Title

Protein and DNA interactions of transcriptional co-regulator LEUNIG_HOMOLOG reveal its functions during early stages of Arabidopsis flower development.

Abstract

Transcriptional co-regulators are key modulators of gene expression, yet their dynamic recruitment and stage-specific roles in development remain incompletely understood. Here, we dissect the regulatory functions of the Arabidopsis *LEUNIG_HOMOLOG* (LUH), a Groucho/Tup1 family co-regulator, during floral development. Using time-resolved proteomics, ChIP-seq, and transcriptomics, we show that LUH broadly interacts with chromatin regulators and transcription factors, including MADS-domain, TALE, and GRF proteins, with interaction networks rewired as flowers transition from meristem maintenance to organ differentiation. LUH directly binds developmental regulators such as *AP1*, *SEP3*, and *STM*, forming complexes that bridge transcription factors with chromatin-modifying enzymes. Stage-specific DNA occupancy patterns reveal a shift in LUH targets from meristem identity genes to organogenesis regulators, aligning with dynamic transcriptional outputs. Comparative analyses with *lug* mutants highlight overlapping yet distinct regulatory programs, with LUH contributing unique functions despite redundancy with LUG. Together, our study uncovers LUH as a versatile, stage-specific co-regulator that coordinates floral meristem activity and organ patterning through dynamic remodeling of protein and DNA interaction networks.