


Breeding 4.0: The Breeding Revolution of Genetic Information Integration and Editing

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Abstract Breeding 4.0 represents a breeding revolution in genetic information integration and editing, and is an important innovation in the field of plant breeding. By integrating genetic and genomic information, Breeding 4.0 introduces highly precise genotype selection and gene editing technologies to improve breeding efficiency and accuracy. This revolutionary breeding method helps accelerate the improvement and optimization of crop varieties to meet the growing agricultural demand and sustainable development challenges. The technology and methods of Breeding 4.0, including the development of genome prediction and selection, the application of high-throughput phenotype determination, and the application of artificial intelligence and machine learning in Breeding 4.0. The application and benefits of Breeding 4.0 are obvious, including examples and advantages of genetically modified breeding and gene editing breeding, as well as the contribution of Breeding 4.0 to sustainable agricultural development. However, Breeding 4.0 faces ethical, legal, and social considerations, as well as technical and methodological challenges. Undoubtedly, Breeding 4.0 is the forefront and future direction of contemporary breeding, providing a foundation for achieving higher-level breeding goals.

Keywords Breeding 4.0; Genetic information; Genotype selection; Gene editing; Sustainable agricultural development

1 Introduction

Breeding has always been a key area in agricultural development, continuously driving the improvement and enhancement of crops. With the progress of science and technology and the deepening of genomic research, breeding has undergone several stages of evolution. Breeding 4.0, as the latest stage of breeding revolution, revolves around the genetic information integration and editing, ushering in a new era of breeding (Wallace et al., 2018).

The core concept of Breeding 4.0 is to apply the genetic information integration and editing in the breeding process. By integrating and analyzing large-scale genetic data, such as genome sequencing and big data analysis, breeders can more accurately understand the genetic background and trait expression of crops, guiding the determination of breeding goals and the selection process. Additionally, the emergence of gene editing technology allows breeders to directly edit the genome of crops, precisely altering target traits and accelerating the breeding process.

Under the guidance of Breeding 4.0, transgenic breeding has become an important application area. By introducing exogenous genes or regulating the expression of endogenous genes, transgenic breeding can confer traits such as disease resistance and stress tolerance to crops, enhancing crop yield and quality. Simultaneously, the rapid development of gene editing technology provides breeders with more precise and efficient tools. This allows for precise modifications at target gene loci, achieving more accurate and fine-tuned crop improvements.

This study will focus on exploring the technologies and methods, applications and benefits, as well as the challenges and future prospects of Breeding 4.0. Through in-depth research on the development of Breeding 4.0, we aim to better understand the significance and impact of this breeding revolution stage, contributing to sustainable agricultural development and food security.

2 Technologies and Methods of Breeding 4.0

2.1 Genetic information integration

The core of Breeding 4.0 lies in the integration of genetic information. By consolidating large-scale genetic data, such as genome sequencing, phenotype data, and environmental information, breeders can obtain comprehensive and accurate genetic backgrounds and trait expression, guiding the formulation of breeding strategies and the selection process. This integration of genetic information utilizes advanced genomics and data analysis technologies, such as genome-wide association study, expression profiling analysis, and machine learning algorithms, to comprehensively understand the genetic characteristics and potential trait expression of crops.

In terms of genome-wide association study, the study “Genome Wide Association Study of Seedling and Adult Plant Leaf Rust Resistance in Elite Spring Wheat Breeding Lines” (PLoS One, 2016) applied the GWAS method to identify resistance genes or QTLs for leaf rust resistance in wheat. A total of 46 QTLs were identified, with approximately 20-30 contributing to field resistance to varying extents (Gao et al., 2016). Similarly, in the study “Genome-wide Association Study of Plant Architecture and Disease Resistance in *Coffea canephora*” (Euphytica, 2022), a genome-wide association analysis was conducted on plant architecture and disease resistance in *Coffea canephora* (de Faria Silva et al., 2022).

In terms of expression profiling analysis, the study “Large-scale Transcriptional Profiling of Lignified Tissues in *Tectona grandis*” (BMC Plant Biol., 2015) conducted extensive transcriptome analysis of lignified tissues in teak (*Tectona grandis*), exploring expression differences across various developmental stages and transcription factors that potentially regulate lignin biosynthesis (Galeano et al., 2015). Similarly, the study “Genetic and Molecular Bases of Cucumber (*Cucumis sativus* L.) Sex Determination” (Mol. Breeding, 2019) delved into the genetic and molecular basis of sex determination in cucumber (*Cucumis sativus* L.), utilizing various methods including transcriptome analysis (Pawełkowicz et al., 2019).

The application of machine learning algorithms in plant breeding has made significant progress. These algorithms can handle and analyze large-scale plant genotype and phenotype datasets, discovering meaningful patterns and thus driving the development of plant science and breeding. Technological advancements have enabled machine learning to play a crucial role in the analysis of various aspects (from biochemistry to yield) of plant phenotypes (van Dijk et al., 2021). Particularly in the field of image analysis, the application of deep learning technology, such as image segmentation, effectively reduces noise and bias, enhancing the accuracy of data analysis. Additionally, machine learning technology has shown tremendous potential in understanding the interactions and evolutionary patterns between plants and herbivores (Soltis et al., 2020).

Furthermore, machine learning technologies have demonstrated their importance in handling high-dimensional multi-omics data, inferring gene regulatory networks, conducting correlation analysis of multi-omics data, and gene discovery. Modern machine learning technologies such as supervised learning, semi-supervised learning, unsupervised learning, and deep learning have been all applied in basic research in botany. In areas like plant phenomics, whole-genome selection-assisted breeding, genotype-to-phenotype prediction, and modeling the interaction between genotype and environment, machine learning technologies have also shown tremendous potential for application (Yan and Wang, 2022).

2.2 Genome editing

Genome editing is another key technology in Breeding 4.0 (Xu et al., 2019). Through genome editing tools such as the CRISPR-Cas9 system, breeders can directly modify specific loci in the crop genome, achieving precise changes to target traits. Genome editing technology is characterized by its efficiency, precision, and repeatability, enabling effective modifications of single or multiple genes. This provides greater flexibility and accuracy in crop improvement.

Bortesi and Fischer (2015) described CRISPR/Cas9 as a tool for specific double-strand DNA breaks, comparing it with other genome editing platforms such as ZFNs and TALENs. They emphasized its application and potential future development in plant breeding.

Schaeffer and Nakata (2015) discussed the evolution of CRISPR/Cas9 from conceptual validation studies to applications in crop trait improvement, highlighting the need for crop-specific vectors and transformation protocols.

Xu et al. (2015) described the use of CRISPR/Cas9-mediated genome editing in rice, focusing on the modification of genetic and “non-transgenic” target genomes.

Ding et al. (2016) provided insights into the latest developments and applications of CRISPR/Cas9 in plant research, discussing the establishment of gene knockout in various plant species and how it can be used for specific mutation/integration and transcriptional control of target genes.

Together, these studies demonstrate the revolutionary impact of the CRISPR-Cas9 system in plant breeding, providing new approaches for genome editing and trait improvement.

2.3 High-throughput phenotypic analysis

High-throughput phenotypic analysis is one of the key methods in Breeding 4.0. By utilizing advanced sensor technology, imaging technology, and automated systems, breeders can efficiently measure and analyze multiple traits of crops, including growth characteristics, physiological indicators, and yield-related traits. High-throughput phenotypic analysis provides high-resolution and large-scale trait data, offering breeders a more accurate basis for crop evaluation and selection.

Early research in high-throughput phenotypic analysis laid the foundational theoretical and technical support for modern plant breeding, driving the development of this field. The molecular technology development in plant breeding, such as the application of RAPDs and microsatellite markers, provided new methods, especially in DNA separation, gene amplification, and data processing automation (Rafalski and Tingey, 1993).

Utilizing genomic strategies has accelerated gene discovery, and combining high-throughput transformation processes with automated analysis methods has provided new avenues for improving plant quality (Mazur et al., 1999). Comparative genomics research has advanced the adaptability of plants to stress, particularly by using high-throughput phenotypic analysis techniques, laying the foundation for the effectiveness of engineering strategies (Cushman and Bohnert, 2000).

The development of DNA sequencing technology, especially the study of the global pattern of gene expression, has brought a revolutionary transformation in plant biology, holding significant importance in the field of plant breeding (Harmer and Kay, 2000).

2.4 Data analysis and artificial intelligence

Breeding 4.0 utilizes data analysis and artificial intelligence to process and interpret large-scale genetic and phenotypic data. By applying machine learning, deep learning, and statistical models, breeders can extract valuable information from massive datasets, identify crucial genetic factors and trait associations, and predict the breeding potential of crops. The technologies of data analysis and artificial intelligence play a crucial role in decision-making and strategy formulation of breeding, enhancing breeding efficiency and accuracy.

Early plant breeding research primarily relied on traditional methods but gradually started incorporating statistical models and computational approaches to optimize the breeding process and gain deeper insights into the characteristics of different varieties. Donald (1968) proposed a plant breeding approach based on model features in his paper “Breeding for Ideotypes of Crop Plants”, where these features influence photosynthesis, growth, and (in cereals) grain production. Shorter et al. (1991) investigated the role of breeding, physiology, and models in assessing the adaptation of plant genotypes to target environments. Smith et al. (1997) explored how models and statistical methods could be used to evaluate different varieties’ responses to biological control agents, thereby improving the effectiveness of biological control. Goldman (1999) discussed the method of using Wisconsin Fast-growing Plants in a cycle selection process, which holds significance for education and research.

With the rapid development of data analysis and artificial intelligence, significant progress has been made in applying these technologies in the field of plant breeding. Khan et al. (2022) discussed how AI is reshaping modern crop breeding by integrating “omics” approaches to better understand crops’ responses to environmental stress. They emphasized the role of AI in high-throughput phenotypic analysis and gene function analysis, highlighting how it improves the accuracy of crop phenotype, genotype, and environmental data. Hilli (2022) emphasized the application of ground and aerial platforms, as well as sensors, in characterizing crop phenotypes under different stress factors. The paper discussed how AI-based technologies enhance traditional breeding programs to meet the growing demands of agriculture. Xing et al. (2022) focused on the role of AI and computer vision (CV) in enhancing phenotype feature analysis in soybean breeding. They discussed how CV provides a high-resolution, cost-effective method for analyzing crop phenotypes, which is crucial for designing breeding programs.

Sagan et al. (2022) proposed a data-driven approach for calibrating hyperspectral big data, which is crucial for high-throughput plant phenotypic analysis and breeding. Their work focuses on the automated calibration workflow for near-ground hyperspectral data.

By comprehensively utilizing genetic information integrating, genome editing, high-throughput phenotypic analysis, and data analysis technologies, Breeding 4.0 provides breeders with more powerful and efficient tools and methods. This accelerates the process of crop improvement, achieving more precise and sustainable breeding goals.

3 Innovations and Advances in Breeding 4.0

3.1 Development of genomic prediction and genomic selection

An important innovation in Breeding 4.0 is the development of genomic prediction and genomic selection. Genomic prediction utilizes genomic and phenotypic data to forecast the genetic value and expression of traits in individual crops. By establishing prediction models, breeders can rapidly and accurately assess the genetic potential of a large number of crop individuals, thereby making better selections for superior varieties. Genomic selection, on the other hand, employs genomic data to guide the breeding selection process. Through genomic selection, breeders can directly choose individuals within the genome that possess the desired traits, accelerating the breeding process and improving selection efficiency.

Recent studies indicate that significant progress and applications of genomic prediction and genomic selection in the field of plant breeding. Buntaran et al. (2022) utilized simulations to assess the response to genomic selection, emphasizing the necessity of selecting entries in plant breeding projects to maximize the genetic gains for the traits of interest. They highlighted the role of genomic prediction in improving prediction accuracy and accelerating the breeding cycle.

Montesinos-López et al. (2022a) demonstrated that using incomplete block designs for series allocation in genomic selection can improve predictions in plant breeding. Compared to random allocation, this method performs better, enhancing the efficiency of resource optimization in breeding programs.

Weiß et al. (2022) explored phenotype selection in maize, and used near-infrared spectroscopy data for prediction. They found that phenotype prediction was minimally influenced by population structure, especially when dealing with diverse germplasm, making it a promising tool in practical breeding.

Montesinos-López et al. (2022b) compared gradient boosting machines and Bayesian threshold BLUP for genomic prediction of categorical traits in wheat breeding. They found that gradient boosting machines generally outperform Bayesian models, indicating the need for further research on this approach in the context of genomic selection.

Feldmann et al. (2022) discussed the impact of different methods for calculating genomic relationship matrices on genomic variance and heritability estimates, proposing a novel matrix that produces accurate estimates in both plants and animals.

These studies represent a sample of innovative research in the field of genomic prediction and selection in plant breeding, showcasing various approaches and their impact on improving breeding programs.

3.2 Application of high-throughput phenotyping

In Breeding 4.0, there have been significant advancements in the application of high-throughput phenotyping. High-throughput phenotyping utilizes advanced sensor technology, imaging technology, and automated systems to efficiently measure multiple traits of crops. Through large-scale, high-resolution trait data, breeders can gain a more accurate understanding of the phenotypic characteristics of crops, guiding breeding decisions and strategy formulation. The application of high-throughput phenotyping makes crop assessment more comprehensive and accurate, accelerating the screening and promotion of superior varieties.

Recent research indicated that in the field of plant breeding, High-throughput phenotyping (HTP) technology is rapidly advancing, particularly in the high-throughput phenotyping of canopy-based traits for major crops in field environments. Here are some key findings:

Kuroki et al. (2022) developed a ground-based high-throughput phenotyping rover for use in size-limited breeding fields. This rover is suitable for small-scale breeding fields commonly found in Japan and other Asian countries. The device, an open-source hardware, can be constructed at a low cost, effectively improving phenotyping efficiency.

To enhance the phenotyping efficiency of small plants, Wu et al. (2022) developed a miniaturized phenotyping platform, MVS-Pheno V2, based on multi-view stereo 3D reconstruction. This platform is suitable for low-stature plants, particularly in breeding and management research related to canopy structure.

Combining high-throughput phenotyping with spatial dependency analysis, Jang et al. (2023) demonstrated its potential application in revealing hidden heterogeneity in breeding fields, which could be valuable for precision agriculture in field management.

Tayade et al. (2022) employed spectral index analysis methods by using various vegetation indices, combined with artificial intelligence and various remote sensing applications. This provides essential tools for high-throughput phenotyping in precision agriculture.

These studies indicate the rapid development of high-throughput phenotyping technology in the field of plant breeding, particularly in crop phenotyping under field conditions. These technologies not only enhance the efficiency of collecting phenotypic data but also provide more accurate data support for breeding programs.

3.3 Application of artificial intelligence and machine learning in Breeding 4.0

Another innovation in Breeding 4.0 is the application of artificial intelligence (AI) and machine learning (ML) in breeding. By employing AI and ML methods, breeders can handle and interpret large-scale genetic and phenotypic data, discovering hidden patterns and correlations. Algorithms of AI and ML can learn from massive datasets and predict the breeding potential of crops, suggesting optimal selection strategies. This data-driven approach provides more accurate and intelligent support for breeding decisions, fostering improvement and innovation in crop varieties.

The latest literature showcases the recent applications and advancements of artificial intelligence and machine learning in the field of plant breeding. These studies not only encompass genome selection and phenotype analysis but also involve the investigation of traits in various crops, demonstrating the significant role of artificial intelligence and machine learning in modern plant breeding.

The study “Machine Learning Applied to the Search for Nonlinear Features in Breeding Populations” indicated that deep learning methods can better identify differences between positive alleles and genetic backgrounds. By employing machine learning methods, the understanding of non-linear interactions in plant breeding datasets is enhanced, leading to improved prediction accuracy, significant reduction in computation time, and enhanced detection of important alleles related to qualitative or quantitative traits (Gabur et al., 2022).

The study “Machine Learning and Ensemble Learning for Transcriptome Data: Principles and Advances” delved into the latest machine learning studies on ensemble learning, RNA-seq technology, and plant genomics and transcriptome analysis. The study has shown that ensemble learning frameworks perform well in machine learning, outperforming traditional statistical methods, and have wide applications in plant attribute classification, gene importance assessment, and molecular breeding. (Wang et al., 2022).

The study “Traits Expansion and Storage of Soybean Phenotypic Data in Computer Vision-Based Test”, based on computer vision (CV) technology, collected phenotypic data of soybeans, and expanded four trait types in the “Guidelines for Testing Plant Variety Specificity, Consistency, and Stability: Soybeans”. The study highlighted the potential of computer vision (CV) technology in large-scale, low-cost, and precise analysis of crop phenotypes, providing accurate phenotype data for breeding program design (Xing et al., 2022).

The study “Computational Intelligence to Study the Importance of Characteristics in Flood-Irrigated Rice” demonstrated the effectiveness of computational intelligence and machine learning in determining the relative importance of variables in flood-irrigated rice. The study has shown the importance of using multiple regression, computational intelligence, and machine learning to predict rice characteristics, especially under flooded irrigation conditions (Silva Júnior et al., 2023).

The study “Perspective for Genomic-Enabled Prediction Against Black Sigatoka Disease and Drought Stress in Polyploid Species” reviewed the challenges and prospects of genomic selection (GS) in polyploid plants, emphasizing the two major threats to banana production: black spot disease and drought. The study proposed bioinformatics tools and artificial intelligence methods, including machine learning, as well as GS schemes applied to banana BSD and drought (Nkoulou et al., 2022).

Through the development of genomic prediction and selection, the application of high-throughput phenotypic determination, and the utilization of artificial intelligence and machine learning, Breeding 4.0 has achieved revolutionary progress in genetic information integration and editing. These innovations and advancements provide breeders with more accurate and efficient tools and methods, driving rapid development and continuous progress in crop breeding.

4 Breeding 4.0 Applications and Benefits

4.1 Examples and advantages of transgenic breeding

Transgenic breeding is a significant application area within Breeding 4.0. By introducing foreign genes into crops, transgenic breeding can confer new traits and advantages to the crops. For instance, herbicide-resistant soybeans and BT cotton are successful examples of transgenic breeding, representing landmark achievements in this field. Herbicide-resistant soybeans possess the characteristic of tolerance to herbicides, enabling farmers to more effectively control weeds (Biotechnology Progress, 1985). On the other hand, BT cotton, through the incorporation of insecticidal genes, exhibits resistance to pests, reducing the need for pesticides (Wilson et al., 1994). Transgenic breeding can improve crop production efficiency and economic benefits by introducing specific genes to enhance disease resistance, stress tolerance, yield, and quality.

In recent years, landmark achievements in transgenic breeding have emerged in the field of plant breeding. For example, Shailani et al. (2020) explored the improvement of rice tolerance to drought and salinity stress through gene stacking technology. This approach achieves transgenic improvement of rice by combining multiple genes with different tolerance mechanisms. Anwar and Kim (2020) investigated the progress of transgenic breeding in enhancing plant tolerance to abiotic stressors such as temperature, drought, and salinity. Their research emphasized the potential of transgenic technology in plant genetic improvement. Galán-Ávila et al. (2021) developed a novel method for transgenic breeding in *Cannabis sativa* L. This study provides an efficient gene transformation approach with significant implications for *Cannabis* breeding, especially concerning targeted genome editing by using the CRISPR/Cas system. These research papers demonstrate the significant progress and applications of transgenic breeding technologies in the field of plant breeding in recent years. Each study has overcome the limitations of traditional breeding, opening up new possibilities for plant breeding.

4.2 Examples and advantages of genome editing breeding

Genome editing is another application area with tremendous potential in Breeding 4.0. One of the landmark papers in genome editing technology was published in 2014 in the journal “Human Molecular Genetics”. This research described the CRISPR-Cas9 system composed of the nonspecific Cas9 nuclease and a set of programmable specific sequence CRISPR RNA (crRNA), which guides Cas9 to cleave DNA, thereby generating double-strand breaks at the target site. Subsequent cellular DNA repair processes lead to the desired insertions, deletions, or replacements at the target site (Zhang et al., 2014). Through CRISPR-Cas9 technology, researchers can precisely modify specific gene sequences in the genome, achieving accurate control over traits. The breakthrough in this technology has revolutionized the field of genome editing, providing new tools and methods for Breeding 4.0.

By utilizing gene editing technologies like CRISPR-Cas9, breeders can precisely modify specific gene sequences in the crop genome, achieving accurate control and improvement of traits. Gene editing can be employed to enhance disease resistance, improve quality characteristics, and increase yield in crops. For instance, Veillet et al. (2019) successfully achieved efficient editing of target bases by targeting the acetyl lactate synthase (ALS) genes of tomatoes and potatoes, by using the CRISPR/Cas9 gene editing tool, creating herbicide-resistant plants. And 12.9% of tomatoes and 10% of potatoes in the first generation of plants do not contain genetically modified ingredients. The study by Yasumoto et al. (2020) demonstrated the application of gene editing in potato breeding by using TALENs and CRISPR-Cas9 technologies. Precise editing of the potato genome was achieved through transient TALEN expression via *Agrobacterium* infection, holding significant implications for crop breeding. Kawall’s research (2021) discussed methods to accelerate modern plant breeding by using gene editing technologies. By altering specific features of rapeseed through gene editing, such as increasing yield and modifying nutritional components, the study showcased the enormous potential of this technology in plant breeding. Nerkar et al. (2022) emphasized the powerful potential of gene editing technology in precisely modifying specific loci in the crop genome, which is a long-term goal for crop breeders. The study also discussed the regulatory approval status of gene-edited crops and the prospects of developing high-yielding stress-resistant crops through precise gene editing.

4.3 The contribution of Breeding 4.0 to the sustainable development of agriculture

The application of Breeding 4.0 has made positive contributions to the sustainable development of agriculture. The use of innovative technologies such as gene editing and transgenic breeding can enhance crop resistance and adaptability, reducing dependence on pesticides and fertilizers, thereby minimizing the negative environmental impact of agriculture. Additionally, Breeding 4.0 can address the growing demand for food by increasing crop yields, improving quality, and enhancing stress tolerance, providing a more sustainable food supply. The innovations and progress in Breeding 4.0 offer new pathways and possibilities for achieving green, efficient, and sustainable agricultural development.

Through the development of applications such as transgenic breeding and gene editing, Breeding 4.0 can offer more choices and solutions for agricultural production. These applications demonstrate significant potential in enhancing crop quality, increasing resistance, improving yields, and making important contributions to the sustainable development of agriculture.

5 Challenges and Prospects of Breeding 4.0

5.1 Considerations of ethical, legal, and social issues

Breeding 4.0 introduces new genetic information integration and editing technologies, triggering a series of considerations regarding ethical, legal, and social issues. For instance, transgenic breeding has sparked controversies related to food safety, environmental impact, and intellectual property rights. The application of gene editing technology also involves ethical concerns and considerations of societal acceptance. Whelan and Lema (2017) explored the application of gene editing technology in plant breeding, with a particular focus on whether these technologies should be considered a form of conventional breeding or be subject to regulations governing genetically modified crops. The research indicates that policymakers should consider safety

information, legal/regulatory definitions, and tools from the social sciences when making decisions. To ensure the sustainable development of Breeding 4.0, a balance between technological innovation and the ethical and legal frameworks of society must be struck, establishing transparent, responsible, and sustainable breeding practices.

5.2 Technical and methodological challenges

Breeding 4.0 faces several challenges on the technical and methodological fronts. Despite significant progress in gene editing technologies such as CRISPR-Cas9, there are still issues to be addressed concerning the precision, efficiency, and safety of gene editing. Additionally, challenges related to high-throughput phenotypic determination and data processing need to be overcome to enhance the analytical and interpretative capabilities in the breeding process. Ongoing research and innovation are essential to address these technical and methodological challenges and drive the continued development of Breeding 4.0.

5.3 Future directions of Breeding 4.0

The future directions of Breeding 4.0 involve further optimizing genetic information integration and editing technologies to enhance their precision and efficiency. Simultaneously, there is a need to intensify research on the ethical and societal impacts of breeding practices to ensure sustainable and responsible applications. Additionally, the integration of technologies such as artificial intelligence and machine learning can provide more accurate data analysis and predictions, accelerating the progress of the breeding process. Breeding 4.0 can also explore cross-disciplinary collaborations with other fields, such as synthetic biology and systems biology, to achieve more innovative and efficient breeding methods. Future iterations of Breeding 4.0 will continue to focus on improving crop yields, adaptability, and quality, making greater contributions to the sustainability of agriculture.

6 Conclusion

Breeding 4.0, as a revolution in genetic information integration and editing, holds significant and far-reaching implications for the field of plant breeding. By amalgamating genetic and genomic information, Breeding 4.0 offers more precise and efficient breeding methods, accelerating the improvement and optimization of crop varieties. Innovative applications such as transgenic breeding and gene editing technologies bring forth new possibilities for breeding, enabling us to precisely manipulate plant genomes to meet the ever-growing demands of agriculture and address challenges in sustainable development.

The significance of Breeding 4.0 is not only evident in the speed and efficiency of crop variety improvement but also in its contribution to sustainable agriculture. Through precise genotype selection and gene editing technologies, Breeding 4.0 can cultivate crop varieties that are more adaptable to environmental changes and resistant to diseases and pests. This reduces reliance on chemical pesticides and fertilizers, enhances crop yield and quality, thereby achieving the goals of sustainable agriculture. Additionally, Breeding 4.0 can offer a variety of nutrient-rich cultivars, meeting the nutritional needs and health preferences of consumers.

Breeding 4.0 marks the next generation of breeding technologies, but with continuous progress in science and technology, we can anticipate the arrival of Breeding 5.0. Breeding 5.0 will further explore genome design, optimize signaling pathways, and introduce new traits and characteristics. Through innovative technologies and methods, Breeding 5.0 is poised to achieve a completely new design of genes, pathways, and traits to further enhance the adaptability, yield, and quality of crops. Breeding 5.0 may involve a broader range of gene editing and regulation technologies, as well as the application of emerging synthetic biology and artificial intelligence.

However, the realization of Breeding 5.0 still requires extensive research and innovation, including a deep understanding of the genome and gene functions, as well as continuous improvements in genetic improvement technologies. At the same time, we need to carefully address the ethical, legal, and societal issues brought about by Breeding 4.0 and 5.0, ensuring the safety and sustainability of breeding technologies. Despite facing numerous challenges, the implementation of Breeding 5.0 represents the future direction of the breeding field, offering limitless possibilities for exploring a more intelligent, efficient, and sustainable agricultural production.

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