

growth, and reproductive strategies in response to environmental fluctuations. Epigenetic regulation therefore provides a potentially rapid and reversible mechanism for enhancing phenotypic plasticity and environmental responsiveness (Gutzat and Mittelsten Scheid, 2012; Springer and Schmitz, 2017).

Wild grasses are especially valuable systems for investigating drought-associated epigenetic adaptation for several reasons. First, many species occupy extensive environmental gradients characterized by substantial variation in precipitation, temperature, and soil moisture availability, resulting in pronounced local adaptation and ecological differentiation. Second, grass genomes are frequently enriched with transposable elements and repetitive DNA, making DNA methylation-mediated genome stabilization and transposon silencing particularly important components of stress adaptation (Sigman and Slotkin, 2016; Wicker et al., 2018). Because environmental stress can alter the activity of transposable elements and the chromatin landscape surrounding them, epigenetic regulation may play a disproportionately important role in grass genome responses to drought (Cavrak et al., 2014; Ito et al., 2011). Third, several wild and semi-wild grasses represent the evolutionary relatives of globally important cereal crops, providing opportunities to translate discoveries from natural systems into crop improvement strategies aimed at enhancing drought tolerance (Springer and Schmitz, 2017). Finally, a limited number of grass species, particularly *Setaria viridis*, offer the experimental tractability necessary to integrate ecological sampling, functional genomics, and epigenetic analyses within a single framework. As a rapidly cycling, transformable C4 grass with extensive genomic resources, *S. viridis* has emerged as a powerful model for elucidating the molecular and epigenetic mechanisms underlying drought adaptation in natural grass populations (Brutnell et al., 2010; Jiang et al., 2013; Sebastian et al., 2014).

This study is therefore organized around a simple proposition: drought adaptation in wild grasses emerges from the interaction of ecological selection, population history, genome architecture, and multi-layered epigenetic regulation. The manuscript emphasizes recent literature, uses a molecular ecology lens throughout, and closes with a detailed *Setaria viridis* case analysis and a forward-looking agenda for conservation, adaptive restoration, and epibreeding.

2 Epigenetic Architecture and Molecular Ecology Framework

2.1 DNA methylation and transposable element regulation in drought adaptation

DNA methylation represents the most extensively studied epigenetic mechanism involved in plant responses to drought stress. In plants, cytosine methylation occurs in three sequence contexts, namely CG, CHG, and CHH, which are maintained through distinct but interconnected pathways. CG methylation is primarily maintained by METHYLTRANSFERASE 1 (MET1), whereas CHG methylation is regulated through the coordinated activities of CHROMOMETHYLASE 3 (CMT3) and SUVH-mediated feedback loops. CHH methylation is largely established and maintained through CMT2 and the RNA-directed DNA methylation (RdDM) pathway, while active DNA demethylation is mediated by DNA glycosylase-dependent mechanisms (Law and Jacobsen, 2010; Du et al., 2015; Bewick et al., 2017; Parrilla-Doblas et al., 2019).

In wild grass species, DNA methylation serves functions beyond simple promoter regulation. It plays a crucial role in silencing repetitive sequences and transposable elements (TEs), thereby maintaining genome stability under environmental stress conditions (Zemach et al., 2013; Sigman and Slotkin, 2016). Because many grass genomes contain exceptionally high proportions of transposable elements, epigenetic regulation of TEs becomes particularly important during drought adaptation. For example, transposable elements account for more than 80% of the wheat genome and substantially influence genome evolution and gene regulation (Wicker et al., 2018). Environmental stresses may induce TE activation or alter chromatin states surrounding TE-adjacent genes, leading to changes in gene expression patterns (Cavrak et al., 2014; Ito et al., 2011). Consequently, drought adaptation in grasses is closely associated with the interaction between epigenetic regulation and genome architecture, highlighting the importance of methylation-mediated control of repetitive genomic regions.

2.2 Histone modifications and chromatin state remodeling under drought stress

Histone modifications constitute a second major layer of epigenetic regulation involved in plant drought responses. Various histone marks influence chromatin structure and accessibility, thereby affecting the transcriptional activity