

EPIGENETIC REGULATION OF AGRONOMIC TRAITS

Our research focuses on how epigenetic mechanisms regulate key developmental processes and genome organization in plants. To address these questions, we employ molecular genetics, biochemical analyses, and advanced epigenomics techniques. We focus on developmental processes that directly impact crop productivity, especially flowering time — a critical factor with major implications for future agriculture. To this end, our work spans both the model plant *Arabidopsis thaliana* and agriculturally important Brassica species (*Brassica rapa* and *Brassica napus*). By bridging fundamental and applied research in plant epigenetics, our work not only advances our understanding of chromatin-based regulation but also contributes to the development of tools for improving crop resilience and adaptability to changing environmental conditions.

RESEARCH LINES

Role of histone demethylases on plant development

We investigate the dynamic epigenetic regulation mediated by H3K27me₃, a repressive histone modification conserved across both plants and animals. H3K27me₃ critically controls transcriptional repression necessary for proper plant development and effective environmental responses. This mark is established by the Polycomb Repressive Complex 2 (PRC2), a specialized histone methyltransferase complex, and is precisely removed by Jumonji-C domain-containing histone demethylases.

H3K27me histone demethylases function as molecular switches, removing repressive marks to activate developmental gene networks at precise times and locations. To unveil the function of these histone demethylases in plant development, we pursue two interconnected research directions. First, we investigate how histone demethylases regulate key developmental processes, including flowering time, flower development, and fruit formation. We recently found that H3K27me₃ histone demethylases exhibit both conserved and distinct roles in regulating flowering time between *Arabidopsis* and Brassica crops.

Second, we study how histone demethylases enable plants to modify their developmental programs in response to environmental cues, particularly light and temperature changes. We examine how these signals are translated into epigenetic modifications that reprogram gene expression and developmental outcomes. Our findings demonstrate that histone demethylases function as molecular integrators, allowing plants to dynamically adjust their epigenetic landscapes in response to environmental signals. This research reveals how plants coordinate internal developmental programs with external environmental information, providing insights into plant adaptation strategies and developmental plasticity mechanisms.

Effect of fluctuating temperatures on chromatin silencing

Plant development occurs at different pace in diverse ambient temperatures but also under constant versus fluctuating temperature conditions. Within the framework of the [CBGP-CEPLAS International Collaborative Scientific Program](#), we are investigating how changes in chromatin states are associated with both short-term and long-term responses to fluctuating ambient temperatures. This research is crucial for gaining a better understanding of how plants adapt to temperature changes, which, in turn, is essential for developing crops that are resilient to the challenges of climate change.

Deciphering the plant epigenome

We leverage state-of-the-art genomic and epigenomic technologies to precisely dissect the function of critical epigenetic modifications within the *Arabidopsis* and *Brassica* genomes. In past years, our research has significantly advanced Brassica epigenomics. Key achievements of Brassica research include: generating the first H3K27me3 genome-wide profile creating a foundational resource; and pioneering studies of epigenetic modifier mutants.

We recently started a collaborative research program with researchers from the [Institute of Vegetables and Flowers \(CAAS, China\)](#) to advance the understanding of Brassica genome complexity. We are performing pan-genomic structural

variation analysis and mapping the three-dimensional organization of the genome. Through this multi-layered genome analysis, we aim to uncover fundamental mechanisms that shape genome evolution and structural diversity in plants.

PROSPECTIVE STUDENTS

We are a dynamic and collaborative research team exploring the molecular and epigenetic mechanisms that shape plant development. Scientists at different career stages work side by side, united by curiosity and a shared commitment to discovery. Mentoring young researchers is a core part of what we do, providing hands-on training that builds both technical expertise and scientific confidence.

Our lab is a place to grow — scientifically and personally. Students are encouraged to think critically, communicate effectively, and pursue innovative ideas that advance plant science. We aim to empower the next generation of scientists to lead impactful research careers in academia, industry, and beyond.