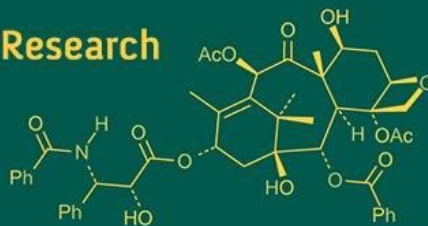
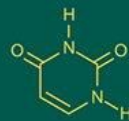
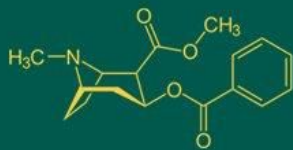


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New plant breeding techniques to boost resilience and sustainability in crop production

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Abstract

Agriculture faces unprecedented challenges due to climate variability, environmental degradation and increasing food demand. Traditional breeding alone cannot meet these challenges because of its slow pace and limited genetic variability. New Plant Breeding Techniques (NPBTs)—including genome editing, genomic selection, pan-genomics, speed breeding, high-throughput phenotyping and de novo domestication—offer precise and accelerated methods for developing climate-resilient and sustainable crop varieties. This review synthesizes recent advances in NPBTs, demonstrating their contributions to drought, heat, salinity and disease tolerance, as well as improvements in nutrient-use efficiency and yield stability. Case studies in rice, wheat, maize, tomato, legumes and sorghum illustrate their real-world applications. Regulatory, ethical and socio-economic considerations are also discussed. Collectively, NPBTs form a synergistic breeding ecosystem that can rapidly generate climate-ready, low-input cultivars essential for global food and nutritional security.

Keywords: New plant breeding techniques, genome editing, genomic selection, pan-genomics, speed breeding, phenotyping, de novo domestication, resilience, climate-smart agriculture

1. Introduction

1.1 (Elaborated Version)

Agriculture today operates under unprecedented ecological and economic pressure. Rising temperatures, erratic rainfall, frequent heatwaves, soil salinization, pest outbreaks and depletion of soil organic matter have collectively destabilized crop productivity across continents. Global cereal yields are increasingly vulnerable to climate extremes, with heat-related losses reported even in high-input production systems. Simultaneously, farmers confront rising fertilizer and pesticide costs, shrinking arable land and tightening environmental regulations aimed at reducing agrochemical dependence. Together, these constraints create an urgent need for crop varieties that are resilient, resource-efficient and capable of sustaining production under variable and stressful environments.

Traditional breeding has served as the backbone of agricultural improvement for over a century. The systematic application of Mendelian genetics, hybrid breeding, heterosis exploitation and selection programs delivered significant gains in yield and adaptability. However, these conventional approaches depend on naturally occurring recombination and long generational intervals, making them inherently slow. Many adaptive traits—such as drought tolerance, heat resilience, nutrient-use efficiency and disease resistance—are complex, polygenic and influenced by thousands of small-effect loci. Improving such traits through classical breeding requires substantial time, large populations and extensive multi-location testing.

Additionally, decades of intensive selection have narrowed genetic diversity in many major crops. Modern high-performing cultivars often share a limited genetic base, reducing their adaptive capacity under rapidly changing climatic conditions. This makes it difficult for traditional breeding systems to introduce novel variation at the pace required by emerging environmental challenges.

New Plant Breeding Techniques (NPBTs) provide a transformative response to these limitations. Genome editing enables precise modification of key genes governing stress responses, growth patterns and metabolic pathways.

Pan-genomics opens access to a much broader range of natural variation present in wild relatives and landraces. Genomic selection allows prediction of complex traits before phenotyping, significantly accelerating genetic gain. Speed breeding shortens generation cycles, enabling faster fixation of beneficial traits. High-throughput phenotyping enhances measurement accuracy of stress responses and strengthens predictive models.

By integrating these approaches, breeders can develop climate-resilient varieties far more rapidly and accurately than through traditional methods alone. NPBTs collectively improve stress tolerance, yield stability and input-use efficiency, positioning them at the center of future sustainable agriculture and global food security strategies.

2. Evolution of Plant Breeding and the Need for NPBTs (Elaborated Version)

Plant breeding has undergone several major technological transitions. Early domestication relied on phenotypic selection for traits such as grain size, shattering resistance and palatability. The rediscovery of Mendel's laws in the early 20th century initiated a scientific era of breeding based on controlled crosses, segregation analysis and heritable variation. Hybrid breeding and the Green Revolution further propelled productivity by exploiting heterosis, dwarfing genes and improved nutrient responses.

Despite these achievements, classical breeding operates within biological constraints. Recombination events are limited, meaning that combining beneficial alleles into a single cultivar often requires many generations of crossing and selection. Breeding cycles for cereals, legumes and horticultural crops may take 8-12 years or more. This pace is increasingly incompatible with the speed at which climatic stresses are intensifying.

Another major limitation is the narrow genetic base of modern cultivars. Many elite varieties are derived from a small set of shared ancestors, leading to genetic bottlenecks. This uniformity increases vulnerability to both abiotic

stresses—such as heat, drought and salinity—and biotic threats including evolving pathogens and insect pests. Although traditional introgression from wild relatives can introduce new variation, it is often hindered by linkage drag, sterility barriers and long backcrossing periods.

Furthermore, phenotyping—the evaluation of plant traits—has historically been a slow and labor-intensive process. Many resilience-related traits, such as water-use efficiency, canopy temperature, root architecture or early stress responses, are difficult to measure accurately using traditional tools, slowing down selection efficiency.

NPBTs directly address each of these limitations. Genome editing allows precise alteration of target alleles without the need for repeated crossing. Pan-genomic resources enable breeders to identify stress-adaptive genes absent from elite varieties. Genomic selection accelerates breeding by using genome-wide markers to predict performance, making phenotyping more strategic rather than exhaustive. Speed breeding drastically reduces generation time, while high-throughput phenotyping provides detailed trait measurements at scale.

Together, these innovations redefine breeding from a largely empirical discipline to a predictive, data-driven field capable of responding to rapid ecological changes. NPBTs therefore represent not just an enhancement of traditional methods but a necessary shift toward modern, climate-resilient crop improvement.

3. Genome Editing Technologies

CRISPR-Cas systems allow targeted modifications such as base editing, promoter editing and multiplex editing. Applications include improving:

- Disease resistance (SWEET gene editing in rice),
- Stress tolerance (editing drought and salinity regulators),
- Plant architecture (yield-related genes),
- Nutrient-use efficiency.

Table 1: Major CRISPR genome editing applications for resilience traits across crops.

Crop	Target Gene(s)	Edited Trait	Outcome	Reference
Rice	SWEET promoters	Bacterial blight resistance	Broad-spectrum resistance	Oliva <i>et al.</i> (2019) ^[23]
Wheat	MLO	Powdery mildew resistance	Durable fungal resistance	Wang <i>et al.</i> (2020) ^[20]
Rice	OsRR22	Salt tolerance	Higher tolerance under saline stress	Yang <i>et al.</i> (2021) ^[39]
Tomato	Multiple domestication genes	Fruit size/architecture	New climate-resilient lines	Zsögön <i>et al.</i> (2018) ^[44]

4. Genomic Selection and Predictive Breeding

Genomic selection (GS) predicts breeding values using genome-wide markers, accelerating improvement of complex polygenic traits. GS allows early selection, reduces

breeding cycle time and supports multi-trait improvement. Integration with speed breeding and phenotyping increases predictive accuracy.

Table 2: Genomic selection approaches and applications in resilience breeding.

Trait Type	GS Application	Crop Example	Impact
Drought tolerance	GS for transpiration efficiency alleles	Sorghum	Faster selection accuracy
Heat tolerance	GS models using canopy temperature	Wheat	Better performance prediction
Yield stability	Multi-environment GS	Maize	Improved stress-zone yields

5. Speed Breeding

Speed breeding accelerates generation advancement through extended photoperiods, controlled temperatures and optimized growth environments. Wheat, chickpea, barley and tomato can complete 4-6 generations annually. This rapid turnover greatly enhances CRISPR allele fixation, GS cycles and mapping population development.

Table 3: Speed breeding generation cycles in major crops.

Crop		Speed Breeding Generations/Year	Source
Wheat	1-2	4-6	Watson <i>et al.</i> (2018)
Barley	1-2	4-5	Hickey <i>et al.</i> (2019)
Chickpea	1	3-4	Varshney <i>et al.</i> (2021)
Tomato	2	4-6	Lemmon <i>et al.</i> (2018)

6. Pan-Genomics, Wild Relatives and De Novo Domestication

Pan-genomes reveal presence-absence variations and rare stress-related alleles lost during domestication. Wild relatives contain adaptive traits—deep roots, salt tolerance,

disease resistance—that can now be introgressed with CRISPR and GS. De novo domestication enables rapid improvement of wild species adapted to extreme environments.

Table 4: Stress-adaptive alleles identified using pan-genomic approaches.

Crop	Newly Identified Alleles	Trait	Source
Rice	Ion transport alleles	Salinity tolerance	Zhou <i>et al.</i> (2020) ^[43]
Tomato	Disease resistance loci	Biotic resistance	Gao <i>et al.</i> (2019) ^[8]
Chickpea	Heat/drought haplotypes	Climate resilience	Ruperao <i>et al.</i> (2021) ^[30]

7. High-Throughput Phenotyping and Digital Breeding

Drone-based, sensor-driven and automated greenhouse platforms capture multi-dimensional traits such as canopy temperature, spectral reflectance, root architecture and stress kinetics. HTP strengthens genomic selection and accelerates stress-resilience screening.

Table 5: High-throughput phenotyping platforms and measured traits.

Platform	Sensors Used	Key Traits Measured
UAV drones	RGB, thermal, multispectral	NDVI, canopy temperature
Field gantries	Hyperspectral, LiDAR	Photosynthetic traits, biomass
Greenhouse conveyors	RGB, fluorescence	Growth rate, early stress responses

8. Applications of NPBTs for Resilience

New Plant Breeding Techniques (NPBTs) are particularly powerful when applied to improve resilience traits—those that determine a crop's ability to survive, adapt and yield under diverse environmental constraints. Resilience encompasses tolerance to abiotic stresses such as drought, heat, salinity and flooding, as well as resistance to pathogens and pests, nutrient-use efficiency and yield stability in fluctuating conditions. These traits are often complex and polygenic, making them difficult to enhance through conventional breeding alone.

NPBTs enable breeders to precisely manipulate stress-responsive genes, assemble favorable allele combinations and rapidly fix these traits using accelerated breeding cycles. Genomic insights supported by pan-genomic resources and high-throughput phenotyping further refine the selection of superior genotypes. Together, NPBTs represent a multidimensional toolkit for developing climate-ready cultivars suited for sustainable agriculture.

8.1 Abiotic Stress Tolerance

Abiotic stresses—especially drought, heat and salinity—are among the most severe constraints on global crop productivity. These stresses often occur simultaneously, intensifying their impact on plant physiology, water relations and metabolic processes. NPBTs offer diverse strategies to enhance tolerance by modifying specific genes, regulatory pathways and physiological mechanisms.

Genome editing using CRISPR-Cas systems has enabled precise modification of drought-responsive genes such as transcription factors in the abscisic acid (ABA) signaling network. For instance, editing ABA receptors or downstream regulators can improve stomatal control, osmotic adjustment and water-use efficiency. Similar approaches target heat tolerance by manipulating heat shock

factors (HSFs) and chaperone proteins that stabilize cellular structures under high temperatures.

Salinity tolerance is improved by editing ion transporters such as HKT and NHX genes, which regulate sodium exclusion and intracellular ion homeostasis. Manipulating these genes helps maintain membrane integrity, osmotic balance and enzyme functionality in saline environments.

Genomic selection (GS) complements genome editing by predicting complex, polygenic resilience traits that involve numerous small-effect loci. Drought and heat tolerance traits—such as canopy temperature depression, osmotic adjustment and transpiration efficiency—are particularly suitable for GS because they are difficult to phenotype directly at large scale.

Speed breeding enhances abiotic stress tolerance by enabling rapid pyramiding of beneficial alleles and accelerating the evaluation of multi-stress response combinations. Breeders can complete multiple selection cycles in a single year, thereby shortening the time required to develop resilient lines.

Together, these NPBTs allow breeders to integrate physiological, molecular and genomic pathways for robust abiotic stress tolerance.

8.2 Biotic Stress Resistance

Biotic stresses—including diseases caused by bacteria, fungi, viruses and insect pests—remain a major cause of yield losses globally. Many pathotypes evolve rapidly, outpacing traditional resistance breeding programs. NPBTs offer durable solutions to this challenge by enabling direct editing of susceptibility genes and enhancing innate immune pathways.

One of the most notable breakthroughs is promoter editing of SWEET genes in rice to confer broad-spectrum resistance to bacterial blight. CRISPR-induced modifications prevent pathogen effectors from hijacking host sugar transport pathways, providing stable resistance without impairing plant fitness. Similarly, knockout of MLO susceptibility genes in wheat and barley confers durable resistance to powdery mildew.

Genome editing also enables the introduction of resistance alleles from wild relatives without the need for lengthy backcrossing, avoiding linkage drag. RNA-guided nucleases and new CRISPR variants such as Cas13 open avenues for antiviral resistance by degrading viral RNA within host cells.

Genomic selection helps breeders identify multi-locus resistance profiles and pyramid several resistance genes simultaneously, improving durability against evolving pathogens. High-throughput phenotyping strengthens this process by capturing detailed disease progression patterns and host responses.

NPBT-based resistance strategies significantly reduce dependence on chemical pesticides, lowering production costs and minimizing environmental impacts.

8.3 Nutrient-Use Efficiency

Increasing nutrient-use efficiency (NUE) is essential to reduce fertilizer dependency, lower input costs and limit nutrient pollution in agricultural systems. NPBTs provide multiple avenues to enhance the uptake, transport and assimilation of key nutrients such as nitrogen (N), phosphorus (P) and potassium (K).

Genome editing enables precise modification of nutrient transporter genes. For nitrogen, altering ammonium (AMT) or nitrate transporter (NRT) genes improves uptake efficiency and enhances nitrogen assimilation pathways. Editing regulators involved in nitrogen metabolism can fine-tune signaling networks to enhance efficiency under low-input conditions.

Phosphorus-use efficiency is improved by modifying PHT1 and other phosphate transporter genes, as well as root architecture regulators that enhance soil exploration and mycorrhizal associations. Pan-genomics helps identify rare alleles associated with efficient phosphorus acquisition from landraces and wild relatives.

Genomic selection accelerates the improvement of complex NUE-related traits such as root system architecture, nutrient remobilization and biomass allocation. High-throughput phenotyping technologies—such as spectral imaging and root imaging systems—allow breeders to quantify nutrient-response traits more accurately and at scale.

Improved NUE not only enhances yield under nutrient-limiting conditions but also contributes to sustainable agriculture by lowering fertilizer consumption and reducing

emissions from nutrient loss.

8.4 Yield Stability

Yield stability is a fundamental trait for ensuring food security, particularly in regions with fluctuating climates. It reflects a plant's ability to maintain consistent productivity across varied environments and under multiple stress combinations.

NPBTs offer several pathways to improve yield stability. Editing genes regulating flowering time, photoperiod sensitivity and developmental plasticity helps synchronize crop growth with local environmental conditions. Modifying architecture-related genes influences traits such as tillering, root depth and canopy structure—traits that affect water-use efficiency, lodging resistance and resource allocation.

Stress-related regulatory genes can be modified to enhance the plant's ability to cope with drought, heat and nutrient stress simultaneously. Multi-gene editing strategies allow simultaneous improvement of traits controlling biomass partitioning, reproduction and stress resilience, leading to stable yields even in unpredictable environments.

Genomic selection enhances yield stability by enabling breeders to predict performance across diverse environments using multi-environment trial (MET) data. Integration with HTP strengthens selection for stability indices, resilience trajectories and stress-adaptive growth patterns.

Speed breeding further accelerates the development of stable-yielding varieties by allowing repeated testing and selection across environments within shorter timeframes.

Together, NPBTs enable breeders to design cultivars with strong yield consistency, reduced sensitivity to climatic variation and improved resilience to environmental shocks.

9. Case Studies

Table 6: Documented case studies demonstrating practical NPBT outcomes.

Crop	NPBT Used	Achieved Trait	Reference
Rice	CRISPR promoter editing	Blight resistance	Oliva <i>et al.</i> (2019) ^[23]
Tomato	De novo domestication	Yield + resilience	Zsögön <i>et al.</i> (2018) ^[44]
Wheat	Speed breeding	Faster resistance pyramiding	Watson <i>et al.</i> (2018) ^[36]
Rice	Pan-genome introgressions	Salinity tolerance	Zhou <i>et al.</i> (2020) ^[43]
Chickpea	Pan-genome + GS	Drought stability	Ruperao <i>et al.</i> (2021) ^[30]

10. Regulatory, Ethical and Socio-Economic Dimensions

Regulation remains one of the most influential factors determining how quickly New Plant Breeding Techniques (NPBTs) can transition from research to widespread agricultural application. Although genome editing enables precise and often non-transgenic modifications, global policies differ considerably in how these technologies are classified and regulated. Countries such as the United States, Japan, Australia and India have adopted more progressive frameworks, allowing genome-edited crops that do not contain foreign DNA—particularly SDN-1 and SDN-2 modifications—to bypass traditional GMO regulations. These nations focus on the final product rather than the breeding process, enabling faster approvals, reduced compliance costs and more rapid commercialization. In contrast, the European Union continues to regulate genome-edited plants under the same stringent legislation applied to GMOs, emphasizing process-based evaluation. This regulatory divergence has created uneven innovation opportunities and global trade complexities.

Beyond regulatory challenges, NPBTs raise several ethical considerations. One major concern involves biodiversity:

while genomic tools allow targeted improvement, overreliance on uniform elite germplasm may inadvertently reduce genetic diversity if not managed responsibly. Another key issue relates to equitable access. Advanced breeding technologies are often concentrated within large private companies or well-funded institutions, potentially widening the technological gap for resource-poor breeders and smallholder farming communities. Intellectual property rights around key technologies—particularly CRISPR patents—also influence who can utilize NPBTs and under what conditions.

Public perception plays an equally critical role. Even when genome editing does not introduce foreign DNA, many consumers view it with the same skepticism associated with genetically modified organisms. Misunderstandings about gene editing, coupled with concerns about corporate control of seeds and potential ecological consequences, can affect market acceptance. Transparent communication, clear labeling policies and public engagement are essential to build trust and ensure informed decision-making.

Socio-economic implications further highlight the transformative potential of NPBTs. Faster breeding cycles,

reduced input requirements and climate-resilient varieties could significantly benefit farmers by lowering production costs and stabilizing yields. However, these benefits must be accessible across diverse socio-economic groups to avoid reinforcing existing inequalities. Collaborative innovation models—linking public sector research, farmer organizations and national breeding programs—can help democratize NPBT outcomes.

Overall, the regulatory, ethical and socio-economic landscape surrounding NPBTs is complex but manageable. Clear, science-based policies combined with inclusive innovation strategies will be critical to ensure that these technologies contribute equitably to sustainable and climate-resilient agriculture.

11. Integrated Discussion

NPBTs work best when integrated. Pan-genomics identifies target alleles; CRISPR installs them; GS predicts polygenic gains; speed breeding accelerates fixation; HTP validates stress responses. Together, they form a rapid, adaptive breeding ecosystem essential for climate-smart agriculture.

12. Conclusion

NPBTs provide the precision, speed and genetic diversity necessary to develop resilient, sustainable crop varieties. Their synergy offers a transformative breeding framework capable of meeting climate challenges and securing global food production. As regulatory frameworks evolve and technological access expands, NPBTs will become foundational tools in climate-smart agriculture.

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