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OPINION

Rethinking gene editing impact in plant breeding as measured by genetic gain

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Abstract

Gene editing (GEd) has transformed the ability to precisely modify plant genomes, offering new opportunities for plant breeding over the past decade. Despite rapid advances in GEd technology, its measurable impact on realised genetic gain in plant breeding programmes remains unknown. This gap reflects a mismatch between editing capability and the biological, operational, and regulatory realities of plant breeding, rather than evidence of technology-related limitations or poor field performance of gene-edited crops. We discuss key constraints of GEd, including genotype-dependent transformation, the multigenic nature of most agronomic traits in crops, integration into plant breeding pipelines, and regulatory and societal considerations. Framing GEd within a systems-level plant breeding framework that integrates selection strategies, speed breeding, advanced editing methods, and access to diverse germplasm provides a realistic pathway to accelerate genetic gain.

Keywords Crop improvement · Food security · Genetic gain · New breeding technologies

1 Introduction

Feeding a growing global population under increasing climate change and climate variability requires innovative approaches to plant breeding. The emergence of gene editing (GEd) over a decade ago has fundamentally reshaped plant breeding (Jinek et al., 2012). GEd enables targeted mutagenesis (precise DNA sequence changes), allele replacement, and regulatory modification with unprecedented precision. Early demonstrations in crops generated considerable optimism about their potential to accelerate plant breeding and enhance global food security. GEd technologies, particularly CRISPR–Cas systems (Clustered Regularly Interspaced Short Palindromic Repeats–CRISPR-associated proteins), have enabled precise modification of genes underlying crop quality traits, as well as responses to plant pathogens and pests, and abiotic stresses (reviewed in Ahmar et al., 2026). Together, this capability highlights the strong potential of GEd to deliver more resilient, market-aligned crops suited to a changing climate.

Despite a rapidly growing body of scientific evidence, relatively few gene-edited cultivars have been introduced or progressed to commercialization. While GEd accelerates the generation of allelic variation, plant breeding success ultimately depends on the effective deployment and evaluation of these alleles within complex plant and cropping systems. The limited translational impact that GEd has achieved so far reflects a misalignment between technological capability and the biological and operational realities of plant breeding. Progress will require a shift toward a systems approach that integrates GEd with quantitative genetics, multi-environment field testing, and breeding programme design. This opinion article examines how GEd can be translated into realised genetic gain and outlines a system-level framework for its integration into plant breeding pipelines.

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2 Precision, speed, and novel variation

GEd offers several advantages over conventional plant breeding. It enables precise modification of specific loci without linkage drag (undesirable traits inherited with target genes), accelerates the delivery of favourable alleles, and allows the development of novel variants not easily found in available germplasm. These features are especially valuable for major-effect genes. Representative examples illustrate this potential. For example, knockout of *TaMLO* genes in wheat confers durable resistance to powdery mildew (Wang et al., 2014). Promoter editing of *IPA1* increases grains per panicle in rice (Song et al., 2022). Multiplex editing of domestication genes in wild tomato species facilitates rapid development of improved ideotypes (Zsögön et al., 2018). Editing of asparagine synthetase (*TaASN*) genes in wheat reduces grain asparagine accumulation and enables the development of ultra-low asparagine lines (Kaur et al., 2026). Emerging base and prime editors further expand the precision of edits, thereby allowing transgene-free modifications and the fine-tuning of quantitative traits.

3 GEd current constraints

3.1 Transformation and genotype dependency

A major limitation of GEd in crops is that the efficiency of plant transformation and regeneration strongly varies among genotypes. Efficient editing requires delivery and regeneration, which remain highly genotype-specific in many crops. Elite breeding lines are often recalcitrant to transformation, requiring editing in model or transformable genotypes, followed by introgression into elite backgrounds. To do this requires multi-year breeding cycles, thereby reducing the time savings offered by GEd. The use of morphogenic regulators (e.g., *Baby boom* and *Wuschel2*) (Lowe et al., 2016), *de novo* meristem induction (Maher et al., 2020), and viral-based delivery systems (Saini et al., 2023) have expanded transformation capacity. These approaches, however, can only be applied to a limited diversity of crop species. Transformation thus remains a central bottleneck limiting the scalability of GEd.

3.2 Multigenic traits

GEd can be applied to complex traits. But the effectiveness of GEd may be difficult to implement in complex genetic architectures. Crop genotype attributes such as potential yield, drought adaptation, and nutrient use efficiency are typically multigenic; i.e., influenced by many loci of small effect, as well as by the genotype-by-environment interactions and epistasis (inter-locus interactions). Even with multiplex or regulatory editing, outcomes remain context-dependent and difficult to predict. Moreover, much of the functional variation underlying quantitative traits resides in regulatory regions rather than coding sequences. High-throughput plant phenotyping and multi-omics data integration are required tools to evaluate the effect of the edited alleles in complex genetic backgrounds. Consequently, GEd alone is unlikely to rival genomic approaches such as genomics-assisted breeding tools, which capture additive genetic variance across the entire genome.

3.3 Integration into plant breeding pipelines

Plant breeding is a multi-stage process involving germplasm screening, population development, multi-environment field testing, seed multiplication, and cultivar deployment. GEd in most cases operates at the earliest stage of this process and does not remove downstream constraints: the edited lines must still undergo extensive field testing. Without deliberate integration into breeding pipeline, GEd risks functioning as an additional upstream step rather than a true accelerator of genetic gain.

4 Integrating GEd within system-level plant breeding frameworks

4.1 Unlock and deploy plant genetic diversity

Modern breeding is often constrained by the narrow genetic base of elite breeding lines. Although landraces and crop wild relatives harbour extensive diversity, their use is limited by linkage drag. GEd provides an alternative by bringing favourable alleles into elite breeding populations. This "allele mining to allele recreation" approach allows breeders to bypass conventional introgression while retaining the adaptive context of elite cultivars. For example, alleles underlying stress tolerance or disease resistance identified in wild relatives can be accurately inserted into high-performing lines without introducing undesirable associated wild traits. Success critically depends on prior identification of causal variants through genomics and functional research. GEd can also enhance the value of genebanks by making previously inaccessible diversity actionable.

4.2 Plant breeding selection strategies

GEd and plant breeding selection approaches address complementary aspects of crop genetic improvement. GEd enables precise modification or mutation of specific alleles, often at loci with known functional effects. For complex

Table 1 Bridging gene editing (GEd) potential and breeding system constraints: current gaps limiting realised genetic gain

Aspect	GEd potential	Breeding system constraint	Implication for genetic gain
Targeting precision	Precise modification of specific gene(s) and regulatory element(s)	Most important agronomic traits are multigenic and influenced by genotype × environment interactions	Limited impact on genetic gain unless combined with other plant breeding approaches
Allele introduction	Rapid creation or recreation of favourable allele(s)	Transformation and regeneration are genotype-dependent; elite germplasm often recalcitrant	Delays in deployment due to need for introgression into elite backgrounds
New variation	Generation or recreation of allele(s) not readily accessible in breeding germplasm	Phenotypic effects depend on genetic background, epistasis	Outcomes are context-dependent and require validation across years and locations
Cycle time	Rapid editing and allele generation at early stages	Breeding pipelines require multi-generation advancement and multi-environment testing	Time gains are reduced unless combined with accelerated breeding strategies (speed breeding)
Genetic diversity	Targeted deployment of alleles identified from diverse germplasm	Functional variants must be identified prior to editing (diversity is not generated *de novo*)	Impact depends on prior discovery of causal variants and access to diversity resources
Integration into plant breeding	Flexible application as a targeted upstream tool	Must be aligned within plant breeding programme design, breeding selection schemes, phenotyping and genotyping pipelines	Realised genetic gain depends on system-level integration rather than editing efficiency alone

multigenic traits, genomic selection (GS) is particularly suitable because it captures genome-wide additive genetic variance across many small-effect loci. For traits controlled by one or a few major-effect genes, marker-assisted selection (MAS) can efficiently track edited alleles. Integrating GEd with GS or MAS allows breeders to simultaneously target key alleles while optimizing the broader genetic background. This integration is all the more necessary because the phenotypic impact of the edited loci is often contingent on both genetic context and environmental interactions.

4.3 Accelerating breeding cycles through speed breeding

Even if GEd successfully generates desirable alleles, the time required for allele fixation, validation, and multi-environment field testing remains a major constraint. Speed breeding, through extended photoperiods and controlled environmental conditions, can significantly shorten generation times and accelerate breeding cycles. Combining GEd with speed breeding enables more rapid progression from edit design to homozygous lines and field evaluation. This is especially valuable for crops with long generation times or complex breeding schemes. Rather than functioning as a stand-alone innovation, editing should be viewed as part of a coordinated element combining allele design, genome-wide selection, accelerated generation turnover, and access to diverse genetic resources. Integration shifts the focus from maximizing editing efficiency to maximizing genetic gain per unit time.

4.4 From gene disruption to allele design

Early applications of GEd techniques focused on gene knockouts, often targeting coding sequences to generate loss-of-function alleles. Although effective for single-gene traits, this approach is less suited for quantitative traits, which are influenced by regulatory variation. Recent advances shift the focus from gene disruption to allele design, including promoter editing, cis-regulatory modification, base and prime editing, and fine-tuning gene expression. These approaches generate quantitative phenotypic variation, providing a closer match to plant breeding needs. For example, cis-regulatory editing of developmental genes in tomatoes allowed engineering of quantitative variation in traits such as inflorescence architecture and fruit size (Rodríguez-Leal et al., 2017). These approaches align more closely with the quantitative nature of most agronomic traits.

4.5 Implications for plant breeding programmes

GEd is most impactful when strategically applied to introduce major-effect alleles, recreate beneficial variants from diverse germplasm, or eliminate deleterious alleles. Integration with genomics-assisted breeding enables simultaneous optimization of targeted loci and multigenic background. Success should be measured in terms of genetic gain per unit time, not simply the number of edited events. Table 1 summarises some key factors shaping the contribution of GEd to genetic gain within breeding systems, highlighting where integration is critical.

5 Regulatory considerations and public acceptance

Regulatory policies and public perception strongly influence the adoption and impact of GEd. Countries differ markedly in how they classify gene-edited crops. Some jurisdictions, such as those of the United States of America and Brazil, exempt certain gene-edited plants from GMO-style regulation when no foreign DNA is present and the changes could, in principle, arise through conventional mutagenesis. In contrast, the European Union has, to date, largely considered most genome-edited crops under existing GMO legislation, although ongoing discussions on "new genomic techniques" may lead to a differentiated framework in the future.

Ultimately, the contribution of GEd to food security *via* sustainable food production will depend to a large extent on its accessibility to breeding programmes in low- and middle-income countries (LMIC). This is for two reasons: (1) transformation capacity, phenotyping infrastructure, and regulatory clarity remain limited in the LMIC, and (2) countries of the Global South have their own needs in terms of breeding targets. Transparent communication about technology, its risks, benefits, and its potential contribution to sustainable agriculture is necessary to build and maintain trust in science and its products. Regulatory clarity and societal support are instrumental of whether gene-edited varieties move beyond experimental stages into widespread cultivation and adoption in farmers' fields.

6 Conclusions

GEd has introduced unprecedented precision into plant breeding, but its transformative potential is constrained by biological, operational, and societal realities. GEd has already demonstrated success for traits controlled by major-effect genes, where causal variants are well defined, and its broader impact on complex traits is likely to increase as technologies, datasets, and breeding integration mature. However, genetic gain is a slow and long-term process. The full contribution of GEd will only become apparent as edited alleles progress through breeding cycles and multi-environment evaluation. A systems approach integrating GEd with selection strategies, speed breeding, next-generation editing, high-throughput plant phenotyping, and expanded genetic diversity provides a realistic pathway to accelerating genetic gain. In this context, GEd is best viewed not as a stand-alone tool, but as a strategy for allele design and deployment within breeding systems. Future progress will require improved transformation systems, scalable next-generation editing, predictive breeding models, and supportive regulatory frameworks. Even with these advances, success will ultimately depend on embedding GEd within robust breeding systems and aligning edits with selection strategies. While gene editing is still under development, we recommend using genomics-based selection along with phenotypic selection tools for multigenic traits, and reserving GEd for traits controlled by major-effect, well-characterised loci.

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Declarations

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