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Research Article

A Strategy for Creating Climate Smart Crops by Applying Gene Editing to Wild Relatives

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Abstract

Climate change poses an unprecedented threat to global food security, with rising temperatures, soil degradation, drought, and emerging pests demanding urgent agricultural adaptation. Conventional plant breeding has successfully increased yields but inadvertently reduced genetic diversity, leaving modern cultivars vulnerable to environmental stresses. This review aims to evaluate a comprehensive strategy for creating climate-smart crops through the application of gene editing to wild relatives, a paradigm known as de novo domestication. By synthesizing current literature and case studies across major crop families, this paper examines the genetic principles underlying domestication traits, the application of CRISPR-Cas9 technology, and the technical and regulatory challenges involved. The results of recent proof-of-concept studies demonstrate that editing a handful of major domestication genes in wild species, such as tomato, rice, and soybean, can transform them into productive, compact crops within years rather than centuries, while preserving their intrinsic stress tolerance. In conclusion, the integration of gene editing with wild relative conservation and high-throughput phenotyping offers a transformative pathway toward resilient, nutritious, and sustainable crops capable of thriving in a changing climate, representing a paradigm shift from defensive breeding to proactive climate adaptation.

Keywords

De Novo Domestication, Plant Breeding, Crop Wild Relatives, Climate Smart Agriculture, Genome Editing

1. Introduction

The 21st century represents agriculture with an unprecedented convergence of challenges. The global population is projected to reach nearly ten billion by the year 2050, requiring substantial increase in food production above current levels [1-3]. Simultaneously, climate change intensifies abiotic stresses (heat, salinity, drought, and flooding) that already reduce crop yields by 20 to 50% annually [1, 2, 4]. The green revolution of the mid-twentieth century achieved remarkable yield gains through semi-dwarf genes and intensive management, but this success came at a cost. Modern cultivars have lost much of the genetic diversity that enabled their wild ancestors to withstand environmental extremes [4].

The fundamental paradox of modern plant breeding is that selection for high yield under optimal conditions has inadvertently eroded stress tolerance. Domestication, the millennia-long process of adapting wild plants for human use, involved selecting for a suite of traits collectively termed the domestication syndrome (loss of reduced branching, uniform germination, seed shattering, compact growth habit, and increased

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fruit size) [5]. While these changes made agriculture possible, they also created bottlenecks that eliminated alleles conferring stress resilience. Wild relatives, by contrast, retain this genetic richness but are unsuitable for cultivation due to their primitive agronomic characteristics.

The development of CRISPR-Cas9 and related technologies has fundamentally altered what is possible in plant breeding. Unlike transgenic approaches that introduce foreign DNA, CRISPR enables precise modification of native genes, allowing breeders to domesticate wild species by correcting their undesirable traits while preserving their stress tolerance [6]. This approach, termed de novo or neo-domestication, collapses a 10,000-year process into a few years of targeted molecular breeding.

This review addresses a specific strategy at the intersection of conservation biology and crop improvement: applying gene editing to wild relatives to create climate-smart crops. The central argument is that wild germplasm, long considered too difficult to use in breeding, represents the most promising resource for developing resilient varieties for climate-challenged environments. By editing a handful of major domestication genes, researchers can rapidly transform stress-tolerant wild species into productive crops. This paper synthesizes current research, examines successful case studies, analyzes challenges, and outlines a path forward for implementing this strategy in mainstream breeding programs. The logical flow moves from the genetic rationale for using wild relatives, through the technological capabilities of CRISPR systems, to concrete case studies, and finally to implementation challenges and future directions.

2. Objectives

The objectives of this review are:

1) To critically evaluate the genetic and agronomic rationale for using crop wild relatives as a starting material for climate-smart crop development through gene editing.
2) To examine the current state of CRISPR-Cas9 and related genome editing technologies applicable to de novo domestication of wild species.
3) To analyze successful case studies of de novo domestication across major crop families, including Solanaceae, Poaceae, and Fabaceae.
4) To identify technical, biological, regulatory, and social challenges limiting widespread adoption of this strategy.
5) To propose an integrated pipeline combining gene editing, speed breeding, and high-throughput phenotyping for efficient de novo domestication.
6) To provide evidence-based recommendations for future research priorities and policy frameworks that would accelerate the development of climate-smart crops derived from wild relatives.

3. Literature Synthesis

3.1. The Genetic Bottleneck of Domestication

Domestication has consistently reduced genetic diversity across virtually all species of crops [7-9]. Maize derived from teosinte (*Zea mays ssp*. parviglumis) lost approximately 30% of its genetic variation during domestication and modern breeding [10]. Bread wheat, rice, soybean, and tomato show similar patterns of diversity loss [11, 12]. This reduction correlates directly with the loss of alleles conferring resistance to biotic and abiotic stress.

The gene pool concept categorizes genetic resources by their cross ability with cultivated crops [8, 13, 14]. The primary gene pool (GP1) includes the cultivated species and its immediate wild ancestors with free cross ability and fertile hybrids. The secondary gene pool (GP2) includes more distant relatives that can hybridize with difficulty, producing partially fertile offspring. The tertiary gene pool (GP3) encompasses species from different genera requiring advanced techniques for gene transfer. Traditional breeding has largely remained within GP1, leaving GP2 and GP3 largely untapped despite their rich stress tolerance traits [8, 9, 12].

3.2. Stress Tolerance Traits in Wild Germplasm

Wild relatives exhibit remarkable adaptations to extreme environments. *Aegilops tauschii*, the D genome donor of bread wheat, demonstrates superior thermo stability of photosynthetic mechanisms and tolerance to saline conditions [1, 15]. Wild barley (*Hordeum spontaneous*) and its perennial relative *Hordeum bulbosum* possess drought tolerance and disease resistance absent from cultivated barley [5]. Wild soybean (*Glycine soja*) produces long non-coding RNAs that confer resistance to pests like insects, a trait largely lost in cultivated soybean [16, 17].

These adaptations arise from natural selection operating in heterogeneous, stressful environments, the opposite of the uniform, high-input conditions under which modern cultivars are chosen. Wild species have evolved diverse mechanisms for coping with water limitations, high temperature, nutrient deficiency, and pathogen pressure [18, 19]. Capturing these mechanisms in cultivated backgrounds has proven challenging through conventional crossing due to linkage drag, where undesirable wild traits remain associated with beneficial ones [4, 20, 21].

3.3. Traditional Introgression Limitations

The conventional approach to using wild relatives involves crossing with elite cultivars followed by repeated backcrossing to recover agronomic performance while retaining the wild trait. This process is time-consuming (taking up to 5 to 10 years or more), inefficient, and often unsuccessful due to

reproductive barriers, hybrid sterility, and recombination suppression [22-24]. Even when successful, the resulting lines typically retain linkage drag, which are the chromosomal segments from the wild parent that reduce yield or quality. Polygenic stress-tolerant traits are particularly difficult to introgression [25-27]. When multiple genes control a trait, each must be transferred and combined without disrupting the recipient genome [10, 26, 28]. The chance of recovering all desirable combinations diminishes exponentially with the number of loci involved [10]. These statistical realities have led breeders to favor major genes when working with wild relatives, leaving complex polygenic traits largely inaccessible [22-24].

3.4. CRISPR-Cas9 and Its Variants for Plant Breeding

Clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated protein nine (Cas9) constitute an adaptive immune system in bacteria that has been repurposed as a programmable genome editing tool. The system's simplicity (a single guide RNA directs the Cas9 nuclease to specific DNA sequences) has democratized genome editing across plant biology [29].

For plant breeding applications, CRISPR-Cas9 enables three primary outcomes:

1) Gene knockout through insertion-deletion mutations that disrupt coding sequences.
2) Precise base editing that converts one nucleotide to another without double-strand breaks.
3) Prime editing that enables targeted insertions or replacements [30].

The development of Cas variants with different protospacer adjacent motif (PAM) requirements has expanded targeting range, while Cas12, Cas13, and Cas14 offer alternative cleavage properties useful for specific applications [31].

3.5. Key Domestication Genes as Editing Targets

De novo domestication focuses on modifying major genes controlling the domestication syndrome. These genes are well characterized in major crops and often share orthologous functions across species, enabling knowledge transfer from model systems to understudied wild relatives [32].

In tomato, the Self-Pruning (SP) gene controls determinacy, the transition from vegetative to reproductive growth. Editing the wild self-pruning ortholog converts sprawling, indeterminate vines into compact, determinate plants suitable for cultivation [4, 33]. SP5G and SP2D regulate flowering time, enabling adaptation to long-day conditions. Multi-Flora (MFT) controls fruit number, and Ovate influences fruit shape. Simultaneous editing of these genes transformed the wild tomato relative Solanum pimpinellifolium into a cultivated type plant with threefold larger fruits and ten-fold more fruit per cluster [14, 33].

In rice, the major domestication genes include PROSTRATE GROWTH1 (PROG1) for erect growth habit, SHATTERING4 (SH4) and qSH1 for reduced seed shattering, grain number, plant height and heading date7 (Ghd7) for yield, and SEMIDWARF1 (SD1) for plant height [34]. Editing these genes in wild rice relatives produces plants with non-shattering panicles, compact architecture, and improved harvest index while retaining stress tolerance.

3.6. Multiplex Editing and Speed Breeding Integration

The efficiency of de novo domestication increases dramatically with multiplex editing. Together, targeting multiple genes using arrays of guide RNAs delivered from a single construct, multiplex enables the correction of several domestication-related deficiencies in one transformation event, reducing the time required to generate agronomically acceptable plants [1].

Integration with speed breeding further accelerates the process. Speed breeding uses extended photoperiods and controlled environments to achieve four to six generations under standard conditions [5, 36]. When combined with rapid generation advance techniques and early trait screening, de novo domestication field-ready lines within two to three years of initiating a project [36].

4. Case Studies

4.1. Tomato (Proof of Concept in Solanaceae)

The first successful domestication of de novo domestication came from tomato. A previous study [33] used CRISPR-Cas9 to edit domestication genes in Solanum pimpinellifolium, the wild ancestor of cultivated tomato. The targeted genes controlled plant architecture (SP), fruit size (FW2.2, FW3.2, LC), and fruit shape (OVATE). The resulting engineered plants exhibited compact growth, three-fold larger fruits, and ten-fold increased fruit number while retaining the wild parent's stress tolerance and nutritional quality [33].

Subsequent work expanded this approach to other Solanaceae species. A recent review [32] highlighted advances in de novo domestication across the family, noting that tomato serves as a model for transplanting domestication gene knowledge to related crops including potato, pepper, and eggplant. The conservation of gene function across the Solanaceae suggests that domestication loci identified in tomato can guide editing in less studied wild relatives [33]. This case dominates and emphasizes that a single transformation event targeting four to six genes can produce a field-ready variety from wild species.

4.2. Rice (Recovering Nutritional Diversity)

Wild rice relatives, including Oryza rufipogon and Oryza

nivara, possess valuable traits for stress tolerance and grain nutrition that were lost or reduced during domestication [37, 38]. A recent study [37] documented that pigmented wild rice contains abundant anthocyanin's, proanthocyanidins, and flavonoids, antioxidants with documented health benefits that are largely absent from modern white rice [37]. Furthermore, another study [38] reported that intensive selection during the green revolution inadvertently resulted in the gradual disappearance of loci governing salinity tolerance, which are still preserved in wild relatives [38]. Additionally, [39] developed chromosome segment substitution lines from crosses between these wild species and elite varieties to incorporate genetic variation for yield, stress tolerance, and disease resistance.

Research has demonstrated that editing domestication genes in Oryza rufipogon can produce plants with non-shattering panicles, erect growth, and increased grain size while maintaining pigmented grain traits [34]. This neo-domestication approach opens possibilities for creating nutritionally enhanced rice varieties adapted to specific environments. The pigmented trait, which has documented health benefits [39], is retained because gene pathways independent of the targeted domestication loci control it.

4.3. Soybean (Novel Non-coding Genetic Mechanisms)

Recent work in soybean has revealed unexpected genetic mechanisms relevant to de novo domestication. A recent study [17] identified two non-coding RNA (lncRNA) genes at a single genetic locus that control multiple domestication-related traits in wild soybean (Glycine soja), including leaf and stem size, pubescence, and insect resistance. These lncRNAs produce small RNAs that inhibit the expression of several protein-coding genes; they are highly expressed in wild soybean due to natural mutation [17].

This discovery has two implications for de novo domestication. First, it demonstrates non-coding genes, expanding the target space beyond protein-coding sequences, can control domestication traits. Secondly, it shows that wild alleles can be reactivated in cultivated backgrounds through gene editing, complementing the approach of editing cultivated alleles into wild species [17, 40, 41]. Reintroducing the wild lncRNA expression pattern into cultivated soybean restored insect resistance without yield penalty [17].

4.4. Emerging Examples in Other Crops

The de novo domestication approach is expanding to additional crop families. In cereals, genome editing-accelerated re-domestication (GEaReD) as a major direction for barley improvement, targeting wild Hordeum vulgare spp. spontaneum and perennial H. bulbosum for direct domestication. The authors outlined specific domestication gene orthologs in barley corresponding to those successfully edited in tomato and rice [5].

In wheat, researchers have successfully demonstrated CRISPR/Cas9 editing of the *TaQ* genes, which alters spike morphogenesis and grain thresh ability [50]. This proof of concept suggests that the D genome sub genome can be domesticated de novo and then combined with existing A and B genomes to create synthetic hexaploid wheat with enhanced stress tolerance.

In legumes, proof-of-concept studies are underway in cowpea (*Vigna unguiculata*), targeting orthologs of tomato domestication genes. The genome of cowpea has been sequenced and annotated, providing foundational resources for editing experiments [42].

5. Challenges

5.1. Technical Challenges

Despite promising proof-of-concept studies, many technical challenges limit widespread adoption of de novo domestication. Transformation and regeneration remain species- and genotype-dependent. Many wild relatives are recalcitrant to Agrobacterium-mediated transformation or tissue culture regeneration, necessitating the development of genotype-independent protocols [4, 43]. This is particularly problematic for perennial species and those with complex genomes. For instance, perennial wild relatives of wheat and barley have proven extremely difficult to transform using current methods [5].

Epistatic interactions between edited genes present another challenge. The phenotypic effect of a domestication gene often depends on genetic background, with interactions that either enhance or mask desired outcomes [10, 32]. In tomato, for instance, the effect of fruit size genes is modulated by background variation, requiring empirical testing of edited lines rather than simple prediction from gene function [33]. Pleiotropy, where a single gene affects multiple traits, can produce unintended consequences when editing domestication loci. The SP gene in tomato, while controlling determinacy, also affects fruit shape and soluble solid content. Off-target editing effects, while generally low with well-designed guide RNAs, require verification through whole-genome sequencing, particularly for applications intended for commercial release. While CRISPR-Cas9 has high specificity, off-target mutations can occur at sequences with three to five mismatches to the guide RNA, necessitating empirical validation for each guide design [44].

5.2. Biological Constraints

Not all domestication traits are controlled by major genes amenable to simple editing. Shattering resistance in some species involves multiple loci with minor effects, requiring more complex engineering strategies [34]. The genetic architecture of stress tolerance in wild relatives is often polygenic, and editing major domestication genes may inadvertently disrupt

stress-responsive pathways. For instance, the PROG1 gene in rice controls both plant architecture and drought response, creating a potential trade-off between domestication and stress tolerance.

Reproductive barriers between species used for de novo domestication and cultivated relatives can complicate introgression of additional traits or integration into existing breeding programs. While de novo domestication produces a freestanding variety rather than requiring crossing, breeders may wish to combine traits from multiple sources, requiring fertility [10]. Hybrid sterility has been documented between de novo domesticated lines and standard cultivars in both tomato and rice [4, 34].

5.3. Regulatory and Social Considerations

The regulatory landscape for genome-edited crops remains fragmented. In the United States, the USDA has clarified that many CRISPR-edited plants without foreign DNA are not subject to biotechnology regulations. The European Union's Court of Justice ruled in 2018 that genome-edited organisms fall under GMO regulations, severely restricting development in member states [45]. Other countries, including Japan, Australia, and Brazil, have adopted intermediate approaches that distinguish between trans genesis and genome editing [15].

Intellectual property presents another consideration. CRISPR-Cas9 patents are held by multiple entities, including the Broad Institute, UC Berkeley, and Corteva. While some licenses are available for research, commercial applications may require royalty payments [46]. The wild relatives themselves are subject to international access and benefit-sharing agreements under the Convention on Biological Diversity and Nagoya Protocol, requiring documentation of provenance and compliance with national laws [13].

Public acceptance remains uncertain. While genome-edited crops without foreign DNA may face less opposition than transgenic GMOs, consumer attitudes vary by region and product. Transparent communication about the distinction between trans genesis and editing, and about the conservation benefit of using wild relatives, can improve public perception [47].

6. Future Perspectives

6.1. Integration with Emerging Technologies

The full potential of de novo domestication will be realized through integration with other accelerating technologies. High-throughput phenotyping using drones, robotics, and computer vision enables rapid evaluation of edited populations for agronomic traits [1, 48]. Machine learning algorithms can predict optimal guide RNA designs and identify candidate domestication genes from pan genome data. Artificial intelligence applications are beginning to enable prediction of epistastic interactions and pleiotropic effects before transformation, reducing the need for extensive empirical screening [49].

Pan genome resources, collections representing the full genetic diversity of a species and its relatives, provide the foundational data for de novo domestication [10]. By sequencing multiple accessions of wild relatives, researchers can identify conserved domestication gene orthologs and predict editing outcomes. The construction of pan genomes for major crop families will accelerate translation from model species to understudied crops [50]. The Solanaceae pan genome project, for example, has already identified domestication gene orthologs across tomato, potato, pepper, and eggplant [4].

6.2. Conservation Implications

De novo domestication has implications for plant genetic resource conservation that extend beyond crop improvement. By creating economic value from wild relatives, the approach provides incentives for their conservation both ex situ in gene banks and in situ in natural habitats [6, 13]. However, careful governance is required to prevent overharvesting or genetic contamination of wild populations.

A previous study [6] reviewed perspectives on gene editing for conservation, noting that CRISPR-based strategies can integrate conservation science with sustainable agriculture. The same technologies enabling de novo domestication can be applied to restore endangered plant species, control invasive plants through gene drive systems, and enhance the resilience of wild populations to climate change. The authors propose a framework for conservation editing that parallels de novo domestication but with goals of population recovery rather than agricultural production [6].

6.3. Toward a Standardized de Novo Domestication Pipeline

A standardized pipeline for de novo domestication would include seven stages [1, 4, 36].

1) *Germplasm identification and collection:* Wild relative accessions with documented stress tolerance are sourced from gene banks or field collections, with attention to provenance documentation for regulatory compliance [13].
2) *Genome sequencing and assembly:* High-quality reference genomes are generated for selected accessions, with annotation of domestication gene orthologs using reference-guided assembly and RNA sequence validation.
3) *CRISPR Design:* Multiplex constructs targeting four to eight domestication loci are designed using computational tools, with off-target prediction and empirical validation in protoplast systems [44].
4) *Transformation and Regeneration:* Optimized Agrobac-

terium or biolistic-based protocols are applied, with regeneration under selective conditions. This stage remains the primary bottleneck for many species [43].

5) *Genotypic and Phenotypic Screening:* Edited plants are screened by PCR, sequencing to confirm on-target edits, and absence of off-target mutations. Primary transformants are advanced under speed breeding conditions [35].
6) *Multi-location Field Evaluation:* Selected lines are evaluated for agronomic performance and stress tolerance across multiple environments relevant to target development regions [48].
7) *Regulatory approval and Variety Release:* Documentation is prepared for regulatory authorities and foundation seed is multiplied for distribution to farmers.

Implementation of this pipeline across multiple crops will require investment in transformation capacity, phenotyping infrastructure, and regulatory science. International collaboration and data sharing will accelerate progress, specifically for minor crops and those from understudied plant families [10].

7. Conclusion

The convergence of genome editing technology with the underutilized genetic diversity of crop wild relatives represents a paradigm shift in plant breeding. De novo domestication collapses the millennia-long process of converting wild plants into crops in the matter of years, enabling rapid creation of climate-smart varieties adapted to specific and particular environments. Proof of concept in tomato, rice, soybean, and other species demonstrates that editing a handful of major domestication genes transforms sprawling, low-yielding wild species into compact, productive plants while preserving their intrinsic stress tolerance and nutritional quality [33, 34].

This strategy directly addresses the challenge of climate change adaptation. Wild relatives have survived and evolved under natural selection in stressful environments; their genetic adaptations are proven and effective. By removing the agronomic barriers that have prevented their direct use, gene editing unlocks this adaptive potential for agriculture [4, 5]. The resulting climate-smart crops can thrive with fewer inputs, tolerate temperature extremes and water scarcity, and provide nutritional security for vulnerable populations.

Challenges remain technical hurdles in transformation and regeneration, biological constraints from epistasis and polygenic traits, regulatory fragmentation, and intellectual property considerations. None appear insurmountable. The trajectory of genome editing technology suggests continued improvements in efficiency, specificity, and ease of use [30, 31]. As regulatory frameworks evolve to distinguish edited from transgenic organisms, the path to field deployment will clarify.

For plant breeding to meet the challenges of the coming decades, it must transcend the limitations of conventional approaches. De novo domestication of wild relatives through gene editing offers a scientifically sound, practically achievable, and urgently needed strategy for creating climate-smart crops. The wild relatives are waiting in gene banks and natural habitats. The tools are ready. The time to act is now. The integration of this approach with conservation biology ensures that the genetic resources enabling climate adaptation will be preserved for future generations of plant breeders [13].

8. Recommendations

Based on the synthesis presented in this review, the following recommendations are proposed for research, policy, and practice:

1) *Expand transformation capacity:* For diverse wild relatives across major crop families, particularly perennial species and those with complex genomes. Investment in genotype-independent regeneration protocols should be prioritized [43].
2) *Develop pan genome Resources:* For underutilized crops (millets, teff, cowpea, cassava) to identify conserved domestication gene orthologs and predict editing outcomes across diverse genetic backgrounds [10].
3) *Investigate Epistatic Networks:* Governing domestication traits using CRISPR-based combinatorial editing and quantitative genetics approaches to enable prediction of interaction effects before transformation [32].
4) *Establish Standardized Phenotyping Protocols:* For evaluating edited lines under multiple stress conditions relevant to climate change scenarios, including combined stress (heat and drought) trials [48].
5) *Create Open-access Repositories:* For guide RNA designs, transformation protocols, phenotypic data, and negative results to accelerate progress across crops and avoid duplication of effort [36].
6) Policy Recommendations:
7) *Develop Regulatory Science Frameworks:* is that distinguish genome-edited de novo domestication products from transgenic organisms based on scientific risk assessment rather than process-based definitions. Harmonization across major agricultural economies would reduce uncertainty for breeders [47].
8) *Clarify the Intellectual Property Landscape:* for CRISPR-Cas9 applications in plant breeding to enable affordable access for public sector and developing country programs. Consideration of patent pools or open-source licensing models is warranted.
9) *Integrate Conservation Planning:* with de novo domestication programs to ensure sustainable use of wild genetic resources. Benefit-sharing mechanisms that return value to source countries and communities should be established [13].
10) Practice Recommendations:
11) *Train the next generation of plant breeders:* in genome editing technologies, computational biology, and wild relative conservation to enable integrated approaches.

Curriculum revisions should reflect the convergence of these disciplines [10].

12) *Establish International Consortia:* focused on de novo domestication for specific crop families, with coordinated efforts across tomato, rice, soybean, wheat, barley, and understudied orphan crops. Shared infrastructure and materials will reduce costs and accelerate progress [4].

Abbreviations

CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats
Cas9	CRISPR-associated Protein 9
GMO	Genetically Modified Organism
GP1	Primary Gene Pool
GP2	Secondary Gene Pool
GP3	Tertiary Gene Pool
lncRNA	Long Non-Coding RNA
PAM	Protospacer Adjacent Motif
PCR	Polymerase Chain Reaction
USDA	United States Department of Agriculture

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Conflicts of Interest

The author declares no conflicts of interest.

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