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Editing crops for a hotter planet: how CRISPR is creating climate-smart agriculture

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Abstract

Rising temperatures, erratic rainfall and expanding soil salinity are steadily eroding the productivity of the crop varieties farmers rely on today. Conventional breeding can respond, but it usually needs eight to twelve years to move a single useful gene into an elite background. Genome editing based on clustered regularly interspaced short palindromic repeats (CRISPR) offers a faster and more targeted route. This article explains how heat, drought and salinity damage plants at the cellular level. It then describes the current editing toolbox of nucleases, base editors, prime editors and expression tuners and reviews genes that have already been edited for climate resilience in rice, maize, wheat, tomato and orphan crops. It also covers the pipeline from candidate gene to field trial, the sharply divergent regulatory positions across countries and the practical limits of single-gene editing for traits that are inherently polygenic.

Keywords: Temperature, conventional, salinity, productivity, genome, breeding

Introduction

Farming has always depended on the weather, but the weather is no longer behaving the way it did when today's major crop varieties were bred. Heat waves arrive earlier, rainfall is less predictable and coastal soils are turning saltier. The numbers are sobering. A synthesis of four independent modelling approaches estimated that, without adaptation, each additional degree Celsius of global mean warming reduces global yields of wheat by about 6 per cent, rice by about 3 per cent, maize by about 7 per cent and soybean by about 3 per cent (Zhao *et al.*, 2017).

At the same time, the world needs more food, not less. Conventional breeding can help, but it is slow. Moving a useful gene from a wild relative into an elite variety usually takes eight to twelve years of crossing and selection and undesirable linked genes are often transferred along with the target gene, a problem known as linkage drag (Kumar *et al.*, 2025). Marker-assisted selection (MAS) has partly addressed these constraints by allowing breeders to track target loci with deoxyribonucleic acid (DNA) markers rather than phenotype alone, thereby shortening selection cycles and reducing donor-genome carryover; even so, MAS still depends on recombination and repeated backcrossing and it remains inefficient for highly polygenic traits such as drought tolerance (Kumar *et al.*, 2025). CRISPR changes that arithmetic. It lets breeders rewrite a specific gene in an elite variety directly, without the long detour of repeated backcrossing. This article looks at what CRISPR can realistically do for climate resilience, which genes are already being edited, what the field data show and where the honest limits lie.

What climate stress actually does to a plant

Before editing a gene, it helps to know what is breaking. Heat, drought and salinity are distinct stresses, but they converge on similar damage inside the cell. Heat stress is most damaging around flowering. Pollen development is highly temperature sensitive and a few hot days at the wrong moment can cause widespread sterility. High night temperatures also shorten the grain-filling period, so grains are lighter. Drought triggers stomatal closure, which conserves water but also restricts carbon dioxide uptake and therefore photosynthesis. Salinity acts twice: first as an osmotic constraint that mimics drought and later as ion toxicity as sodium accumulates in leaves (Balasubramaniam *et al.*, 2023).

All three stresses generate reactive oxygen species (ROS). At low concentrations these molecules act as signals, but in excess they damage membranes, proteins and chloroplasts (Sachdev *et al.*, 2021). Importantly, these stresses rarely occur alone. Combined drought and heat produces responses that cannot be predicted by adding the two single-stress responses together, which matters a great deal when choosing editing targets (Sato *et al.*, 2024). Figure 1 summarises how each stressor maps onto physiological damage and then onto editable genes.

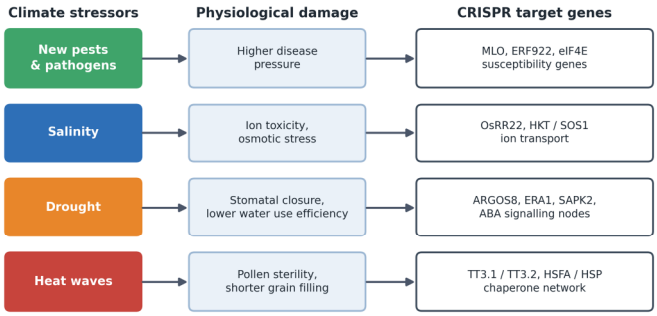

Figure 1. From climate stressors to physiological damage and the corresponding CRISPR target genes discussed in this article

The CRISPR toolbox, briefly

Most people picture CRISPR as molecular scissors and the original CRISPR-associated protein 9 (Cas9) system does work that way. A guide ribonucleic acid (guide RNA) directs the Cas9 protein to a matching DNA sequence, Cas9 cuts both strands and the cell repairs the break imperfectly. The resulting small insertions or deletions usually knock the gene out. That is useful when the goal is to remove a negative regulator or a susceptibility gene.

But knocking genes out is a blunt instrument and the toolbox has grown considerably. Base editors change a single DNA base pair, C to T or A to G, without cutting both strands. Prime editors use a reverse transcriptase (RT) fused to a nicking Cas9 and can write short, defined sequences, including small insertions and deletions (Anzalone *et al.*, 2020). Prime editing was demonstrated in rice and wheat soon after it was first developed in human cells (Lin *et al.*, 2020). A catalytically dead Cas9 (dCas9) can also be fused to activation or repression domains, letting breeders turn a gene up or down instead of destroying it. Figure 2 compares these four modes.

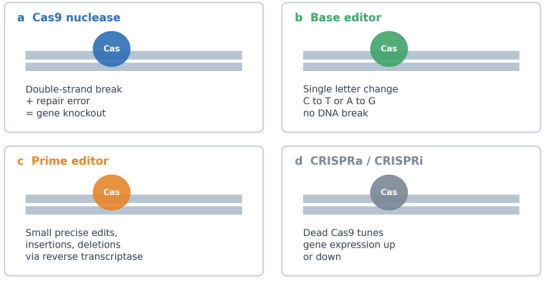

Figure 2. The main CRISPR editing modes used in crop improvement, namely nuclease-based knockout, base editing, prime editing and transcriptional tuning with a catalytically dead Cas9 (dCas9)

The distinction matters for climate traits. Stress-tolerance genes are often dose sensitive. Complete loss of function can protect the plant under stress but cost yield in a favourable season. Base editing and promoter tuning allow more subtle adjustments, which is often what a breeder actually wants. Table 1 sets out the practical trade-offs.

Table 1. Comparison of the main genome editing approaches used in crops

Approach	What it does	Typical use in climate traits	Main limitation
Cas9 nuclease	Double-strand break; repair errors cause knockout	Removing negative regulators or susceptibility genes	No precise substitution; off-target risk
Base editors (C to T, A to G)	Single base-pair change without a double-strand break	Fine-tuning enzyme activity or splice sites	Limited range of base changes and narrow target windows
Prime editing	Writes short defined sequences using a reverse transcriptase (RT) fusion	Installing favourable alleles found in landraces	Lower efficiency in many crop species
dCas9 activation or repression	Alters expression without changing the coding sequence	Adjusting the dose of a stress-response gene	Requires the editing construct to be retained in the genome, so the effect is lost in transgene-free segregants
Promoter or cis-element editing	Alters regulatory sequence	Creating a continuous range of expression levels	Needs good knowledge of the promoter

Genes that are already being edited

Heat. The clearest recent example in rice comes from the THERMO-TOLERANCE 3 (TT3) locus, where researchers identified two genes with opposing effects, TT3.1 and TT3.2. TT3.1 encodes a RING-type E3 ubiquitin ligase. Under heat stress it relocates from the plasma membrane to endosomes and promotes the degradation of TT3.2 and the resulting reduction in mature TT3.2 protects chloroplasts from thermal damage. Combining the tolerant TT3.1 allele with a reduced-function TT3.2 allele raised grain yield under field heat stress (Zhang *et al.*, 2022). The benefit came from adjusting the balance between two genes, not from simply deleting one. Broader reviews describe a layered network of heat shock transcription factors, chaperones and membrane-associated sensors, many of which are now realistic editing targets (Xing *et al.*, 2024; Xiong *et al.*, 2025).

Drought. The most cited field example remains maize ARGOS8. Rather than knocking the gene out, the researchers used CRISPR-Cas9 with homology-directed repair (HDR) to insert the moderate constitutive maize GOS2 promoter upstream of ARGOS8 or to replace the native promoter with it, so that the gene was expressed more widely. ARGOS8 is a negative regulator of ethylene signalling and reduced ethylene sensitivity is associated with better performance under water deficit. In multi-location field trials the edited lines produced roughly five bushels per acre more grain, about 0.3 tonnes per hectare, than controls under flowering-stage drought, with no yield penalty under well-watered conditions (Shi *et al.*, 2017). The gain is modest and that honesty is useful. The reverse experiment is equally informative. Knocking out SlMAPK3 in tomato reduced drought tolerance, showing that editing can also establish which genes are genuinely protective before a breeding programme is committed (Wang *et al.*, 2017).

Salinity. Rising sea levels and irrigation-driven salt accumulation are pushing salinity up the priority list. CRISPR-Cas9 knockout of OsRR22, a transcription factor acting in cytokinin signalling, produced rice lines with markedly better shoot growth and survival under salt stress at the seedling stage, while agronomic performance under non-saline conditions was essentially unchanged (Zhang *et al.*, 2019). The evaluation was carried out under controlled salt treatment rather than in multi-season saline field trials, so the result should be read as a promising proof of concept.

Disease under a shifting climate. Warmer and wetter conditions expand the range of many pathogens, so disease resistance is part of climate resilience. Loss of function of the Mildew resistance Locus O (MLO) genes in wheat confers strong powdery mildew resistance, but has historically been accompanied by stunted growth and yield loss. By editing the locus to create a specific allele, Tamlo-R32, which carries a large targeted deletion that alters expression of the neighbouring gene TaTMT3B, researchers obtained resistance without the growth penalty (Li *et al.*, 2022). Figure 3 shows how such discoveries move from the laboratory to a field-tested line and Table 2 collects the main published examples.

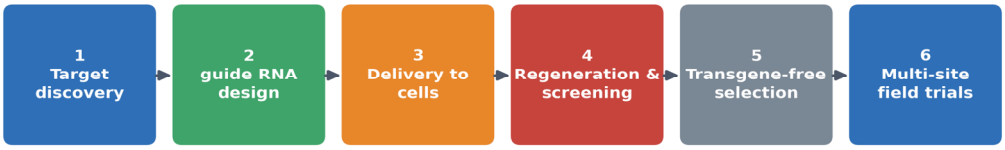

Figure 3. Workflow from target gene discovery through guide RNA design, delivery, regeneration, selection of transgene-free plants and multi-site field evaluation

Table 2. Selected CRISPR-edited genes linked to climate resilience in crops

Crop	Gene or locus	Edit type	Stress addressed	Reported outcome	Reference
Rice	TT3.1 / TT3.2	Allele combination (tolerant TT3.1 with reduced-function TT3.2)	Heat	Higher grain yield under field heat stress	Zhang *et al.* (2022)
Maize	ARGOS8	Promoter insertion or replacement (GOS2 promoter)	Drought	About 5 bushels per acre (about 0.3 t/ha) gain under flowering-stage drought; no penalty under well-watered conditions	Shi *et al.* (2017)
Rice	OsRR22	Knockout	Salinity	Improved seedling growth and survival under salt stress	Zhang *et al.* (2019)
Wheat	MLO (Tamlo-R32)	Targeted deletion	Powdery mildew	Resistance without growth or yield penalty (Tamlo-R32 allele)	Li *et al.* (2022)
Tomato	SlMAPK3	Knockout	Drought	Reduced drought tolerance, confirming a protective role	Wang *et al.* (2017)
Groundcherry	SP, SP5G, CLV1	Knockout	Rapid domestication	Improved plant architecture and fruit size in an orphan crop	Lemmon *et al.* (2018)

Figure 4 places the reported magnitudes side by side, which is a useful corrective to over-optimistic headlines.

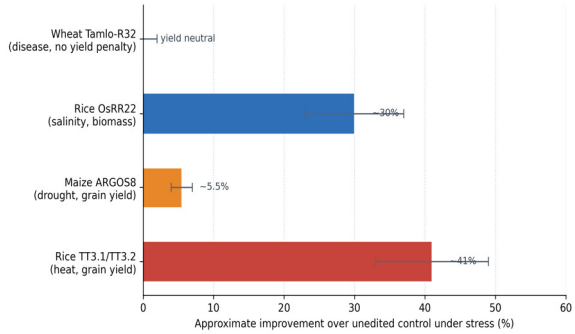

Figure 4. Approximate improvement of selected edited lines over unedited controls under the relevant stress. Values are indicative and drawn from the studies cited in Table 2. Trial conditions differ between studies, so the bars should be compared with caution.

Orphan crops and the equity question

Most editing effort has gone into rice, maize, wheat and tomato. Yet the crops that feed many climate-vulnerable regions, such as millets, teff, cowpea and groundcherry, receive far less attention. CRISPR offers a shortcut here. Instead of domesticating a wild species over centuries, researchers can edit the small number of genes that control plant architecture, flowering time and fruit size. Lemmon *et al.* (2018) did exactly this in groundcherry, improving several domestication traits within a few generations. This is arguably where CRISPR could matter most. Orphan crops are often already tolerant of heat and poor soils. What they lack is yield and harvestability and those traits respond well to targeted edits.

Regulation, cost and public trust

A genome-edited plant that carries no foreign DNA can be indistinguishable from one carrying a naturally occurring mutation. Regulators have reacted very differently. Several countries, including Argentina, Brazil, Japan and the United States, assess such plants case by case and generally exempt transgene-free edits from the rules applied to genetically modified organisms (GMOs) (Entine *et al.*, 2021). The European Union, following a 2018 Court of Justice ruling, has treated them as GMOs, although legislative reform on new genomic techniques has been under negotiation since 2023. Because regulatory status is changing in several jurisdictions, readers should check current national rules rather than rely on any single review.

Regulation is not the only barrier. Transformation and regeneration remain difficult in many important genotypes and intellectual property around Cas enzymes complicates deployment in low-income countries. Public acceptance also depends heavily on framing: new plant breeding technologies are more likely to be accepted when the benefit is visible to farmers and consumers rather than only to seed companies (Qaim, 2020).

What CRISPR cannot do

Some honesty is needed. Climate resilience is not a single trait. Yield under stress depends on many loci, on root architecture, on phenology and on how the crop interacts with soil biology and such polygenic traits remain difficult to improve by manipulating one locus at a time (Kumar *et al.*, 2025). A single edit rarely delivers a large gain, as the ARGOS8 result shows. Editing also cannot substitute for irrigation infrastructure, soil management, crop diversification or emissions reduction. There is a trade-off risk as well. Genes that protect against stress often slow growth and plants that close their stomata early save water but fix less carbon. The most valuable edits are those that decouple protection from cost, as the wheat MLO work achieved (Li *et al.*, 2022). Finally, most published results come from controlled environments or a small number of field sites. Multi-year, multi-location testing under realistic combined stress is the step that turns a promising line into a usable variety and it is the step most often missing.

Conclusion

CRISPR will not, on its own, climate-proof agriculture. What it does change is the speed and precision of the response. Breeders can now test a hypothesis about a stress-tolerance gene within a few seasons instead of a decade and they can install a favourable allele in an elite variety without dragging in unwanted linked genes. The examples in Table 2 show that the gains are real but usually incremental and that the most successful edits are those guided by a clear mechanistic understanding of the trait. The near-term priorities are straightforward: mine natural alleles from landraces and install them by prime editing, use multiplex editing for polygenic traits, extend transformation to more genotypes and to orphan crops and test candidate lines across multiple years and sites (Atia *et al.*, 2024). Genome editing is also most powerful when it is embedded in, rather than separated from, existing molecular breeding pipelines, where marker-assisted selection and genomic selection are used to move validated edits into locally adapted backgrounds (Kumar *et al.*, 2025). Used sensibly, CRISPR is best understood as a way to make breeding faster and more precise, not as a replacement for it. On a hotter planet, speed is exactly what breeding programmes need.

Conflict of Interest

The authors declare no competing or conflict of interest.

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