

DNA methylation changes are predicted to occur more selectively, particularly within transposable element-rich regions and promoter-adjacent regulatory sequences. Repeated drought exposure may induce persistent epigenetic modifications that remain detectable after recovery, thereby contributing to drought stress memory. Such memory-associated loci may exhibit sustained chromatin accessibility or retention of active histone marks, allowing more rapid and robust transcriptional responses during subsequent drought events (Auge et al., 2023). These observations support the hypothesis that epigenetic memory functions as an adaptive mechanism enabling wild grasses to cope with fluctuating environmental conditions.

3.4 Adaptive interpretation and implications for grassland resilience

The interpretation of epigenetic variation in natural populations requires careful distinction between environmentally induced responses and genuinely adaptive modifications. Not all drought-induced epigenetic changes necessarily contribute to improved fitness. Therefore, adaptive significance should only be inferred when epigenetic features are consistently associated with drought tolerance across multiple accessions, persist following stress recovery, reappear during repeated stress cycles, correlate with environmental conditions at collection sites, or are experimentally validated through functional analyses (Springer and Schmitz, 2017; Fortes and Gallusci, 2017).

Several candidate regulatory modules are expected to play central roles in drought adaptation in *S. viridis*. These include ABA biosynthesis and signaling pathways, aquaporin-mediated water transport systems, late embryogenesis abundant (LEA) proteins, reactive oxygen species scavenging enzymes, and developmental regulators controlling flowering and reproductive success under water limitation. In addition, epigenetic regulators such as MET1, CMT2, CMT3, DRM2, AGO4, DDM1, and ROS1-like demethylases may directly influence the establishment and maintenance of adaptive chromatin states (Du et al., 2015; Zemach et al., 2013). Collectively, these findings highlight the potential of *S. viridis* as a powerful model for understanding how epigenetic mechanisms contribute to ecological resilience and drought adaptation in wild grass species.

4 Conservation, Epibreeding, and Future Directions

The conservation implications of drought epigenomics in wild grasses are substantial. If wild populations contain adaptive combinations of genotype and epigenotype shaped by local drought regimes, then conservation units should not be defined solely by neutral genetic structure. Instead, sampling strategies should deliberately capture climatic heterogeneity, especially along rainfall, aridity, and disturbance gradients. For seed banking and restoration, this means recording source moisture conditions, maternal environment, and regeneration procedures, because one practical risk is that *ex situ* propagation under benign conditions may erase or dilute ecologically relevant epigenetic states even when DNA sequence diversity is retained. In degraded drylands and encroached grasslands, restoration success may therefore depend not only on selecting locally adapted genotypes, but also on preserving environmentally calibrated regulatory states.

Epibreeding is the translational extension of this logic. In wild and semi-wild grasses, epibreeding should not be framed as replacing conventional breeding, but as adding a regulatory dimension to it. Three routes look most promising. The first is selection on stable natural epialleles that co-segregate with drought performance. The second is the deliberate use of stress priming, recurrent drought selection, or synthetic epigenetic populations to enrich favorable regulatory states before introgression or deployment. The third is epigenomic prediction, in which methylation and accessibility profiles are incorporated into models of drought performance alongside genotype and climate-of-origin data. This is especially attractive in complex, TE-rich grass genomes where many adaptive effects may be regulatory rather than coding.

Targeted epigenome editing offers a more direct future route. The RdDM literature now makes clear that locus-specific methylation can be induced in plants by engineered RNAs, hairpin constructs, or direct tethering of methylation machinery to specific loci, including CRISPR-based approaches. This is conceptually important for drought adaptation because it allows researchers to test whether methylation at a candidate promoter, enhancer, or TE actually changes phenotype without altering the underlying DNA sequence. For wild-grass research, that means moving from association to causality at candidate drought loci. In breeding terms, epigenome editing is