

**Review Article****Synthetic Rice Genome and Epigenetic Engineering: Emerging Strategies for Climate-Resilient Crops: Review Article****Rouya Mohammed Ahmed¹, Raghda Salim Sultan¹**¹Department of Biotechnology, College of Science, University of Baghdad, Baghdad, Iraq**Corresponding author:** Raghda Salim Sultan

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Email: raghda.s@sc.uobagdad.edu.iqDOI: <https://doi.org/10.71428/JHB.2026.0205>**Abstract**

Rice (*Oryza sativa*) is among the most important staple food crops in the world, serving as a main source of food security for approximately one-half of the world's population. Nevertheless, its cultivation is becoming compromised due to climate change, as repeated drought and saline soils, along with erratic temperatures, pose heavy restrictions on its yield. Traditional breeding and genetic engineering have contributed to enhancing crop performance; however, they are still constrained by the complex stress-responsive networks and by the time taken to develop tolerant cultivars. In order to overcome these challenges, technologies on the horizon, synthetic genomics and epigenetic engineering, are becoming game-changers in crop science. Synthetic genomics permits the refactoring and partial reassembly of plant genomes, thereby allowing new gene circuits to be built in, synthetic chromosomes to be installed, and multiplex editing via CRISPR-mediated alterations to increase drought tolerance or salinity resistance or boost photosynthesis in rice. Concurrently, epigenetic changes such as DNA methylation and histone modification, as well as non-coding RNA-mediated regulation, can impose a more dynamic and reversible layer of control on gene expression by modulating stress responses while leaving the actual DNA sequence unaltered. Emerging evidence indicates that certain epigenetic marks are capable of being 'remembered' across generations and could influence long-term resilience to stress. This review emphasizes the use of synthetic genomics-based epigenetic regulation as a new horizon in climate-resilient rice improvement.

Keywords: Synthetic Genomics; Epigenetics; CRISPR; DNA methylation; Climate Resilience.**Introduction**

Rice (*Oryza sativa*) is one of the most important staple crops in the world, providing almost a fifth of dietary energy intake for more than half of the world's human population and an important source of income for tens of millions of smallholder farmers in Asia, Africa, and other tropical/sub-tropical regions (1). But the continued sustenance of rice production in the near future is now being put under pressure. Global Need to Feed the World's

Population: Growth in global population would create a rapid and large-scale increase in demand for rice by 2050, while climate change is escalating the frequency and magnitude of environmental stresses (2). Episodes of severe droughts and saltwater intrusion leading to coastal soil salinization, coupled with occurring high temperatures during sensitive reproductive stages like flowering and grain setting, have been proven on various occasions to reduce yields by up to 50-60% in sometimes vulnerable

production systems (3). In traditional breeding, despite the great successes in creating new improved varieties over decades, old varieties remain mostly unchanged due to low genetic variance within elite germplasm, time-consuming multi-generation selection, and problems of concomitant amelioration of multiple traits controlled by various polygenic networks (4). In the same vein, first-generation genetic engineering approaches based on introducing or altering single genes tend to be of limited success when it comes to stress tolerance, since plant responses to drought, salinity, and heat are mediated by large and complex regulon networks, not discrete gene switches (5). In this regard, developments in synthetic genomics offer powerful new opportunities. And as opposed to using available allelic variation, the new field of synthetic genomics is now allowing for the redesign or even construction of genomic regions from scratch and rewiring metabolic and signaling networks that result in improved stress tolerance (6). Recent advancements in long-read sequencing technologies, pan-genome construction, and CRISPR-based multiplex genome editing now make it possible to precisely edit multiple loci regulating photosynthetic efficiency, ion transport, and hormone-signaling networks (7). In parallel, epigenetic engineering provides an additional layer

of regulation for controlling gene expression. Epigenetic pathways, such as cytosine methylation, histone modifications, and small RNAs, are involved in the plastic response of plants to environmental challenges that modulate gene transcription without changing the primary DNA sequence (8). A proportion of environmentally driven epigenetic marks are heritable, some for several generations, effectively forming ‘stress memories’ which can confer on offspring of polluted plants a level of stress resistance. Thus, the objective of this study is to provide a critical overview and unification of the recent advances in synthetic genomics (SynGen) and epigenetic engineering in general as well as in rice as a model or staple crop (9).

Conceptual Framework

The conceptual paradigm of this review is based on the convergence of these two realms of complementary innovation: Synthetic genomics and epigenetic governance. Whereas synthetic genomics concentrates on the rational redesign of genetic circuits, including multiplexed CRISPR editing, synthetic promoters, and even complete Generation IV-like chromosomes, epigenetic engineering enables arbitrated control over these circuits in an entirely reversible and often stress-responsive manner (10).

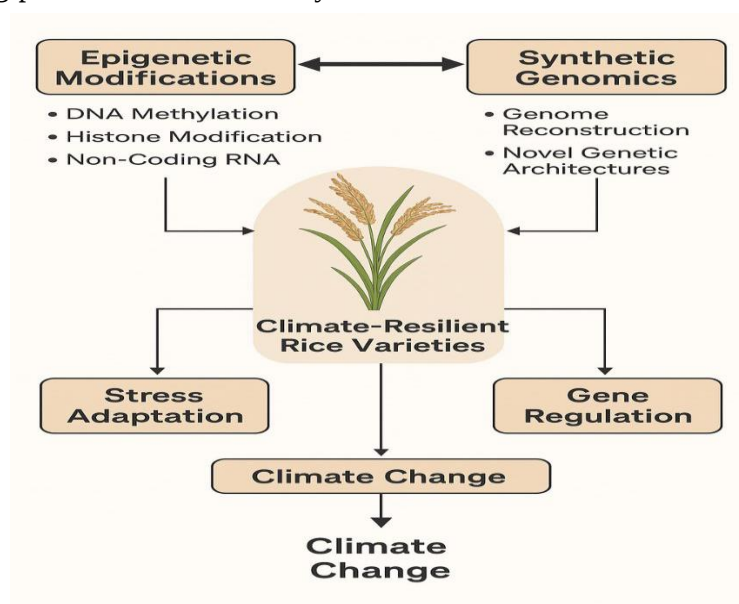


Figure 1. Conceptual framework of integrating synthetic genomics and epigenetic engineering in rice.

As depicted in Figure 1, the left panel corresponds to the genomic engineering layer that represents tailored modifications and synthetic constructs for stress-related pathways. In the middle, the epigenetic regulation layer (including three types of DNA methylation, CG, CHG, and CHH) is performed by histone acetylation or methylation, as well as small RNAs, to maintain transcriptional steadiness during adverse environments. The right panel represents the expected result, that is, enhanced physiological performance of rice plants under drought, salinity, or high temperature stress. The aim of this section is to present a simplified model that expresses genome-scale design and epigenetic plasticity in terms of conceptual entities so as to highlight the least-risk path for achieving true resilience: The case where both layers are tackled together rather than independently (11).

Scope and Novelty

Until recently, most synthetic genome building efforts have been focused on model systems such as yeasts and *Arabidopsis thaliana* for their fast growth and genetic amenability (12). Nonetheless, rice is now increasingly taking center stage due to its world significance, small genome size compared with other cereals, and the growing availability of high-quality reference sequences and the pan-genome data (13). Community-created pan-genomes of rice have revealed extensive structural and regulatory variations among the indica-japonica subspecies and among landraces adapted to different agro-ecological settings (14). This diversity is likely to serve as a useful basis for the design of synthetic genomic parts whose use can be extended to other environments. On the other hand, high-throughput CRISPR pipelines capable of targeting multiple loci at one time can be used to reprogram complex traits, like drought tolerance, ion transport, and photosynthetic efficiency (15). The innovation of these methods in rice is the development of species-oriented design strategies. Stress-induced promoters, for example, help create a conditional

environment in which the synthetic circuits cannot be activated unless a stressful condition is present, and therefore prevent fitness costs to the host under non-stressful conditions (16).

Methodological Foundations

Synthetic Genomics Toolkit

- Synthetic genomics in rice has developed with rapid strides by virtue of the amalgamation of sequencing technology, computational design, and multiplex genome-editing systems. The development of high-quality long-read sequencing technologies, such as PacBio and Oxford Nanopore, has enabled near-complete assembly of reference genomes and pan-genomes that include the full range of genetic diversity across indica, japonica, and traditional landraces (17). These assemblies provide a reference for structural variation, regulatory hotspots, and candidate loci that can be synthetically re-designed for stress resilience.
- CRISPR-based multiplex editing has become one of the most powerful tools in rice synthetic genomics. While single-locus editing is possible, with multiplex CRISPR technology researchers can target many genes or regulatory elements at once and re-code entire pathways involved in photosynthesis, ion homeostasis, or hormone signaling. Recent uses have combined the editing of photosynthetic genes to make them more efficient under fluctuating light or drought (18).
- A second key component of the synthetic genomics repertoire is the construction of synthetic regulatory elements. Stress-responsive promoters and synthetic enhancers might be used to ensure that engineered circuits only function when conditions are unfavorable, avoiding unnecessary energy expenditure in good conditions (19). The inclusion of insulator sequences is designed to minimize regulatory crosstalk between synthetic and endogenous gene networks, while copy number control ensures that

stable expression is achieved in future field generations (20).

- This subsection provides an overview of the major genomic tools—sequencing, multiplex editing, and regulatory part design—that establish the basis for successful application of synthetic biology to rice in order to develop resilient stress-tolerant cultivars that are robust in the field.

Epigenetic Engineering Toolkit

- Epigenetic manipulation provides a new complementary and more rapidly adjustable approach in the crop production pool, characterized by changes in gene expression that do not involve any alteration in the nucleotide sequence itself. In rice, all layers of epigenetic regulation (DNA methylation, histone modifications, and small RNAs) interact in complex ways to regulate the stress-responsive pathways and silence transposable elements (TEs) under unfavorable conditions (21).
- DNA methylation at cytosine sites includes mainly CG, CHG, and CHH (where H represents any nucleotide besides G) and is catalyzed by MET1, CMT3, and DRM2. Stress-caused methylation changes can have both activating and suppressing impacts on certain loci, affecting phenotypic plasticity. For example, drought and salinity stress have been associated with differential methylation at the promoters of ion transport and transcription factor genes in rice (22).
- Histone modifications bring yet another level of regulation. For example, marks like H3K4me3 modulate active transcription, while generators of H3K27me3 and H3K9me2 are players in gene silencing. Chromatin accessibility and 3D genome architecture during drought-responsive H3K9ac were demonstrated to reorganize marking in rice (23). The two above-mentioned uranium-induced histone modifications are of a reversible nature, enabling plants to fine-tune their transcriptional programs in changing environments.
- Small RNAs, such as microRNAs (miRNAs) and 24-nt small interfering RNAs (siRNAs), additionally modulate epigenetic regulation by directing DNA methylation and post-transcriptional silencing of stress-responsive targets. In rice, a few miRNAs were characterized to directly regulate stress signaling pathways that connect environmental signals and rapid regulatory changes (24).
- Recent developments in synthetic biology have brought dCas9-based epigenome editors, which comprise Cas9 proteins that are catalytically dead and linked to methyltransferases, demethylases, or histone acetyltransferases. These programmable systems allow locus-specific and reversible modulations of chromatin states, and can be used to either turn on or off the expression of stress-related genes without changes in DNA sequence (25).
- In this subsection, we aim to overview the online news major approaches of epigenetic engineering (i.e., DNA methylation, histone modifications and RNA-mediated pathways), with a focus on the synthetic potential to stabilize stress tolerance in rice without compromising genome integrity.

3D Genome Dynamics

Three-dimensional (3D) genome organization is an essential but less understood dimension in plant stress biology. Methods such as Hi-C and chromatin conformation techniques have shown that the rice genome undergoes global topological reorganization in response to either drought or salinity stress (26). These changes involve paragraphing of chromatin loops, the exchange between A and B compartments in the genome, and changing long-range interactions between enhancers and promoters. This dynamic remodeling determines whether essential stress-responsive genes are available to the transcriptional machinery and, in turn directly influences the ability of the plant to initiate rapid defense responses. From the perspective of synthetic biology, manipulation of 3D genome dynamics represents unprecedented

opportunities. Synthetic enhancers or designed regulatory modules may also be located in genomic neighborhoods when it is adjacent to the target loci, to increase stress-inducible responses. Likewise, insulation features are potential factors that can be incorporated to fix desirable topological domains and reduce unwanted crosstalk with other pathways. New studies have shown that the histone acetylation mark H3K9ac is frequently enriched in regions of stress-induced topological remodeling (27). This

would imply that 3D genome engineering and epigenetic editing can be used to “lock in” beneficial chromatin states, which are resilient across stress cycles (both responsive and stable). The purpose of this subsection is to emphasize the contribution of 3D chromatin organization toward stress adaptation and illustrate how synthetic genomics can use topological applications to construct better regulatory circuits in rice.

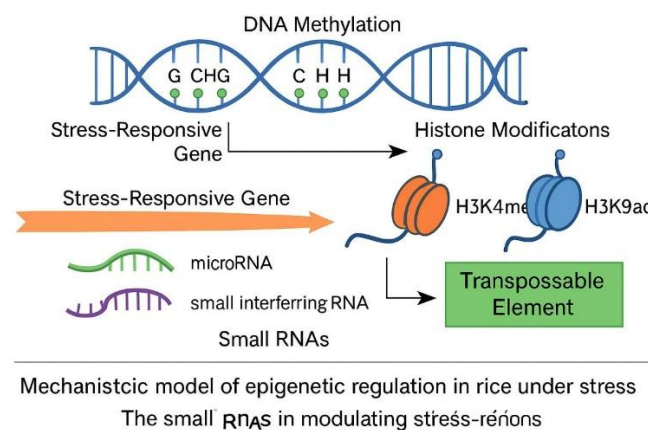


Figure 2. A mechanistic model for epigenetic regulation in rice responses to stress.

Figure 2 represents DNA methylation at CG/CHG/CHH contexts, H3K4me3, H3K27me3 and H3K9ac modifications, and the action of small RNAs in regulating stress-responsive genes and silencing transposable elements, which contribute synergistically to rice in adapting to drought, salt or heat stress (28).

Integration of Synthetic and Epigenetic Approaches

One of the key messages of this review is that synthetic genomics and epigenetic control are not isolated strategies or mutually exclusive options, but they complement each other in providing a powerful combination that can be implemented as an integrated approach for crop improvement. Synthetic genomics (such as new circuits, synthetic promoters, or multiplex editing) gives the structural frame, while epigenetic engineering maintains and

stabilizes their activity in dynamic fields where rice plants are growing (29). For instance, the artificial regulatory network can be established to induce genes responding to drought stress (e.g., OsDREB2 or SNAC1) in response to water deficit. But these circuits are likely to be silenced, or expressed with variable patterns without epigenetic strengthening. Pairing synthetic constructs with engineered epigenetic marks - for example, site-specific DNA demethylation or histone acetylation – also holds the potential to render these constructs stable over multiple cycles of stress followed by recovery (30). On the contrary, epigenetic alterations that develop in response to stress may be transient and flexible. Synthetic genomics provides the means to “hard-wire” these favorable regulatory states into engineered networks so that desirable responses are not only inducible, but are also robustly transmitted

in future generations. Thus, this dual-layer approach combines fast response with long-term stability and represents one of the most long-standing challenges in a climate-resilient breeding program. Here, we show how synthetic genomics and epigenetics merge

in a long-lasting integration – fast activation from the synthetic circuits empowered by an aesthetic of memory – paving the way for a robust approach to deliver climate-resilient rice lines ready for deployment (31).

Table 1. Comparison of Synthetic Genomics and Epigenetic Engineering Technologies in Rice

Aspect	Synthetic Genomics	Epigenetic Engineering
Mechanism	De novo design or large-scale genome editing to create synthetic circuits, genes, or chromosomes	DNA methylation, histone modifications, and non-coding RNAs regulating gene expression without changing DNA sequence
Precision	High when using multiplex CRISPR/Cas9; potential off-target edits remain a challenge	Locus-specific targeting possible with CRISPR-dCas9 epigenetic modifiers; often reversible
Advantages	Enables introduction of novel traits, pathway rewiring, and genome-scale redesign	Dynamic and reversible regulation; potential for stress “memory” and transgenerational inheritance
Limitations	Technically complex, costly, potential regulatory and ethical barriers	Variable stability of modifications; may fade across generations or environments
Examples in Rice	Synthetic apomixis for hybrid seed production (Dan et al., 2024); multiplex photosynthetic gene editing (Patel-Tupper et al., 2024)	DNA methylation regulating drought/salinity tolerance (Li et al., 2025; Yin et al., 2024); histone acetylation under drought (Chang et al., 2024)

Climate Resilience and Field Application and Transgenerational Stability

Although progress in synthetic genomics and epigenetic engineering is promising in controlled environments, achieving stable field-ready traits remains challenging. Laboratory results showing improved drought, salinity, and heat tolerance often fail to translate consistently under diverse field conditions. Multi-environment trials and long-term monitoring are essential to evaluate yield stability, water-use efficiency, and transgenerational epigenetic inheritance. Standardized field-relevant indicators—such as survival rate, Na⁺/K⁺ balance, and grain yield stability—should guide assessment across locations and seasons. Linking laboratory success to field validation and ensuring durable inheritance of engineered traits are crucial steps for integrating synthetic and epigenetic tools into mainstream rice breeding programs (32).

Ethical, Social, and Regulatory Considerations

The implementation of synthetic genomics and epigenetic engineering in rice improvement demands not only technical success but also ethical responsibility and social acceptance. Biosafety and regulatory preparedness remain the key concerns, as synthetic circuits or epigenetically modified traits could potentially interact with wild relatives or be misclassified under current GMO laws. Establishing unified international regulations, transparent risk assessment, and effective communication with farmers and consumers are essential to gain public trust. Moreover, equitable access to these technologies must be ensured through open-source databases, fair intellectual property frameworks, and participatory breeding initiatives so that smallholder farmers, especially in developing regions, can benefit equally from scientific innovation (33).

Future Perspectives and Challenges

The future of synthetic and epigenetic engineering in rice relies on global collaboration, cost-effective genome editing platforms, and field validation across diverse environments. Although multiplex CRISPR and dCas9-based epigenome editing show promise, challenges such as off-target effects, limited field trials, and variable heritability of artificial epigenetic marks still hinder large-scale application. Establishing standardized evaluation criteria, long-term multi-site testing, and transparent regulatory policies will be crucial to translate laboratory breakthroughs into resilient rice cultivars. Ultimately, combining international cooperation with open-access data sharing and public awareness will determine whether these technologies can secure sustainable rice productivity under accelerating climate pressures (34).

3D Genome Dynamics

A newly discovered category of epigenetic regulation in rice is the three-dimensional (3D) structure of the genome, which influences proximity among genes, promoters, and enhancers in nuclear organization. Chromatin is not randomly arranged; it's neatly looped, and its constituents are held in various higher-order compartments that affect which regulatory elements can speak to each other. Recent Hi-C analyses in rice have shown that stress signals such as drought and salinity can lead to massive restructuring of the chromatin loops and compartments (35).

Small RNAs & TE Control

Small RNAs form a central part of epigenetic regulation in rice and provide fast, sequence-specific gene regulation. General mechanisms: By and large, the targets of miRNAs are stress-responsive transcription factors at the post-transcriptional level, in this way ensuring stringent control of major pathways such as ABA signaling and ion homeostasis during drought (and salinity) stress. 24-nt siRNAs, in contrast, are the mobile signal that guides the RNA-directed DNA methylation (RdDM)

pathway to establish additional methyl marks at locations throughout the genome and help shape long-term transcriptional programs (36). In addition to modulating defence-related genes, small RNAs are also a key component in the regulation of TE silencing and genome stability. Environmental stresses may trigger TEs, resulting in genome instability and possibly gene breakdown. In rice, 24-nt siRNAs target methylation of TE loci to block their mobilization and maintain genome integrity through stress cycles (37).

Design Constraints for Synthetic Circuits

Effective introduction of synthetic circuits in rice does not only rely on editing efficiency but also on design constraints that affect functionality under field conditions. Perhaps the most important is that of promoter selection. Although strong expression can be achieved using constitutive promoters, these often impose growth costs in a normal environment. By contrast, stress-inducible promoters are active under only unfavorable conditions, thereby saving energy and minimizing pleiotropic effects. Thus, the choice of promoter is now critical to the optimization of response and agronomic suitability (38).

Multiplex CRISPR Quality Control

Although CRISPR-based editing has emerged as a foundational tool for synthetic genomics, the complexity of multiplex editing also presents greater potential for off-target modifications. Editing many loci at once increases the likelihood of off-target modifications that could disrupt non-corresponding genes or regulatory elements and result in unknown phenotypes. These are particularly problematic in rice breeding because unintended changes in yield- or stress-related pathways can damage field performance. To minimize such risks, tight quality control (QC) pipelines are crucial. Prediction tools are available to design guides with low off-target potential by scanning the rice genome for near matches. The predictions need to be tested experimentally by amplicon deep sequencing with

base-level resolution for both target and theoretical off-targets (39).

Field-Relevant Metrics

For it to be possible for both synthetic and epigenetic innovation in rice to progress beyond the proof-of-concept stage, it is essential that research outputs are reported using standard field-relevant parameters. Far too often, research papers focus on molecular changes or laboratory stress assays and do not clearly relate these to agronomic performance. Developing a common set of evaluation criteria would enable comparisons between studies and make it clear which methods are most suitable for breeder pipelines (40). Primary traits should include grain yield under drought or salinity stress, because of farmer's perspective, yield stability is the most crucial trait. Survival percentiles under acute stress in fish also offer an additional resilience index. Na^+/K^+ ratio is a common physiological indicator for salinity stress, and WUE integrates the responses of physiology with agronomy to drought. Lastly, grain quality traits (amylose content, chalkiness, and protein content) will make sure that the enhancement of stress tolerance does not carry a penalty in terms of consumer or market acceptance (41).

Conclusion

The review underlines that the convergence of synthetic genomics and epigenetic engineering is a game-changing pathway for rice improvement in the era of climate change. Although conventional breeding and genetic engineering technology have both played key roles in yield and stress tolerance improvement, they are unable to deal with the multigenic responses mandated by climate-induced stresses. Thus, using synthetic genomics, one can engineer new genetic architectures and pathways that do not have to be limited by the constraints of natural variation, while epigenetic control adds a flexible and reversible layer of regulation over stress-responsive genes. Together, they constitute a dual strategy that improves structural genome capacity and dynamic gene expression regulation.

For rice, a staple food for almost half of the world's population, synthetic and epigenetic technologies can be applied to generate stress-resistant varieties (drought-, salt-, and heat-resistant). The heritability of environmentally induced epigenetic states across generations raises the prospect that memory may be stored, and crops 'hardened' against stress in subsequent generations. On the other hand, synthetic genome design enables implementation of new pathways—such as optimized photosynthesis or stress-inducible circuits—impossible by means of breeding. Some challenges remain, including the need for field validation, cost-effective editing platforms transferable to developing-country breeders, and issues related to ethics, biosafety, and regulation. Future success will depend on international collaboration, the establishment of open-access genomic and epigenomic databases, and the development of clear regulatory policies. By combining the design power of synthetic genomics with the regulatory precision of epigenetics, a new trajectory for climate-resilient rice can be envisioned for researchers and breeders. This not only ensures the sustainability of one of the world's most important staple crops but also sets a precedent for broader agricultural innovation and a model for addressing food security in an era of climate change

Conflict of interest: NIL

Funding: NIL

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