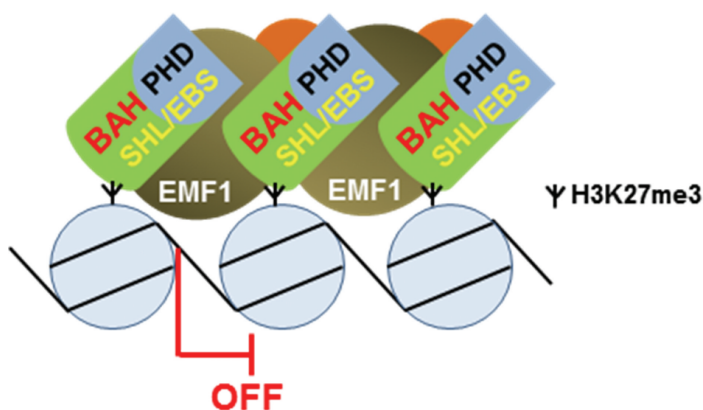


## A plant-specific reader-effector complex interprets an epigenome mark for transcriptional silencing

With the support of the National Natural Science Foundation of China, the research team led by Prof. He YueHui (何跃辉), from Shanghai Center for Plant Stress Biology, Chinese Academy of Sciences (CAS), identified a novel plant-specific reader-effector complex that interprets the epigenome mark histone 3 lysine-27 trimethylation (H3K27me3) and mediates transcriptional silencing in the experimental model plant *Arabidopsis thaliana*, which was published in *Nature Genetics* (2018, 50: 1254–1261; <https://doi.org/10.1038/s41588-018-0190-0>).

Polycomb group (PcG) proteins mediate genome-wide transcriptional silencing through chromatin-associated mechanisms in both plants and animals. PcG proteins are often assembled into two complexes: Polycomb Repressive Complex 1 (PRC1) and PRC2. PRC2 is an H3K27 methyltransferase complex and deposits the repressive epigenome mark H3K27me3 that is read and interpreted by PRC1 in animals, resulting in chromatin compaction and transcriptional silencing. PRC2 subunits are evolutionarily conserved in plants and animals; however, several core components of PRC1 found in animals are missing in plants, including Polycomb (Pc), the reader of H3K27me3 and Polyhomeotic (Ph), the protein essential for chromatin compaction. The H3K27me3 marks are widely spread in plant genomes; hence, how plants interpret this repressive mark for transcriptional repression is largely unclear. In *Arabidopsis*, it was found that LIKE HETEROCHROMATIN PROTEIN 1 (LHP1), the only homolog of animal HP1 proteins, can recognize H3K27me3, but loss of *LHP1* function leads to only moderate morphological defects. Thus, in plants there must be other H3K27me3 readers to interpret this mark for transcriptional silencing.

He's Group, in collaboration with Prof. Renyi Liu's bioinformatics team, found that two homologous BAH (Bromo adjacent homology) domain-containing proteins, EARLY BOLTING IN SHORT DAYS (EBS) and SHORT LIFE (SHL), read the H3K27me3 mark in the *Arabidopsis* genome. Furthermore, EBS and SHL, through the BAH domains, physically associate with EMBRYONIC FLOWER 1 (EMF1), a plant-specific protein to mediate chromatin compaction for transcriptional silencing. The BAH-EMF1 (EBS/SHL-EMF1) complex reads H3K27me3 to mediate genome-wide transcriptional silencing, functioning as a reader-effector complex. BAH-EMF1 complexes are found not only in eudicots, but also in monocots such as rice, suggesting its conservation across higher plants. The findings from this study uncover a novel molecular mechanism to interpret the epigenome mark H3K27me3 for transcriptional silencing, and further our understanding of gene regulation in plants.



**Figure** BAH-EMF1 (SHL/EBS-EMF1) complexes read the H3K27me3 mark and mediate chromatin compaction for transcriptional silencing.