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“Chromatin Dynamics at the Onset of Plant Developmental Programs”

Plant life-long organogenesis involves sequential, time and tissue specific expression of developmental genes. This requires opposite activities of Polycomb Group (PcG) and trithorax Group complexes, respectively responsible for repressive Histone 3 trimethylation at lysine 27 (H3K27me3) and activation-related H3K4me3. While genome-wide profiles of these modifications have been reported in plants, little is known on their dynamics during specific developmental processes. Moreover, the mechanisms that switch the state of genes from repressed to active (or active to repressed) in a specific manner have remained elusive. We use a combination of genome-wide, genetic and molecular interaction analyses to elucidate such mechanisms. (i) We found that the stage and tissue specific transcriptional regulator ULTRAPETALA1 (ULT1) activates hundreds of genes in a manner antagonistic to the CLF PcG Histone Methyl Transferase. We identified physical interactors of ULT1 among chromatin factors, transcription factors and components of the basal transcription machinery, indicating that ULT1 likely functions as a linker between chromatin remodeling and transcriptional regulation. (ii) In a developmental series including Arabidopsis leaf and three stages of flower development, we assessed distributions of H3K27me3 and H3K4me3, along with expression changes. We found that chromatin marks levels are highly dynamic over the time series. Our results reveal H3K4me3 as greater predictor over H3K27me3 for transcription dynamics and unveil unexpected chromatin dynamics for gene activation. Notably, early activation of PcG target genes is dominated by increases in H3K4me3. I will discuss how both our datasets contribute to resolve the mechanisms at plant chromatin that proceed to regulate developmental gene expression.