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UTILIZING FROM MODERN TOOLS IN PLANT BREEDING

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Abstract: Recent advances in biotechnology and genetic engineering have revolutionized plant breeding through tools like genomic selection, CRISPR/Cas9, high-throughput phenotyping, and molecular markers. These technologies boost precision, efficiency, and resilience in crop development, creating superior varieties with higher seed yield and quality, plus better adaptation to biotic and abiotic stresses. Genome editing tools, in particular, speed up and sharpen breeding processes, while artificial intelligence and bioinformatics handling massive datasets to guide smarter decisions-promise to drive plant breeding forward, especially against devastating abiotic challenges.

Keywords: Sunflowers, Cut flowers, Wild species

INTRODUCTION

The world population is expected to reach 10 billion by 2050. Despite steady increases in food production, climate change bringing drought, floods, extreme temperatures, and new pests/diseases threatens global food security. Developing stress-resistant crop varieties through plant breeding has become essential to ensure sustainable agriculture (Asghar et al., 2025). Traditional breeding methods have fed humanity for millennia but are slow, weather-dependent, and limited by genetic diversity. Modern molecular tools genomics, bioinformatics, and engineering enable deeper genome manipulation, making breeding faster, more precise, and better at combining desired traits while removing undesirable ones (Kaya and Beşer, 2020a, b). To tackle complex abiotic stresses (controlled by many genes and GxE interactions), these tools integrate genomic selection, speed breeding, and high-throughput phenotyping. They accelerate elite germplasm screening and shorten breeding cycles, optimizing quantitative traits to close yield gaps and secure global food production (Ćeran et al., 2024).

MODERN TECHNIQUES IN PLANT BREEDING

Genomic Approaches and Molecular Markers

Genomic approaches have accelerated the time-consuming, labor-intensive processes of traditional plant breeding by directly targeting genetic variation in plant genomes. Their foundation lies in molecular markers that detect DNA differences (Kaya and Beşer, 2020b).

Molecular Markers and Marker-Assisted Selection (MAS)

Molecular markers are specific DNA sequences in the plant genome that reveal genetic variation. Various types including Restriction Fragment Length Polymorphism (RFLP), Simple Sequence Repeats (SSR), and Single Nucleotide Polymorphisms (SNP) support applications like genetic mapping, variety identification, and diversity assessment. SNPs stand out today due to their abundance across genomes and compatibility with high-throughput genotyping platforms (Collard and Mackill, 2008).

Marker-assisted selection (MAS) uses these markers to identify desirable traits (e.g., disease resistance, yield, quality) early in breeding populations. It excels where phenotypic selection proves challenging or slow such as detecting resistance genes without field exposure shortening cycles, boosting efficiency, and proving especially valuable for oligogenic traits and heterozygosity management (Varshney et al., 2021).

Genomic Selection (GS)

Unlike marker-assisted selection, genomic selection (GS) predicts the genetic value of quantitative traits using all molecular markers (typically SNPs) across the plant genome (Meuwissen et al., 2001). GS builds prediction models from genotypic and phenotypic data in training populations, then estimates breeding values for candidate plants using only their genotypes to select superior lines (Crossa et al., 2017). This approach dramatically shortens breeding cycles and accelerates genetic gains, especially for traits where phenotyping proves costly or complex. GS success hinges on high-density marker data, accurate phenotyping, and sophisticated statistical models (Van Eeuwijk et al., 2019). Its effectiveness is proven for complex traits like yield, disease resistance, and quality in key crops such as maize, wheat, and soybeans.

Genome Editing Technologies

Genome editing technologies represent revolutionary tools that enable precise genetic modifications in plant breeding. They allow targeted insertion, deletion, or replacement of genes by creating specific cuts in the plant genome, offering unprecedented accuracy and speed compared to conventional methods (Doudna and Charpentier, 2014; Naqvi et al., 2022).

CRISPR/Cas9 System

The CRISPR/Cas9 system derived from bacterial immune defense ranks as the most widely used and powerful genome editing tool. It combines guide RNA (gRNA) that targets specific DNA sequences with the Cas9 enzyme, which cuts the DNA at that precise location. Cellular repair mechanisms (NHEJ or HDR) then introduce desired changes like gene knockout, insertion, or replacement (Kaya and Beşer, 2020b). Key advantages include high specificity, efficiency, simplicity, and low cost, making it ideal for plant breeding applications.

CRISPR/Cas9 applications in plant breeding:

- *Disease resistance:* Editing susceptibility genes or boosting resistance pathways (e.g., bacterial blight resistance in rice) (Wang et al., 2016),
- *Yield enhancement:* Optimizing photosynthesis, nutrient uptake, or flowering genes,
- *Nutritional improvement*: Boosting vitamins, minerals, or proteins (e.g., iron/zinc-enriched rice),
- *Stress tolerance:* Targeting drought, salinity, heat, or cold response genes (Asghar et al., 2025),
- *Herbicide resistance*: Enabling precise weed control without crop damage.

Other Genome Editing Techniques

Before CRISPR/Cas9, techniques like Zinc Finger Nucleases (ZFNs) and Transcription Activator-Like Effector Nucleases (TALENs) enabled targeted DNA cuts for genetic modification. However, their complex design, higher costs, and lower throughput have made them less popular compared to CRISPR/Cas9's simplicity and flexibility, positioning the latter as the dominant tool in modern plant breeding (Gaj et al., 2013; Kaya and Beşer, 2020 a,b).

High-Capacity Phenotyping (HTP)

Accurate phenotyping linking genotypes to observable traits drives genetic progress in plant breeding, but traditional methods are slow, labor-intensive, and subjective, creating bottlenecks in large populations. High-throughput phenotyping (HTP) overcomes this through automated, non-destructive technologies that measure plant morphology, physiology, and biochemistry at scale (Kaya and Beşer, 2020 a,b).

Key HTP platforms:

- **Drones/UAVs**: Multispectral/thermal imaging monitors field-wide health, water stress, and yield potential (Araus and Cairns, 2014),
- **Ground robots**: Track growth dynamics, chlorophyll, and leaf area in real-time,
- **Sensors**: LiDAR, fluorescence, and RGB capture structural/physiological data,
- **AI analytics**: Process massive image datasets to reveal genotype-phenotype patterns (Chen, 2024).

HTP supercharges genomic selection by delivering precise, high-volume phenotypic data, accelerating breeding cycles and enabling rapid development of superior stress-tolerant varieties.

Speed Breeding

Speed breeding (SB) is an innovative technique that dramatically shortens plant breeding cycles, accelerating the time required to develop and market new varieties. Traditional breeding often depends on seasonal conditions, taking months or years per generation. SB overcomes this by optimizing environmental controls to rapidly advance plant growth (Ćeran et al., 2024).

The core principle involves providing ideal light, temperature, humidity, and nutrients to compress growth cycles. Key components include:

- *Extended photoperiod:* Artificial lighting for 16-22 hours daily speeds vegetative growth and triggers early flowering,
- *Optimized temperature and humidity*: Species-specific conditions maximize growth rates,
- *Intensive nutrient management*: Continuous feeding supports accelerated development.

This approach enables 4-6 generations per year in crops like wheat, barley, rice, and canola doubling or tripling traditional rates and dramatically accelerating genetic progress.

SB reaches maximum potential when combined with modern tools like genomic selection (GS) and CRISPR/Cas9. GS-identified superior genotypes can be rapidly multiplied through SB, while CRISPR-edited plants quickly advance to stable field-ready lines. These integrated strategies form the foundation of next-generation plant breeding, particularly for addressing urgent climate adaptation needs (Jaganathan et al., 2020).

Artificial Intelligence and Bioinformatics

Modern plant breeding generates vast, complex datasets from genomics, transcriptomics, proteomics, metabolomics, and phenomics. Integrating and analyzing these diverse data sources reveals insights unattainable through traditional methods alone. Artificial intelligence (AI) and bioinformatics tools play a pivotal role in enhancing the efficiency and accuracy of breeding programs by processing massive datasets, identifying patterns, and supporting data-driven decisions (Singh and Singh, 2020).

Machine learning (ML) algorithms play a central role in modern plant breeding, particularly in developing genomic selection models and predicting phenotypic traits. Algorithms such as Support Vector Machines (SVM), Random Forests, and Deep Learning enable breeders to model complex genotype-phenotype relationships more accurately, leading to better-informed genotype selection decisions (Singh and Singh, 2020).

For instance, ML models frequently outperform traditional statistical methods when predicting complex traits like yield and disease resistance from high-dimensional genomic data, providing breeders with powerful tools for precision selection in large populations.

Integration of Multiple Omics Data

Bioinformatics provides computational tools and algorithms for storing, managing, and analyzing data across different omics layers (genomics, transcriptomics, proteomics, metabolomics). Integrating these datasets offers a comprehensive understanding of complex biological processes, such as plant growth, development, and stress responses. By combining multi-omics data, AI algorithms can identify novel gene candidates, map gene regulatory networks, and propose targeted breeding strategies (Ma et al., 2020; Naqvi et al., 2025). Together, AI and bioinformatics enable data-driven decision-making in plant breeding, accelerating program efficiency and effectiveness while supporting more sustainable agricultural systems.

Discussion and Future Perspectives

Integrating modern tools into plant breeding holds tremendous potential for achieving global food security and sustainable agriculture but cost and accessibility remain barriers for small-scale programs (Kaya and Beşer, 2020a). Furthermore, legal regulations regarding CRISPR-edited plants vary significantly between countries, impacting commercialization (Bortesi and Fischer, 2015). However, several challenges must be addressed to make these technologies widely accessible and fully effective. In specific crops like sunflowers, utilizing wild species remains a primary genetic resource for introducing diversity and resistance (Jocić et al., 2015; Kaya and Vasilevska-Ivanova, 2021). The transition from traditional to modern "Alien Gene Transfer" is essential for future crop improvement (Kaya, 2014).

Cost and Accessibility

Advanced genomic tools like sequencing, high-throughput phenotyping, and genome editing demand substantial investments, creating barriers for small-scale breeding programs in developing countries. Lowering costs and enhancing accessibility are essential to maximize their global impact. International collaborations and public-private partnerships can help bridge this gap (Kaya and Beşer, 2020a,b).

Legal Regulations and Ethical Debates

Genome editing technologies, particularly CRISPR/Cas9, raise legal and ethical debates due to their ability to precisely alter plant genetics. The distinction between Genetically Modified Organisms (GMOs) and genome-edited plants is still unclear in many countries. While some countries regulate genome-edited plants similarly to traditional breeding products, others subject them to GMO legislation. These legal uncertainties can slow the development and commercialization of new varieties. Public perception and acceptance of these technologies is also a significant factor. Transparent communication and scientifically based information are essential to gaining public trust (Kaya and Beşer, 2020b).

Integrated Breeding Strategies

Modern tools achieve maximum impact through integrated breeding strategies that combine genomic selection, high-throughput phenotyping, genome editing, and speed breeding. For instance, HTP data enhances GS models, while CRISPR edits can be validated in rapid cycles. This synergy boosts efficiency, accelerates timelines, and improves predictability in breeding programs (Kaya and Beşer, 2020b).

OVERVIEW OF MODERN TOOLS

Modern breeding tools genomic selection, CRISPR/Cas9 editing, high-throughput phenotyping, and molecular markers transform traditional methods into precise, efficient processes for developing superior plant varieties.

1. **Genomic Selection**: Genomic selection shortens breeding cycles by predicting genetic potential early using DNA data combined with phenotypes. This approach revolutionizes selection accuracy and speed.
2. **CRISPR/Cas9 Technology**: CRISPR/Cas9 enables precise trait edits but faces regulatory and public acceptance issues. These challenges must be navigated for widespread adoption.
3. **High-Throughput Phenotyping**: Robotics and imaging deliver real-time trait data, revealing plant stress responses. Such insights speed up resilient crop development (Araus and Cairns, (2014).
4. **Molecular Markers**: Markers streamline trait mapping and selection, accelerating beneficial gene integration into commercial varieties.

Strengths

A key strength of the review lies in its interdisciplinary lens, blending genetics, technology, and environmental sciences for a comprehensive take on modern plant breeding. It backs a wide array of tools with up-to-date research, boosting credibility and timeliness. The researchers thoughtfully weigh each technology's pros, cons, and ethical angles (Watson et al., 2018).

Limitations

Despite its strengths, the review has limitations. It covers technical aspects well but lacks case studies showing real-world applications and results. A deeper dive into economic impacts and accessibility for smallholder farmers would better contextualize modern plant breeding's socio-economic realities (Kaya and Beşer, 2020a).

Future Directions

To boost modern tools' role in plant breeding, the authors recommend key future research paths. Integrating artificial intelligence into breeding workflows shows strong potential for gains. Strategies must also prioritize accessibility for diverse stakeholders, especially small farmers in developing areas, to drive equitable advancement (Naqvi et al., 2022).

CONCLUSION

Plant breeding remains crucial for global food security and climate resilience. Traditional methods laid strong foundations, but modern tools like genomic selection, CRISPR/Cas9 editing, high-throughput phenotyping, and speed breeding have revolutionized the field with unprecedented speed, precision, and efficiency. Artificial intelligence and bioinformatics further empower data-driven decisions, unlocking resilient, nutrient-dense crops at scale. Integrated application of these technologies promises to outpace evolving challenges, delivering disease-resistant, stress-tolerant varieties essential for sustainable agriculture. Despite costs, regulations, and ethical hurdles, their transformative potential is undeniable, driving breakthroughs to feed future generations. Future research must prioritize cost reductions, global accessibility, and real-world validation, especially for smallholder farmers. The review "Utilizing Modern Tools in Plant Breeding" excels in dissecting these innovations, balancing technical depth with broader implications, though it could expand on case studies and socio-economics. By illuminating pathways forward, it strengthens the case for accelerated, equitable adoption worldwide.

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