



Epigenetic Regulation of Drought Adaptation in Wild Grass Species

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Abstract This study synthesizes current knowledge on the epigenetic regulation of drought adaptation in wild grass species, with emphasis on DNA methylation, RNA-directed DNA methylation, histone modifications, chromatin accessibility, non-coding RNAs, and stress memory. We argue that epigenetic regulation should be treated not as an isolated molecular layer, but as part of a molecular ecology framework in which repeat-rich grass genomes, local climatic heterogeneity, transposable element control, developmental state, and population history jointly shape drought-responsive phenotypes. Mechanistically, the strongest conserved themes are: maintenance and remodeling of CG, CHG, and CHH methylation by MET1, CMT/SUVH, and RdDM pathways; dynamic coupling between DNA methylation and heterochromatin marks such as H3K9 methylation; the involvement of active chromatin states and accessibility changes in rapid stress-responsive transcription; and the potential for within-generation and, in some cases, transgenerational stress memory. From a molecular ecology perspective, we propose that the next generation of studies in wild grasses should combine environmental gradient sampling, common gardens, reciprocal transplants, and multi-omics assays such as whole-genome bisulfite sequencing, ATAC-seq, ChIP-seq or CUT&Tag, RNA-seq, and small RNA-seq. We then develop a detailed case analysis for *Setaria viridis* as an ideal wild-grass model for drought epigenomics and outline a publication-ready workflow integrating WGBS, ATAC-seq, histone profiling, and transcriptomics. Finally, we discuss how epigenetic knowledge can inform conservation genomics, restoration, epibreeding, and targeted epigenome editing, while also emphasizing key limitations, including causality, tissue heterogeneity, epigenetic resetting, and the still-limited number of direct field-based studies in natural wild-grass populations. Together, the evidence supports a transition from correlative stress epigenetics to predictive eco-epigenomics for dryland conservation and climate-resilient grass improvement.

Keywords Drought adaptation; Wild grasses; Eco-epigenomics; DNA methylation; RNA-directed DNA methylation; Chromatin accessibility; Stress memory; *Setaria viridis*; Conservation genomics; Epibreeding

1 Introduction

Grasslands and rangelands are under escalating pressure from climate change, drought, land degradation, and woody encroachment. Recent global assessments have emphasized that large fractions of the world's rangelands are already degraded, and climate-driven drought is increasingly interacting with land-use change to alter ecosystem structure, productivity, hydrology, and biodiversity. Because grasses dominate many open biomes and frequently determine both forage production and belowground carbon dynamics, understanding the biological basis of drought resilience in wild grass species is a conservation problem as much as a plant biology problem (Fortes and Gallusci, 2017). Furthermore, the increasing frequency and intensity of extreme drought events are expected to impose strong selective pressures on natural plant populations, making the identification of adaptive mechanisms a priority for both ecosystem conservation and climate-resilient agriculture (Auge et al., 2023).

At the same time, epigenetics has become central to plant environmental biology because it offers a mechanistic framework through which plants translate external stress signals into altered patterns of gene regulation without changing their underlying DNA sequence. Reviews published over the past decade have converged on the view that plant environmental memory can involve multiple interconnected mechanisms, including DNA methylation, histone modifications, chromatin remodeling, RNA-mediated regulation, and persistent stress priming across developmental stages or even generations (Law and Jacobsen, 2010; Du et al., 2015; Crisp et al., 2016; Lämke and Bäurle, 2017; Auge et al., 2023). In plants, these mechanisms are particularly important because sessile organisms cannot escape unfavorable environmental conditions and must continuously adjust their physiology,