

REVIEW

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Gene editing applications, opportunities and challenges for crop improvement in Africa a review

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Abstract

Gene editing, particularly CRISPR/Cas-based new genomic techniques (NGTs), offers significant opportunities for accelerated crop improvement in developing African countries, ensuring food security, livelihoods, climate resilience, and economic growth. This review critically evaluates the scientific basis, applications, breeding value, technical capacity, and regulatory developments of gene editing in major African crops. Recent evidence shows that it has shown significant progress in improving disease resistance, nutrient use efficiency, climate resilience, grain quality, and yield traits in teff, maize, wheat, banana, cassava, and sorghum and other important crops with active research in Kenya, Nigeria, Ghana, Uganda, South Africa, and Ethiopia. Key findings highlights CRISPR/Cas9 remains the dominant editing platform, while base editing, prime editing, and multiplex genome engineering are expanding opportunities for precise trait modification in major and orphan crops. Evidence to date shows measurable gains include improved resistance to banana Xanthomonas wilt through *MusaDMR6* editing, enhanced cassava disease resistance, and drought-tolerant *ARGOS8*-edited maize. However, most African gene-editing pipelines remain at pre-release or at reserach stage because of limited transformation and phenotyping capacity, fragmented regulatory implementation, inadequate funding, and social and institutional constraints and weak seed-delivery systems. Compared with product-based regulatory approaches in Argentina, Brazil, Japan, and the United Kingdom, African framework remains less harmonized and enabling. Future priorities focus on harmonizing *SDN-1/SDN-2* regulatory pathways, participatory public engagement mechanisms, strengthening biosafety and research infrastructure, applying AI-assisted guide RNA design, pangenomics, machine learning, epigenome editing, and de novo domestication, and expanding research on orphan crops such as finger millet, cowpea, and enset that underpin food security but remain under-researched. By focusing on crop-specific examples and well-documented breeding targets, this review aims to provide a scientifically grounded perspective on how gene editing can complement conventional and emerging precision breeding approaches to support sustainable and climate-resilient agriculture in Africa.

Keywords Gene editing, CRISPR tools, Precision breeding, Major crops



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1 Introduction

Agriculture plays a pivotal role in the African economy, providing employment for the majority of the population and contributing substantially to the gross domestic product, with crop production accounting for the largest share [30, 48, 98]. Major crops include cereals such as maize, wheat, sorghum, millet, and teff; root and tuber crops such as cassava and sweet potato; bananas; legumes including common beans, cowpea, chickpea, lentil, and groundnut; and oil and cash crops such as soybean, sesame, and sunflower, cultivated across diverse African agro-ecological zones [40, 103]. Among these, Maize (1st), Cassava (2nd), Sorghum (3rd), Teff (4th in Ethiopia), Banana/Plantain (5th) are key drivers of continental for ensuring food security, accelerating sustainable economic development, supports the livelihoods and regulating food supply in sub-Saharan Africa [30].

However, productivity is constrained by biotic stresses, including diseases, insect pests, and weeds; abiotic stresses such as drought, heat, salinity, and poor soil fertility; post-harvest losses; limited access to improved varieties; and increasing climate variability resulting low yield to the global average [30]. Specifically, Sub-Saharan Africa (SSA) is becoming increasingly vulnerable to climate change due to its extreme dependence on agriculture, and limited adaptive capacity [7]. To address the constraints, conventional breeding has contributed substantially to crop improvement with good results; its progress is often slow, labor-intensive, and economically inefficient, and limited by narrow genetic diversity, long breeding cycles, and complex polygenic traits. These limitations are a compelling reason to increase an interest in new genomic techniques (NGTs), particularly CRISPR/Cas-based gene editing, which enables precise, rapid, and versatility targeted modification of endogenous genes without introducing foreign DNA and can be integrated with high-throughput phenotyping and predictive breeding approaches [19, 28, 31, 35, 65]. Gene editing therefore provides opportunities to develop crops with improved yield, nutritional quality, disease resistance, and tolerance to drought, heat, and other stresses while complementing conventional breeding to the continent agriculture system.

Globally, the development and application of gene editing varies depending on their research capacity, funding, and infrastructure. In this regard, Countries such as China, the United States, and Brazil have advanced rapidly due to strong investment, adequate infrastructure, supportive regulatory systems [19, 27, 29, 45]. African countries, including South Africa, Ethiopia, Kenya and Nigeria, have initiated gene-editing research, and are carefully developing and reviewing regulatory frameworks developed and/or revised in line with recommendations from the African Union [72, 85, 86]. Nevertheless, adoption remains uneven because of limited infrastructure and funding, technical capacity gaps, knowledge gaps, regulatory uncertainty, fragmented policy implementation, and low public awareness [1, 78, 85, 90, 92].

Recent African research has applied gene editing to major food crops, including maize, wheat, sorghum, millet, barley, teff, cassava, banana, and legumes (common bean) [72, 85]. However, most applications remain at research or pre-release stages, and translating laboratory innovations into farmer benefits remains challenging, particularly in low-resource farming systems. Strengthening transformation and phenotyping infrastructure, shortage of skilled personnel, technical capacity, regulatory harmonization, investment, and public engagement is therefore essential for realizing the potential of

NGTs. Previous studies have broadly examined genome editing in African agriculture [1, 31, 90], this review provides a crop-focused synthesis emphasizing food-security relevance, priority traits, and practical deployment pathways. It evaluates applications, opportunities, and challenges across major African crops, integrating scientific, regulatory, infrastructural, socioeconomic, and adoption considerations. Additionally, this review explores the cross-crop comparison of editing tools and efficiencies, a comparative review that includes Africa, the European Union, the UK, Japan, Argentina, and Brazil, and an evaluation of orphan and indigenous crops that are not currently available in gene editing pipelines. In particular, it develops a trait-priority perspective for teff, cassava, banana, sorghum, maize, and wheat and summarizes gene-editing concepts, precision-breeding approaches, and workflows relevant to crop improvement.

2 Methodology

This review employed a narrative review approach rather than a fully systematic review. However, a structured and transparent literature search process was used to improve reproducibility and reduce selection bias. Relevant articles were identified by combining keywords related to 'CRISPR/Cas9', 'gene editing', 'genome editing', 'new genomic techniques (NGTs)', 'precision breeding', 'primary editing', 'major African crops', 'orphan crops', 'conventional crop breeding', 'gene editing regulatory systems', 'capacity building', 'biosafety', 'regulation' and 'socio-economic impacts'. The review was limited by the scarcity of Africa-specific evidence, rapidly evolving regulatory frameworks, crop-specific technical constraints, and limited access to unpublished research. Future studies should emphasize Africa-based validation, risk assessment, economic evaluation, and documentation of African-led genome-editing research.

2.1 Search strategy and selection criteria

Literature searches were conducted between January and March 2026 using journal articles potentially indexed in databases (Web of Science, Scopus, PubMed) and other database sources such AGRIS, and Google Scholar, regulatory and policy documents from FAO, CGIAR, ISAAA, African biosafety agencies, and government sources from Ethiopia, Kenya, Nigeria, Uganda, and South Africa. The search focused mainly on publications from 2016 to 2026, while seminal earlier studies were included where necessary to support established scientific concepts and historical context. Approximately 867 records were initially identified, and after duplicate removal and screening for relevance, accessibility, and methodological adequacy, 192 full-text sources were assessed for eligibility. Finally, 111 peer-reviewed articles, reviews, policy documents, biosafety guidelines, and institutional reports were included in the synthesis.

The studies consider those explicit inclusion criteria: peer-reviewed, English-language, published 2016–2026 (or the actual range used), directly addressing gene editing in African-relevant crops or African policy/regulatory context. The explicit exclusion criteria were non-plant systems, duplicate reports, and non-peer-reviewed opinion pieces without citable data (except the defined grey-literature carve-out already stated). Studies were screened by title, abstract, and full text, and relevant data on crops, traits, editing technologies, target genes, regulatory context, outcomes, and challenges were extracted and thematically synthesized. The numbers of records identified, screened, assessed for eligibility, and included in the review, along with the reasons for exclusion based on the

predefined inclusion and exclusion criteria are summarized in the PRISMA flow chart Fig. 1.

3 Gene editing technologies and workflow in plant breeding

Plant Gene editing refers altering the DNA sequence of a specific gene (small DNA segments) with a plant. While, genome editing is a broad term is the modification of genomic DNA at a specific target site in a wide variety of cell types and organisms, including insertion, deletion and replacement of DNA, resulting in inactivation of target genes, acquisition of novel genetic traits and correction of pathogenic gene mutations. Small insertions, deletions, and single nucleotide changes (SDN-1 and SDN-2 type edits), the resulting genetic changes are often indistinguishable from those caused by conventional mutagenesis or natural polymorphisms, although larger edits or the presence of transgene integration (SDN-3) would be distinguishable [50].

Early molecular breeding platforms such as zinc finger nucleases (ZFNs) and transcription activator-like effector nucleases (TALENs) laid the basis for targeted genome modification in an entire genome of an organism's genome (DNA), but they were limited by cost, technical complexity, and limited scalability [33, 100]. Genome-editing technology selection for African crop improvement should be guided by the target trait, desired genetic change, crop genotype, PAM availability, transformation capacity, and breeding objective rather than by the dominance of CRISPR/Cas9 alone. Cas9 is particularly effective for loss-of-function mutations, whereas Cas12a provides complementary PAM flexibility and multiplexing potential; base editors enable precise nucleotide substitutions, prime editors facilitate more complex sequence modifications, and Cas13 offers opportunities for RNA-level regulation and viral disease management. Multiplex editing is especially promising for complex traits such as drought tolerance, disease resistance,

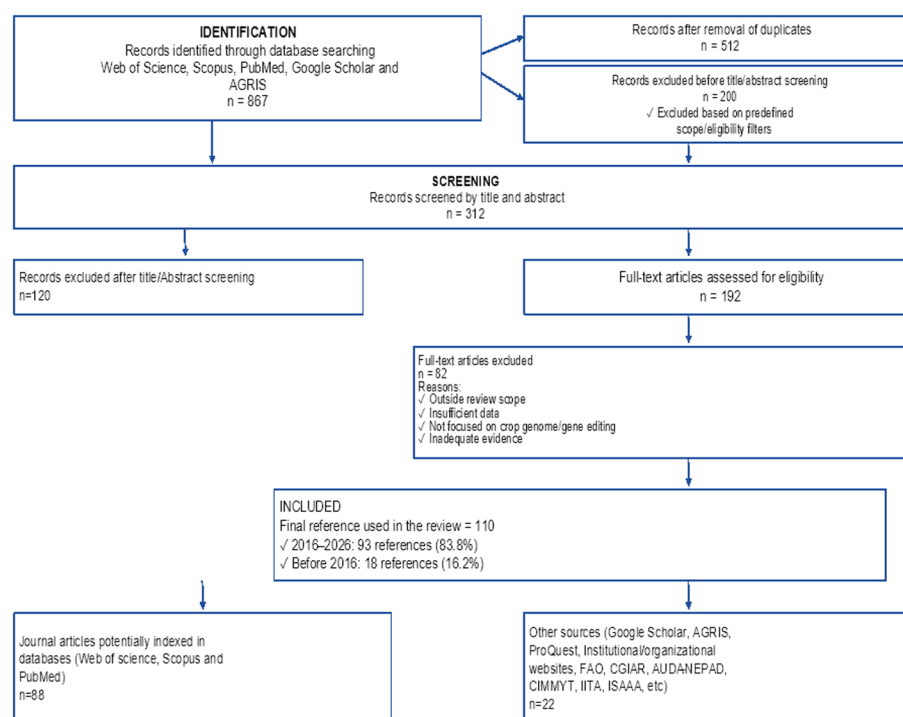


Fig. 1 PRISMA-flow chart for the review

nutrient-use efficiency, and yield stability, although editing efficiency remains highly dependent on genotype and delivery systems [54]. African breeding programs should prioritize technologies according to biological suitability, technical feasibility, cost, scalability, and compatibility with locally adapted germplasm [18, 48, 56, 97]. The comparison of gene-editing technologies such as CRISPR/Cas9, Cas12a, Cas13, CasΦ, Base editors, Prime editing and Multiplex editing are summarized in Table 1.

New genomic techniques (NGTs) include advanced gene-editing approaches such as CRISPR/Cas systems, which employ site-specific nucleases to induce efficient and programmable double-strand breaks (DSBs) at predefined genomic locations [15, 22]. CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) originated as an adaptive immune system in bacteria, whereas Cas9 (CRISPR-associated protein 9) is an RNA-guided endonuclease that cleaves DNA at sequences complementary to a designed guide RNA [39, 46]. As a precision-breeding technology, gene editing enables breeders to introduce targeted modifications into plant DNA with greater precision, speed, and efficiency than conventional breeding approaches, without necessarily incorporating foreign DNA [9, 34, 48]. In plant-breeding applications, CRISPR/Cas9 typically uses a single guide RNA (sgRNA), which combines the functions of CRISPR RNA (crRNA) and trans-activating crRNA (tracrRNA) into a single molecule to direct Cas9-mediated DNA cleavage [22]. The resulting DSBs are primarily repaired through non-homologous end joining (NHEJ), which generates targeted mutations and gene knockouts, or through homology-directed repair (HDR), which enables precise sequence modifications [74, 101]. Recent innovations, including base editing and prime editing, have further expanded the scope of genome editing by enabling specific nucleotide changes without generating conventional double-strand breaks [9, 52]. Importantly, the resulting genetic changes are DNA-level mutations that may be indistinguishable from naturally occurring or conventionally induced mutations because the mutations themselves do not contain information about the technology used to generate them [83, 104]. More broadly, precision breeding integrates advanced genetic and genomic approaches, including genome editing, genomic selection, marker-assisted selection, doubled haploids, and rapid cycling, to accelerate genetic gain and shorten breeding cycles compared with traditional breeding and mutation-based approaches [5]. Editing efficiency is further influenced by guide RNA design, promoter selection, Cas nuclease expression levels, chromatin accessibility, and the method of delivering editing reagents, resulting in substantial variability among species and target loci [17, 38, 51, 94, 111]. Emerging approaches, including morphogenic regulator-assisted transformation, viral vector-mediated delivery, nanoparticle-based systems, and transient RNP delivery, offer promising opportunities to improve editing efficiency while reducing transgene integration and associated regulatory complexity [17, 19]. Therefore, developing genotype-independent transformation platforms, rapid regeneration systems, and high-efficiency DNA-free editing methods should be considered a critical research priority for enabling the widespread deployment of genome editing in African crop improvement programs. The resulting lines are then evaluated through breeding programs and field trials to assess trait stability, agronomic performance, and regulatory compliance [9, 34, 48]. Applications such as editing virus-susceptibility genes in cassava and banana and modifying resistance-related genes in cereals and legumes demonstrate the potential of these technologies to accelerate the development of improved crop varieties [33, 100]. Gene

Table 1 Comparison of genome editing systems relevant to crop improvement

Gene editing technology	Target	PAM/mechanism	Typical edit type	Advantage for African crop breeding	Best-fit application in African crops	Current limitation	References
CRISPR/Cas9	DsDNA	NGG PAM, DSB	Knockout, indel (SDN-1/2)	Most mature, widely validated, cheapest reagents	Loss-of-function traits; disease resistance, and functional validation of candidate genes in African crops	Requires PAM near target; NHEJ-driven, less precise	[17, 112]
CRISPR/Cas12a	DsDNA	T-rich PAM, staggered DSB	Knockout, multiplexing	Simpler multiplex gRNA arrays; useful for polyploid crops (e.g., hexaploid wheat, tetraploid teff-related species)	Multiplex trait improvement and targeting loci that are difficult to access with conventional Cas9	Lower activity in some monocots without optimization	[106, 108]
Base editing	RNA	No PAM (RNA target)	RNA knockdown, viral interference	Direct antiviral tool—relevant to CBSD/CMD in cassava, BSV in banana without altering genomic DNA	Conversion of known favorable alleles associated with stress tolerance, disease resistance and other agronomic traits	Transient effect, delivery still developing in plants	[23, 57, 63, 76]
Prime editing	DsDNA	Compact ortholog	Knockout	Small size eases viral-vector/nanoparticle delivery—useful where transformation infrastructure is limited	Precise allele replacement and complex sequence modifications	Less validated in crop systems to date	[9, 56]
CRISPR/Cas13	DsDNA	No DSB	Single-nucleotide substitution	Precise SNP correction/introduction without DSB-associated risks; suited to quality traits (e.g., cyanogen reduction, herbicide tolerance)	RNA-virus resistance and transient gene regulation, particularly for economically important viral diseases of African crops	Narrow editing window, potential bystander edits	[6, 107]
Multiplex CRISPR	dsDNA	No DSB, uses pegRNA/RT	Insertions, deletions, all base substitutions	Broadest precision; can install specific beneficial alleles	Drought tolerance, disease resistance, and multi-trait improvement where several genes or pathways contribute to the phenotype	Larger construct, lower efficiency in monocots, limited African-crop data	[2, 109]
	DsDNA	Multiple gRNAs/system	Simultaneous multi-gene edits	Enables stacking of multiple traits (e.g., disease resistance + drought tolerance) in one generation		Higher off-target risk, more complex screening	

editing efficiency, current evidence in African countries and interpretation are displayed in Table 2.

The systematic workflow for gene editing in plant breeding begins with the identification of target genes associated with desired traits. A major constraint limiting the practical application of CRISPR/Cas-based gene editing in developing African countries is the inefficiency of delivery systems and plant transformation procedures. Current delivery methods include *Agrobacterium*-mediated transformation, particle bombardment, protoplast transfection, and DNA-free delivery of ribonucleoprotein (RNP) complexes, each differing in editing efficiency, genotype dependency, cost, and scalability [19]. In crops such as sorghum, teff, pearl millet, cowpea, and enset, low transformation frequencies, genotype-specific regeneration responses, somaclonal variation, and difficulties in recovering fertile edited plants remain important bottlenecks that restrict the translation of laboratory protocols into routine breeding pipelines [17, 60]. Following delivery into plant cells, programmable nucleases such as CRISPR/Cas9 generate targeted DNA lesions that are repaired by endogenous plant DNA-repair pathways, primarily through NHEJ for gene knockout and, in appropriate circumstances, HDR for precise sequence modification [74, 93, 101]. Edited cells are subsequently regenerated into whole plants through tissue culture and subjected to molecular screening to confirm the intended edits and identify unwanted modifications. The major steps and applications of genome editing in representative African crops, as summarized by Arora and Narula [10] and Ndudzo et al. [67], are presented in Fig. 2.

4 Applications of gene editing in major African crops

Africa's diverse agro-ecological conditions are favorable for crop production, yet productivity remains constrained by biotic and abiotic stresses, low-input production systems, limited access to improved germplasm, and slow conventional breeding cycles [98]. Genome editing is a complementary precision breeding strategy to address these constraints by directly modifying genes or regulatory regions associated with agricultural performance, stress responses, nutritional quality, and developmental processes [19, 95]. Importantly, its value across African-priority crops does not arise from CRISPR/Cas9 alone, but from the application of common editing strategies, particularly gene knockout, targeted allele modification, promoter editing, and multiplex editing, to different biological constraints.

4.1 Improvement of yield and agronomic traits

Across major African crops, genome editing for yield improvement increasingly follows several common strategies. Targeted knockout of genes that negatively regulate desirable agronomic traits is widely used, while precise allele replacement or regulatory-region editing can be employed where complete loss of gene function would be undesirable. These approaches are particularly relevant to plant architecture, flowering time, biomass partitioning, grain development, and adaptation to local environments.

In cereals such as maize, wheat, sorghum, and barley, targeted editing of yield- and stress-related genes has demonstrated potential to enhance productivity while maintaining desirable agronomic traits [81, 102, 109]. A prominent strategy involves modifying genes controlling plant height and architecture. In teff, where lodging is a major production constraint, research in Ethiopia has considered editing orthologs of semi-dwarfing

Table 2 Gene editing efficiency, current evidence in African countries

Indicator	Current evidence on status in African countries	Examples	Explanation	References
Editing efficiency	Highly crop- and genotype-dependent. In an East African banana/plantain study, targeted <i>PDS</i> mutations were confirmed in 100% of sequenced edited events in the cultivars studied	Banana (<i>Musa</i> spp.): 18/18 sequenced events contained indels; 52/77 <i>Sukali Ndiizi</i> and 16/17 <i>Gonja Manjaya</i> events were albino phenotypes	Demonstrates that high editing efficiency is technically achievable in an African staple crop, although this result should not be interpreted as an average for African crops	[49]
Mutation efficiency	In the same banana study, mutation efficiency at the target site was 100% among the 18 events sequenced; however, simultaneous editing of both target sites was lower and genotype-dependent	<i>Sukali Ndiizi</i> : 2/10 events had indels at both target sites; <i>Gonja Manjaya</i> : 6/8 events had indels at both sites	Shows that successful editing of one target does not necessarily mean efficient multiplex editing	–
Yield improvement	Quantitative yield gains from field-tested African genome-edited crops remain limited/not yet well established. Current programs mainly target disease resistance, stress tolerance, quality and yield-related traits	MLN-resistant maize, disease-resistant banana, Striga-resistant sorghum and improved cassava are among the major African genome-editing programs	Genome editing has strong potential to protect yield from losses, but there are insufficient multi-location field data to provide a reliable continental percentage increase in yield [79, 90]	
Number of edited crops	No single authoritative number exists, because studies count crops, varieties, events, traits and projects differently. Major African programs have involved banana, maize, sorghum, cassava, cowpea, yam, rice and other crops	Examples include MLN-resistant maize, BXW-resistant banana, Striga-resistant sorghum, cassava disease/quality improvement and edited yam	The appropriate measure for a review is therefore the number of crop species/projects documented, rather than claiming a precise total number of “edited crops”	[8, 90]
Regulatory approvals/frameworks	By 2024, Nigeria and Kenya had specific national frameworks/guidelines for genome editing; Burkina Faso, Ghana and Malawi had also developed genome-editing-related regulatory provisions, while several other countries were still developing or discussing frameworks	Nigeria’s framework was established first; Kenya subsequently published genome-editing guidelines	Regulatory development is progressing, but it remains fragmented across countries	–

Table 2 (continued)

Indicator	Current evidence on status in African countries	Examples	Explanation	References
Commercial regulatory approval of gene-edited crops	Very limited/no clearly documented commercial release of a purely gene-edited crop in Africa in the cited literature. Most African products remain in laboratory, contained, confined-field or pre-commercial development stages	MLN-resistant maize and other edited staple crops are progressing toward commercialization, but the literature describes them as being in development rather than established commercial products	This is an important distinction: approval of a regulatory framework is not the same as approval of a gene-edited crop for commercial cultivation	[79, 90]

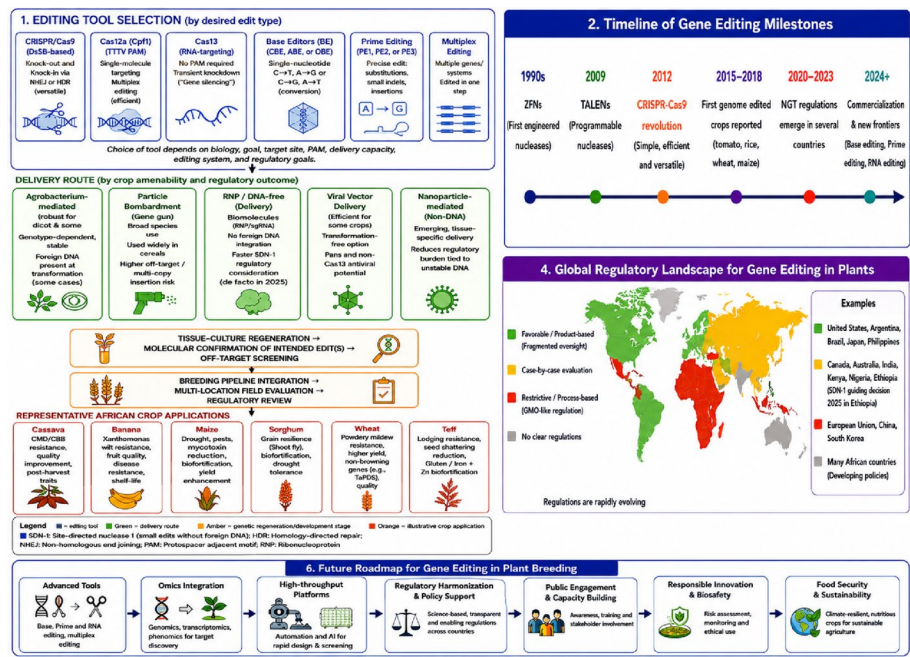


Fig. 2 Gene Editing tools and delivery systems in African crop improvement

genes, including SbSD1 and TefSD1, to reduce plant height and strengthen stems, following the broader principles underlying semi-dwarfing in rice and wheat. In Kenya, CRISPR/Cas9-based genome editing has been established in banana, providing opportunities for functional genomics and identification of genes associated with biotic and abiotic stress tolerance and nutritional traits [90].

CRISPR/Cas9-based approaches have also been investigated for nutritional improvement, with progress reported in enhancing iron, zinc, carotenoids, and amino acids in crops such as camelina, grape, potato, rapeseed, rice, sweet potato, tomato, and wheat [58]. In cassava, CRISPR/Cas9-mediated editing has been established through targeting the PDS gene [69], while manipulation of flowering-related pathways has been proposed

to facilitate controlled crosses and accelerate breeding [47, 69, 73]. CRISPR/Cas9-based approaches to generate cassava resistant to cassava brown streak disease (CBSD) have also been attempted in Uganda [36]. Maize was among the early crops in which genome editing was used to introduce gene variants associated with traits such as herbicide tolerance and grain biofortification [82].

A second strategy involves modification of genes regulating developmental timing and reproductive traits. Editing flowering-related pathways can accelerate generation turnover and facilitate rapid breeding, particularly in crops with long or environmentally constrained reproductive cycles. These approaches can be combined with speed breeding, genomic selection, and rapid generation advancement, allowing genome editing to contribute both directly to yield improvement and indirectly to shortening breeding cycles [95].

A third strategy involves modifying genes associated with resource allocation and yield stability. Rather than increasing yield potential alone, editing can help maintain productivity under drought, heat, nutrient limitation, or disease pressure. For example, editing ARGOS8 in maize has been associated with improved drought tolerance and yield stability under water-limited conditions [21, 24, 81]. Similar approaches are being investigated in wheat, sorghum, barley, and other cereals through manipulation of genes involved in stress signaling, plant architecture, and carbon allocation [81, 102, 109].

The application of these strategies is strongly influenced by transformation capacity and breeding background. Transformation of elite maize lines used as parents of commercial hybrids has historically been a major bottleneck [90]. Advances involving cell-morphogenesis or developmental-regulator genes have substantially improved transformation efficiency in recalcitrant elite germplasm [59, 60]. Maize lethal necrosis (MLN), which first appeared in Kenya in 2011 and subsequently spread to surrounding countries, remains an important constraint in eastern Africa [13, 61, 77]. Consequently, successful target-gene modification must ultimately be achieved in agronomically relevant germplasm and incorporated into locally adapted breeding pipelines.

Furthermore, integrating gene editing with rapid breeding and genomic selection can shorten breeding cycles, which is particularly important in African contexts where time, infrastructure, and financial resources are limited [95]. Successful deployment therefore requires alignment with continental agricultural priorities, regulatory frameworks, institutional capacity, transformation efficiency, access to elite germplasm, and the ability of breeding programs to convert edited events into farmer-acceptable varieties [67, 72, 85].

4.2 Resistance to biotic stresses and tolerance to abiotic stresses

Biotic and abiotic stress improvement represents one of the most broadly transferable applications of genome editing across African crops [68]. Major climate-related constraints include drought, heat, salinity, and irregular rainfall [12, 66]. Across staple crops, CRISPR/Cas9 has demonstrated strong potential to enhance abiotic stress tolerance and biotic stress resistance while maintaining or improving yield and quality [105, 107, 109]. Unlike conventional breeding, which may require repeated introgression of resistance alleles and introduce undesirable linked traits, genome editing can directly modify susceptibility genes, resistance regulators, stress-responsive genes, and signaling components.

For biotic stress resistance, one important strategy is the knockout or modification of host susceptibility genes required by pathogens to establish infection. In cassava, genome editing has been explored to reduce susceptibility to cassava brown streak disease and cassava mosaic disease, while editing of metabolic genes can reduce cyanogenic compounds [47, 69]. In banana, modification of *MusaDMR6* has been associated with enhanced resistance to Banana Xanthomonas Wilt, while targeted modification of endogenous viral sequences provides a strategy for reducing the effects of endogenous Banana Streak Virus [49, 88, 89]. In wheat, CRISPR/Cas-based modification of resistance-associated loci has generated lines with strong resistance to powdery mildew [102]. In maize, genome-editing approaches are being investigated for resistance to maize lethal necrosis, an important disease in eastern Africa [21, 24, 81].

Editing endogenous stress-signaling and regulatory pathways provides a complementary strategy for improving abiotic stress tolerance. Modification of *SAL1* in wheat has enhanced drought resilience at the seedling stage, whereas editing *ARGOS8* in maize has improved drought tolerance [21, 102]. Gene editing enables manipulation of transcription factors, signaling proteins, hormone-regulated pathways, and negative regulators of stress responses, allowing plants to maintain growth under adverse environments. Yield losses due to *Striga* in sorghum range from 30 to 100% in affected fields in Kenya and Ethiopia [70], while cassava brown streak disease causes annual losses estimated at \$100 million in East Africa [20].

Additional examples demonstrate the breadth of these applications. In cassava, gene editing has reduced susceptibility to major viral diseases, lowered toxic cyanogenic compounds through *MeCYP79D1* mutagenesis, and facilitated improved flowering for accelerated breeding [47, 69]. In banana, CRISPR/Cas9 has enabled resistance to Banana Xanthomonas Wilt through *MusaDMR6* editing, permanent inactivation of endogenous Banana Streak Virus, and delayed fruit ripening through *MaACO1* targeting [49, 88, 89, 91]. These findings highlight the potential of genome editing to strengthen climate resilience, disease resistance, drought tolerance, food safety, and productivity in crops important to food security in sub-Saharan Africa [41].

Importantly, multiplex genome editing offers an additional advantage for complex stress traits because disease resistance, drought tolerance, nutrient-use efficiency, and yield stability are often controlled by multiple genes. Simultaneous modification of several targets could therefore generate more durable phenotypes than editing a single locus. However, multiplex editing increases the need for careful target selection, molecular characterization, and evaluation of possible pleiotropic effects. Overall, genome editing for stress improvement can be organized around three complementary strategies: (i) knockout or modification of host susceptibility genes, (ii) enhancement of endogenous defense pathways, and (iii) manipulation of stress-responsive regulatory networks. Their practical value will ultimately depend on whether enhanced resistance or tolerance is maintained under field conditions without compromising yield, quality, or farmer-preferred traits.

4.3 Nutritional quality and biofortification

Genome editing provides a cross-crop strategy for improving nutritional quality by directly modifying metabolic pathways controlling micronutrient accumulation, provitamin synthesis, protein composition, and anti-nutritional compounds. This is particularly

important in Africa, where dependence on staple crops can contribute to micronutrient deficiencies and where conventional biofortification may require lengthy breeding cycles [14, 75, 80].

One major approach is modification of genes regulating nutrient uptake, transport, storage, and metabolic conversion. Targeted editing has been investigated to increase iron and zinc accumulation and improve the nutritional composition of staple crops. Similar strategies have been reported across diverse crops, including rice, wheat, potato, sweet potato, tomato, rapeseed, and other food and industrial crops [75, 80]. CRISPR/Cas9-based approaches have also been investigated for increasing iron, zinc, carotenoid, and amino-acid content in several crops [58]. A second strategy involves editing biosynthetic pathways for vitamins and health-promoting metabolites. Modification of pathway-regulating genes can increase compounds such as provitamin A carotenoids, while targeted manipulation of metabolic enzymes can alter amino-acid composition and protein quality. These approaches are particularly relevant to maize and other cereal-based diets in Africa because improving the nutritional value of widely consumed staples could benefit large populations without requiring major changes in food preferences or production systems [14, 75]. A third strategy is the reduction of anti-nutritional or toxic compounds. Genome editing can improve nutritional quality by removing or reducing compounds that interfere with nutrient absorption or food safety. Cassava provides an important example, where editing of MeCYP79D1 has been investigated to reduce cyanogenic compounds [47, 69]. Such approaches can simultaneously contribute to food safety and nutritional improvement. The broader significance of these applications is that nutritional improvement can be integrated with other breeding objectives. An edited genotype could potentially combine enhanced micronutrient accumulation with disease resistance, drought tolerance, or improved yield through multiplex editing.

Overall, evidence across African-priority crops indicates that genome editing should be viewed as a trait-oriented precision-breeding platform rather than a crop-specific technology. The same basic strategies gene knockout, precise allele modification, promoter/regulatory editing, and multiplex targeting can be adapted to improve plant architecture, yield stability, stress resistance, nutritional quality, and food safety across different crops. The principal differences among crops are therefore the biological target, genetic architecture of the trait, transformation efficiency, availability of elite germplasm, and capacity to evaluate and deploy the resulting materials. This cross-crop perspective provides a more useful framework for assessing the contribution of genome editing to African agriculture than describing individual crops in isolation.

5 Opportunities for African countries

5.1 Complementarity with conventional and precision breeding

Plant breeders have conducted extensive research to address major crop biotic and abiotic constraints through traditional plant breeding methods and to improve crop traits, but this is a time-consuming, laborious and costly process [96, 99]. Despite these efforts, significant productivity challenges remain, to address the challenges using advanced gene editing techniques in major African crops for target modification of crop traits in collaboration with international gene editing research projects [72, 90]. Gene editing does not replace conventional breeding but complements it by accelerating trait introgression and enabling precise modification of elite varieties. Integration with genomic

selection, speed breeding, and phenomics can substantially shorten breeding cycles. This requires pre-existing elite germplasm, crossing strategies, and backcrossing pipelines to place edits into agronomically superior backgrounds. Without strong breeding pipelines, edited alleles may not perform precisely. Therefore, African public breeding programs need resources to use rapid introduction strategies (speed breeding, double haploid) and combine editing with genomic selection approaches [96].

Gene editing offers substantial economic opportunities for African countries by increasing crop productivity, reducing production losses and input costs, and improving resilience to climate-related shocks, with potential welfare gains for smallholder farmers [75]. Faster breeding cycles could further reduce the time and cost of developing improved varieties, increasing the efficiency of agricultural research and technology delivery [19, 75]. Realizing these benefits will require affordable access to edited varieties, efficient seed systems, supportive regulatory frameworks, public–private partnerships, and sustained investment in local biotechnology and breeding capacity [44].

5.2 Adaptation to local agro-ecologies

African agriculture is characterized by diverse environments, is often with small-scale farming systems. Gene editing can provide solutions that target locally important traits, crops, and landraces, thereby improving adoption and maximizing impact [72, 90].

5.3 Capacity building and regional collaboration

Growing investment in biotechnology infrastructure, human capacity development, and regional research networks provides an opportunity to mainstream gene editing in African crop improvement programs. Public–private partnerships and South–South collaborations can further accelerate progress, as government and international research centers have active genome editing research relevant to Africa [72, 90]. Regional laboratory centers with mobile phenotyping units and cloud-based bioinformatics platforms can accelerate knowledge transfer. African collaborations with multilateral centers including CGIAR centers, CIMMYT, ICRISAT, universities, and international donors, along with selected national research institutions, are crucial for decentralized capacity, regional Hubs, and partnerships actively involved in working on gene editing collaborations, training and early product development [67, 72, 90]. These projects are still mostly in the experimental or pre-release stages, but represent a viable pipeline for national crops. Ethiopia, for example, has encouraged a clear regulatory framework for genome-edited products, publishing guidelines in 2025 that distinguish which products require full GMO-style regulation and which can be treated differently, such as SDN-1-type edits without foreign DNA) [85, 90]. In this regard, By 2025 Ethiopia has already approved biotech maize and cotton varieties by 2025, demonstrating its commitment to modern biotechnology in commercial agriculture and its broad focus on regulatory compliance. Platforms such as OFAB Ethiopia (Open Forum on Agricultural Biotechnology) and the International Training Partnership have further enhanced stakeholder engagement and knowledge transfer [72]. These policy measures are essential to modernize regulatory processes and promote responsible gene editing technology adoption; the policies proposed are well implemented and accompanied by capacity building. However, civil society groups remain somewhat marginalized, and public discourse varies by

region and crop type, highlighting the importance of clearly communicating risks and demonstrating benefits to smallholder farmers, while also building broad trust [15, 85].

Overall, new insights from Africa indicate that improved regulatory clarity is helping to shorten the “valley of death” between research and deployment of gene-edited crops, while reinforcing genome editing as a complement to, rather than a replacement for, existing conventional breeding pipelines [85]. In parallel, orphan and underutilized crops are increasingly recognized as realistic targets for precision genome editing, with continental reviews and policy discussions prioritizing both staples and locally important crops for traits that address production constraints and socio-environmental challenges poorly served by conventional breeding alone [72, 90]. Countries and crops selected based on production volume, food security importance, and documented gene editing research activity as reported in AUDA-NEPAD [11] and ISAAA AfriCenter [43]. Currently, African countries have several ongoing gene editing research projects in collaboration with international research centers and are working hard to improve resistance to biotic stresses and abiotic tolerance, to ensure food security and improve nutritional quality in Africa as indicated in Table 3.

6 Challenges and constraints

Despite substantial progress in genome editing of African crops, important knowledge gaps and practical challenges remain, particularly in understanding the genetic basis of complex, polygenic traits and Africa-specific genetic diversity, as well as in genome annotation, target-gene validation, and efficient transformation and regeneration systems. Progress is further constrained by limited research infrastructure, funding, specialized expertise, genomic and bioinformatics resources, and multi-location field validation. The limited transition of edited crops from laboratory studies to field testing, regulatory approval, and commercialization also creates uncertainty about their stability, environmental interactions, and benefits to smallholder farmers. Addressing these gaps requires investment in African genomic resources and research capacity, improved editing and transformation systems, robust field evaluation, harmonized science-based regulatory frameworks, and stronger integration of genome editing with conventional breeding and farmer-defined priorities [1, 8, 71, 79, 90].

6.1 Scientific and technical challenges

High-quality gene editing in Africa requires well-equipped molecular biology laboratories; suitable regulatory systems for implementation; and trained biosafety personnel. Several universities and research institutions in some countries on the continent have improved their laboratories, although gaps remain in crop-specific sequencing, long-term tissue culture capacity, and in-country high-throughput sequencing and bioinformatics capabilities, most do not have a dedicated laboratory [72, 85, 90]. In several African settings, researchers have limited access to such facilities, while equipment maintenance and replacement can also be difficult. Abkallo et al. [1] specifically identify limited access to laboratories, equipment and molecular-biology reagents as major obstacles to genome editing in Africa. Therefore, it is essential to invest in long-term human capacity development, including postgraduate training, technical staff, and laboratory management, to build organized laboratories, which are critical to realizing the full potential of gene editing for crop improvement in Africa [67].

In Africa, many crops are recalcitrant to transformation or regeneration, which slows desirable trait introgression [72, 90]. Delivery methods such as *Agrobacterium*-mediated transformation, particle bombardment or RNP (ribonucleoprotein) delivery each have their advantages and limitations [19, 67]. For limited crops, efficient transfection protocols may require parallel investment in tissue culture facilities or the exploration of novel delivery methods, and Transformation-Free Editing are emerging approaches, as such RNP delivery, viral vectors, nanoparticles, and pollen magnetofection can reduce reliance on tissue culture and associated regulatory burdens [25]. Overall, technical challenges and resource-intensive requirements persists major obstructions to widespread adoption of gene-editing technologies in Africa.

Off-target edits occur when the CRISPR/Cas9 complex cleaves DNA at sites similar but not identical to the intended target sequence. Several factors influence off-target risk, including guide RNA design, nuclease delivery method, and the chromatin accessibility at potential off-target loci. While not off-targets themselves, genomic context and chromatin state modulate editing efficiency and specificity, requiring careful empirical validation for each sgRNA [16, 64, 107]. Off-target effects, which are influenced by factors such as chromatin accessibility and genomic context, can destabilize the genome and even affect cell survival, including unanticipated double-strand breaks (DSBs), single-nucleotide variations (SNVs), and large chromosomal rearrangements. While there are many bioinformatic tools and experimental strategies for designing sgRNAs, the potential for off-target effects can be minimized by using highly diverse and molecularly engineered lines [55, 64]. Claims about the precision of CRISPR/Cas systems are now supported by empirical evidence, although discussions about their limitations remain important for balanced interpretation [26, 110].

Phenotypic prediction is a prerequisite for breeders efficiently use genomic tools. High-throughput phenotyping is critical to evaluate edited lines across various environments and manage genotype by environment interactions. Africa has diverse agricultural ecosystems, and multi-site and multi-season trials are needed to ensure that edited alleles provide agricultural benefits under local conditions [1]. Several studies have predicted phenotypic diversity and variability in different crop; limited multi-location and multi-season trials remain a bottleneck for identifying traits amenable to genome editing. Investments in sensor platforms, data pipelines, and training are urgent for strengthening continental phenotyping capacity.

6.2 Regulatory developments relevant to plant breeding

Recent regulatory developments distinguish between transgenic and certain gene-edited crops, explaining what has changed compared to previous frameworks and discussing the implications for breeding programs and field deployment [32, 72, 85]. Differences in regulatory treatment across domestic, regional, and international markets complicate breeding and commercialization strategies. These regulatory expectations and market strategies explain why alignment across markets remains challenging for breeders [83, 90]. In comparison, Kenya (leader in research with MLN-resistant maize), Nigeria (leader in biosafety guidelines), and Ethiopia (newest guidelines, 2025), noting their different stages of development and how they benchmark against global forerunners like the USA, Canada, and Argentina [42].

Table 3 CRISPR/Cas genome editing system research, editing status, target gen and target traits in major priority crops in Africa

Country/region	Crop	Specific trait/application	Target gene	Editing system	Editing status	Institution	Publication year	Commercial stage
Kenya	Sorghum	Striga resistance	LGS1 editing	CRISPR/Cas9	Greenhouse and field-oriented research	KALRO; SSSFA consortium; CIMMYT partners	2023–2025	
	Maize	Drought tolerance	ARGOS8-like targets under investigation	CRISPR/Cas9	Experimental	KALRO; university collaborations	2023–2025	Research
	Maize	MLN resistance	Not publicly specified	CRISPR/Cas9	Laboratory and proof-of-concept research	KALRO; CIMMYT	2022–2024	Research
Ethiopia	Banana	Disease resistance	Candidate resistance genes under evaluation	CRISPR/Cas9	Early-stage development	Ethiopian Institute of Agricultural Research (EIAR); regional biotechnology partners	2023–2025	Research
	common beans	Faster cooking / quality improvement	Not publicly specified	CRISPR/Cas9	Conceptual and exploratory research	EIAR; university research groups	2024–2025	Research
	Sorghum	Striga resistance	LGS1	CRISPR/Cas9	Collaborative research	EIAR; SSSFA; Kenyan partners	2023–2025	Research
Rwanda	Teff	Yield and stress tolerance	Candidate domestication and architecture genes under consideration	CRISPR/Cas9	Capacity building and pilot trials planned	EIAR; Addis Ababa University; biotechnology initiatives	2024–2025	Pre-research/pilot
	Ethiopian mustard	Trait improvement	Not publicly specified	CRISPR/Cas9	Early-stage infrastructure development	EIAR	2024–2025	Pre-research
	Coffee	Disease resistance and quality improvement	Not publicly specified	CRISPR/Cas9	Early-stage research planning	Jimma University; EIAR	2024–2025	Pre-research
	Cassava	CMD and CBSD resistance	nCBP-1 / nCBP-2	CRISPR/Cas9	Advanced experimental research	Rwanda Agriculture and Animal Resources Development Board (RAB); international cassava partners	2020–2024	Research
	Maize	Drought tolerance	Candidate stress-response genes	CRISPR/Cas9	Experimental	RAB	2023–2025	Research
	Potato	Late blight resistance	StDMR6-1 and related susceptibility genes	CRISPR/Cas9	Proof-of-concept and confined research	RAB; regional potato research programs	2022–2024	Research

Table 3 (continued)

Country/region	Crop	Specific trait/application	Target gene	Editing system	Editing status	Institution	Publication year	Commercial stage
Cameroon	Beans	Productivity and stress tolerance	Not publicly specified	CRISPR/Cas9	Priority-setting stage	IRAD Cameroon	2024–2025	Research planning
	Cocoa	Black pod disease resistance	Candidate susceptibility and defense-related genes	CRISPR/Cas9	Exploratory laboratory research	IRAD; cocoa biotechnology collaborations	2023–2025	Research
South Africa (R&D stage)	Banana/Plantain	Black Sigatoka resistance	Musa DMR6-like targets under evaluation	CRISPR/Cas9	Experimental	CARBAP; regional banana research networks	2022–2025	Research
	Cassava	Disease and pest resistance	nCBP-related targets under consideration	CRISPR/Cas9	Exploratory	IRAD Cameroon	2023–2025	Research
	Cassava	Disease resistance	Candidate resistance genes	CRISPR/Cas9	University-based experimental research	University of Pretoria; ARC partners	2022–2025	Research
	Wheat	Disease resistance and yield improvement	MLQ, TaGW2, and related targets under investigation	CRISPR/Cas9	Experimental	ARC-Small Grain; university collaborators	2021–2025	Research
	Grapes	Drought tolerance	Candidate ABA and stomatal regulation genes	CRISPR/Cas9	Experimental	Stellenbosch University; ARC Infuitec-Nietvoorbij	2023–2025	Research
	Sorghum, Millet	Drought, <i>Striga</i> , and nutritional improvement	Candidate stress-response genes	CRISPR/Cas9	Target identification stage	ARC; university research groups	2024–2025	Research planning

Table 3 (continued)

Country/region	Crop	Specific trait/application	Target gene	Editing system	Editing status	Institution	Publication year	Commercial stage
General/multi-country across Africa	Banana	Xanthomonas wilt resistance	DMR6 and related susceptibility genes	CRISPR/Cas9	Advanced experimental research	ILITA; NARO Uganda; regional Musa partnerships	2021–2025	Research
	Cassava	CMD / CBSD resistance	nCBP-1 / nCBP-2	CRISPR/Cas9	Multi-location experimental research	ILITA; national agricultural research systems	2020–2025	Research
	Maize	Biofortification	PSY1, crtRB1, and carotenoid-pathway targets	CRISPR/Cas9	Experimental	CIMMYT; national partners	2021–2025	Research
	Wheat	Yield enhancement and disease resistance	TaGW2, MLO, and related targets	CRISPR/Cas9	Research and development	CIMMYT; African wheat improvement networks	2021–2025	Research
	Yam	Abiotic stress and pest/disease resistance	Candidate stress and resistance genes	CRISPR/Cas9	Emerging research area	ILITA Yam Improvement Program	2023–2025	Research

Source: Countries and crops selected based on production volume, food security importance, and documented gene editing research activity as reported in AUDA-NEPAD [11]; Genome Africa [35]; ISAAA AfriCenter [43]; ACBIO [4]; Mmbando [62]

6.3 Regulatory, legal, and governance challenges

Publication of guidelines is a major step, but their implementation across agencies (variety release committees, biosafety authorities, and seed regulators) remains critical. Key challenges include the capacity to review molecular dossiers, differentiate SDN-1 edits from transgenic events, and coordinate with trade and seed frameworks [84]. In this regard, Ethiopia publishes new guidelines aims how to implement genome-edited products, but training, laboratory accreditation, and transparent timelines remain bottlenecks.

6.4 Seed systems, variety release, and intellectual property of gene edited crops

More than half of African smallholders access seed through informal networks. Introducing edited varieties requires robust seed multiplication, quality control, and accessible distribution systems with extensive agricultural extension services. Intellectual property (IP) considerations for CRISPR tools, edited alleles, or proprietary markers can complicate public breeding efforts; open-access licensing and stewardship models can mitigate barriers [90, 95].

However, intellectual property (IP) represents a major challenge for CRISPR/Cas-based gene editing in Africa because overlapping patents covering editing systems, delivery technologies, and edited traits can create licensing costs and freedom-to-operate (FTO) constraints for public breeding programs [46, 87]. These barriers may disproportionately affect orphan crops such as teff, enset, Bambara groundnut, finger millet, and pigeonpea, where limited commercial markets may not justify costly licensing arrangements [37]. Differences among national and regional IP systems, including ARIPO and OAPI, further complicate commercialization and cross-border seed dissemination, despite some research-use and humanitarian licensing provisions [53]. Strengthening public-sector IP capacity, regional licensing mechanisms, open-science initiatives, and public–private partnerships will therefore be important for improving FTO and ensuring equitable access to genome-editing technologies. This critically insists that financial models and public investment are necessary to ensure edited varieties are affordable and accessible to farmers, and that breeders will determine real-world benefits are necessary.

6.5 Ethical, social, and participatory governance of gene editing

In developing African countries, public understanding and acceptance of gene editing varied. Some stakeholders view genome editing as distinct from older GMO technologies (especially those without foreign DNA), while others view it as integrated. Ethical considerations including farmer choice, benefit sharing, and stakeholder engagement are essential to improving desired crops traits. Overall, transparent, participatory governance and open communication are critical to address these concerns [29, 72, 85].

6.6 Socio-economic and adoption challenges of gene editing

Editing efforts must focus on smallholder-prioritized traits such as yield stability, reduced lodging in teff in Ethiopia, Striga resistance in sorghum, drought tolerance, disease resistance, and nutritional quality for other crops [72, 85]. Sometimes misalignment between lab projects and farmer needs wastes resources and reduces adoption. Therefore, participatory varietal selection and on-farm trials are essential to align researchers with farmers' needs. NGOs and civil society groups in Africa and beyond have different

perspectives; some are skeptical of any genetic modification, while others support evidence-based adoption. In addition critics, including some civil society organizations (e.g., AFSafrica, 2023), argue that genome editing is a costly distraction from agro ecological approaches, farmer-managed seed systems, and public investment in basic infrastructure. These critiques emphasize that complex; patented biotechnologies may not address the immediate needs of the majority of smallholders who lack access to inputs, extension services, and reliable markets. We then counter this by arguing for a complementary, not replacement, approach. This shows that there is a lack of understanding and awareness regarding gene editing, and a lack of a clear operational process in Africa. Effective risk communication, demonstration trials, and transparent regulatory processes can build trust.

Gene editing technologies offer unprecedented opportunities for improving African crops, their successful deployment requires rigorous molecular screening, ecological risk assessment, biodiversity conservation measures, robust food safety evaluation, and transparent public engagement. Addressing these issues proactively will be critical for ensuring that gene-editing innovations contribute to sustainable agriculture, food security, and societal acceptance across diverse African agroecological systems.

7 Prioritizing traits by production constraint for high-impact applications in Africa

Yield losses caused by key stresses in African staple crops are extreme. For example, Striga in sorghum can result in losses of up to 100%, maize lethal necrosis can cause up to 90% loss, and cassava brown streak disease can lead to losses of up to 100% and specific gene-editing projects have been mapped to address these challenges [3]. African farmers prioritize traits that enhance yield stability and resilience under biotic and abiotic stress. Priority traits in developing African countries focus mainly on major production and nutritional stresses [67, 90, 95]. In teff, priorities include reduced lodging and panicle shattering, particularly in Ethiopia. In sorghum and maize, key traits include disease resistance, Striga resistance, and drought tolerance. In banana, priorities include resistance to bacterial and viral diseases. In common bean, reducing cooking time is a major target. In cassava, priorities include resistance to CMD and CBSD, higher starch and yield, and reduced cyanogenic compounds. In potato, late blight resistance is a key target. In grape, drought tolerance is important. In wheat and enset, priorities include higher protein and micronutrient content and disease resistance. In maize, improving nutritional quality is a major priority. Gene editing accelerates improvement relative to conventional mutagenesis [19, 109].

8 Policy, capacity building, and investment priorities

Actions include establishing clear processes and timelines, training staff, enabling public-sector access to facilities, integrating gene editing with genomic selection and multi-environment phenotyping, encouraging public-private models for smallholder access, and promoting participatory approaches for traditional crops such as teff, particularly in Ethiopia [85, 90]. Capacity development should emphasize retraining and upskilling scientists to integrate gene editing with conventional breeding and phenotyping, rather than focusing solely on retention [90, 95]. This aligns capacity development more closely with technological advancement in plant breeding.

9 Conclusion

Gene editing and precision breeding technologies are a critical toolkit for Africa to become more resilient to pests and diseases and adapt to climate change. To achieve this, the continent is preparing to move towards regulatory transparency and early approvals for engaging with modern biotechnology. Realizing its benefits requires coordinated investment in capacity development, breeding integration, regulatory clarity, and inclusive governance. With These elements through national policy, donor investments, public sector leadership, and international cooperation in place, gene editing can contribute meaningfully to sustainable and equitable agricultural transformation in Africa. In conclusion, the successful deployment of gene-edited crops in Africa requires clear and harmonized regulatory frameworks, strengthened research infrastructure, and specialized technical capacity. Gene editing should be integrated into breeding programs, with emphasis on climate-resilient and orphan crops important for food security and nutrition. Public–private partnerships, affordable technology access, farmer participation, and transparent communication are essential to ensure that the benefits of gene editing reach smallholder and marginalized farmers.

Abbreviations

ARC	Agricultural Research Council
CARBAP	African Centre for Research on Bananas and Plantains
CBSD	Cassava Brown Streak Disease
CIMMYT	International Maize and Wheat Improvement Center
CMD	Cassava Mosaic Disease
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats
EIAR	Ethiopian Institute of Agricultural Research
FT	Flowering locus t
IITA	International Institute of Tropical Agriculture
IRAD	Institute of Agricultural Research for Development
KALRO	Kenya Agricultural and Livestock Research Organization
LGS1	Low germination stimulant 1
MLN	Maize lethal necrosis
nCBP	Novel cap-binding protein
RAB	Rwanda Agriculture and Animal Resources Development Board
SSSfA	Striga Smart Sorghum for Africa

Author contributions

All authors were contributed in planning, designing and conducting the review **.* Mr. Gebremeskel Mequanint handled conceptualization, investigation, methodology, supervision, original draft writing, editing and reviewing, and visualization and all authors read and approved the final manuscript. Adane Wondmaneh and Birkneh Kuru contributed to conceptualization, investigation, methodology editing and reviewing.

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