

A histone modifier that facilitates an epigenetic switch

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A depiction of the double helical structure of DNA. Its four coding units (A, T, C, G) are color-coded in pink, orange, purple and yellow. Credit: NHGRI

Epigenetic regulation of gene expression is associated with switching between chromatin states characterized by distinct histone modifications.

But how these states are faithfully inherited through DNA replication is still poorly understood.

In this study, researchers characterized a gene from an early flowering Arabidopsis mutant and showed that the [mutated gene](#) encodes a protein that modifies chromatin—that is it affects the chemical modifications of the histone proteins that surround the DNA in our cells. This class of modifier had not been well characterized in plants before.

Further, they find that the modifier protein physically associates with a well-known class of chromatin modifiers—called Polycomb proteins.

Polycomb proteins add an epigenetic mark (methylation) at a specific point (lysine residue at position 27) in the amino acid sequence of a histone protein that packages the DNA and this leads to silent chromatin.

The addition of this epigenetic mark can only happen when another nearby site (lysine residue at position 36) in the amino acid sequence is not modified. They are mutually exclusive- that is only one of these specific sites can be modified with the epigenetic mark at any one time.

Interestingly, the newly discovered modifier [protein](#) facilitates removal of the epigenetic mark at lysine 36, thus allows Polycomb to add the epigenetic mark at lysine 27. The physical association of the two activities helps generate a switch of active chromatin to silent chromatin.

Understanding [basic principles](#) of how [genes](#) are regulated by [chromatin](#) will help in many other studies of plant growth and development and in future plant biotechnology.

This project was started over 20 years ago by a Ph.D. student (Claire Hutchison) in the group of Professor Dame Caroline Dean and resumed through collaboration with Dr. Xiaoqi Feng's lab at the John Innes Center and Professor Justin Goodrich at the University of Edinburgh.

More information: Rebecca H. Bloomer et al. The Arabidopsis epigenetic regulator ICU11 as an accessory protein of Polycomb Repressive Complex 2, *Proceedings of the National Academy of Sciences* (2020). [DOI: 10.1073/pnas.1920621117](https://doi.org/10.1073/pnas.1920621117)

Provided by John Innes Centre

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