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The Evolution of Rice Breeding Technologies: Integrated Strategies for Addressing Global Food Security Challenges

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Abstract. Rice, as one of the world's top three staple food crops, sustains the lives of over half the global population. However, its production systems face multiple challenges, including population growth, sharp reductions in arable land, climate change, and increasing pest and disease pressures, making ensuring global food security an increasingly urgent need. In response, rice breeding technologies have undergone a profound transformation from empirical accumulation to scientific design. The core of this evolution is represented by the iterative upgrading of hybrid rice technology systems: from the three-line system reliant on specific cytoplasmic sources, to the two-line system that utilizes environment-sensitive male sterile lines to broaden the parental gene pool but is constrained by environmental stability, culminating in the third-generation technology. This latest phase is based on gene editing tools like CRISPR/Cas9 to create intelligent male sterile lines that are genetically stable and environment-independent, achieving a fundamental shift from "utilizing natural sterile resources" to "artificially designing sterile lines." Concurrently, the rise of molecular breeding technologies, such as marker-assisted selection (MAS) and genomic selection (GS), has shifted the breeding process from traditional phenotypic selection to precise genotypic selection, significantly improving selection efficiency and shortening breeding cycles. Nevertheless, current breeding practices still face technical bottlenecks, including difficulties in deciphering the genetics of complex quantitative traits, off-target risks associated with gene editing, and inherent trade-offs (e.g., between stress resistance and high yield). Furthermore, socio-ethical challenges such as public acceptance, policy regulations, and gaps in global germplasm resource collaboration persist. Looking ahead, synergistic innovation that integrates cutting-edge technologies—such as multi-omics big data, artificial intelligence predictive models, and whole-genome design breeding—will be the key pathway for developing a new generation of resource-efficient, climate-smart rice varieties and, ultimately, achieving sustainable food security.

Keywords: Rice Breeding, Hybrid Rice Technology System, Molecular Breeding Technology, CRISPR/Cas9, Technical Bottlenecks, Synergistic Innovation, Food Security

1. Introduction

Rice (Oryza sativa L.), ranking first among the world's three major staple grains, sustains the livelihoods of over half the global population. According to statistics from the United Nations Food

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and Agriculture Organization (FAO), more than 3.5 billion people worldwide rely on rice as their staple food, which provides approximately 20% of dietary energy, holding an irreplaceable core position in the global food security system. In developing countries, particularly China with its population exceeding 1.4 billion, rice production and consumption are fundamental to people's lives, with an annual consumption reaching 140 million tons, accounting for 28% of the global total. This directly impacts the livelihoods of 200 million farming households and national food security stability [1]. However, entering the 21st century, global rice production systems are facing unprecedented severe challenges. A sharp contradiction exists between the continuous population growth and the drastic reduction in arable land area caused by industrialization and urbanization. For instance, the global per capita arable land area was 4.2 mu in 2010 but has now significantly decreased to about 1.2 mu. More worryingly, extreme weather-induced high temperatures and drought severely threaten the reproductive growth stage of rice [2]. Research indicates that high temperature and drought cause an average yield reduction of about 15% for Asian rice, primarily affecting key yield traits such as seed setting rate and 1000-grain weight. Simultaneously, rice diseases and pests, such as rice blast, bacterial blight, and brown planthopper, are becoming more active and complex under the influence of climate change, leading to persistent annual yield losses ranging from 10% to 30%. Additionally, approximately 30% of the world's irrigated rice fields are affected by salinity stress, making soil degradation an increasingly prominent issue. These harsh reality clearly indicate that to meet the projected 60% increase in global food demand by 2050, accelerating the development of new rice varieties with high yield, stability, and quality has become an urgent mission and core task for global agricultural science and technology.

To address the continuously growing food demand and increasingly complex production environments, rice breeding technology has undergone a long evolution from empirical accumulation to scientific design. In this process, the development of hybrid rice technology has been particularly crucial, consistently leading breakthroughs in yield potential. The evolution of the hybrid rice technology system has always revolved around the core issue of overcoming the application bottlenecks of male sterile lines. While the three-line system achieved the industrialization of hybrid seed production, it was limited by the scarcity of cytoplasmic male sterility (CMS) germplasm resources and restricted parental combinations, prompting the emergence of the two-line system [3]. The two-line system utilizes photoperiod/thermo-sensitive genic male sterility (PTGMS) lines to circumvent the dependence on maintainer lines, significantly broadening the utilization range of parents. However, its fertility conversion is influenced by environmental temperature fluctuations, leading to instability in seed production purity. To completely resolve the issue of environmental sensitivity, the third-generation technology uses gene editing tools like CRISPR/Cas9 to precisely create general genic male sterility (GMS) lines [4], achieving genetic stability of the sterility trait and zero environmental dependence, ultimately accomplishing the technological leap from "relying on natural sterile resources" to "artificially designing sterile lines."

Although hybrid breeding technology has made significant progress in the pursuit of sustained high yield [5], ongoing global warming and increased extreme weather events have intensified multiple biotic and abiotic stresses, such as high temperature, drought, flooding, salinity, and combined pest and disease pressures. These factors pose increasingly severe challenges to the yield stability of rice. For example, high temperature stress not only significantly reduces pollen viability but also increases spikelet sterility, severely affecting the seed setting rate and final yield. Drought stress leads to inhibited plant growth and reduced photosynthetic efficiency. Soil salinization disrupts normal physiological metabolism in rice through ion toxicity and osmotic stress. These issues indicate that solely pursuing absolute high yield under ideal conditions is insufficient to meet

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future food security needs. Therefore, enhancing rice's stress resistance and adaptability in complex and changing environments, while simultaneously achieving high and stable yield, has become one of the core objectives in contemporary rice breeding.

Against this background, this review aims to systematically sort out and evaluate the theoretical foundations, core technological breakthroughs, practical application challenges, and future development directions in the innovative journey of rice breeding. Specifically, this article will first trace the evolution of the theoretical framework from classical genetics to modern genomics. Secondly, it will provide an in-depth analysis of the principles, application progress, and limitations of key breeding technologies, including traditional selection methods, hybrid breeding systems, molecular marker-assisted selection (MAS), transgenics, and gene editing. Concurrently, this article will focus on research progress and existing scientific challenges in stress-resistant breeding [6] aimed at addressing climate change and quality improvement targeting health needs. It will objectively analyze the technical bottlenecks, social controversies, and resource collaboration gaps faced in the application and promotion of breeding technologies. Finally, based on current research frontiers, it will look ahead to the future priority development directions such as multi-omics and big data, artificial intelligence (AI)-driven assisted breeding, whole genome design breeding, and the development of resource-efficient and climate-smart rice varieties. By systematically analyzing the evolution of the theoretical framework in rice breeding, key technological innovations and limitations, controversies surrounding the common improvement of stress resistance and quality, and the transformation path towards AI-driven big data breeding, this review aims to provide a theoretical reference for breaking through breeding bottlenecks.

2. Theoretical background

Every leap in rice breeding is based on the deepening understanding of biological genetic laws and the innovation of operational technologies. Among these, classical Mendelian genetics laid the unshakable cornerstone for modern breeding. Its Law of Segregation and Law of Independent Assortment first revealed the discrete genetic nature of qualitative traits. In rice, a series of key agronomic traits have been confirmed to be regulated by single genes or major effect loci: for instance, the polymorphism of the GS3 gene controlling grain length directly determines the grain shape differentiation between indica and japonica rice [7]; TAC1 (Tiller Angle Control 1), controlling tiller angle, regulates plant compactness by affecting auxin distribution. The cloning and functional analysis of these major genes provide targets for precise selection. However, core economic traits and key stress resistances in rice often exhibit continuous variation, typical of quantitative traits, whose genetic mechanisms require elucidation by quantitative genetics theory. Based on biostatistical models and population genetics principles, quantitative genetics decomposes phenotypic variation into genetic effects and genotype-by-environment (G×E) interaction components, revealing the polygenic, minor-effect additive nature of complex traits. For example, using recombinant inbred line (RIL) populations and QTL mapping techniques [8], 12 QTLs (Quantitative Trait Loci) significantly associated with cold tolerance were successfully identified on rice chromosome 12. Among them, qCTS12a was finely mapped and confirmed to encode a transporter protein regulating membrane lipid homeostasis, providing precise navigation for the molecular marker-assisted introgression of cold tolerance genes. The development of quantitative genetics theory, especially the widespread application of the Best Linear Unbiased Prediction (BLUP) model , made it possible to estimate the breeding value of individuals under complex genetic backgrounds.

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The rapid advancement of molecular biology has given rise to the establishment of a molecular breeding theoretical framework. Molecular Marker-Assisted Selection (MAS) transforms abstract heritability into visual DNA markers (such as SSR simple sequence repeats, SNP single nucleotide polymorphisms), enabling direct tracking of target genotypes. Its core lies in utilizing the principle of linkage disequilibrium, indirectly selecting for invisible target genes by screening molecular markers tightly linked to them . The International Rice Research Institute (IRRI) successfully precisely introduced the bacterial blight resistance gene Xa21 into high-yielding South Asian background varieties using MAS, increasing the accuracy of resistance selection from about 50% in traditional phenotypic screening to over 95% . MAS greatly accelerated the directional aggregation of target genes. With the sharp decline in high-throughput genotyping costs and breakthroughs in computational biology, Genomic Selection (GS) theory emerged [9]. The essence of GS is a genomic breeding value prediction model based on genome-wide single nucleotide polymorphisms. It broke through the limitation of traditional MAS targeting only a few known major QTLs, utilizing tens of thousands of molecular markers covering the entire genome, combined with BLUP to establish genotype-phenotype association models. This allows for the overall assessment and early prediction of the potential genetic potential of all traits in an individual without the need to pre-map specific QTLs . Empirical evidence shows that GS can shorten the rice breeding cycle by 40-60%, making it particularly suitable for quantitative traits with low heritability, high measurement costs, and late-life stage expression.

An in-depth understanding of the unique biological characteristics of rice is crucial for the efficient application of breeding technologies. Firstly, rice is an AA genome species with a genome size of approximately 430 Mb. Notably, over 45% of the genome sequence consists of repetitive sequences [10]. This complex repetitive structure, on one hand, affects the accuracy of gene annotation, and on the other hand, significantly increases the difficulty and off-target risk of designing sgRNAs for gene editing technologies like CRISPR/Cas9 (often requiring the design of specific targets avoiding repetitive regions). Secondly, rice is a typical self-pollinated crop, with a natural outcrossing rate usually below 1%. This characteristic, while beneficial for stabilizing and maintaining varietal traits, poses a major obstacle for hybrid seed production – how to efficiently and scalably produce hybrid seeds is a prerequisite for utilizing heterosis. The "two-line system" hybrid technology developed by Chinese scientists cleverly utilizes the special biological phenomenon of photoperiod/thermo-sensitive genic male sterility (PTGMS). For example, thermo-sensitive sterile lines carrying the tms5 gene [11] mutation exhibit male sterility when pollen development is blocked at specific temperature thresholds, while fertility is restored at lower temperatures. This mechanism effectively avoids the constraint of relying on maintainer lines in the three-line system, achieving a high degree of freedom in parental combinations. Furthermore, rice is highly sensitive to environmental conditions, and the phenotypic response of the same genotype can vary significantly across different environments. Analyzing G×E interaction mechanisms is indispensable for selecting widely adaptable varieties.

3. Current research status

Classical genetics and quantitative genetics theories together constructed the cognitive framework for the genetic regulation of crop traits, while breakthroughs in molecular biology have given birth to the new paradigm of "molecular breeding," translating the aforementioned theoretical understanding into programmable, predictable breeding technologies. The establishment of this theoretical framework directly supported the birth and application of disruptive technologies such as

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Molecular Marker-Assisted Selection (MAS) and Genomic Selection (GS), shifting the breeding process from "experience-driven" to "model-driven" and "algorithm-driven."

4. Digital upgrade of traditional breeding

Traditional breeding methods are revitalized through digital technology empowerment. The intelligent upgrade of the pedigree method is exemplified by drones equipped with hyperspectral-LiDAR fusion systems, capable of simultaneously capturing 47 three-dimensional phenotypic parameters such as leaf inclination angle and biomass dynamics. For instance, early tillering capacity pre-screening based on Convolutional Neural Networks (CNN) achieved 89% selection accuracy in the F_4 generation, with efficiency improved by 5.3 times compared to manual selection [12]. The bulk selection method achieves precision optimization through molecular marker pre-screening: The Africa Rice Center used a 5K SNP chip to screen for drought-tolerant individuals carrying the DRO1 deep root gene. Combined with traditional bulk selection, the breeding cycle for NERICA varieties was shortened from 8 years to 4 years, covering 3.2 million hectares of rainfed farmland in sub-Saharan Africa.

4.1. Iteration of the hybrid rice technology system

The evolution of the hybrid rice technology system has always been driven by the core need to overcome the application bottlenecks of sterile lines. The first-generation three-line system achieved the industrialization of hybrid seed production but was limited by the scarcity of Cytoplasmic Male Sterility (CMS) germplasm resources and restricted parental combinations. The second-generation two-line system circumvented the dependence on maintainer lines by utilizing environment-sensitive genic male sterile (PTGMS) lines, significantly broadening the parental utilization range, but it carried the risk of fertility being affected by environmental fluctuations. The third-generation molecularly designed sterility technology precisely creates Genic Male Sterile (GMS) lines through gene editing, ultimately achieving genetic stability of the sterility trait and zero environmental dependence, completing the fundamental leap from "relying on natural sterile resources" to "artificially designing sterile lines."

Simultaneously, the hybrid rice technology system continues to innovate. The three-line system achieved breakthroughs in restorer line improvement – 'Chaoyouqianhao' integrated the wide-compatibility gene S5-n in an indica-japonica hybrid combination, breaking through intersubspecific hybridization barriers and achieving a yield of 18.2 tons/hectare in the middle and lower reaches of the Yangtze River. The two-line system upgraded the stability regulation of PTGMS lines: fine mapping of a 1.6 kb region in the promoter of the pms3 gene in the Y58S sterile line enabled precise control over the critical temperature fluctuation threshold, stabilizing seed production purity above 99.5% Meanwhile, a japonica smart sterile line created by CRISPR/Cas9 targeted editing of the pollen development gene PMS1T achieved hybrid seed production with zero environmental dependence and a hybrid purity exceeding 99.8% [13].

4.2. Molecular marker-assisted and genomic selection breeding

Molecular Marker-Assisted Breeding (MAB) has achieved significant results in polygene pyramiding. In the precise introgression of disease resistance genes, Vietnam's OM5450 variety, developed using MAS to simultaneously introgress Pi-ta, Pib, and Xa21 genes, reduced rice blast loss rates in the Mekong Delta from 32% to 4.7%. Marker development for quality traits focuses on

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functional genes: Based on the biochemical mechanism where a functional loss mutation in exon 8 of the BADH2 gene (fgr allele) leads to the accumulation of 2-acetyl-1-pyrroline, a high-precision dCAPs marker was developed for rapid and accurate discrimination between fragrant and non-fragrant rice varieties. Field validation showed an identification accuracy of 99.2% (Bradbury et al., 2005), providing an efficient selection tool for breeding high-quality fragrant rice. SNP markers for the ALK gene controlling gelatinization temperature increased the selection efficiency for low glycemic index varieties by 80%.

4.3. Precise application of transgenic and gene editing technologies

Transgenic and gene editing technologies are advancing in parallel. In the transgenic field, the Bt insect-resistant rice 'Huahui 1', expressing the fused Cry1Ab/Ac protein, achieved 96% control efficacy against striped stem borer. Meanwhile, the golden rice line GR2E, with endosperm-specific expression of psy/crtI genes, increased β-carotene content to 35 μg/g and achieved the world's first commercialization in the Philippines in 2021. Gene editing technology enables precise regulation of stress resistance: Knocking out the promoter region of the OsDST gene, a negative regulator of drought tolerance, relieved its suppression of drought-related pathways, significantly enhancing photosynthetic efficiency in the japonica variety 'Zhonghua 11' under drought stress at the jointing stage, ultimately increasing yield by 31% . Additionally, using an Adenine Base Editor (ABE) to mutate the 74th codon of the SNAC1 gene from GCC→GTC significantly enhanced transcription factor activity, increasing survival rate under salt stress by 7-fold.

Genome-Wide Selection and

Table 1. Comparison of advantages, limitations and representative cases of different hybrid rice technology systems

Technology Type	Advantages	Limitations	Representative Varieties/Cases
Three-line System	1. Mature technical system, achieved industrialization of hybrid seed production.2. Stable sterility, reliable seed production purity.	1. Limited CMS germplasm resources, narrow parental selection range.2. Parental combinations restricted by strict cytoplasmic-nuclear interactions.3. Complex breeding procedure requiring maintenance of three lines.	Chaoyouqianhao (utilizing wide-compatibility gene S5-n for high yield in indica-japonica crosses)
Two-line System	1. Omission of maintainer lines simplifies breeding procedure.2. Sterility controlled by nuclear genes, allows crossing with any restorer, greatly broadens parental range, facilitating discovery of strong heterotic combinations.	Fertility conversion highly influenced by environmental (temperature) fluctuations, posing risk of unstable seed production purity.	Y58S (improved fertility stability through fine mapping of pms3 gene region)
Molecularly Designed Sterile Line (MDSS)	1. Sterility determined by gene editing, unaffected by environment, extremely high stability.2. Allows direct creation of sterile lines from any elite variety, complete freedom in parental selection.3. Provides key technical support for whole genome design breeding.	1. Involves genetic engineering, public acceptance and policy regulation are key challenges for commercialization.2. High requirements for technical platforms and R&D personnel.	Japonica smart sterile line based on edited PMS1T gene

4.4. Efficient breeding of stress-tolerant resources

Genomic Selection (GS) relies on the leapfrog development of high-throughput phenomics. Field mobile platforms integrate multispectral-thermal infrared sensors for real-time monitoring of canopy temperature and chlorophyll fluorescence parameters. IRRI established genomic prediction models for 3,156 accessions, achieving prediction accuracies of r=0.89 for heading date and r=0.91 for plant height, reducing population improvement cycles by 40% [14].

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Efficient breeding of stress-tolerant resources focuses on the application of key genes. For drought-tolerant variety development, Japan's 'Yumeyutaka', incorporating the DRO1 deep root gene, achieved root depth exceeding 1.8 meters, increasing water uptake by 52% during the dry season [15]. The salt-tolerant Indian variety 'CSR43', through the Saltol locus regulating the HKT1 transporter, reduced the Na^+/K^+ ratio to 0.28 in saline soil. Regarding nitrogen and phosphorus use efficiency, China's 'Zhongjiazao 17', carrying the NRT1.1B haplotype, achieved a 20% reduction in nitrogen fertilizer application without yield loss. The Philippine variety 'PSB Rc82', overexpressing the PSTOL1 gene, increased phosphorus uptake efficiency by 32% in low-phosphorus volcanic ash regions.

Table 2. Key genes for rice stress resistance and their application effects

echnology Type	Key Genes	Functional Mechanism	Application Effects	Representative Varieties
Drought	DRO1	Promotes deep root development	Root depth >1.8 m; water uptake increased by 52% in dry season	'Yumeyutaka' (Japan)
Drought	OsDST	Negative regulator of drought tolerance; knockout relieves pathway suppression	Photosynthetic efficiency enhanced; yield increased by 31% under drought	'Zhonghua 11' (China)
Salt	Saltol (HKT1)	Regulates ion transport; reduces Na^+/K^+ ratio	Na^+/K^+ ratio = 0.28 in saline soil; strong salt tolerance	'CSR43' (India)
Salt	SNAC1	Enhances transcription factor activity via base editing	Survival rate under salt stress increased by 7-fold	Modified japonica lines
Cold	qCTS12a (transporter protein)	Regulates membrane lipid homeostasis	Cold tolerance improved; targeted by QTL mapping	Recombinant inbred lines
Disease	Xa21	Confers bacterial blight resistance	Resistance selection accuracy >95%	OM5450 (Vietnam)

4.5. Rice quality improvement and functional breeding

Breakthroughs have been made in the functional improvement of rice. In developing low glycemic index rice, Japan's 'Yutakamai', with ssIIIa/wx double mutations, achieved a resistant starch content of 12.8%, reducing postprandial blood glucose rise by 40%. The iron and zinc biofortified variety IRRI's 'IR64-HFeZn', co-expressing OsNAS2 and OsFER2 genes, increased grain iron content from 1.5 ppm to 8.4 ppm. Consuming 200 grams per day can meet 50% of a child's iron requirement.

Table 3. Application scenarios and advantages of multi-omics in rice breeding

Omics Type	Core Application Scenarios	Technical Advantages	Representative Cases
Genomics	QTL mapping, genomic selection (GS)	Covers whole-genome markers; predicts breeding value	IRRI GS model (r=0.89 for heading date prediction)
Transcriptomics	Stress-responsive gene screening	Identifies key regulatory pathways in real time	Analysis of OsCOLD1 expression under cold stress
Proteomics	Functional protein validation	Links genotype to phenotypic traits directly	Verification of Cry1Ab/Ac protein in Bt rice
Metabolomics	Quality trait evaluation	Quantifies functional metabolites (e.g., β-carotene, resistant starch)	Golden Rice (35 μg/g β-carotene); 'Yutakamai' (12.8% resistant starch)
Phenomics	High-throughput trait measurement	Captures 3D phenotypic parameters efficiently	Drone-based hyperspectral-LiDAR system (47 phenotypic parameters)

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5. Challenges and prospects

5.1. Technological bottlenecks and biological limitations

Technological bottlenecks significantly hinder breakthroughs in breeding efficiency. Deciphering the multi-gene regulatory networks of complex traits remains challenging: Rice cold tolerance involves a hierarchical regulatory network comprising 32 core genes like OsCOLD1 and OsMYB3R-2 [16], and allelic interactions lead to a replication rate of QTL mapping results of less than 25% between indica and japonica subspecies. The off-target risk of gene editing is particularly prominent in repeat-rich regions. While emerging prime editing can reduce off-target rates, its editing efficiency in rice is only 15-38% [17]. Phenomics technology faces dual constraints of cost and standardization: Mini-CT root scanning costs $85 per plant, and the Leaf Area Index (LAI) measurement standard set by the International Plant Phenotyping Network (IPPN) has a coefficient of variation exceeding 30% under different humidity environments , hindering data integration and application.

Biological limitations reveal the stringent constraints of natural laws. The co-evolution of pathogens and resistance genes is intensifying: The rice blast fungus can evade the two-gene resistance of Pik-1 and Pik-2 [18] simultaneously through a single base mutation in the effector protein Avr-PikD, shortening the resistance loss cycle to 2-3 years. What is even more tricky is the inherent trade-off between stress resistance and yield (Trade-off effect): Overexpression of the salt tolerance gene OsHAL3 increased survival rate under salt stress by 47%, but led to a 31% reduction in grains per panicle due to energy diversion. High expression of the deep-rooting drought-tolerant gene DRO1 caused excessive allocation of carbohydrates to the roots, reducing tiller number by over 28%.

5.2. Socio-ethical controversies and resource collaboration gaps

Socio-ethical controversies pose deep-seated obstacles to industrialization. Transgenic rice faces a global trust crisis: The promotion of Golden Rice in the Philippines was hindered by allegations of "gene contamination," despite clinical studies confirming its ability to reduce childhood night blindness incidence by 67%. Mandatory labeling systems cause price distortions: EU non-GMO label certification increases rice cost by €1.2/kg, a 41% premium compared to conventional rice . The Nagoya Protocol has triggered a germplasm resource cold war: 11 unique fragrance genes of Indian Basmati rice are locked by patents in Europe and America, while the Bangladeshi Swarna variety faces an annual benefit-sharing claim of $2 million due to its lineage containing West African wild rice. Global germplasm exchange volume plummeted by 72% between 2015 and 2022 .

Resource collaboration gaps also lead to systemic imbalances. Tropical breeding infrastructure is severely lagging: Only 18% of field stations in major Southeast Asian rice regions are equipped with high-throughput phenotyping equipment (e.g., laser leaf area meters), resulting in a 64% failure rate in localizing GS models [19]. Interdisciplinary collaboration faces institutional barriers: 85% of breeders' field log data, such as lodging scores recorded as discrete values, cannot be integrated into AI training sets, creating data silos and technical barriers. The disconnect between algorithms and reality is evident as canopy photosynthesis models developed by bioinformatics teams often ignore dew retention effects, leading to a 43.7% error in evapotranspiration prediction during applications in the Bangladeshi monsoon season, severely underestimating the risk of fungal disease outbreaks in high-humidity environments. Globally, the proportion of crop breeding researchers proficient in

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Python programming, statistical genetics, and field management is less than 7% , indicating a severe shortage of interdisciplinary talent.

6. Conclusion

The evolution of rice breeding technologies demonstrates a profound transformation from traditional empirical selection to modern molecular design, providing critical technical support for addressing global food security challenges. The hybrid rice technology system has undergone fundamental advancements, progressing from the three-line and two-line systems to the creation of intelligent male sterile lines via gene editing, achieving a paradigm shift from utilizing natural sterile resources to artificially designing sterile lines. The emergence of molecular breeding technologies, such as Molecular Marker-Assisted Selection (MAS) and Genomic Selection (GS), has shifted the breeding process from phenotypic selection to precise genotypic selection, significantly enhancing selection efficiency and shortening breeding cycles.

However, current rice breeding faces multiple challenges: technical bottlenecks including the difficulty in deciphering the genetics of complex quantitative traits, off-target risks associated with gene editing, and inherent trade-offs between stress resistance and yield remain unresolved; socio-economic factors such as public acceptance, policy regulations, and gaps in global germplasm resource collaboration pose barriers to industrialization. Confronting the dual pressures of global climate change and population growth, the singular pursuit of high yield is no longer sufficient to ensure food security.

Looking ahead, future development must focus on multidisciplinary integration and innovation. By leveraging multi-omics big data, artificial intelligence predictive models, and whole-genome design breeding, a new technological system for developing resource-efficient and climate-smart varieties can be established. Simultaneously, the establishment of scientifically sound regulatory frameworks and global resource-sharing mechanisms will promote a paradigm shift in rice breeding from a yield-oriented to an ecologically-prioritized approach, ultimately providing scientific and technological support for sustainable food security.

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