IN BRIEF

Remodeling Chromatin in an ARID Environment.

The control of gene expression is of fundamental importance for cellular life. In Eukaryaotes, linear DNA is wrapped around nucleosomes that constitute a physical barrier to active transcription. Chromatin remodeling complexes modulate the composition, stability and positioning of nucleosomes therefore allowing regulatory factors to access DNA and ultimately regulate gene expression. Chromatin remodelers are defined by a conserved ATPase domain that fine-tunes DNA-nucleosome interactions (reviewed in Clapier and Cairns, 2009). The imitation switch (ISWI) family remodelers are characterized by additional SANT and SLIDE domains that bind DNA and histone tails (Boyer et al., 2004). ISWI remodelers form multiple distinct protein complexes and, were shown to move or restructure nucleosomes.

The plant model organism Arabidopsis thaliana contains two redundant ISWI remodelers, chromatin remodeling 11 and 17 (CHR11/17), which are required for the formation of evenly spaced nucleosomes in gene bodies (Li et al., 2014). CHR11/17 interact with the DTT (DNA binding homebox and different transcription factors)-domain proteins ringlet 1 and 2 (RLT1/2) and play a major role during plant development (Li et al., 2012). In this issue of The Plant Cell, Tan et al., (2020) identify new CHR11/17 interaction partners and show that these ISWI remodelers are recruited to specific chromatin locations by the DNA/histone binding protein ARID5.

Immunoprecipitation followed by mass spectrometry uncovered a CHR11/17 protein interaction network consisting of three independent complexes (see Figure). Yeast-two hybrid assays revealed direct interactions between RLT1/2 and CHR11/17, between RLT1/2 and ARID5 but not between CHR11/17 and ARID5, suggesting that RLT1/2 act as a bridge between CHR11/17 and ARID5. Consistently, the phenotype of ARID5 loss-of-function plants was similar to the rlt1/rlt2 double mutant (see Figure). In line with additional roles for CHR11/17, outside of the CHR/RLT/ARID complex, the phenotypes of the arid5 and rlt1/2 mutants were not as pronounced as the chr11/17, consistent with the additional roles for CHR11/17 outside the CHR/RLT/ARID complex. The crystal structure of ARID5 PHD (plant homeodomain) and ARID domains (top right) revealed a dual-binding cassette for trimethylated H3K4 and AT-rich DNA, which are responsible for recruiting CHR11/17 to chromatin (bottom right). (Adapted from Tan et al. [2020] Figures 1, 2 and 5)

Characterization of the CHR11/17 interaction network and recruitment to chromatin. CHR11/17 are part of three independent protein complexes (top left). Arabidopsis thaliana plants deficient for ARID display a similar phenotype as the rlt1/rlt2 double mutant (bottom left). However, this phenotype is weaker compared to the chr11/17, consistent with the additional roles for CHR11/17 outside the CHR/RLT/ARID complex. The crystal structure of ARID5 PHD (plant homeodomain) and ARID domains (top right) revealed a dual-binding cassette for trimethylated H3K4 and AT-rich DNA, which are responsible for recruiting CHR11/17 to chromatin (bottom right). (Adapted from Tan et al. [2020] Figures 1, 2 and 5)
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