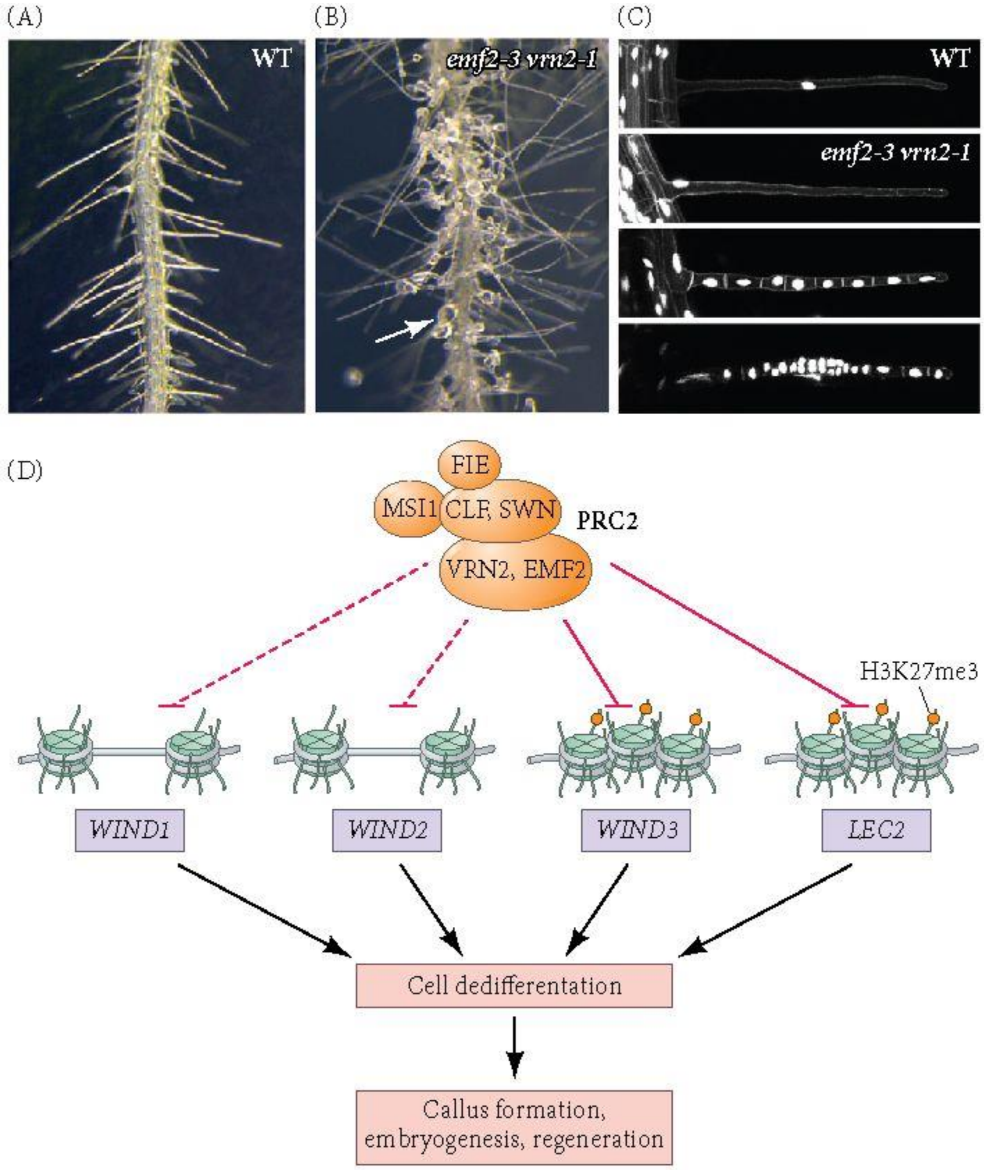
<Further Development 24_03>

Epigenetic Control of Plant Regeneration

The sudden nature of an injury demands a rapid regenerative response, which suggests the involvement of molecular mechanisms that can affect global changes in the genomic architecture of a cell—such as the result of epigenetic modifications. As you learned in Chapter 3 (see Figure 3.10), the epigenetic state of a cell refers to how accessible chromatin is for gene expression, and epigenetic changes are largely accomplished through alterations in DNA methylation and modification to histones (Xu and Huang 2014; Ikeuchi et al. 2015a). Prior to injury, epigenetic marks are in place to maintain cell differentiation while also repressing multipotency and regenerative abilities. For instance, pharmacological inhibition or loss of histone deacetylases in *Arabidopsis thaliana* converts differentiated leaves and shoots into embryonic-like structures (Tanaka et al. 2008). As in animals, DNA methylation often yields an opposite effect on chromatin accessibility as compared with histone acetylation. Importantly, reduced methylation due to the loss of *DNA METHYLTRANSFERASE1* (*MET1*) has been shown to enhance shoot regeneration (Li et al. 2011).

Among the most well characterized groups of epigenetic histone modifiers are the Polycomb proteins, which play a conserved role in gene silencing across eukaryotic life (Golbabapour et al. 2013; Derkacheva and Hennig 2014; Liu et al. 2015). In *A. thaliana*, loss of POLYCOMB REPRESSIVE COMPLEX2 (PRC2)[i] function causes the reprogramming of differentiated root hair cells into a proliferative callus and embryonic-like structures (Figure 1; Ikeuchi et al. 2015b). PRC2 normally functions by trimethylating lysine 27 of histone H3 (H3K27me3), which serves to repress the expression of several known regulators of reprogramming and regeneration, such as *WIND3*, *LEC2*, *STM*, *WOX5* and *11*, and most important, *WUS* (Ikeuchi et al. 2016). Taken together, these studies demonstrate that epigenetic modifications that lead to a more euchromatic architecture (more acetylation and less methylation) are important mechanisms to promote the dedifferentiation of cells toward a more regenerative state.



From M. Ikeuchi et al. 2015. *Nat Plants* 1: 15089.

Figure 1 Relieving epigenetic repression to allow regeneration. (A,B) Loss of PRC2 function in an *emf2-3 vrn2-1* mutant results in ectopic callus formation on lateral roots (arrow). (C) Compared with wild-type root hairs (top panel), PRC2-deficient lateral root hairs exhibited uncontrolled cell proliferation over time (lower three panels). In these images, the nuclei are white. Root hairs are usually single cells. (D) Schematic of the stem cell-promoting genes that PRC2 normally represses.

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[i] Loss of POLYCOMB REPRESSIVE COMPLEX2 in this report was determined by examining a double mutant for EMBRYONIC FLOWER2-3 and VERNALIZATION2-1, which are two of at least six proteins that form this repressive complex.