

especially appealing where reversible or regulatory tuning is desired and where sequence modification is either unnecessary or undesirable.

Several challenges remain. Causality is still the central bottleneck. Many epigenetic marks mirror altered transcription instead of driving it. Tissue heterogeneity can blur signal, especially in leaves and meristems. Developmental stage strongly conditions the methylome and chromatin landscape, making time-resolved sampling essential. In grasses, repetitive DNA complicates mapping and interpretation. Population structure can also produce false adaptive signals if methylation is analyzed without genetics. Finally, transgenerational claims require particular caution because many stress-associated marks are reset, diluted, or contingent on repeated exposure. A rigorous field will therefore require pangenome-aware references, repeated-stress designs, recovery sampling, and explicit modeling of genotype, environment, and life history.

The most productive research agenda for 2026 and beyond is, in my view, clear. It should combine wild-population sampling across eco-climatic mosaics, long-read or pangenome-enabled methylome mapping, accessibility and histone profiling in stress time series, small-RNA analysis, fitness-linked common gardens, and targeted validation in tractable model grasses such as *Setaria*. That agenda is sufficiently mechanistic for molecular ecology, sufficiently ecological for conservation biology, and sufficiently translational for epibreeding.

Figure 1 showing how epigenetic information can inform seed collection, drought-resilient restoration, conservation prioritization, adaptive management, and regulatory breeding pipelines.

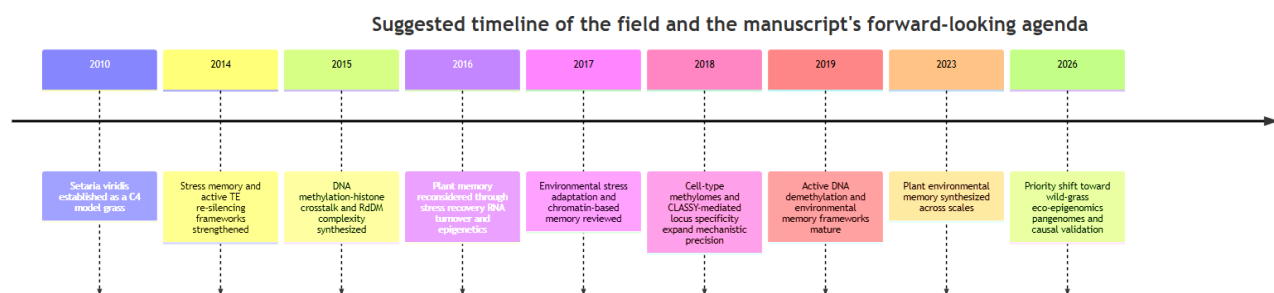


Figure 1 Conservation and epibreeding decision framework

5 Conclusions and Open Questions

Drought adaptation in wild grasses is not explained adequately by DNA sequence variation alone. The literature now supports a layered model in which drought cues are filtered through methylation pathways, histone-state transitions, accessibility changes, and small-RNA systems that collectively shape transcription, physiology, and potentially stress memory. This is especially relevant in grasses because of their ecological dominance in drylands and the regulatory importance of TE-rich genomes. The most secure mechanistic conclusions concern methylation pathway architecture, RdDM-mediated TE and stress regulation, and coupling between heterochromatin marks and gene control.

The main limitation of the current evidence base is taxonomic unevenness. Direct, multi-layer drought epigenomic datasets remain denser in model plants and crop systems than in truly wild grass populations, and integrated WGBS–ATAC–histone–RNA drought atlases are still rare for wild grasses. For that reason, *Setaria viridis* emerges as the most practical near-term organism for deriving causal, ecologically relevant insight that can later be transferred to less tractable taxa.

The most pressing open questions are these: Which epigenetic changes in wild grasses are adaptive rather than reactive? How stable are drought-associated states across development, dormancy, and seed regeneration? What fraction of field-relevant variation is controlled by cis-acting genetic differences versus environmentally induced epigenetic plasticity? How important are TE-adjacent regulatory changes in repeat-rich grass genomes? And can conservation and breeding programs deliberately preserve or induce beneficial regulatory states without