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Study reveals distinct roles of H3K27me3 and H3K36me3 in winter wheat vernalization

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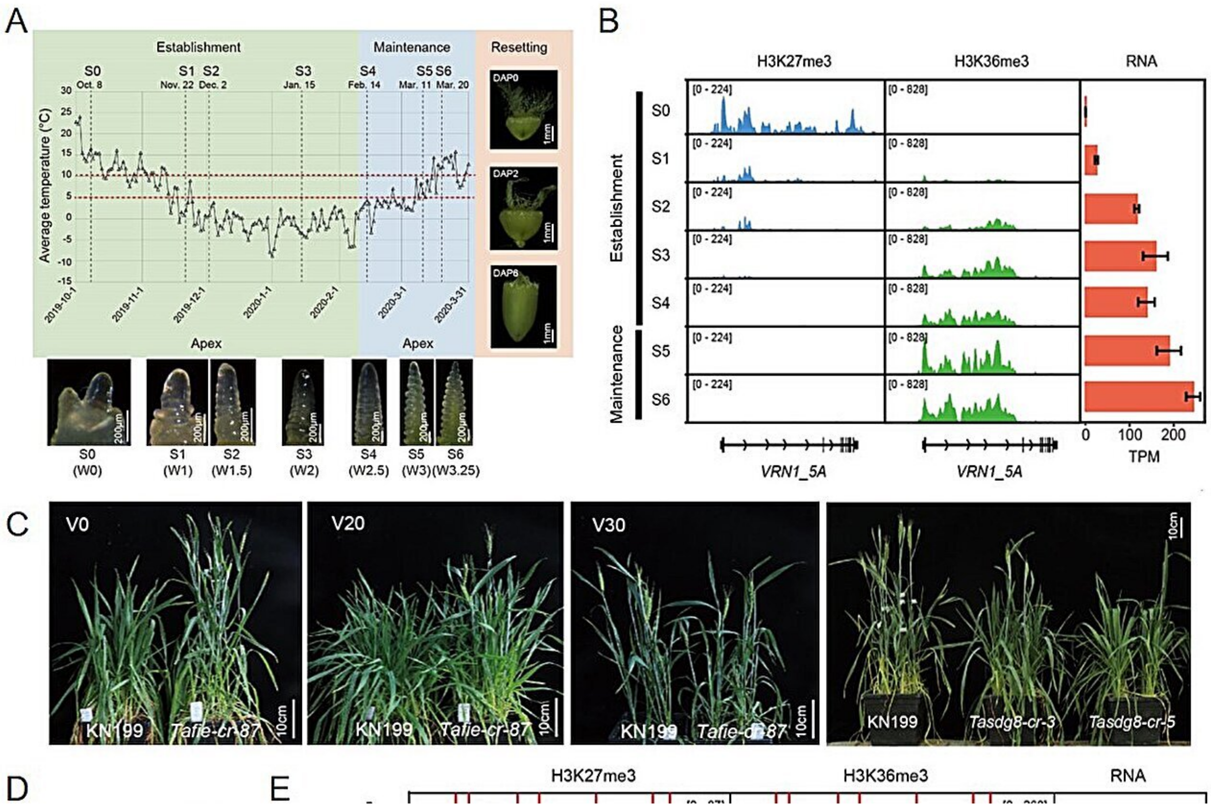

Distinct roles of H3K27me3 and H3K36me3 in vernalization response, maintenance, and resetting in winter wheat. Credit: Science China Press

Vernalization is the phenomenon whereby plants require prolonged exposure to low temperatures to flower. This ensures that overwintering plants undergo reproductive growth under suitable light and temperature conditions, thereby securing yield.

Wheat is primarily classified into winter wheat, which requires vernalization to flower, and spring wheat, which does not. Studying vernalization in wheat and understanding its regulatory mechanisms are of significance for improving the adaptability of wheat varieties.

A research team led by Prof. Jun Xiao at the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, utilized RNA-seq, ATAC-seq, and CUT&Tag technologies to profile the transcription and chromatin dynamics of field-grown winter wheat during the response, maintenance, and resetting of vernalization.

The findings were published online in *Science China Life Sciences*, under the title "Distinct roles of H3K27me3 and H3K36me3 in vernalization response, maintenance, and resetting in winter wheat."

The study revealed that the main vernalization gene in wheat, VRN1, was regulated by repressive H3K27me3 and active H3K36me3 with a distinct pattern.

Using CRISPR technology, the researchers generated mutants of the "writers" of H3K27me3 and H3K36me3, namely Tafie-cr-87 and Tasdg8-cr-3/5, respectively. These mutants exhibited early and late flowering phenotypes and influenced the expression of VRN1 during vernalization response, maintenance, and resetting processes respectively, demonstrating the specific regulatory roles of H3K27me3 and H3K36me3 on VRN1.

Similarly, the key vernalization gene FLC in Arabidopsis is regulated by both H3K27me3 and H3K36me3, but in a completely opposite manner to VRN1.

Given this mirrored transcription and histone modification pattern between VRN1 and FLC, the researchers identified 212 VRN1-pattern-like genes and 585 FLC-pattern-like genes as potential vernalization-mediated flowering regulators using RNA-H3K27me3-H3K36me3 patterns.

Among these, TaFUL3 and TaTOE1 contain sequence variations significantly associated with flowering, with TILLING mutants showing altered heading time, suggesting their roles in flowering regulation.

More information: Xuemei Liu et al, Distinct roles of H3K27me3 and H3K36me3 in vernalization response, maintenance, and resetting in winter wheat, *Science China Life Sciences* (2024). DOI: 10.1007/s11427-024-2664-0

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