

# Epigenome modification is involved in the Rosaceae DAM-mediated bud dormancy control

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**Abstract**

Bud dormancy facilitates the winter survival of woody perennials and instigates vigorous plant growth during the spring season. In Rosaceae fruit trees, a short photoperiod and chilling prompt the induction of bud dormancy in autumn. Prolonged chilling triggers the dormancy release and a transition to a quiescent state during winter, followed by subsequent warm periods that stimulate bud break. In Rosaceae, *DORMANCY-ASSOCIATED MADS-box (DAM)* genes, which encode SVP/AGL24-clade MADS-box transcription factors, have been identified as potential regulators of dormancy. Previous research has highlighted the contribution of epigenome modifications to bud dormancy regulation in various woody perennials. To substantiate these findings, our recent study revealed the involvement of a histone modification, H3K4me3, in the control of dormancy mediated by SVP/DAM. Additionally, through transcriptome analysis employing *DAM*-overexpressing lines, we observed that elevated *DAM* expression promotes the siRNA production pathway while inhibiting gibberellin biosynthesis, lipid catabolism, and cell division in the dormant vegetative meristem. Furthermore, we discovered a higher accumulation of small RNAs within the promoter regions of *DAM*-targeted genes in *DAM*-overexpressing lines compared to the wild-type. In summary, our results suggest that *DAMs* are capable of modifying epigenomes by regulating histone modification and facilitating siRNA-induced gene silencing, thereby influencing various metabolic processes.