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PERSPECTIVE

Bridging the Translational Divide: A Vision for AI-Guided Genome Editing from Bench to Field in Cereal Crops

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Abstract

The mix of AI and CRISPR gene editing is changing how we upgrade grain crops, which feed much of the world. In this inaugural perspective, we propose a transformative framework to close the gap between computational prediction and field performance. Rather than presenting new data, we call for a paradigm shift toward explainable AI, digital twins, federated learning, and breeder-centric platforms. We argue that only through integrated, transparent, and collaborative systems can we realize the full promise of precision breeding for global food security. Still, translating computational predictions into successful crop performance in the field often fails or exhibits rapid performance decline. Here's A critical analysis of the primary failure points - finding targets, making edits and growing plants, then testing them in different fields - and proposes a practical framework that fits the tricky biology of grains such as wheat, corn, and rice. We pull together realistic standards for picking models (focusing on transparent AI instead of hidden algorithms, testing under unexpected stresses), handling edits safely (methods for complex, repeated DNA patterns, designing with cell structure in mind, checking thoroughly for unintended changes), plus getting trials set up right (solid checks of genes meeting environments, repeating tests across locations, planning seed production to field timing smartly). We lay out a step-by-step process using clear AI to spot key traits, link gene edits with safety checks for side effects, while running virtual tests to predict how crops perform in different climates and genetics. Moving beyond conceptual proposals, we define a set of verifiable metrics to track progress from lab work to real-world use. Turning scattered tips into fixed rules helps avoid costly mistakes later, speeds up creating tough grain varieties, and makes results easier to verify worldwide. This piece speaks directly to those wanting practical steps matched to actual farming needs, answering calls for fresh approaches in crop research.

Keywords: CRISPR genome editing, cereal breeding, explainable artificial intelligence (XAI), genotype-by-environment (G×E).

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1 Introduction

1.1 The Imperative for Cereal Crop Innovation

This editorial outlines a forward-looking roadmap to overcome these barriers, advocating for a new breed of translational science that unites computational innovation with agronomic reality. With Earth's population nearing 10 billion by 2050, growing food is getting tougher due to wild weather and shrinking land and water [1]. Wheat, rice, and corn fuel more than half the world's diet - so improving these plants isn't optional, it's essential for survival [2]. For years, scientists relied on classic crossbreeding, a method taking ten-plus years just to make one improved strain - is labor-intensive and time-consuming [3]. But climate chaos moves faster; droughts hit harder now, heat waves linger longer, while bugs and diseases adapt quicker than ever [4]. Old techniques aren't keeping up - their benefits have stalled. Consequently, there is an urgent need for more efficient and precise methods to build resilient grains.

1.2 The Technological Vanguard: AI and Genome Editing

In this fast-moving space, two forces are joining - artificial intelligence and CRISPRedits. Instead of just working side by side, they are converging synergistically. Machine learning, a part of AI, digs through huge piles of biological data - not just genes but activity and traits - to spot hidden links. It can guess what a gene does or which tweaks might boost yield, doing it faster than any human ever could. While that's happening, tools like base editors let scientists make exact DNA changes on purpose. These edits aren't random; they aim at things like drought survival or better nutrition uptake. What used to take decades now happens quicker, sometimes in one go. Breeders don't only pick plants anymore - they build them. With each test feeding back into the system, discoveries lead straight to real crops, no lag. The Figure 1 illustrates an integrated workflow combining multi-omics data, environmental metadata, and trait physiology to prioritize gene targets in cereals using explainable AI. predictive models extract causal regulatory features and rank candidate loci for editing based on trait relevance, network centrality, and environmental robustness. This pipeline reduces false positives, improves biological interpretability, and accelerates the transition from computational prediction to experimental validation.

To enhance conceptual clarity, the target-discovery method must clearly illustrate the hierarchical structure of the input data. This encompasses genetic variants, transcriptome profiles, protein levels, metabolite signatures, and chromatin accessibility states, in addition to comprehensive environmental descriptors including temperature, soil physicochemical properties, humidity, and stress-specific metadata. Integrating these diverse data types is crucial, since multi-omics signatures frequently demonstrate context-dependent regulation that AI models cannot decipher without environmental context [5, 6]. The updated figure must visually distinguish the XAI module—employing techniques as SHAP, integrated gradients, or attention-weight visualization—to illustrate the relationship between feature attribution maps, biological inputs, and trait predictions [22, 23]. The pipeline must incorporate a definitive ranking phase that prioritizes candidate genes based on criteria including causal network centrality, functional conservation, genotype–environment robustness, and anticipated pleiotropic risk, succeeded by a validation layer comprising in silico simulations, molecular assays (qPCR, reporter constructs), and phenotypic evaluations [14, 17].

For clarity, the updated version of Figure 1 follows these principles and now distinguishes between data inputs, the XAI interpretation engine, candidate-ranking modules, and the sequential validation steps necessary for translation to experimental systems.

1.3 The Translational Gap in Cereals

Even with such huge potential, there's still a deep divide between data and actual farming - especially for grain crops. One moment an AI spots a likely gene with strong backing, while CRISPR tweaks it perfectly indoors - but then the new plant fails to demonstrate improved performance under field conditions [12]. That's the main roadblock: smart computer forecasts or greenhouse wins don't turn into tougher, reliable crops out in the wild. And honestly, it's not because tools like AI or gene editing are broken - it's more that big grains have messy biology which breaks the rules those techs rely on. 1.3 Plants such as bread wheat (Triticum aestivum, a hexaploid AABBDD genome) or oats (Avena sativa, a hexaploid AACCDD genome) have complex genetic structures - loaded with repeating sections - that make it tough to spot genes or tweak them [19]. On top of that, how genes behave can shift big time depending on weather, dirt type, or farming methods; this strong link between genetics

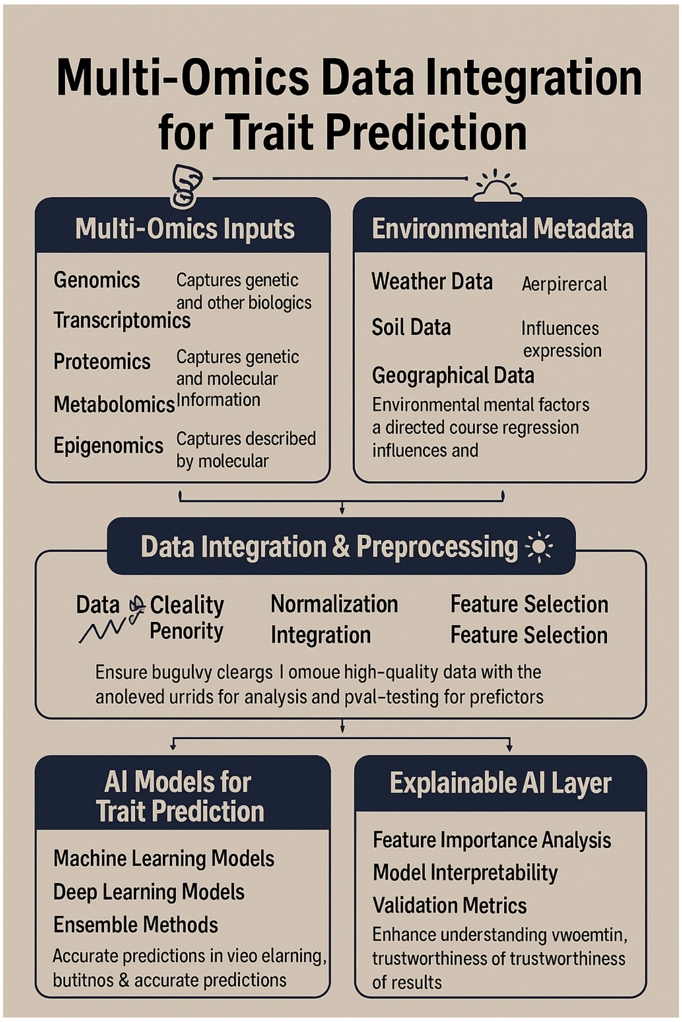

Figure 1. AI-enabled target discovery pipeline integrating multi-omics inputs (genomics, transcriptomics, proteomics, metabolomics, epigenomics) with environmental metadata to generate biologically interpretable predictions. Explainable AI (XAI) modules—such as SHAP and attention-based attribution—highlight key regulatory features driving model outputs. Ranked candidate loci are prioritized using trait relevance, network centrality, and predicted environmental robustness. Final targets undergo multi-tier validation, including in silico simulations, molecular assays, and phenotypic evaluation under controlled and field conditions.

and surroundings messes up lab results when applied out in real fields where grains actually grow [30].

1.4 A Critical Framework for Cereal Breeding

A fresh look at how we breed grain crops - this piece steps back to examine the whole process, focusing on smart methods used for wheat, corn, and rice. Instead of hyping up tech advances, it zeroes in on real roadblocks: biology limits, flawed algorithms, clunky logistics. The divide between theory and field results won't close without a shift - driven by interdisciplinary collaboration, openness, choices that help actual plant breeders. What's needed? Clear strategies, doable benchmarks, tools that hold up under pressure. Each part of the breeding chain gets broken down, tested through real-world examples, then rebuilt smarter. Solutions aren't standalone fixes - they link together, targeting weak spots head-on. We therefore propose a structured yet adaptive framework designed not merely to inform, but to inspire and orchestrate cross-disciplinary collaboration across the public and private sectors.

2 The Cereal Challenge: Complexity in the Crosshairs of Precision Tools

Below, we dissect the key challenges and propose actionable principles—not merely technical fixes—for a new era of cereal breeding. The dream of smart breeding - AI picking a goal while CRISPR makes it happen - encounters significant challenges in applied agricultural contexts with grain plants. Traits that help these crops thrive also trip up even the sharpest high-tech fixes.

2.1 The Precision Toolkit: AI and CRISPR

AI plus CRISPR. These technologies retain significant potential. Not just picking genomes anymore - AI's doing more now. Take Graph Neural Networks (GNNs), they're starting to map out how biology really works, linking genes, proteins, and chemicals together to guess things like crop output or drought survival [35]. When it comes to gene edits, CRISPR isn't alone anymore - it's got help from base editors (BEs) and prime editors (PEs). Those let scientists swap one DNA letter at a time - or make tiny cuts - without dangerous breaks in both strands, which matters a lot when working with top-tier plant lines [7, 11, 21]. Big wins include boosting rice yields fast by tweaking several genes at once [36], or giving wheat armor against diseases [32] - proof this combo can shake up farming.

Recent implementations of explainable AI (XAI) in cereals illustrate its effectiveness for trait prediction. SHAP (SHapley Additive exPlanations) was utilized to elucidate a random forest model forecasting wheat grain yield based on hyperspectral data, identifying critical wavelength bands associated with photosynthetic efficiency [28]. A convolutional neural network (CNN) analyzed root architectural features from rhizotron pictures in maize and associated them with drought-responsive genes, offering breeders viable genetic targets [27]. These examples illustrate how XAI transcends a 'black box' approach to provide physiologically interpretable insights for prioritizing genome editing.

The Figure 2 outlines the sequential progression from computational guide RNA design through gene editing, regeneration, greenhouse evaluation, and multi-location field trials. AI-supported prediction modules assess off-target risks, pleiotropic effects, and genotype-by-environment interactions prior to deployment. The integrated workflow increases edit reliability, minimizes late-stage attrition, and ensures that engineered cereal lines meet agronomic performance standards across diverse environments.

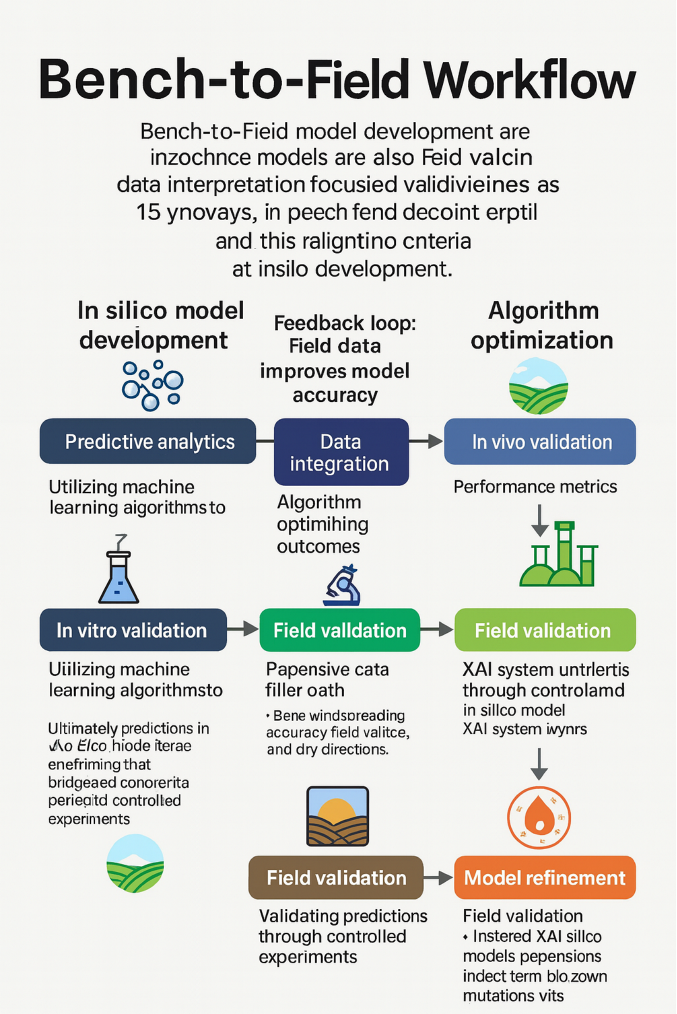

Figure 2. Bench-to-Field workflow for AI-Guided CRISPR editing in cereal crops.

2.2 The Cereal Arena: Unique and Daunting Challenges

Applying this toolkit to cereals presents unique hurdles that directly challenge their core assumptions:

Bread wheat's DNA is split into six sets - three nearly identical versions of most genes, one from each ancestor (A, B, D). When just one version gets changed, the plant usually stays the same because the others still work fine [34]. That throws off current editing tools. For artificial intelligence, guessing what happens when one gene spot changes becomes really tough. Systems built for organisms with only two gene copies struggle here - they don't handle extra copies or how they interact across different spots in the code. Genome editing faces big challenges because these genetic codes are so complex and full of repeats - checking every possible mistake becomes overwhelming, even impossible at times. Getting the right result usually means tweaking several gene copies at once, which makes designing and testing guide RNAs way harder.

The G×E Gauntlet: Cereals grow in way more diverse settings than most garden-type crops. So a gene that helps handle dry spells in watered, high-tech farms in California might flop - or backfire - in rainy but poor-soil areas of South Asia. Because results shift based on location, it's tough for AI tools to predict outcomes accurately - especially since they usually learn from neat test plots and fail when faced with complex, uncontrolled environments [18]. Any fix worth using needs to work reliably, no matter how conditions change.

Initial 'Digital Twin' or crop simulation platforms are being combined with genomics to forecast G×E interactions. The Agricultural Production Systems Simulator (APSIM) has been integrated with genomic prediction models to simulate the yields of several wheat genotypes across both historical and prospective climate scenarios throughout Australia, effectively finding lines with consistent performance [15]. The CropGym environment employs reinforcement learning to train AI agents with the DSSAT crop model, facilitating in silico optimization of maize ideotypes for specific conditions [31]. These instruments provide high-throughput virtual field experiments, thereby diminishing the expenses and duration associated with actual testing.

The Phenotyping Bottleneck for Complex Traits: Although drone, satellite, or sensor-based tools quickly track things like plant height, canopy size, or greenness scores, they miss key factors behind cereal output and quality - instead of capturing those, we're left guessing. Things such as kernels per head, root shape, how well plants grab nutrients, or protein levels in grains stay hidden [8]; because of this gap, machines learning from weak, shallow datasets stumble when trying to link genes to real-world results. Without rich, detailed measurements, even smart algorithms struggle - so for major crop improvements, today's AI runs on incomplete info. That missing piece blocks deeper understanding needed to connect genetic code with actual performance.

3 Deconstructing the 'Data-to-Field' Pipeline: Three Critical Failure Points in Cereals

The dream path from raw info to real-world use breaks down at three key spots - each one a place where good options fall away. While some ideas start strong, they don't make it past these hurdles. Where data turns into action, holes appear that kill progress. Though early stages show promise, results often vanish before reaching practice. Because gaps exist between steps, potential gets wasted along the way.

3.1 The Target Discovery Gap

The hunt starts by using smart algorithms to study layers of genetic info - spotting key genes plus how they're controlled in tricky traits. But right here's where things start wobbling. Many powerful AI systems act like sealed boxes - you get an output without providing interpretable decision pathways. The integration of XAI layers during the discovery phase enables breeders and geneticists to elucidate the impact of certain omics traits or environmental variables on model predictions, hence enhancing confidence in the biological validity of chosen targets [9].

For someone growing better crops, just knowing a result looks good on paper isn't enough - they need to know why it makes sense biologically before spending years and cash on new varieties [9]. When you can't see inside, doubt kicks in - and that slows everything down. 3.1 Yet once scientists spot a potential gene, testing it in crops like wheat takes ages - lots of work, big costs. This forms a jam: fast computer predictions hit the slow pace of real-world biology checks. Take Fusarium resistance in wheat - one single gene test might need three or more years just to grow and study the altered plants across its triple genome copies.

3.2 The Editing Execution Gap

Even if you're sure about your target, actually making the edit can still go wrong. But in plants with multiple chromosome sets, hitting every matching gene copy is tough - either knock them all out or tweak each one right. If only some get edited, outcomes are messy or useless, which burns up effort and materials. On top of that, how well an sgRNA works depends a lot on nearby DNA packaging - like chemical tags and openness - and those shift around and don't show up clearly in AI tools built from data in different organisms [20]. A particularly significant challenge is Negative pleiotropy - tweaking a gene for one good thing, like bigger grains, might mess up something else important, say shorter plants or weaker stems that fall over easily. Because today's AI usually learns just single gene effects, it often misses how changes ripple through the whole system, so even if the edit works in theory, it can fail badly in real farming.

3.3 The Field Validation Gap

Moving out of labs or greenhouses into messy, real farming setups. That's what some call the G×E challenge. When a modified crop shines in steady, perfect settings, it might flop once hit by actual field chaos - weather swings, soil differences, bugs - it happens all the time [12]. But here's the catch: how well it works depends heavily on the base plant variety it gets added to. 3.3 An allele that helps one type of wheat could lose its effect due to gene interactions in another, wrecking hopes for quick genetic fixes. On top of biology's roadblocks comes the real-world gap known as the Valley of Death. Moving from just a handful of modified plants to enough uniform seeds for widespread testing takes years and piles of effort. That stage still drags on forever, even though early lab steps have gotten much faster.

Quantitative studies highlight the magnitude of this translational gap. A meta-analysis of plant biotechnology outcomes indicated that about 5-10% of genes found in laboratory investigations (e.g., through RNA interference or model plant mutants) lead to enhanced agronomic features when incorporated into elite crop varieties in field circumstances [13]. In the context of genome editing in cereals, although the success rates for generating edits are elevated, a review indicated that a considerable percentage of edits targeting complex traits such as yield or drought tolerance exhibit inconsistent or negligible effects in multi-environment field trials, frequently attributable to unforeseen pleiotropy or G×E interactions [10]. This attrition rate underscores the urgent necessity for improved predictive models.

4 Bridging the Gap: An Integrated Framework for Cereal Crops

To translate promise into practice, we advocate for four pillars of innovation, each designed to bridge a specific translational gap. To tackle these issues, we're shifting focus - going for a system that's joined up, clear, and focused on breeders. It runs on four linked parts, each feeding into the next, turning raw info into real-world results.

4.1 From 'Black Box' to 'Glass Box' with Explainable AI (XAI)

To build trust and facilitate biological insight, the field must champion Explainable AI (XAI). Because trust matters - and real-world understanding helps - this approach should get more attention. Instead of guessing what's inside, tools like SHAP or LIME show how decisions happen [22]. Think of a farmer seeing which DNA bits a neural net paid attention to when judging gene roles. Or imagine getting a list of climate factors that shaped a crop output guess. Rather than treating AI like magic, transparency turns it into a teammate. Breeders can then check results, question them, and mix in their own knowledge. 4.1 Focusing on cause, not just patterns, next-gen tools need to use smarter systems that track real influences. Tools such as Bayesian models can untangle messy gene interactions by showing which genes steer others - these top controllers usually make better spots to edit DNA.

4.2 Taming Complexity In Silico with Digital Twins

Digital twins represent more than a modeling tool; they are a dynamic testing ground for predictive breeding, enabling in silico stress trials that would be impossible in the field [14, 15, 30]. To address the G×E challenge and negative pleiotropy, we must get better at predicting these complex outcomes in silico. The most promising frontier in this domain is the concept of the digital twin—a dynamic, computational replica of a crop genotype growing in a specific, simulated environment [17]. Instead of waiting for real-world tests, scientists mix DNA details with advanced growth simulations. These models test many genetic tweaks in different fake weather and dirt setups. Because of this, researchers spot changes that work well - not just once, but reliably under shifting conditions. That's key when building grain crops ready for climate ups and downs. On top of that, these virtual systems can link up with smart learning tools. Such tools weigh common breeding conflicts - say more harvest versus richer nutrition - and craft clever edit combos. The goal? Better overall performance without obvious drawbacks.

4.3 Closing the Data Loop with Federated Learning and Advanced Phenomics

One way forward? Change how we create and share information. In cereal breeding - where data is scattered and locked up - new methods can help. Think decentralized training: computers learn together but keep data local [24]. No files move; only insights are combined. So instead of trading secrets, teams tweak one joint model. Picture seed companies plus research labs improving drought resistance in wheat - all while guarding their unique plant lines. 4.3 At the same time, speeding up how fast we get info from farms is key. Instead of waiting, live updates from high-tech tools like drones, sensors, or robots flow straight into AI setups. This builds a model that keeps changing, shaped by fresh results from actual crop behavior out in the fields. Because it retrains itself nonstop, it gradually picks up on how genes and environments interact. With each round of breeding, its guesses become sharper.

Federated learning is an emerging application for genomic prediction in wheat, enabling multiple international breeding institutes to collaboratively enhance a global yield prediction model without disclosing sensitive germplasm data, resulting in a 15% improvement in prediction accuracy over local models [25].

4.4 The Breeder-in-the-Loop: Human-Centric Decision Platforms

One key thing - closing the distance between raw numbers and real farms - needs a new mindset. Smart breeding isn't about replacing breeders with machines; it's about boosting their deep know-how. The best setups will work like partner tools, putting breeders in charge when decisions land. This way, computer guesses get checked against hands-on insight and actual soil-level truth. 4.4 These tools need to respond to user actions, so people can check results, tweak settings using gut feeling, or bring in subtle know-how algorithms miss. Doing it this way builds confidence, helps teams start using them faster, while keeping a breeder's instinct alive - the kind earned over years, something lines of code just won't replicate.

5 Discussion

As we stand at the convergence of data science and genome editing, the question is no longer what is possible, but how to responsibly realize it. This requires a cultural shift toward open science, shared failure, and iterative learning. The mix of AI and gene tweaking in grain crops isn't just tech progress - it might flip how we improve plants, shifting from fixing problems later to designing them ahead. But that change brings some real friction. In theory, AI and editing go hand-in-hand: one guesses what could work using patterns, while the other tests those ideas directly through edits. Still, deep down, these fields pull in different directions. A single guess from an AI might hint at what's likely - yet it's never guaranteed. Unlike that, tweaking DNA follows strict cause and effect, changing living systems for good. If you trust a faulty forecast, effort drains fast while progress stalls for years, possibly messing up natural gene patterns along the way. That's why real experts must stay involved, linking smart software hunches with actual farm or lab outcomes.

The scientific community must prioritize the systematic documentation of negative results, jotting them down, then using those lessons. Right now, nearly every botched outcome - like when an AI forecast fails real-world testing - is often not published or deposited in public databases, leading to a publication bias. That habit warps the whole picture, making tech seem further along than it is while others blindly trip over identical pitfalls. And honestly? We can't keep burning resources like this. We suggest building a fresh setup - one that supports early-stage, open-access data banks for confirmed 'no effect' gene links. That kind of hub could seriously boost upcoming AI systems by showing them clear cases where things fall flat. It shows how vital breeders really are - not only picking top performers but also reading subtle balances and handling setbacks machines still can't handle. So having people involved isn't just a stopgap fix while tech improves - it's a lasting must-have to guide smart tools through real-world trial and error. Moreover, the integration of AI and genome editing must be guided by ethical and governance frameworks that ensure equity, transparency, and sustainability. Public trust will depend not only on scientific success but also on inclusive dialogue with farmers, policymakers, and consumers [2, 37].

6 Conclusion and a Roadmap for Translational Cereal Breeding

In closing, we envision a future where AI and genome editing are seamlessly woven into the fabric of cereal breeding. This will not happen by chance, but by design—through explainable systems, digital foresight, shared intelligence, and human wisdom. We invite the community to join us in building this integrated pathway from lab to field, for a more resilient and nourished world.

The integration of artificial intelligence with precision genome editing holds significant promise for cereal crop improvement, yet its translation from theoretical potential to practical application remains challenging. This study has rigorously analyzed the ongoing translational gaps—from target identification and editing implementation to field validation—that obstruct the development of climate-resilient cultivars. We contend that these issues arise not from a lack of technological capability, but from a discord between advanced computational tools and the complex, polyploid biology of grains cultivated in diverse conditions.

The suggested framework—rooted in explainable AI (XAI), in silico digital twins, federated learning architectures, and human-in-the-loop decision platforms—offers a systematic approach to close this gap. The fundamental breakthrough is the establishment of a closed-loop, predictive breeding cycle in which computational ideas are physiologically interpretable, meticulously validated in virtual environments, and perpetually enhanced with empirical data, all under the strategic oversight of plant breeders.

To convert this conceptual framework into expedited genetic advancement, we delineate the subsequent specific, cooperative measures for the international research community:

1. **Establish Consortia for Cereal-Specific Digital Twin Development.**
   We advocate for the establishment of multinational consortia to create and authenticate open-source digital twin systems for wheat, rice, and maize. These platforms must incorporate genotype-to-phenotype models (e.g., APSIM, WOFOST) with genomic prediction algorithms to simulate the performance of modified gene networks across extensive, simulated environmental gradients [16, 29]. A flagship study may concentrate on simulating the effects of modifying drought-responsive transcription factors in key worldwide agricultural regions, therefore pinpointing potential changes with the greatest likelihood of sustained performance prior to initiating laboratory experiments.
2. **Champion FAIR Data Ecosystems with**

Mandatory Reporting of Negative Results.
The forecasting ability of AI is inherently limited by the quality and extent of its training data. The community must implement and uphold FAIR (Findable, Accessible, Interoperable, Reusable) data principles for all omics, phenomics, and environmental metadata [33]. It is essential for journals and funding organizations to encourage or require the publication of negative results and replication studies in centralized repositories (e.g., hosting datasets demonstrating "gene edit - no effect"). This would rectify the existing positive-result bias and generate the "failure-aware" datasets essential for training resilient, generalizable AI models [26].

3. **Launch Pilot Federated Learning Networks for Complex Trait Prediction.**
To utilize global genetic diversity while safeguarding proprietary germplasm, experimental federated learning networks should be created among public institutions and breeding enterprises. These networks would jointly train models on intricate features such as heat tolerance or nitrogen usage efficiency without disclosing raw genomic data, as evidenced by groundbreaking research in genomic prediction [25]. This method democratizes access to advanced analytics and consolidates distributed knowledge to address shared concerns.

4. **Develop and Standardize Field-Readiness Metrics (FRMs).**
The community must establish a standardized set of Field-Readiness Metrics (FRMs) that transcends basic characteristic measurement. These would be multi-dimensional metrics assessing an altered line's performance stability (G×E variance), yield reduction under stress, lack of pleiotropic flaws, and scalability of seed production. FRMs would offer a standardized, quantitative framework for evaluating translational efficacy from greenhouse to agricultural implementation.

This framework facilitates a predictive and participative breeding paradigm for long-term vision. In this future, a breeder can query a system to create a wheat ideotype for a specific climate scenario, obtain a prioritized shortlist of multi-gene edits with articulated biological rationale and simulated performance confidence intervals, and commence a targeted editing pipeline with significantly diminished risk of field failure.

The implementation of this integrated approach is expected to reduce the varietal development cycle by a minimum of 30–50%. It accomplishes this not by expediting a singular phase, but by systematically eradicating the expensive, time-intensive iterative cycles of field trial attrition. By rendering failure foreseeable and preventable in silico, we can concentrate physical resources on the most promising genetic treatments. This is the critical measure required to swiftly implement grains capable of enduring climatic fluctuations, thereby guaranteeing food security for an expanding global populace amid progressively difficult circumstances.

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Conflicts of Interest

The author declares no conflicts of interest.

Ethical Approval and Consent to Participate

Not applicable.

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