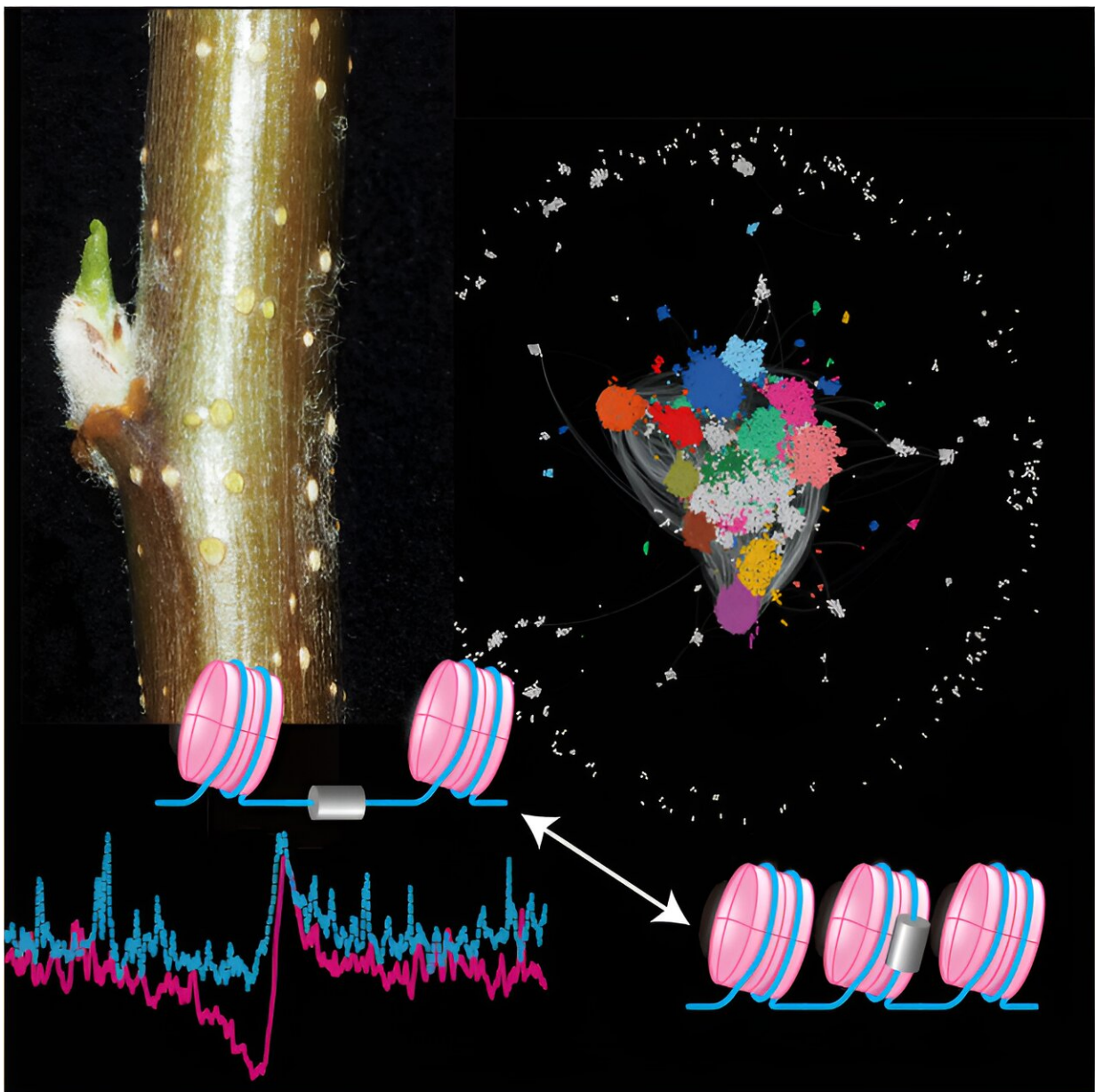


Survival tactics: AI-driven insights into chromatin changes for winter dormancy in axillary buds

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Scientists in Japan investigate how apple axillary buds sense environmental conditions and enhance survival under harsh circumstances. Their study analyzes changes in chromatin structures and transcription to unravel the mechanisms behind seasonal adaptation in plants. Credit: Takanori Saito from Chiba University

Evolution has enabled plants to survive under adverse conditions. The winter bud of a plant is a crucial structure that establishes adaptability. Depending on environmental and intrinsic conditions, buds can transition between growth and dormancy. The three dormancy phases are determined by signals triggering each phase: ecodormancy, influenced by environmental factors; paradormancy, promoted by other plant organs; and endodormancy, maintained by internal signals within the bud.

Paradormant buds enter endodormancy in response to changes in day length and/or low temperature in autumn, while endo- and eco-dormant phases occur in response to chilling temperatures. The transition from para- to endodormancy is a protective phenomenon for the bud. The epigenetic mechanism that triggers endodormancy is under-researched.

In a study published in [Tree Physiology](#) on June 21, 2024, Assistant Professor Takanori Saito and his colleagues explore the [epigenetic modifications](#) in chromatin structures and transcriptional changes that enable temperature recognition in "Fuji" apple axillary buds.

The results were further interpreted by deep-learning artificial intelligence (AI) models and statistical analysis. This research was co-authored by Dr. Shanshan Wang, Dr. Katsuya Ohkawa, Dr. Hitoshi

Ohara, and Dr. Satoru Kondo from the Graduate School of Horticulture at Chiba University.

One of the objectives of this study was to understand differently expressed genes (DEGs) in the transition phase from para- to endodormancy. Genes related to the cellular response to hypoxia, the defense response to [abscisic acid](#) (ABA), and circadian rhythm were activated at the initial stage of bud dormancy. Further, the authors revealed that nucleosome depletion was not correlated with the transcriptional pattern.

"In contrast, among the DEGs, although a nucleosome position shift in the putative promoters was observed, a difference in nucleosome occupancy between the upregulated and downregulated genes in most gene bodies was not observed during the axillary bud dormancy phase transition," explains Dr. Saito.

Cis-regulatory elements (CREs) are short DNA sequences that influence gene expression. The authors further examined the relationship between transcriptional changes and CREs using a deep-learning AI model. Elaborating on these results, Dr. Saito says, "CREs related to the [cell cycle](#), circadian rhythm, and the TATA box were found. In particular, the importance of the circadian rhythm for downregulated genes was also concomitant with the transcriptional changes." The data further revealed that COL9 signal were possibly involved in altering CO levels to trigger bud dormancy.

While most AI-based epigenetic studies use large datasets, their model uses a small dataset. Despite this, Bayesian [statistical analysis](#) linked epigenetic changes to [gene transcription](#) involved in winter bud regulation. The AI approach from this study can enhance epigenetic analysis, particularly for non-model plants with less developed genome databases.

Dr. Saito says, "The collective results of our study using DL showed that the cold-driven circadian rhythm-based machinery in axillary bud dormancy induction is tuned by single-nucleosome oscillations."

Looking ahead, these findings can enable the development of more efficient strategies to maintain a sustainable production of crops, plants, and trees to counter the effects of global warming.

More information: Saito, T et al. Deep learning with a small dataset predicts chromatin remodelling contribution to winter dormancy of apple axillary buds, *Tree Physiology* (2024). [DOI: 10.1093/treephys/tpae072](https://doi.org/10.1093/treephys/tpae072)

Provided by Chiba University

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