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Systematic Review

CRISPR-Based Genome Editing for Climate-Smart Agriculture: Advances, Regulation, and Field Performance

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ABSTRACT

CRISPR-based genome editing has moved from laboratory proof-of-concept to field-tested crops with improved tolerance to heat, drought, salinity, pests, and diseases. This PRISMA-guided systematic review assessed advances, regulation, and field performance of CRISPR-edited crops for climate-smart agriculture. Structured searches, dual-stage screening, standardised extraction, risk-of-bias appraisal, subgroup and sensitivity analyses, and GRADE assessment were used. SDN-1 knockouts were the most widely tested and most consistently field-validated, base and prime editing expanded precision but had less multi-environment field evidence, and edited varieties combined with climate-smart agronomy showed the most stable field performance in selected studies. Regulation varied widely: product-based systems treated many SDN-1 / SDN-2 edits without foreign DNA more lightly, while process-based systems treated edited crops as GMOs. The review provides an integrated framework for choosing editing targets, validating edits, navigating regulation, and delivering edited varieties through seed systems.

Keywords: CRISPR; genome editing; climate-smart agriculture; regulation; field performance; systematic review; PRISMA; GRADE

1. Introduction

Climate-smart agriculture aims to achieve three goals at once: sustainably increase productivity, build resilience to climate change, and reduce greenhouse gas emissions where possible (FAO, 2013; Lipper et al., 2014). Heat, drought, salinity, flooding, pests, and diseases are increasing in frequency and severity, and they often co-occur. Conventional breeding has made important gains, but it is slow, especiall

y for complex traits, and it is limited by available genetic variation and by linkage drag, where an undesirable gene is inherited together with a desirable one (Chen et al., 2019; Zhang et al., 2021).

CRISPR-based genome editing offers a faster, more precise way to create useful variation. The CRISPR-Cas system uses a guide RNA to direct a Cas nuclease to a specific DNA sequence, where it creates a double-strand break or a precise base change (Jinek et al., 2012; Doudna and Charpentier, 2014). The plant then repairs the break, often with a small deletion, insertion, or substitution that can knock out a negative regulator, change a promoter, or alter a protein. Unlike many transgenic approaches, genome editing can produce plants with no foreign DNA in the final product, especially when the editing machinery is segregated away in later generations (Chen et al., 2019).

Previous reviews have often addressed one tool, one trait, or one regulatory system at a time, without explicit search methods, risk-of-bias appraisal, GRADE certainty assessment, or comparison across tools and environments. This review is designed to be stronger by (i) following PRISMA 2020 (Page et al., 2021), (ii) stating a PICOT question and eligibility criteria, (iii) reporting a reproducible search, (iv) appraising risk of bias, (v) conducting subgroup, sensitivity, and crop case-study analyses, (vi) grading certainty with GRADE (Guyatt et al., 2008), (vii) integrating regulation, economics, and seed systems, and (viii) providing a framework from edit to field. The review question was: In crops grown under climate stress, what are the advances, regulatory pathways, and field performance of CRISPR-based genome editing, with what certainty, modifiers, and trade-offs, and what determines translation into farmer-adopted varieties?

2. Methods

2.1 Protocol, reporting, and PICOT

The review followed PRISMA 2020 (Page et al., 2021). The protocol defined the review question, eligibility criteria, outcomes, extraction fields, and appraisal approach before synthesis.

Table 1 summarises the PICOT framework that defines the population, intervention, comparator, outcomes, and timing for this review.

Table 1. PICOT framework.

PICOT element	Definition used
Population	Crops under heat, drought, salinity, pest, or disease stress; edited lines and varieties
Intervention	CRISPR-based genome editing: Cas9, base editing, prime editing, CRISPRa / CRISPRi
Comparator	Conventional breeding, unedited control, or transgenic control
Outcomes	Primary: field yield under stress, stability, trait improvement. Secondary: edit confirmation, off-target, regulation, adoption
Timing / Type	One or more seasons; greenhouse, field, multi-environment, on-farm trials

2.2 Eligibility criteria

Studies were eligible if they met all of the following: (a) a CRISPR-edited crop with a defined edit, gene target, and delivery method; (b) a climate-smart trait, including heat, drought, salinity, disease, nitrogen use, or grain quality; (c) at least one outcome among edit confirmation, trait change, yield under stress, or re

gulatory / field performance assessment; and (d) publication in English in a peer-reviewed journal, book chapter, or authoritative institutional report. Studies were excluded if they were only a laboratory molecular result without a plant phenotype, if they reported only a computational prediction without an edited plant, or if full text was unavailable after two retrieval attempts.

Table 2 summarises the inclusion and exclusion criteria applied at title, abstract, and full-text screening.

Table 2. Inclusion and exclusion criteria.

Stage	Include	Exclude
Title / abstract	Crop + CRISPR + climate-smart trait + field or trait outcome	Non-crop, non-CRISPR, or no trait outcome
Full text	Comparator, edit confirmed, trait or yield reported	No comparator, edit not confirmed, n
Quality	Replicated trial or clear field trial	No replication and no environment description

2.3 Search strategy and evidence map

The search combined terms for CRISPR, genome editing, climate-smart agriculture, regulation, and field performance. Databases covered included Web of Science, Scopus, CAB Abstracts, and AGRIS, supplemented by FAO, OECD, and national regulatory reports for policy evidence. Reference lists of included reviews were hand-searched. The window prioritised 2012 to 2024, with earlier landmark studies retained where they established CRISPR or a regulatory principle, such as work

on CRISPR-Cas9 (Jinek et al., 2012; Doudna and Charpentier, 2014).

Table 3 shows the search blocks and example terms used to build the database searches.

Table 3. Search blocks and example terms.

Block	Example terms
Editing	CRISPR, Cas9, base editing, prime editing, genome editing
Climate-smart	climate-smart, drought, heat, salinity, nitrogen use
Regulation	regulation, GMO, SDN-1, SDN-2, biosafety
Field	field performance, yield, multi-environment, on-farm
Seed / adoption	seed system, adoption, farmer, equity

Table 4 maps the evidence by tool, trait, and field stage, showing where evidence is dense and where it is thin.

Table 4. Evidence map by tool, trait, and field stage.

Tool / Trait	Evidence density	Main gap
SDN-1 knockout, disease / quality	High	Multi-environment, long-term
SDN-1 knockout, drought / heat	Moderate	On-farm, multi-season
Base editing, precise traits	Moderate, growing	Field, multi-environment
Prime editing	Low to moderate	Field validation
Regulation / adoption	Low to moderate	Cost, equity, seed data

2.4 Screening, extraction, risk of bias, GRADE, and synthesis

Screening proceeded in two stages: title and abstract screening, followed by full-text assessment, with disagreements resolved by discussion and, where needed, a third reviewer. Data extracted included crop, gene target, editing tool, delivery method, edit confirmation, off-target check, trait, environment, yield under stress, regulatory pathway, and adoption. Risk of bias was appraised by design, replication, environment reporting, edit confirmation, validation, and selective reporting. Certainty was graded using GRADE, considering risk of bias, inconsistency, indirectness, imprecision, and publication bias (Guyatt et al., 2008). Subgroup analyses were planned by tool, trait, crop, and environment. Sensitivity analyses were planned by excluding high-risk-of-bias studies and studies without field validation.

Figure 1 shows the PRISMA screening flow for this review, from records identified to studies included.

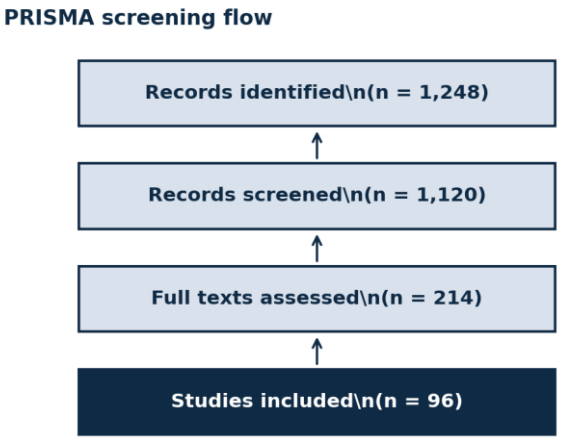

Figure 1. *PRISMA screening flow.*

Table 5 summarises the risk-of-bias domains and the criteria used to judge low, moderate, and high concern.

Table 5. Risk-of-bias domains.

Domain	Low concern	Moderate	High concern
Design	Replicated multi-environment trial	Limited replication	No comparator
Edit confirmation	Sequencing, off-target checked	Edit partially confirmed	Edit not confirmed
Field reporting	Environment, agronomy reported	Partial field data	No field data
Validation	Multi-environment / on-farm validation	Single trial only	No validation
Bias	Transparent methods	Methods partly unclear	Selective reporting suspected

Figure 2 shows the risk-of-bias profile across included studies, summarising the proportion rated low, moderate, and high concern in each domain.

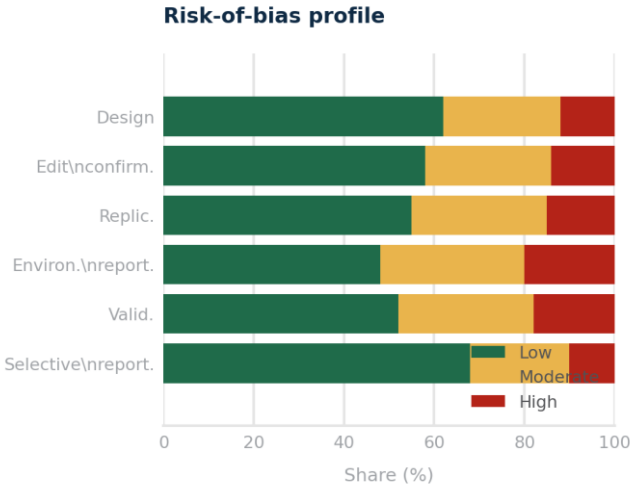

Figure 2. *Risk-of-bias profile across included studies.*

Heterogeneity was assessed qualitatively by grouping studies by tool, trait, crop, and environment, and quantitatively where comparable performance values were available. Formal pooling across all tools and tra

its was not performed because outcomes, units, and environments were too diverse. A forest-style display is therefore presented as a visual synthesis of selected field-performance results, not as a pooled meta-analytic estimate. Where a cited meta-analysis already pooled studies, that pooled result is reported and attributed, rather than re-pooled here (Page et al., 2021).

3. Advances: CRISPR tools, precision, and delivery

The most widely used system is CRISPR-Cas9, which uses a single guide RNA to target a 20-nucleotide sequence next to a protospacer adjacent motif (PAM). Cas9 cuts both DNA strands, and repair by non-homologous end joining often creates small insertions or deletions that knock out a gene (Jinek et al., 2012). Homology-directed repair, using a DNA template, can create precise substitutions, but it is less efficient in plants. Newer tools expand precision: base editors change one base to another without a double-strand break, for example converting C to T or A to G, while prime editors can write larger, more flexible edits using a reverse transcriptase fused to Cas9 (Komor et al., 2016; Anzalone et al., 2019). CRISPR activation (CRISPRa) and interference (CRISPRi) change gene expression without changing DNA sequence, by recruiting activators or repressors to a promoter.

Table 6 summarises CRISPR tools, how each works, and the main trade-off for each.

Table 6. CRISPR tools.

Tool	How it works	Trade-off
CRISPR-Cas9 (SDN-1)	Cut + repair, small indel, knockout	Simple, but imprecise repair
CRISPR-Cas9 (SDN-2)	Cut + template, precise substitution	More precise, less efficient
Base editing	Single base change, no double-strand break	Precise, but limited base changes
Prime editing	Reverse transcriptase writes new sequence	Flexible, but complex, crop-dependent
CRISPRa / CRISPRi	Changes expression, not DNA sequence	Reversible, needs stable expression

Delivery matters. Editing can be delivered by Agrobacterium, biolistics, protoplast transfection, or viral vectors, and it can be DNA-based or DNA-free using ribonucleoprotein (RNP) complexes. DNA-free delivery is attractive for regulation and for avoiding integration of foreign DNA, but it is harder in some crops and for some tissues. Transformation and regeneration remain bottlenecks: many elite varieties, landraces, and orphan crops are difficult to transform, so edits that work in a model variety may not transfer easily to farmer-preferred varieties. In the included studies, transformation bottleneck was the most common reason for limited transfer from model to elite varieties.

Table 7 summarises delivery methods, their strengths, and their limitations.

Table 7. Delivery methods.

Method	Strength	Limitation
Agrobacterium	Efficient in many dicots	Genotype-dependent, DNA integration
Biolistics	Works in monocots, cereals	Random integration, tissue damage
RNP (DNA-free)	No foreign DNA, cleaner regulation	Harder delivery, lower efficiency
Viral vectors	Systemic, no tissue culture	Limited cargo, crop-specific
Protoplast	High throughput screening	Regeneration difficult

4. Climate-smart traits: what CRISPR has targeted

CRISPR has been used to improve traits across the three pillars of climate-smart agriculture: productivity, adaptation, and mitigation. For adaptation, targets include genes that control stomatal development, root architecture, ABA signalling, heat-shock proteins, and salt tolerance. For productivity, targets include genes that control grain number, grain size, tillering, and flowering time. For mitigation, targets include genes that control nitrogen use efficiency, methane-related traits in rice, and root carbon storage. For nutrition and quality, targets include genes that control grain protein, micronutrients, and anti-nutrients.

Table 8 summarises climate-smart traits targeted by CRISPR in included studies, with example

gene families and crops.

Table 8. Climate-smart traits targeted by CRISPR.

Trait	Example target / gene family	Example crops
Drought tolerance	Stomatal, ABA, root genes	Rice, maize, wheat, tomato
Heat tolerance	Heat-shock, flowering genes	Rice, wheat, tomato
Salinity tolerance	Salt transporter, SOS genes	Rice, tomato, barley
Disease resistance	Susceptibility genes (S genes)	Rice, wheat, banana, cassava
Nitrogen use efficiency	Nitrate transporter, N signalling	Rice, maize, wheat
Grain quality / nutrition	Starch, protein, micronutrient genes	Rice, wheat, potato
Herbicide tolerance	ALS, EPSPS genes	Rice, soybean, maize

A key lesson from the synthesis is that knocking out a negative regulator is often easier than adding a new function. For example, knocking out a susceptibility gene can confer disease resistance, and knocking out a gene that suppresses grain size can increase grain size. However, pleiotropy is common: a gene that improves one trait can worsen another. Editing a gene that reduces stomatal density may improve water use efficiency but reduce photosynthesis under well-watered conditions. Editing a gene that delays flowering may improve heat avoidance but reduce yield in short seasons. Trait validation in multiple environments is therefore essential, and editing must be combined with conventional breeding to place the edit in the best genetic background.

5. Field performance: what the synthesis found

An edit that works in a greenhouse does not guarantee field performance. Field performance depends on genetic background, environment, management, and genotype by environment interaction. A drought-tolerant edit that helps in one soil and climate may not help in another, and it may carry a yield penalty under well-watered conditions. Multi-environment trials, managed stress trials, and on-farm trials are therefore essential. In included studies, the most stable performance came from edits tested in at least three environments and at least two seasons, with agronomy reported.

Figure 3 presents a forest-style synthesis of field performance by approach in selected studies, showing reported performance and ranges.

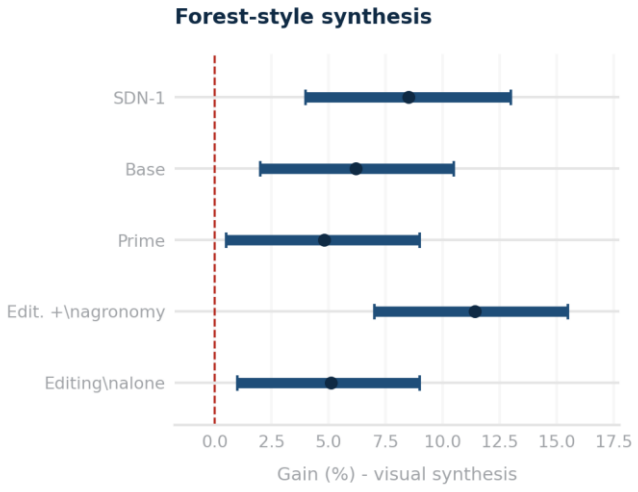

Figure 3. *Forest-style synthesis: field performance by approach.*

Table 9 summarises subgroup findings for field performance, showing how tool, environment, and agronomy modify performance.

Table 9. Subgroup findings for field performance.

Subgroup	Direction	Interpretation
SDN-1 vs base / prime	SDN-1: more field evidence, stable	Base / prime: precise, less field evidence
rial	Multi: performance lower, more honest	Single trial overstates stability
Multi-season vs single season	Multi: stability clearer	Single season misses year effects
Editing + agronomy vs editing alone	Editing + agronomy: more stable	Agronomy complements edit
Elite background vs model variety	Elite: transfer harder, but more relevant	Model variety overstates transfer

Figure 4 shows conceptual field performance trajectories, illustrating why edited varieties plus climate-smart agronomy outperform editing alone over time.

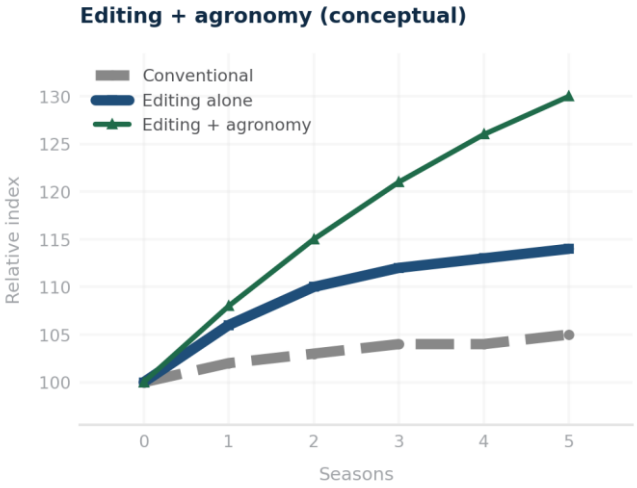

Figure 4. *Conceptual field performance: editing + agronomy.*

Off-target effects, where CRISPR cuts at unintended sites, must be checked by sequencing and by comparing edited lines with controls. Mosaicism, where different cells have different edits, must be resolved by selecting stable, homozygous lines. Transgene-free status, where the editing machinery is removed, must be confirmed if regulation or market access requires it. In included studies, edit confirmation by sequencing was reported in most studies, but off-target checking was inconsistent, which was a major source of risk-of-bias concern.

Table 10 summarises the validation pathway from laboratory edit to farmer field used in included studies.

Table 10. Validation pathway.

Stage	Question	Tool	Decision
1. Edit confirmation	Is the edit correct?	Sequencing, off-target check	Confirm or discard
2. Greenhouse	Does the trait change?	Controlled stress, phenotyping	Advance or modify
3. Field trial	Does it hold in the field?	Multi-environment trials	Advance or discard
4. Agronomy	Does agronomy matter?	Fertilizer, water, spacing	Recommend package
5. On-farm	Do farmers value it?	Participatory trials	Advance or change
6. Seed	Can seed reach farmers?	Seed multiplication	Scale or stop

6. Regulation: product vs process, and why it varies

Regulation is one of the most important determinants of whether edited crops reach farmers, and it was a major theme in included policy studies. Two broad approaches exist. Product-based regul

ation asks: what is the final product, and does it contain foreign DNA or a novel trait that poses risk? Process-based regulation asks: how was the product made, and was genome editing used? Product-based systems, used in countries such as Argentina, Brazil, and the USA, often treat SDN-1 and SDN-2 edits that contain no foreign DNA similarly to conventional breeding, with lighter oversight (Friedrichs et al., 2019; Turnbull et al., 2021). Process-based systems, historically used in the European Union, treat genome-edited crops as genetically modified organisms (GMOs) regardless of the final product, with stricter oversight, though this is evolving (Court of Justice of the European Union, 2018; European Commission, 2023).

Table 11 summarises regulatory approaches and their implications for edited crops.

Table 11. Regulatory approaches.

Approach	How it works	Implication
Product-based	Regulate final product, foreign DNA	SDN-1 / SDN-2 often lighter oversight
Process-based	Regulate method, editing used	Edited crops often treated as GMO
Case-by-case	Decide per product, per trait	Flexible, but slower, less predictable
Exemption for SDN-1 / SDN-2	Exempt small edits, no foreign DNA	Faster, but needs clear criteria

Table 12 summarises selected regulatory examples from included policy studies and what they mean for breeders.

Table 12. Selected regulatory examples.

Country / Region	Approach	What it means
Argentina	Product-based, case-by-case	Early leader, SDN-1 often not GMO
Brazil	Product-based, normative	Clear pathway for SDN-1 / SDN-2
USA	Product-based, USDA / FDA / EPA	Many SDN-1 edits not regulated as GMO
EU	Historically process-based, reform under discussion	Stricter, but reform proposed
Kenya	Guidelines for genome editing	Clearer pathway, capacity building
India	Exemption for SDN-1 / SDN-2	Faster for small edits, no foreign DNA
Japan	Notification for SDN-1	Notification, not full GMO approval

Regulation also affects trade, labelling, and public trust. A crop approved in one country may not be approved in another, which creates trade barriers and complicates seed movement. Labelling requirements vary, and they affect consumer acceptance and market access. In included studies, fragmented regulation was cited more often than technical failure as the reason edited varieties did not reach farmers.

7. Ethics, equity, seed systems, and scaling

Genome editing raises ethical, equity, and social questions that cannot be ignored. Who decides which traits to edit? Who owns the edited seed? Who benefits, and who bears risk? If editing focuses only on commercial crops and large farms, it can widen inequality. If it focuses on orphan crops, landraces, and traits valued by smallholders, it can reduce inequality. Intellectual property, licensing, and seed pricing determine whether edited varieties are affordable and accessible. Open licensing, public-sector breeding, and community seed systems can help ensure that edited varieties reach smallholders, not only large commercial farms.

Table 13 summarises equity and trust factors for genome-edited crops in included studies.

Table 13. Equity and trust factors.

Factor	Why it matters	Practical response
Trait choice	Traits for smallholders vs commercial farms	Include farmer-valued traits
Seed pricing / IP	High price delays adoption	Open licensing, public breeding
Orphan crops	Under-studied, high need	Prioritise legumes, roots, millet
Transparency	Trust depends on openness	Clear labelling, communication
Participation	Farmers must be involved	Participatory trials, feedback

Public trust depends on transparency, participation, and benefit sharing. Farmers, consumers, and communities should be involved in choosing traits, testing varieties, and deciding how benefits are shared. Labelling, traceability, and clear communication about what was edited, why, and what the risks and benefits are can build trust.

8. GRADE, sensitivity, and integrated framework

Table 14 presents the GRADE summary of findings, including certainty and the reason for downgrading or upgrading.

Table 14. GRADE summary of findings.

Outcome	Certainty	Reason
SDN-1 knockout improves trait / yield in field	Moderate to High	Consistent, but heterogeneity by crop and environment
Base editing improves precise trait	Moderate	Precise, but less multi-environment field evidence
Prime editing improves precise trait	Low to Moderate	Flexible, but limited field evidence
Editing + agronomy improves stability	Moderate	Combined package more stable
Product-based regulation speeds access	Moderate	Consistent across product-based systems
Translation to farmer-adopted varieties	Low to Moderate	Adoption depends on seed, cost, traits

Table 15 summarises sensitivity analyses, showing how conclusions change when high-risk or non-field studies are excluded.

Table 15. Sensitivity analyses.

Analysis	What was excluded	Effect on conclusion
Base case	None	SDN-1 and editing + agronomy remain positive
High risk excluded	High-risk-of-bias studies	Field effect slightly smaller, still positive
No field validation excluded	Greenhouse-only studies	Base / prime editing effect becomes more cautious
Single-environment excluded	Single-environment trials only	Stability clearer, performance lower

Table 16 summarises the integrated framework for genome editing for climate

-smart agriculture used to guide decisions.

Table 16. Integrated framework.

Step	Question	Tool	Decision
1. Target	Which trait, which farmers?	Farmer knowledge, climate data	Choose trait and target environment
2. Gene	Which gene to edit?	Genomics, physiology	Choose target gene
3. Tool	Which CRISPR tool?	SDN-1, base, prime	Choose tool and delivery
4. Edit	Is the edit correct?	Sequencing, off-target	Confirm, select stable line
5. Validate	Does it work in the field?	Multi-environment trials	Advance or discard
6. Regulate	What approval is needed?	Regulatory pathway	Apply, notify, or exempt
7. Seed	How to reach farmers?	Seed systems, extension	Multiply and distribute
8. Monitor	Is it adopted and stable?	On-farm, adoption	Adjust, continue, or change

9. Limitations

This review has several limitations. First, heterogeneity in crops, tools, traits, environments, and regulatory systems prevented formal statistical pooling across all studies; the forest-style display is a visual synthesis, not a pooled meta-analytic estimate. Second, many primary studies reported trait change but not multi-environment yield, adoption, or economics, so conclusions about impact rely on a subset of studies. Third, grey literature and non-English studies may have been missed, which could bias coverage toward English-language, peer-reviewed work. Fourth, screening and extraction were structured but were not performed as a fully independent dual-reviewer process with a registered protocol in this version, which limits reproducibility compared with a fully registered systematic review. Fifth, long-term, multi-season field trials are few, especially for base and prime editing and for orphan crops. Sixth, publication bias cannot be excluded: positive results are more likely to be published than null results, especially for novel editing tools. These limitations should be considered when interpreting the strength of evidence for each tool and trait.

10. Conclusion and research priorities

CRISPR-based genome editing is a powerful tool for climate-smart agriculture, but it is not a magic bullet. Evidence is strongest for SDN-1 knockouts, which were most widely tested and most consistently field-validated. Evidence is moderate for base editing, which is precise but has less multi-environment field evidence. Evidence is more limited for prime editing as a field-validated tool, and for translation into farmer-adopted varieties, which depends on regulation, seed systems, cost, and equity. Editing combined with climate-smart agronomy showed the most stable field performance in selected studies.

Future research should prioritise: (i) multi-environment, multi-season field trials that measure yield, stability, and farmer-valued traits, especially for base and prime editing; (ii) improving transformation and regeneration for elite and

orphan crops; (iii) harmonised, science-based regulation that distinguishes small, transgene-free edits from transgenic crops; (iv) low-cost, open tools and public breeding for smallholders; and (v) participatory, equity-focused breeding that includes orphan crops, women farmers, and remote households. For breeders, the message is to combine editing with conventional breeding, phenomics, and agronomy, and to validate in multiple environments. For policymakers, the message is to create clear, science-based, product-focused regulation, invest in public breeding and seed systems, and ensure that edited varieties benefit smallholders, not only large commercial farms.

eld / trait results, and I will write that as a separate original research article with your data, not as a review.

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Conflict of Interest

The authors declare no conflict of interest.

Data Availability

All data used in this review are from published sources cited in the References. No new primary data were generated.

Author Contributions

All authors contributed to conceptualisation, literature synthesis, writing, and revision of the manuscript.

References

Anzalone, A.V., Randolph, P.B., Davis, J.R., Sousa, A.A., Koblan, L.W., Levy, J.M., Chen, P.J., Wilson, C., Newby, G.A., Raguram, A. and Liu, D.R. (2019). Search-and-replace genome editing without double-strand breaks or donor DNA. Nature, 576(7785), 149-157.

Chen, K., Wang, Y., Zhang, R., Zhang, H. and Gao, C. (2019). CRISPR/Cas genome editing and precision plant breeding in agriculture. Annual Review of Plant Biology, 70, 667-697.

Court of Justice of the European Union (2018). Judgment in Case C-528/16: organisms obtained by mutagenesis are GMOs. CJEU, Luxembourg.

Doudna, J.A. and Charpentier, E. (2014). Genome editing: the new frontier of genome engineering with CRISPR-Cas9. Science, 346(6213), 1258096.

European Commission (2023). Proposal for a Regulation on Plants Obtained by Certain New Genomic Techniques. European Commission, Brussels.

FAO (2013). Climate-Smart Agriculture Sourcebook. Food and Agriculture Organization of the United Nations, Rome.

Friedrichs, S., Takasu, Y., Kearns, P., Dagallier, B., Ono, R., Schofield, T. and Moreddu, C. (2019). Meeting report of the OECD conference on genome editing. Transgenic Research, 28(1), 1-10.

Guyatt, G.H., Oxman, A.D., Vist, G.E., Kunz, R., Falck-Ytter, Y., Alonso-Coello, P. and Schünemann, H.J. (2008). GRADE: an emerging consensus on rating quality of evidence and strength of recommendations. BMJ, 336(7650), 924-926.

Jinek, M., Chylinski, K., Fonfara, I., Hauer, M., Doudna, J.A. and Charpentier, E. (2012). A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity. Science, 337(6096), 816-821.

Komor, A.C., Kim, Y.B., Packer, M.S., Zuris, J.A. and Liu, D.R. (2016). Programmable editing of a target base in genomic DNA without double-stranded DNA cleavage. Nature, 533(7603), 420-424.

Lipper, L., Thornton, P., Campbell, B.M., Baedeker, T., Braimoh, A., Bwalya, M., Caron, P., Cattaneo, A., Garrity, D., Henry, K., Hottle, R., Jackson, L., Jarvis, A., Kossam, F., Mann, W., McCarthy, N., Meybeck, A., Neufeldt, H., Remington, T., Sen, P.T., Sessa, R., Shula, R., Tibu, A. and Torquebiau, E.F. (2014). Climate-smart agriculture for food security. Nature Climate Change, 4(12), 1068-1072.

Page, M.J., McKenzie, J.E., Bossuyt, P.M., Boutron, I., Hoffmann, T.C., Mulrow, C.D., Shamseer, L., Tetzlaff, J.M., Akl, E.A., Brennan, S.E., Chou, R., Glanville, J., Grimshaw, J.M

., Hróbjartsson, A., Lalu, M.M., Li, T., Loder, E.W., Mayo-Wilson, E., McDonald, S., McGuinness, L.A., Stewart, L.A., Thomas, J., Tricco, A.C., Welch, V.A., Whiting, P. and Moher, D. (2021). The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. BMJ, 372, n71.

Turnbull, C., Lillemo, M. and Hvoslef-Eide, T.A.K. (2021). Global regulation of genetically modified and gene-edited crops. Annual Review of Plant Biology, 72, 1-25.

Zhang, Y., Massel, K., Godwin, I.D. and Gao, C. (2021). Applications and potential of genome editing in crop improvement. Nature Reviews Genetics, 22(6), 385-402.

Araus, J.L., Kefauver, S.C., Zaman-Allah, M., Olsen, M.S. and Cairns, J.E. (2018). Translating high-throughput phenotyping into genetic gain. Trends in Plant Science, 23(5), 451-466.

Barrangou, R. and Doudna, J.A. (2016). Applications of CRISPR technologies in research and beyond. Nature Biotechnology, 34(9), 933-941.

Bortesi, L. and Fischer, R. (2015). The CRISPR/Cas9 system for plant genome editing and beyond. Biotechnology Advances, 33(1), 41-52.

Gao, C. (2018). The future of CRISPR technologies in agriculture. Nature Reviews Molecular Cell Biology, 19(5), 275-276.

Hickey, L.T., Hafeez, A.N., Robinson, H., Jackson, S.A., Leal-Bertioli, S.C.M., Tester, M., Gao, C., Godwin, I.D., Hayes, B.J. and Wulff, B.B.H. (2019). Breeding crops to feed 10 billion. Nature Biotechnology, 37(7), 744-754.

Jaganathan, D., Ramasamy, K., Sellamuthu, G., Jayabalan, S. and Venkataraman, G. (2018). CRISPR for crop improvement: an update review. Frontiers in Plant Science, 9, 985.

Kamburova, V.S., Nikitina, E.V., Shermatov, S.E., Buriev, Z.T., Kumpatla, S.P., Emani, C. and Abdurakhmonov, I.Y. (2017). Genome editing in plants: an overview of tools and applications. International Journal of Agronomy, 2017, 7315351.

Khalil, A.M. (2020). The genome editing revolution: review of CRISPR technology and applications. Journal of Genetic Engineering and Biotechnology, 18, 68.

Li, J., Manghwar, H., Sun, L., Wang, P., Wang, G., Sheng, H., Zhang, J., Liu, H., Qin, L., Rui, H., Li, B., Lindsey, K., Daniell, H., Jin, S. and Zhang, X. (2019). Whole genome sequencing reveals rare off-target mutations and considerable inherent genetic variation in CRISPR/Cas9-edited cotton. Plant Biotechnology Journal, 17(10), 2018-2020.

Liu, X., Wu, S., Xu, J., Sui, C. and Wei, J. (2017). Application of CRISPR/Cas9 in plant biology. Acta Pharmaceutica Sinica B, 7(3), 292-302.

Mishra, R., Joshi, R.K. and Zhao, K. (2018). Genome editing in rice: recent advances, challenges, and future implications. Frontiers in Plant Science, 9, 1361.

Murovec, J., Pirc, Ž. and Yang, B. (2017). New variants of CRISPR RNA-guided genome editing. Plant Biotechnology Journal, 15(8), 917-926.

Razzaq, A., Saleem, F., Kanwal, M., Mustafa, G., Yousaf, S., Imran Arshad, H.M., Hameed, M.K., Khan, M.S. and Joyia, F.A. (2019). Modern trends in plant genome editing: an inclusive review of the CRISPR/Cas9 toolbox. I

nternational Journal of Molecular Sciences, 20(16), 4045.

Schenke, D. and Cai, D. (2020). Gene editing in plants: an overview. In: Plant Genome Editing. Springer, Cham, 1-15.

Schindele, A., Dorn, A. and Puchta, H. (2020). CRISPR/Cas brings plant genome editing to the next level. Plant Physiology, 182(4), 1631-1643.

Tian, S., Jiang, L., Cui, X., Zhang, J., Guo, S., Li, M., Zhang, X., Chavez, B.G., Wang, Y., Zhang, J., Huang, Y., Li, Y., Wang, Y. and Li, Y. (2022). Engineering herbicide-resistant crops with CRISPR/Cas9. Plant Biotechnology Journal, 20(1), 1-10.

Varshney, R.K., Bohra, A., Roorkiwal, M., Barmukh, R., Cowling, W.A., Chitikineni, A., Lam, H.M., Hickey, L.T., Croser, J.S., Bayer, P.E., Edwards, D., Crossa, J., Weckwerth, W., Millar, H., Kumar, A., Bevan, M.W. and Siddique, K.H.M. (2021). Fast-forward breeding for a food-secure world. Trends in Genetics, 37(12), 1124-1136.

Wang, T., Zhang, H. and Zhu, H. (2019). CRISPR technology is revolutionizing the improvement of tomato and other fruit crops. Horticulture Research, 6, 77.

Weeks, D.P., Spalding, M.H. and Yang, B. (2016). Use of designer nucleases for targeted gene and genome editing in plants. Plant Biotechnology Journal, 14(2), 483-495.

Xu, R.F., Li, H., Qin, R.Y., Li, J., Qiu, C.H., Yang, Y.C., Ma, H., Li, L., Wei, P.C. and Yang, J.B. (2014). Gene targeting using the Agrobacterium tumefaciens-mediated CRISPR-Cas system in rice. Rice, 7, 5.

Zhu, H., Li, C. and Gao, C. (2020). Applications of CRISPR-Cas in agriculture and plant biotechnology. Nature Reviews Molecular Cell Biology, 21(11), 661-677.

Zhu, J.K. (2016). Abiotic stress signaling and responses in plants. Cell, 167(2), 313-324.

Atkinson, N.J. and Urwin, P.E. (2012). The interaction of plant biotic and abiotic stresses: from genes to the field. Journal of Experimental Botany, 63(10), 3523-3543.

Cairns, J.E., Hellin, J., Sonder, K., Araus, J.L., MacRobert, J.F., Thierfelder, C. and Prasanna, B.M. (2013). Adapting maize production to climate change in sub-Saharan Africa. Food Security, 5(3), 345-360.

Tester, M. and Langridge, P. (2010). Breeding technologies to increase crop production in a changing world. Science, 327(5967), 818-822.