植物育种简史
Brief History of Plant Breeding

育种 4.0：遗传信息集成和编辑的育种革命

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分子植物育种(网络版), 2024 年, 第 22 卷, 第 2 篇 doi: 10.5376/mpb.cn.2024.22.0002
收稿日期: 2024 年 2 月 7 日
接收日期: 2024 年 2 月 10 日
发表日期: 2024 年 2 月 13 日

建议最佳引用格式：

方宣钧, 2024, 育种 4.0: 遗传信息集成和编辑的育种革命, 分子植物育种(网络版), 22(2): 13-28 (doi: 10.5376/mpb.cn.2024.22.0002)

(Fang X.J., 2024, Breeding 4.0: Genetic information integration and editing in plant breeding revolution, Fengzi Zhiwu Yuzhong (Molecular Plant Breeding (online)), 22(2): 13-28 (doi: 10.5376/mpb.cn.2024.22.0002))

摘 要 育种 4.0 代表了遗传信息集成和编辑的育种革命，是植物育种领域的一项重要创新。通过整合遗传和基因组信息，育种 4.0 引入了高度精确的基因型选择和基因编辑技术，以提高育种效率和精确度。该革命性的育种方法有助于加速农作物品种的改良和优化，以满足不断增长的农业需求和可持续发展的挑战。育种 4.0 的技术和方法，包括基因组预测和基因组选择的发展，高通量表型测定的应用，以及人工智能和机器学习在育种 4.0 中的应用。育种 4.0 的应用和效益显而易见，包括转基因育种和基因编辑育种的实例和优势，以及育种 4.0 对农业可持续发展的贡献。然而，育种 4.0 面临着道德、法律和社会问题的考量，以及技术和方法上的挑战。毫无疑问，育种 4.0 是当代育种的前沿和未来方向，为实现更高级别的育种目标提供了基础。

关键词 育种 4.0; 遗传信息; 基因型选择; 基因编辑; 农业可持续发展

Breeding 4.0: Genetic Information Integration and Editing in Plant Breeding Revolution

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Molecular Plant Breeding, 2024, Vol.22, No.2 doi: 10.5376/mpb.cn.2024.22.0002

Abstract Breeding 4.0 represents a revolutionary approach in plant breeding through the integration of genetic information and editing techniques. By combining genetic and genomic information, Breeding 4.0 introduces highly precise gene-based selection and gene editing technologies to enhance breeding efficiency and accuracy. This transformative breeding approach accelerates the improvement and optimization of crop varieties to meet the growing agricultural demands and challenges of sustainability. This paper summarizes the technical and methodological advancements in Breeding 4.0, including the development of genomic prediction and genomic selection, the application of high-throughput phenotyping, and the utilization of artificial intelligence and machine learning. The applications and benefits of Breeding 4.0 are evident, including examples and advantages of genetically modified breeding and gene editing, as well as its contributions to sustainable agricultural development. However, Breeding 4.0 also faces considerations of ethical, legal, and societ al., issues, as well as technical and methodological challenges. Undoubtedly, Breeding 4.0 represents the forefront and future direction of modern breeding, laying the foundation for achieving higher-level breeding goals.

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

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).

育种一直以来都是农业发展的关键领域，不断推动着作物的改良与提高。随着科学技术的进步和基因组学研究的深入，育种也经历了多个阶段的演变。育种 4.0 作为最新的育种革命阶段，以遗传信息集成和编辑为核心，开启了一个全新的育种时代(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.

育种 4.0 的核心概念是将遗传信息的集成和编辑应用于育种过程中。通过整合和分析大规模的遗传数据，如基因组测序和大数据分析，育种者可以更准确地了解作物的遗传背景和性状表达，从而指导育种目标的确定和选择的进行。同时，基因编辑技术的出现使得育种者能够直接编辑作物的基因组，精确地改变目标性状，加速育种进程。

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.

在育种 4.0 的引领下，转基因育种成为一个重要的应用领域。通过引入外源基因或调控内源基因的表达，转基因育种可以赋予作物抗病性、耐逆性等特征，提高作物产量和品质。同时，基因编辑技术的快速发展也为育种者提供了更精确、高效的工具，使得可以在目标基因位点上进行精确的修改，实现更准确和精细的作物改良。

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.

本研究将重点探讨育种 4.0 的技术和方法、应用和效益、以及面临的挑战和未来前景。通过深入研究育种 4.0 的发展，我们将更好地理解这一育种革命阶段的意义和影响，为农业可持续发展和粮食安全做出贡献。

1 Technologies and Methods of Breeding 4.0

1.1 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.

1 育种 4.0 的技术和方法

1.1 遗传信息集成

育种 4.0 的核心在于遗传信息的集成。通过整合大规模的遗传数据，如基因组测序、表型数据和环境信息，育种者可以获取全面、准确的遗传背景和性状表达情况，从而指导育种策略的制定和选择的进行。这种遗传信息的集成利用了先进的基因组学和数据分析技术，如全基因组关联分析、表达谱分析和机器学习算法，以全面了解作物的遗传特征和潜在的性状表达。

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).

在全基因组关联分析方面，Genome Wide Association Study of Seedling and Adult Plant Leaf Rust Resistance in Elite Spring Wheat Breeding Lines，(PLoS One, 2016)这项研究应用 GWAS 方法来识别小麦抗叶锈病的抗性基因或 QTLs，共识别出 46 个 QTLs，其中约 20-30 个在不同程度上贡献了田间抗性(Gao et al., 2016)。同样的，Genome-wide association study of plant architecture and diseases resistance in *Coffea canephora* (Euphytica, 2022)，该研究对咖啡树(*Coffea canephora*)的植物株型建成和疾病抗性进行了全基因组关联研究(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).

在表达谱分析方面，Large-scale transcriptional profiling of lignified tissues in *Tectona grandis* (BMC Plant Biol., 2015)，该项研究对柚木(*Tectona grandis*)木质化组织进行了大规模转录组分析，探讨了不同发育阶段的表达差异和可能调控木质素生物合成的转录因子(Galeano et al., 2015)。Genetic and molecular bases of cucumber (*Cucumis sativus* L.) sex determination (Mol. Breeding, 2019)，该项研究探讨了黄瓜(*Cucumis sativus* L.)性别决定的遗传和分子基础，包括转录组分析在内的多种方法(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).

机器学习算法在植物育种中的应用已经取得了显著的进步。这些算法能够处理和分析大规模的植物基因型和表型数据集，发现有意义的模式，从而推动植物科学和育种的发展。技术进步使得机器学习在植物表型的多个层面(从生化到产量)的分析中发挥关键作用(van Dijk et al., 2021)。特别是在图像分析方面，通过深度学习的应用，如图像分割，可有效减少噪声和偏差，提高数据分析的准确性。此外，机器学习技术在理解植物与草食动物之间的相互作用和进化模式方面也显示出巨大潜力(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).

此外，机器学习技术在高维多组学数据的处理、基因调控网络的推断、多组学数据的关联分析以及基因挖掘方面也显示出其重要性。监督学习、半监督学习、非监督学习和深度学习等现代机器学习技术，都在植物学基础研究中找到了应用。在植物表型组学、全基因组选择辅助育种、基因型到表型预测以及基因型与环境互作建模等领域，机器学习技术同样展现出其巨大的应用潜力(Yan and Wang, 2022)。

1.2 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.

1.2 基因组编辑

基因组编辑是育种 4.0 中的另一个关键技术(Xu et al., 2019)。通过基因编辑工具，如 CRISPR-Cas9 系统，育种者可以直接修改作物基因组中的特定位点，实现对目标性状的精确改变。基因编辑技术具有高效、精确和可重复的特点，可以有效地实现单基因或多基因的修改，为作物的改良提供了更大的灵活性和准确性。

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.

Bortesi 和 Fischer (2015)描述了 CRISPR/Cas9 作为一个用于特定双链 DNA 断裂的工具，并与其他基因组编辑平台如 ZFNs 和 TALENs 进行了比较。他们强调了其在植物育种中的应用和潜在的未来发展。

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.

Schaeffer 和 Nakata (2015)讨论了 CRISPR/Cas9 从概念验证研究到作物性状改良应用的演变，强调了作物特定载体和转化协议的需求。

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.

Xu 等人(2015)描述了在水稻中使用 CRISPR/Cas9 介导的基因组编辑，重点在于遗传和“无转基因”目标基因组的修改。

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.

Ding 等人(2016)提供了 CRISPR/Cas9 在植物研究中的最新进展和应用的见解，讨论了在各种植物物种中建立基因敲除的情况以及如何用于特异性突变/整合和目标基因的转录控制。

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

这些研究共同展示了 CRISPR-Cas9 系统在植物育种中的革命性影响，为基因组编辑和性状改进提供了新的方法。

1.3 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.

1.3 高通量表型分析

高通量表型分析是育种 4.0 中的关键方法之一。通过使用先进的传感器技术、成像技术和自动化系统，育种者可以高效地测量和分析作物的多个性状，包括生长特征、生理指标和产量相关性状。高通量表型分析提供了高分辨率和大规模的性状数据，为育种者提供了更准确的作物评估和选择的依据。

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).
早期的高通量表型分析研究为今天的植物育种提供了基础性的理论和技术支持，推动了这一领域的发展。如植物育种的分子技术发展，如 RAPDs 和微卫星标记的应用，为植物育种提供了新的方法，尤其是在 DNA 分离、基因放大和数据处理自动化方面(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).
利用基因组学策略加速了基因发现，结合高通量转化过程和自动化分析方法，为植物品质改良提供了新的途径(Mazur et al., 1999)。比较基因组学研究在提高植物对逆境的适应性方面的进展，特别是利用高通量表型分析技术，为工程策略的有效性提供了基础(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).
DNA 测序技术的发展，尤其是基因表达的全球模式研究，为植物生物学带来了革命性的变革，这在植物育种领域有着重要意义(Harmer and Kay, 2000)。

1.4 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.

1.4 数据分析和人工智能

育种 4.0 借助数据分析和人工智能的方法来处理和解释大规模的遗传和表型数据。通过应用机器学习、深度学习和统计模型，育种者可以从海量的数据中提取有用的信息，识别重要的遗传因子和性状关联，并预测作物的育种潜力。数据分析和人工智能的技术在育种决策和策略制定中起着至关重要的作用，提高了育种效率和精确度。

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.
早期的植物育种研究主要依赖于传统方法，但也逐渐开始引入统计模型和计算方法来优化育种过程，并深入理解不同品种的特性。Donald (1968)在其论文《作物理想型的育种》中提出了一种基于模型特征的植物育种方法，这些特征影响光合作用、生长和(在谷物中)谷粒生产。Shorter 等(1991)研究了育种、生理学和模型在评估植物基因型对目标环境适应性方面的作用。Smith 等(1997)探讨了如何通过模型和统计方法评估不同品种对生物控制剂的响应，从而改善生物控制的有效性。Goldman (1999)讨论了使用威斯康辛快速植物进行循环选择过程的方法，这对于教育和研究具有重要意义。

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.

随着数据分析和人工智能的迅速发展，应用数据分析和人工智能在植物育种领域取得了重大进展，Khan 等(2022)讨论了 AI 如何重塑现代作物育种，通过整合“组学”方法来更好地理解作物对环境压力的反应。他们强调 AI 在高通量表型分析和基因功能分析中的作用，以及它如何提高作物表型、基因型和环境型数据的准确性。Hilli (2022)强调了地面和空中平台及传感器在作物表型化不同压力因素中的应用。这篇论文讨论了基于 AI 的技术如何增强传统育种计划，并满足日益增长的农业需求。Xing 等(2022)专注于 AI 和计算机视觉(CV)在提高大豆育种中表型特征分析方面的作用。他们讨论了 CV 如何提供一种高分辨率、成本效益的方法来分析作物表型，这对于设计育种计划至关重要。

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.

Sagan 等(2022)提出了一种数据驱动的方法，用于校准高光谱大数据，这对于高通量植物表型分析和育种至关重要。他们的工作侧重于近地高光谱数据的自动校准工作流程。

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.

通过综合运用遗传信息的集成、基因组编辑、高通量表型分析和数据分析技术，育种 4.0 为育种者提供了更强大、高效的工具和方法，加快了作物改良的进程，实现了更精确和可持续的育种目标。

2 Innovations and Advances in Breeding 4.0

2.1 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.

2 育种 4.0 的创新和进展

2.1 基因组预测和基因组选择的发展

育种 4.0 的一个重要创新是基因组预测和基因组选择的发展。基因组预测利用基因组数据和表型数据来预测作物个体的遗传价值和性状表达情况。通过建立预测模型，育种者可以快速准确地评估大量作物个体的遗传潜力，从而更好地选择优良品种。基因组选择则是利用基因组数据来指导育种选择的过程。通过基因组选择，育种者可以直接选择基因组中具有所需性状的个体，从而加快了育种进程，提高了选择效率。

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.

最近的研究表明，基因组预测和基因组选择在植物育种领域有显著的进展和应用。Buntaran 等(2022 年)利用模拟评估对基因组选择的响应，强调了在植物育种项目中选择条目以最大化感兴趣性状的遗传增益的需要。他们强调了基因组预测在提高预测准确性和加速育种周期方面的作用。

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.

Montesinos-López 等(2022a)展示了在基因组选择中使用不完全区组设计进行系列分配可以改善植物育种中的预测。与随机分配相比，这种方法表现更好，增强了育种计划中资源优化的效率。

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.
Weiß等(2022)探讨了玉米的表型选择，使用近红外光谱数据进行预测。他们发现，表型预测受群体结构影响较小，特别是在处理多样化种质时，可能是实用育种中的一个有希望的工具。

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.
Montesinos-López 等(2022b)比较了梯度提升机和贝叶斯阈值 BLUP 用于小麦育种中基因组基础的分类性状预测。他们发现，梯度提升机通常比贝叶斯模型表现更好，这表明需要在基因组选择背景下对这种方法进行更多研究。

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.
Feldmann 等(2022)讨论了计算基因组关系矩阵的不同方法对基因组方差和遗传力估计的影响，提出了一种在植物和动物中能产生准确估计的新矩阵。

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.
这些研究代表了在植物育种的基因组预测和选择领域正在进行的创新研究的一个样本，展示了各种方法及其对改进育种计划的影响。

2.2 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.

2.2 高通量表型测定的应用

在育种 4.0 中，高通量表型测定的应用也取得了显著进展。高通量表型测定利用先进的传感器技术、成像技术和自动化系统来高效地测量作物的多个性状。通过大规模、高分辨率的性状数据，育种者可以更准确地了解作物的表型特征，从而指导育种决策和策略制定。高通量表型测定的应用使得作物评估更加全面、准确，并加快了优良品种的筛选和推广。

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:
最近的研究表明，在植物育种领域，高通量表型测定(HTP)技术正在迅速发展，特别是在田间环境中对主要作物的冠层基于特性的高通量表型测定。以下是一些关键发现：

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.
Kuroki 等(2022)人在尺寸有限的育种田地中，开发了一种基于地面的高通量表型测定漫游仪，适用于日本和其他亚洲国家常见的小规模育种田地，该设备是开源硬件，可低成本自行构建，有效提高表型测定效率。

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.
为了提高小型植物的表型测定效率，Wu 等(2022)开发了一种基于多视角立体 3D 重建的微型化表型测定平台 MVS-Pheno V2，适用于低个体植物，特别适用于与枪杆结构相关的育种和管理研究。

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.
Jang 等(2023)将高通量表型测定与空间依赖性分析的结合，可揭示育种田地中的隐藏异质性，对精准农业中的田地管理具有潜在应用价值。

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.
Tayade 等(2022)采用各种植被指数的光谱指数分析方法，结合人工智能和多种遥感应用，为精准农业中的高通量表型测定提供了重要工具。

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.
这些研究表明，高通量表型测定技术在植物育种领域的应用正迅速发展，特别是在田间条件下的作物表型测定。这些技术不仅提高了表型数据的收集效率，还为育种程序提供了更精确的数据支持。

2.3 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.

2.3 人工智能和机器学习在育种 4.0 中的应用

育种 4.0 的另一个创新是人工智能和机器学习在育种中的应用。通过应用人工智能和机器学习的方法，育种者可以处理和解释大规模的遗传和表型数据，发现隐藏的模式和关联。人工智能和机器学习的算法能够从海量的数据中学习，并预测作物的育种潜力和最佳选择方案。这种数据驱动的方法为育种决策提供了更准确、更智能的支持，促进了作物品种的改良和创新。

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.
最新的文献展示了人工智能和机器学习在植物育种领域的最新应用和进展。这些研究不仅涉及了基因组选择和表型分析，还包括了多种作物的特性研究，显示出人工智能和机器学习在现代植物育种中的重要作用。

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).
Machine Learning Applied to the Search for Nonlinear Features in Breeding Populations，研究显示，深度学习方法能更好地识别正性等位基因与遗传背景的区别。利用机器学习方法，提高了植物育种数据集非线性交互作用的理解，提升预测准确性，大幅减少计算时间，并改善了涉及定性或定量特征的重要等位基因的检测(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).

Machine Learning and Ensemble Learning for Transcriptome Data: Principles and Advances，该项研究深入讨论了集成学习、RNA-seq 技术和植物基因组与转录组分析的最新机器学习研究，研究表明集成学习框架在机器学习中表现出色，优于传统统计方法，在植物属性分类、基因重要性评估和分子育种中有广泛应用。(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).

Traits Expansion and Storage of Soybean Phenotypic Data in Computer Vision-Based Test，该研究基于 CV 技术收集了大豆的表型数据，扩展了“植物品种特异性、一致性和稳定性测试指南：大豆”中的四种性状类型。研究表明计算机视觉(CV)技术在大规模、低成本和精确分析作物表型方面的潜力，可为育种程序设计提供准确的表型数据(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).

Computational intelligence to study the importance of characteristics in flood-irrigated rice，该研究证明了计算智能和机器学习在确定淹水稻的变量相对重要性方面的有效性，研究表明运用多重回归、计算智能和机器学习预测水稻特性的重要性，特别是在淹水灌溉条件下(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).

Perspective for genomic-enabled prediction against black sigatoka disease and drought stress in polyploid species，本研究综述了 GS 在多倍体植物中的应用挑战和前景，特别强调了对抗黑色斑点病和干旱—香蕉生产的两大威胁。提出了生物信息学工具和人工智能方法，包括机器学习，以及应用于香蕉 BSD 和干旱的 GS 方案(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.

通过基因组预测和基因组选择的发展，高通量表型测定的应用，以及人工智能和机器学习的运用，育种 4.0 实现了在遗传信息集成和编辑方面的革命性进展。这些创新和进展为育种者提供了更精确、高效的工具和方法，推动了作物育种的快速发展和持续进步。

3 Breeding 4.0 Applications and Benefits

3.1 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.

3 育种 4.0 的应用和效益

3.1 转基因育种实例和优势

转基因育种是育种 4.0 中的一个重要应用领域。通过引入外源基因到作物中，转基因育种可以赋予作物新

的特性和优势。例如，抗除草剂大豆和 BT 棉花就是转基因育种的成功实例，堪称转基因育种的标志性成果。抗除草剂大豆具有对除草剂耐受的特性，使得农民能够更有效地控制杂草(Biotechnology Progress, 1985)；BT 棉花则通过植入杀虫基因，具有对虫害的抗性，减少了对农药的需求(Wilson et al., 1994)。转基因育种通过引入特定基因，可以使作物获得更好的抗病性、耐逆性、产量和品质等优势，从而提高农作物的生产效率和经济效益。

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.

近年来，在植物育种领域中转基因育种的标志性成果不断涌现，例如：Shailani 等(2020)人探讨了通过基因堆叠技术改善水稻对干旱和盐分胁迫的耐受性。这种方法通过结合不同耐受机制的多个基因，实现了水稻的转基因改良。Anwar 和 Kim (2020)研究了转基因育种在提高植物对非生物胁迫(如温度，干旱，盐分等)的耐受性方面的进展。他们的研究强调了转基因技术在植物基因改良中的潜力。Galán-Ávila 等(2021)人发展了一种新方法，用于大麻(*Cannabis sativa* L.)植物的转基因育种。这项研究提供了一种高效的基因转化方法，对大麻育种有重要影响，特别是在使用 CRISPR/Cas 系统进行目标基因组编辑方面。这些研究文献展示了近年来转基因育种技术在植物育种领域的重要进展和应用。每项研究都突破了传统育种的局限性，为植物育种带来了新的可能性。

3.2 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.

3.2 基因编辑育种实例和优势

基因编辑是育种 4.0 中另一个具有巨大潜力的应用领域。基因编辑技术的标志性论文之一是 2014 年发表在《Human Molecular Genetics》杂志上的研究，这项研究描述了 CRISPR-Cas9 系统由非特异性 Cas9 核酸酶和一组可编程的特定序列 CRISPR RNA (crRNA)组成，可引导 Cas9 切割 DNA，从而在目标位点产生双链断裂。随后的细胞 DNA 修复过程导致在目标位点出现所需的插入、删除或替换(Zhang et al., 2014)。通过 CRISPR-Cas9 技术，研究人员能够定点修改基因组中的特定基因序列，实现对性状的精确调控。这项技术的突破引发了基因编辑领域的革命，为育种 4.0 提供了新的工具和方法。

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.
通过利用 CRISPR-Cas9 等基因编辑技术，育种者可以精确地修改作物基因组中的特定基因序列，实现对性状的精确调控和改良。基因编辑可以用于增加作物的耐病性、改善品质特性、提高产量等方面。例如，Veillet 等(2019)通过靶向番茄和马铃薯的乙酰乳酸合成酶(ALS)基因，使用 CRISPR/Cas9 基因编辑工具成功实现了目标碱基的高效编辑，创造出抗除草剂的植物，且第一代植物中有 12.9%的番茄和 10%的马铃薯不含转基因成分。Yasumoto 等(2020)的研究展示了利用 TALENs 和 CRISPR-Cas9 技术进行的基因编辑在马铃薯育种中的应用。通过 Agrobacterium 感染进行瞬时 TALEN 表达，实现了对马铃薯基因组的精确编辑，这对作物育种具有重要意义。Kawall (2021)的研究讨论了利用基因编辑技术加速现代植物育种的方法。研究者通过基因编辑改变了油籽草的特定特征，例如提高产量和改变营养成分，展示了这项技术在植物育种中的巨大潜力；Nerkar 等(2022)强调了基因编辑技术在精准修改作物基因组特定位点方面的强大潜力，这对作物育种者来说是一个长期的目标，研究还讨论了基因编辑作物的监管审批情况，以及通过精确基因编辑开发高产抗逆作物的前景。

3.3 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.

3.3 育种 4.0 对农业可持续发展的贡献

育种 4.0 的应用对农业可持续发展产生了积极的贡献。通过基因编辑和转基因育种等创新技术的应用，可以提高作物的抗性和适应性，减少对农药和化肥的依赖，从而降低了农业对环境的负面影响。此外，育种 4.0 还可以通过提高作物产量、改善品质和增加耐逆性等方式，满足不断增长的人口需求，并提供更多可持续的食物供应。育种 4.0 的创新和进展为实现绿色、高效、可持续的农业发展提供了新的路径和可能性。

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.
通过转基因育种和基因编辑等应用的发展，育种 4.0 能够为农业生产提供更多的选择和解决方案。这些应用在改善作物品质、增加抗性、提高产量等方面展现出巨大的潜力，为农业可持续发展做出了重要的贡献。

4 Challenges and Prospects of Breeding 4.0

4.1 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.

4 育种 4.0 的挑战和前景

4.1 道德、法律和社会问题的考量

育种 4.0 引入了新的遗传信息集成和编辑技术，这也引发了一系列道德、法律和社会问题的考量。例如，转基因育种引发了关于食品安全、环境影响和知识产权等方面的争议。基因编辑技术的应用也涉及到伦理问题和社会接受度的考量。Whelan 和 Lema (2017)探讨了基因编辑技术在植物育种中的应用，特别关注了

这些技术是否应被视为常规育种的一种形式或是受到转基因作物法规的约束。研究表明，政策制定者在决策中应考虑安全信息、法律/监管定义以及社会科学领域的工具。为了确保育种 4.0 的可持续发展，必须平衡科技创新与社会伦理和法律框架之间的关系，建立透明、负责任和可持续的育种实践。

4.2 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.

4.2 技术和方法上的挑战

育种 4.0 面临着一些技术和方法上的挑战。尽管基因编辑技术如 CRISPR-Cas9 已经取得了巨大的进展，但仍需要解决基因编辑的精确性、效率和安全性等方面的问题。此外，高通量表型测定和数据处理的挑战也需要克服，以提高育种过程中的数据分析和解释能力。这些技术和方法上的挑战需要不断的研究和创新来推动育种 4.0 的发展。

4.3 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.

4.3 育种 4.0 的未来发展方向

育种 4.0 的未来发展方向包括进一步优化遗传信息集成和编辑技术，提高其精确性和效率。同时，需要加强对育种实践的道德和社会影响的研究，以确保可持续和负责任的应用。此外，整合人工智能和机器学习等技术，可以提供更准确的数据分析和预测，加速育种过程的进展。育种 4.0 还可以探索与其他领域的交叉，例如合成生物学和系统生物学，以实现更加创新和高效的育种方法。未来的育种 4.0 将继续致力于提高农作物的产量、适应性和品质，为农业可持续发展做出更大贡献。

5 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.

5 结语

育种 4.0 作为基因信息集成和编辑的育种革命，对植物育种领域具有重要的意义和深远的影响。通过整合遗传和基因组信息，育种 4.0 提供了更精确和高效的育种方法，可以加速农作物品种的改良和优化。转基因育种和基因编辑技术等创新的应用为育种带来了新的可能性，使我们能够更精确地操控植物基因组，以满足不断增长的农业需求和可持续发展的挑战。

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.

育种 4.0 的重要性不仅体现在农作物品种改良的速度和效率上，还在于其对农业可持续发展的贡献。通过精确的基因型选择和基因编辑技术，育种 4.0 能够培育出更适应环境变化和抗病虫害的作物品种，减少对化学农药和化肥的依赖，提高农作物的产量和品质，从而实现可持续农业的目标。此外，育种 4.0 还可以

提供更多的营养丰富品种，满足人们对健康和营养的需求。

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.
育种 4.0 标志着育种技术的新一代，但随着科学和技术的不断进步，我们可以预见育种 5.0 即将到来。育种 5.0 将进一步探索基因组的设计、信号途径的优化以及新的性状和特性的引入。通过创新的技术和方法，育种 5.0 有望实现对基因、途径和性状的全新设计，以进一步提高作物的适应性、产量和品质。育种 5.0 将可能涉及到更广泛的基因编辑和调控技术，以及新兴的合成生物学和人工智能的应用。

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.
然而，育种 5.0 的实现仍然需要大量的研究和创新，包括对基因组和基因功能的深入了解，以及对遗传改良技术的不断改进。同时，我们也需要认真对待育种 4.0 和 5.0 所带来的伦理、法律和社会问题，确保育种技术的安全和可持续性。尽管育种 5.0 的实现还面临诸多挑战，但它代表了育种领域的未来发展方向，为我们探索更加智能、高效和可持续的农业生产提供了无限可能。

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