SNF subfamily of chromatin remodeling ATPases is conserved in the plant and animal kingdoms. In metazoans, these ATPases form part of a chromatin remodeling complex consisting of one ATPase subunit, two SWI3 subunits, and one SNF5 subunit.

Bezhani et al. (pages 403–416) used global gene expression studies, double mutant analysis, and protein interaction assays to investigate the functional relationship between the SWI/SNF ATPases BRAHMA (BRM) and SPLAYED (SYD) in Arabidopsis. The results showed that these two SWI/SNF ATPases have unique and shared targets and interaction partners and that they have a remarkable degree of regulatory specificity. Protein interaction studies between individual subunits of the Arabidopsis core SWI/SNF chromatin remodeling complex suggest the occurrence of multiple distinct SWI/SNF core complexes in different plant tissues. Gene expression profiling analysis suggested that the two ATPases control expression of a limited number of genes and that their functional overlap may be biased toward the control of hormonal signaling. Double mutant analysis showed that SYD and BRM are redundantly required during embryo development.

Two Protein Kinases Required for ABA Signaling in Arabidopsis

Numerous studies have indicated that phosphorylation is an important component of ABA signaling. Fujii et al. (pages 485–494) identify two protein kinases in Arabidopsis, SNF1-RELATED PROTEIN KINASE2.2 (SnRK2.2) and SnRK2.3, that are required for the control of responses to ABA during seed germination, dormancy, and seedling growth. An snrk2.2 snrk2.3 double mutant (but not single mutants) exhibited strong ABA-insensitive phenotypes in seed germination and root growth inhibition as well as changes in seed dormancy. ABA-induced expression of several genes whose promoters contain an ABA response element (ABRE) was reduced in the double mutant, which also had a greatly reduced level of a 42-kD kinase activity capable of phosphorylating peptides from ABRE binding factors (ABFs). This suggests that SnRK2.2 and SnRK2.3 function redundantly in ABA signaling to activate ABRE-driven gene expression through the phosphorylation of ABFs.

Many elements of this story have been known or suspected for some time. This study is significant because it provides solid genetic evidence for the role of these two kinases in ABA signaling and introduces a well-defined genetic model for further investigation of the pathway (e.g., toward the identification of upstream components that activate the SnRKs and additional components that influence downstream gene expression).

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