Research Achievements and Prospects of Rice Molecular Module Design (Postprint)

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Abstract

China has over 8,000 years of cultivation history of cereal crops, and the related breeding knowledge has exerted important influence worldwide. In the 1990s, as one of the initiating countries, China participated in the “International Rice Genome Project”, successively completing the sequencing of japonica rice chromosome 4 and the fine map of the indica rice “93-11” genome. With support from the rice functional genomics project under the Ministry of Science and Technology’s “973” Program, significant progress has been made in the analysis of important agronomic traits in rice. The Strategic Priority Research Program (Category A) of the Chinese Academy of Sciences, “Molecular Module Design Breeding Innovation System”, taking rice as the entry point, through molecular module analysis of complex traits such as high yield, stable yield, high quality, and high efficiency, explored the establishment of a molecular module design breeding technology system to drive the analysis of complex traits and development of design breeding technologies for animals and plants including wheat, soybean, and fish. After nearly five years of effort, a rice germplasm resource bank and genome database have been established, a batch of molecular modules with important breeding value have been obtained, and internationally influential achievements have been accomplished in areas such as coordinated improvement of high yield and high quality in rice, perception and resistance to low temperature, balance between broad-spectrum durable disease resistance and yield, nitrogen-efficient utilization, and mechanisms of heterosis for high-yield traits, with the molecular module design breeding technology system receiving experimental validation. Related achievements were selected for the “Top Ten Advances in Chinese Life Sciences” in 2015 and 2017, the “Top Ten Advances in Chinese Science” in 2016, and the First Prize of the National Natural Science Award in 2017. This has demonstrated the leading role of the Chinese Academy of Sciences in basic research and technology development for crops such as rice.

Full Text

Special Topic: Designer Breeding by Molecular Modules

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Achievements and Prospects of Molecular Module-Based Designer Breeding in Rice

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Abstract

Cultivation of cereal crops including rice started in China over 8,000 years ago, and Chinese knowledge of crop breeding has profoundly influenced global agriculture. In the 1990s, as a founding member, China participated in the International Rice Genome Project, completing the sequencing of chromosome 4 of japonica rice and the fine map of the indica rice '93-11' genome. With support from the Ministry of Science and Technology's '973' Program on rice functional genomics, significant progress has been made in dissecting important agronomic traits in rice. The Strategic Priority Program (Category A) of the Chinese Academy of Sciences (CAS), "Innovative System of Designer Breeding by Molecular Modules," uses rice as a model crop to dissect molecular modules controlling complex traits including yield, yield stability, grain quality, and nutrient use efficiency, and to develop molecular module-based designer breeding systems. The program also aims to set rice as a reference to promote the study of complex traits and designer breeding of other related crops and animals such as wheat, soybean, and fish. Through nearly five years of collaborative effort, the program has built shared national rice germplasm libraries and genomic databases, dissected a series of molecular modules applicable in designer breeding, and established a theoretical framework for simultaneous improvement of both yield and quality traits, cold perception and resistance, balancing broad-spectrum durable disease resistance with yield, nitrogen use efficiency, and heterosis of yield traits. Such achievements have experimentally validated the concept of Designer Breeding by Molecular Modules. The importance of these achievements were highlighted by selection as among the "Top Ten Advances in Chinese Life Sciences" in 2015 and 2017, the "Top Ten Advances in Chinese Sciences" in 2016, and winning the First Prize of the National Natural Science Award in 2017.

Keywords: rice, cereal crops, complex traits, molecular modules, molecular module-based designer breeding
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The ancient Chinese comprehensive scientific and technological work *Tiangong Kaiwu* (1637) states that "among all crops that nourish humanity, rice accounts for seven-tenths," illustrating that rice has been the staple food for Chinese people for millennia. Cereal crop cultivation in China has a history of over 8,000 years [1], and related breeding knowledge and technologies have exerted significant global influence. Since the 20th century, rapid accumulation of scientific knowledge and disciplinary development have driven innovations in breeding theory and technology: Mendelian genetics in the early 20th century propelled the development of genetic breeding (hybrid breeding) theories and techniques; molecular biology established in the 1950s based on the DNA double helix structure laid the foundation for molecular breeding (including later transgenic technologies); and the development of genomics in the 1990s has made designer breeding possible.

China is among the first countries to launch plant genomics research. In 1998, as a major founding member, China participated in the International Rice Genome Sequencing Project. Since 1999, under the Ministry of Science and Technology-funded "Rice Functional Genomics" research program, Chinese scientists have made important progress in genetic material technical methods, technical routes, and genetic dissection of simple traits. In 2004, the precise sequencing of chromosome 4 of japonica rice 'Nipponbare' was completed, along with a series of comparative genomics studies. In 2000, the "Super Hybrid Rice Genome Project" was launched, and in 2002, the draft genome of the super hybrid rice parental indica variety '93-11' was first completed, with its precise sequencing finished in 2005. These studies pioneered a new field using rice as a model crop to dissect the regulatory networks of complex traits.

Breakthroughs in Genetic Regulatory Networks for Complex Traits in Rice

To address the low genetic diversity in existing varieties, we collected major rice resource materials worldwide and evaluated their key agronomic traits, obtaining a collection of elite donor materials harboring molecular modules for complex traits such as high yield, stability, superior quality, and high efficiency. We dissected a series of molecular modules including grain width modules GW7 and GW8 [2,3], grain length and width module GLW7/OsSPL13 [4], cold tolerance module COLD1 [5], disease resistance module Pigm [6], and nitrogen use efficiency module NITR1.1 [7]. Through genome-wide association analysis of rice genetic resources, we mined allelic variations and superior alleles of these molecular modules, tested their biological effects in uniform genetic backgrounds, and elucidated genotype-phenotype relationships. We also deciphered the mechanism of heterosis for rice yield traits [8], providing fundamental materials for compiling the most authoritative, web-based open database for rice designer breeding. Some of these achievements have been published in leading journals including *Cell*, *Nature*, *Science*, and *Nature Genetics*. Notably, the study on rice cold perception and resistance mechanisms (COLD1) and the research on genetic and epigenetic regulation mechanisms balancing broad-spectrum durable disease resistance with yield (Pigm) were selected as among the "Top Ten Advances in Chinese Life Sciences" in 2015 and 2017, respectively, while the heterosis mechanism study was selected as a "Top Ten Advance in Chinese Sciences" in 2016.

The "Innovative System of Designer Breeding by Molecular Modules" includes: (1) dissecting molecular modules to compile an encyclopedia of molecular modules that can guide designer breeding; (2) elucidating the coupling effects among molecular modules; and (3) establishing "genome-wide navigation" molecular module-based designer breeding technologies.

Solutions for Simultaneous Improvement of Rice Yield and Quality

Through nearly two decades of development, China has achieved a series of breakthroughs in cloning genes related to yield and quality and in their simultaneous improvement. Multiple genes controlling rice yield and/or quality have been cloned, such as GS3, Ghd7, GW8, GW7, DEP1, IPA1, and LGY3 [2,3,9-13]. Some of these genes have been successfully utilized in molecular design breeding for high yield and superior quality. For example, Li Jiayang's team used the ideal plant architecture gene IPA1 to increase rice yield while maintaining grain quality through molecular design, developing a series of new high-yielding and high-quality varieties [12].

Studies have shown that GW8 and GW7 have tremendous potential for simultaneous improvement of rice yield and quality. The GW8 gene encodes the OsSPL16 protein, a positive regulator controlling grain width and yield. Introducing its superior allele into elite quality varieties can increase yield by 14% while maintaining quality, while introducing it into high-yielding varieties can significantly improve grain quality without yield penalty. GW7 is a gene controlling grain quality. Pyramiding superior alleles of GW7 and GS3 into high-yielding indica rice can simultaneously improve both grain quality and yield. GW8 can directly bind to the promoter of GW7 and regulate its expression. Pyramiding superior alleles of GW8 and GW7 in high-yielding rice achieves a balance between high yield and superior quality. LGY3 encodes a MIKC-type MADS-box family protein, OsMADS1, that controls both rice yield and quality. Introducing its superior allele into high-yielding hybrid rice can significantly improve grain quality while increasing yield by more than 7%. Pyramiding this allele with the high-yield gene dep1 in conventional rice can not only significantly improve grain quality but also increase yield by over 10%. These achievements have profound implications for both theoretical research and breeding applications in simultaneous improvement of rice yield and quality.

Molecular Mechanisms of Rice Cold Perception and Resistance

Japonica (geng) and indica (xian) are the two cultivated subspecies of rice. Generally, japonica rice is characterized by drought and cold tolerance, while indica rice is tolerant to humidity and heat. Rice itself originated as a tropical and subtropical crop and is highly sensitive to low temperatures. During artificial domestication and selection, the cultivation area needed to expand toward regions with lower annual accumulated temperature, making improved cold tolerance a fundamental requirement for northward expansion of rice cultivation.

Cold tolerance in rice is a complex trait controlled by multiple genes. During long-term artificial domestication and selection, QTLs beneficial to humans were screened and retained in specific genetic backgrounds. Based on the distinct differences in cold adaptation between japonica and indica rice, we constructed a genetic population using the indica material '93-11' and japonica material 'Nipponbare', and map-based cloned the important cold tolerance QTL gene COLD1. Using near-isogenic lines, we verified the contribution of japonica COLD1jap to rice tolerance under low temperature stress. COLD1jap overexpression lines showed significantly enhanced cold tolerance, while the cold tolerance was reduced in the loss-of-function mutant cold1-1 and antisense transgenic lines. By analyzing genomic information from 127 rice materials from different cultivation regions and their cold tolerance levels, we identified seven single nucleotide polymorphisms (SNPs) in the COLD1 gene. The second SNP (SNP2) is located in the fourth exon of COLD1, where cytosine or thymine is present in indica rice, while adenine is found in japonica rice. Cold tolerance experiments demonstrated that only when SNP2 in COLD1 is adenine can it complement the cold tolerance defect of cold1-1, indicating that this specific SNP2 is directly associated with cold tolerance in japonica rice. Rice materials with adenine at SNP2 are distributed in Northeast China, Japan, Korea, and other regions with low annual accumulated temperature. Evolutionary analysis revealed that the adenine at SNP2 originated from wild rice in China and was retained during artificial domestication and selection of japonica rice [5]. Similar findings were observed during the booting stage, where two SNPs in the CTB4a promoter conferred stronger cold tolerance to japonica rice during its adaptation to low temperature environments in temperate regions [14]. COLD1 is a nine-transmembrane protein localized to the plasma membrane and endoplasmic reticulum membrane. COLD1 can interact with the G-protein α subunit RGA1, and the japonica COLD1 protein (COLD1jap) can enhance RGA1 enzyme activity. Upon low temperature stimulation, COLD1 participates in G-protein signal transduction, activates Ca2+ channels, and triggers downstream cold defense responses, thereby conferring cold tolerance to japonica rice. These results outline a relatively complete pathway from environmental cold perception at the cell membrane, through cytoplasmic biochemical reactions, to the regulation of specific defense gene expression in the nucleus, explaining the molecular and cellular mechanisms of cold tolerance in japonica rice.

Genetic and Epigenetic Regulation Mechanisms Balancing Broad-Spectrum Durable Disease Resistance and Yield in Rice

Rice blast is the most severe disease of rice, known as the 'cancer' of rice production, which widely infects rice, wheat, and other Poaceae crops, and was listed as the top fungal disease in 2012 [15]. In China, rice blast affects over 80 million mu annually, causing yield losses of 10-20%. Consequently, rice variety certification in China has implemented a 'one-strike veto' system for blast resistance. The most economical and effective approach in production is breeding new varieties with broad-spectrum resistance, but there has long been a lack of broad-spectrum and durable blast resistance genes that can be effectively applied in breeding. Typical resistance genes often lose their effectiveness within a few years of release, while pyramiding multiple resistance genes frequently reduces yield and quality [16].

To address this long-standing theoretical and practical problem, we collaborated with breeders to establish natural disease nurseries for blast resistance evaluation across different ecological regions. Through multi-year, multi-location screening, we obtained a collection of broad-spectrum and durable blast-resistant materials. Among them, 'Gumei 4' showed the most outstanding resistance, superior to internationally known broad-spectrum resistance genes such as Pi-2, Pi-9, and Pizt, with over 30 years of field resistance records demonstrating maintained effectiveness. The 'Gumei 4' variety contains a broad-spectrum resistance locus named Pigm [17], mapped to chromosome 6. The Pigm locus comprises 13 NLR-type resistance genes. Functional dissection revealed that this locus encodes functional NLR receptor proteins PigmR and PigmS. PigmR is constitutively expressed and can form homodimers, conferring broad-spectrum resistance against all tested blast pathogen races, but at a cost—reduced yield. The other NLR receptor protein, PigmS, can competitively bind with PigmR to form heterodimers, suppressing the resistance function of PigmR. During long-term rice evolution and domestication, PigmS expression is regulated epigenetically, with its specific high expression in pollen benefiting rice yield and compensating for the yield penalty caused by PigmR. Due to the low-level expression of PigmS, a 'sanctuary' is provided for pathogens, reducing selection pressure and slowing the evolution of pathogen virulence against PigmR, thereby endowing the Pigm locus with durable resistance [6]. Consequently, varieties bred using the Pigm locus possess broad-spectrum resistance without compromising final yield.

This study discovered a novel mechanism by which plants epigenetically and exquisitely regulate a pair of functionally antagonistic immune receptor proteins to coordinate the balance between broad-spectrum disease resistance and yield. This represents a major breakthrough in plant immunity and crop broad-spectrum resistance mechanisms, establishing foundational work for crop disease resistance and providing new theories and effective molecular technologies to resolve the conflict between high resistance and yield, facilitating the breeding of new high-yield and high-resistance varieties [18,19]. This achievement has been applied in molecular breeding for disease resistance by over 40 breeding institutions including Longping High-tech, Fengle Seed Industry, Qinyan High-tech, and the China National Rice Research Institute. Using specific molecular markers for Pigm, we have rapidly bred and improved a large collection of broad-spectrum and durable blast-resistant rice materials. Among them, the early indica rice variety with high resistance developed by the China National Rice Research Institute has been extended to over 10 million mu, and Longping High-tech has had four broad-spectrum disease-resistant new varieties approved through national certification, demonstrating tremendous application value.

Molecular Modules for Nitrogen Use Efficiency and Breeding of Green Super Rice

Nitrogen is an essential nutrient for organisms and one of the core factors determining crop biomass and yield. For a long time, the agricultural production model focused primarily on pursuing yield has led to excessive application of chemical fertilizers. Statistics show that global nitrogen fertilizer application exceeds 120 million tons annually. China's annual fertilizer consumption is over 60 million tons, accounting for 33% of total world consumption—three times the world average—while fertilizer use efficiency is only about 30% [20]. Nitrogen fertilizer use has greatly contributed to crop yield increases, but excessive application not only raises agricultural production costs but, more importantly, causes environmental disasters including climate change, soil acidification, and water eutrophication. Consequently, nitrogen pollution is considered one of the greatest environmental challenges facing humanity in the 21st century, with estimated annual costs for nitrogen pollution control in the European Union alone ranging from €70 to €320 billion. On the other hand, the growing population demands greater food production. Therefore, how to increase crop yields while reducing nitrogen fertilizer application has long been a challenge for scientists, and breeding new crop varieties with high nitrogen use efficiency is key to solving this series of problems.

Research has revealed molecular modules for high nitrogen use efficiency including NRT1.1A, NRT1.1B, and ARE1 [7,21,22]. NRT1.1B encodes a nitrate transporter protein that differs by only one amino acid between indica and japonica rice, with significant differentiation between the two subspecies. The indica-type NRT1.1B exhibits higher nitrate uptake and transport activity. In near-isogenic lines containing the indica-type NRT1.1B, key genes in the nitrate assimilation process are significantly upregulated, while they are suppressed in nrt1.1b mutant materials, indicating that NRT1.1B in indica rice affects nitrate uptake, transport, and assimilation, thereby conferring higher nitrogen use efficiency. Therefore, a natural variation of a single base in NRT1.1B is an important cause of the difference in nitrogen use efficiency between japonica and indica rice. Introducing the indica-type NRT1.1B into japonica varieties and conducting field experiments at three locations (Beijing, Shanghai, and Changsha) showed that japonica varieties containing the indica-type NRT1.1B achieved 30-33% higher yield and 30% higher nitrogen use efficiency under half nitrogen application compared to controls; under normal nitrogen application, they showed 8-10% yield increase and about 20% improvement in nitrogen use efficiency [7]. NRT1.1B has tremendous application value for improving nitrogen use efficiency in japonica rice [7].

In response, a commentary article in *Nature Plants* on this achievement stated: "This study not only reveals the molecular mechanism underlying the difference in nitrogen use efficiency between rice subspecies, but more importantly, it provides an important gene resource for breeding green super rice" [23]. In collaboration with the Jiaxing Academy of Agricultural Sciences, we have used molecular module-based designer breeding technology and NRT1.1B to develop multiple green rice lines with promising application prospects. In Zhejiang, continuous two-year large-scale planting tests on 50-100 mu plots achieved yields of 860-900 kg per mu. In 2017, the "National Green Super Rice Third-Party Evaluation" organized by Huazhong Agricultural University showed that among the four submitted lines tested at medium nitrogen level (100 kg per hectare, compared to the average 180 kg per hectare in Hubei, representing an 80 kg nitrogen reduction), the highest yield reached 678 kg (compared to the national average rice yield of 453 kg per mu in 2015), ranking 1st, 2nd, 5th, and 9th among 25 submitted materials nationwide. These results demonstrate that the molecular module-based designer breeding technology system has broad application prospects in green super rice breeding.

Mechanism of Heterosis for Rice Yield Traits

Heterosis is a biological phenomenon where hybrid F1 generations exhibit superior performance over both parents in adaptability, yield, and resistance. Over the past 50 years, breeders have utilized heterosis and male sterility principles to select and improve effective hybrid combinations, developing numerous high-yielding hybrid rice varieties through three-line and two-line systems, such as 'Shanyou 63' and 'Liangyou Peijiu', which have substantially increased China's rice production. The mechanism underlying heterosis is a complex genetic phenomenon whose basis has remained unclear. By collecting 1,495 hybrid rice varieties and conducting genomic analysis and field evaluation of yield traits in 17 representative genetic populations, we comprehensively and systematically identified major genetic loci controlling rice heterosis and dissected its molecular genetic mechanism [8,24] using a series of new technologies from quantitative genetics, genomics, and computational biology. The study revealed that most of these genetic loci exhibit incomplete dominance in the heterozygous state, and through hybrid breeding, novel genotype combinations are generated that efficiently achieve optimal combinations of flowering time, plant architecture, and yield components in F1 hybrids, creating heterosis. For example, in traditional three-line hybrid rice combinations, the male parent (restorer line) accumulates numerous superior alleles with excellent comprehensive trait configuration. On this basis, a few alleles from the female parent (male sterile line/maintainer line) further improve seed setting rate, flowering time, and panicle grain number (such as the hd3a gene) and plant architecture (such as IPA and tac1 genes), realizing the superior performance of F1 hybrids. These findings are significant for advancing precise molecular designer breeding practices in both hybrid and conventional rice.

Molecular Module-Based Designer Breeding Achieves Rich Results

"Genome-Wide Navigation" Molecular Module-Based Designer Breeding Technology Validated The "Genome-wide Navigation" molecular module-based designer breeding technology scans and detects the genome to efficiently predict genotype combinations that are missing or need improvement in current commercial varieties. Based on existing molecular modules and their interactions, it designs optimal routes for variety improvement and uses genomic information to rapidly and accurately predict which individuals in hybrid populations have aggregated numerous superior genotypes, providing breeders with optimal strategies and solutions for developing ideal varieties [25]. Using this technology, we have identified molecular modules missing or needing improvement in major varieties from Northeast China, the middle and lower Yangtze River regions, and the Huang-Huai rice cultivation areas. By introducing one, two, or more molecular modules into different varieties lacking these modules and combining with genome-wide selection, we have developed over 30 designer rice new varieties, four of which have passed national certification. These studies validate the feasibility of molecular module-based designer breeding technology. The development and extension of these molecular module varieties have effectively addressed deficiencies in existing rice varieties in China's major rice-producing regions, providing important impetus for rice production in these areas. Simultaneously, it has established and improved the innovative system of molecular module-based designer breeding with rice as the primary model, which will ultimately drive the upgrading of other major crop varieties and lead the development of China's emerging seed industry.

Molecular Module Varieties Demonstrate Tremendous Production Potential The Northeast rice region is China's premium rice production base and commodity grain base, contributing up to 70% of commercial grain. In recent years, factors such as genetic degradation of major varieties and frequent blast outbreaks have severely affected rice production. Using molecular module-based designer breeding theory and technology, our team has developed new multi-module coupled varieties 'Zhongke 804' and 'Zhongke 902'. Zhongke 804 uses 'Jijing 88' as the chassis variety, coupling grain shape module GS3, blast resistance module Pi5, and others, and passed national variety certification in 2017, being suitable for cultivation in the first accumulated temperature zone of Northeast China. Zhongke 902 uses 'Kongyu 131' as the chassis variety, coupling blast resistance modules Pizt, Pi35, Pb1, Pi21, and fragrance module Badh2, and passed Heilongjiang provincial variety certification in 2017. It is expected to become a major variety in the third accumulated temperature zone of Heilongjiang, solving bottleneck problems in rice production across 35 million mu in this region.

The middle and lower Yangtze River rice region is a major rice production area in southern China, where major varieties have seriously degraded in recent years. By coupling ipa1-2D and blast resistance modules PiZ and Pi5, we developed high-yielding, blast-resistant new hybrid japonica combinations 'Jiayou Zhongke' 1, 2, and 3, which successfully passed provincial variety certification. Jiayou Zhongke 1 features high yield, multiple resistances, early maturity, dwarf stature, and large panicles. In 2017, a demonstration on 14,000 mu in Shuyang, Jiangsu, achieved an average yield of 850 kg per mu, representing an increase of over 200 kg per mu compared to local major varieties. Jiayou Zhongke 2 possesses indica plant architecture with japonica grain quality, featuring high yield, multiple resistances, early maturity, and superior quality. Jiayou Zhongke 3 achieved a yield of 917.7 kg per mu in an 11,000 mu demonstration in Shuyang, Jiangsu in 2016. The development and extension of the Jiayou Zhongke series of module-based new varieties have achieved a perfect combination of superior quality, high yield, and multiple resistances, contributing to Academician Li Jiayang's team winning the First Prize of the National Natural Science Award in 2017. The series of achievements have been reported by more than 10 news media outlets including *People's Daily*, *Guangming Daily*, Xinhua News Agency, and CCTV.

To address the critical need for improving hybrid rice quality, we performed genome-wide pyramiding of multiple modules for high yield, superior quality, disease resistance, and high efficiency, developing a new inter-subspecific hybrid rice combination 'Zhongheyou 1'. This variety has strong adaptability, being cultivable from the Huang-Huai rice region to the middle and lower Yangtze River regions, combining indica appearance with japonica taste, achieving a perfect combination of high yield and superior quality that effectively solves the problem of poor grain quality in hybrid rice. It achieved a measured yield of 937.6 kg per mu, representing a 20.8% increase over the control 'Xudao 3', with quality reaching national grade 2 standard, and received national variety certification in 2018. Meanwhile, to address the lack of direct-seeded rice varieties in the Huang-Huai region, we used 'Wuyunjing 8' as the chassis variety and introduced modules for early maturity, blast resistance, and stripe virus resistance to develop the high-quality, high-yielding japonica variety 'Zhongkeyan 1', which also received national variety certification in 2018.

Under the support of the Strategic Priority Program, we have assembled a research team integrating basic research, technology development, and breeding, established rice germplasm resource banks and genomic databases, obtained a collection of molecular modules with important breeding value, and achieved internationally influential results in simultaneous improvement of yield and quality, cold perception and resistance, balancing broad-spectrum durable disease resistance with yield, nitrogen use efficiency, and the mechanism of heterosis for yield traits. The molecular module-based designer breeding technology system has been experimentally validated. Related achievements were selected as among the "Top Ten Advances in Chinese Life Sciences" in 2015 and 2017, the "Top Ten Advances in Chinese Sciences" in 2016, and won the First Prize of the National Natural Science Award in 2017, demonstrating CAS's leading role in basic research and technological development for rice and other crops.

Future Directions

However, rice is a complex living system. In addition to gene-gene interactions, trait formation involves gene-environment interactions. Our understanding of genetic networks underlying complex traits remains limited, the number of important genes available for designer breeding is relatively small, and we lack mathematical models at the genomic level to detect or predict the biological effects of gene-gene or gene-environment factor interactions. These are the constraints in establishing and perfecting a modern breeding innovation system from "molecular modules" to "designer varieties". The next phase should focus on three aspects: (1) Using computational biology and machine learning approaches to reveal molecular networks regulating agronomic traits. We will fully utilize rice germplasm resources and genomic data, expand international exchange and cooperation, and jointly apply functional genomics technologies and genome editing to accelerate the discovery and utilization of germplasm and gene resources, clarifying gene variation, functional changes, and regulatory networks. (2) Achieving precise variety design with green molecular design as the goal. We will systematically evaluate yield, quality, stress resistance, and nutrient use efficiency traits in rice germplasm resources, construct mathematical models at the genomic level to detect or predict biological effects of gene-gene or gene-environment factor interactions, and enable prediction of genotype and environmental factors and their coupling effects to establish demand-oriented crop design solutions and promote precise crop design. (3) Applying the rice molecular design model to wheat variety design in this complex genome crop. We will promote the transformation from traditional breeding to efficient, precise, and directed molecular designer breeding, ultimately facilitating the modernization, scaling, and efficient development of rice and other grain production.

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Note: Figure translations are in progress. See original paper for figures.