Chromatin Remodeling and Gene Expression

Nucleosome Structure is the Normal State
- Histone Core: H2a, H2B, H3, H4
- Core DNA: ~150bp
  - Acts as a repressive state
  - Must be remodeled for active gene expression

Remodeling Process
- Alterations in chromatin structure that either activate or deactivate gene expression
- Involves transcription factor that actively recruit remodeling complexes
- May be coupled to DNA replication
- Involves histone modification
  - Specific lysine residues are modified by
    - Acetylation (by histone acetylases (HATs))
    - Methylation (by methylases)
    - Ubiquination mediated protein degradation
- Recruitment of remodeling complexes
  - Swi/Snf family
    - Contains helicases that twist DNA on the nucleosomes
    - DNA slides on the histones
    - DNA is more accessible to the transcription factors
The Phaseolin (Phas) Complex in Common Bean

- Major storage protein
- Tandemly repeated complex at a single locus
- Contains three TATA boxes
  - TATA boxes are protected from the TBP by histone core of nucleosomes

Phas Cis-elements

- Spatial (seed) expression requires 295 bp upstream of transcription start site
  - Does not include other modulating sequences
- Negative regulator of premature gene expression
  - NRS1: -391 to -295
  - NRS2: -518 to -418
- Matrix attachment region (MAR)
  - Where DNA binds to the nuclear protein matrix
    - 5’ centered at ~ -800 bp (acts as an enhancer)
    - 3’ site: centered at ~ +2500 bp
PvALF Activation of Phas Gene Expression

- **PvALF Activation**
  - Protein acts as a transcription factor
    - Member of the VP1 and AB13 family of transcription factors
  - Modifies chromatin structure of the Phas promoter
    - TATA boxes become accessible to TBP
    - Does not activate transcription by itself
    - Thought to prime the system for ABA-induced gene expression

The Active Phas Complex

- Experiments show that all major cis-elements occupied from early to mid-seed maturation
  - But protocol cannot distinguished fully/partially occupied sites
    - Gives impression all sites are occupied (caution)
- Model suggest that various cis-elements are occupied differentially

Transition to the Silent State

- Protein binding to the promoter decreased after mid-maturation
- ROM1
  - bZIP factor that binds ACGT sequence
  - Probably antagonistic to PvALF
- PvALF itself may be involved in stage specific developmental repression
  - May have a role in histone deacteylation
Figure 1. Proposed interactions between chromatin and transcription factors in *phox* activation. A. The closed chromatin structure over the *phox* promoter prevents TBP access in vegetative tissues. B. Non-histone negative regulators reinforce the repressed status. C. PvALF-mediated recruitment of remodeling factors results in a relaxed structure during embryogenesis. D. ABA-mediated signal transduction actuates transcription activators that mediate recruitment of the basal transcription machinery to the *phox* promoter. E. Heterogeneous DNA-protein arrays yield module-specific expression in the embryo (C, cotyledon; H, hypocotyl; R, radicle). F. The repressive state is re-established during seed maturation.
Model Depicting the Sequential Events and Ordered Modification of Chromatin over the phas Promoter during Potentiation and Activation. Histone modifications associated with various phas promoter states are shown as symbols at right. Experimentally verified and putative pathways leading to phas activation are shown as blue (solid) and red (dotted) lines, respectively. (A) In the repressed state during vegetative growth, the promoter is envisaged as being heterochromatic, with nucleosomes bearing dimethylated H4-K20. (B) ALF-mediated potentiation of phas (1), possibly through recruitment of a complex with histone acetyltransferase (HAT) activity; H3-K9 and H4-K12 are acetylated. Histone modifications may recruit a chromatin-remodeling complex such as SWI/SNF, resulting in a decrease in histone–DNA interactions. (C) Addition of ABA triggers the assembly of the ABA signaling cascade components (2) that interact with the ABRE within the phas promoter (3), leading to the recruitment of RNA Pol II and GTFs (4). New histone code modifications (H3-K4 trimethylation, H3-K14 and H4-K5 acetylation) are incorporated in the actively transcribed phas chromatin with the loss of histone H4-K20 dimethylation. During active phas transcription, histone displacement and redeposition of variant histones may take place that result in the deposition of new histone modifications at the phas chromatin. Although a marked increase in H4-K5 acetylation was evident during activation, a similar increase occurred when only ABA was added (see Figure 4E), suggesting that this modification may reflect events other than activation. The original repressive chromatin status of phas is restored at the end of seed maturation, and canonical histones are deposited into the phas chromatin through DNA replication during seed germination and vegetative growth.