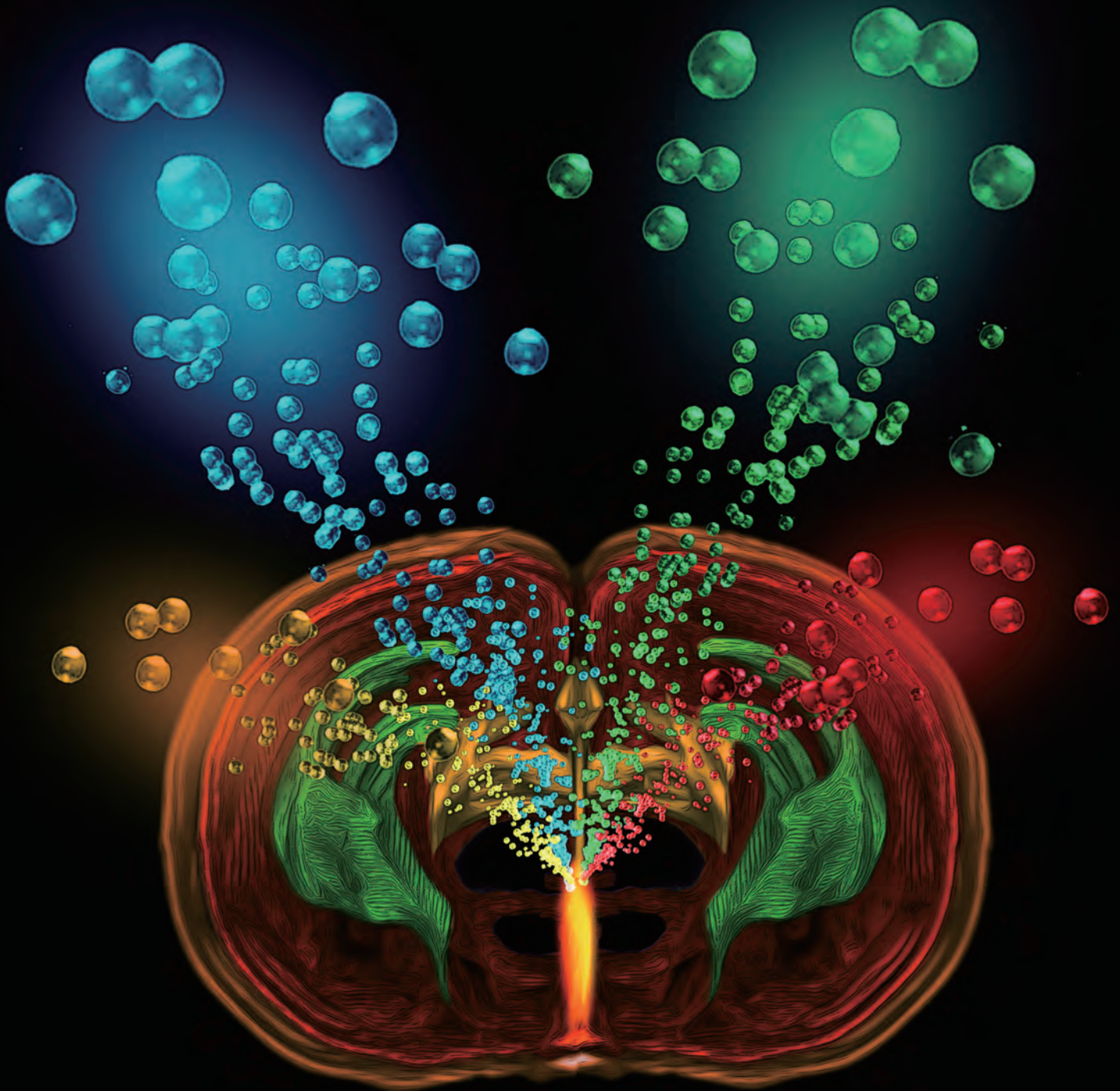


# 2025 Annual Report

Institute of Genetics and Developmental Biology  
Chinese Academy of Sciences

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**Cover description:** The multi-lineage origins of the hypothalamus across species. During the early patterning phase of hypothalamic development, distinct neural progenitor domains emerge, which drive the generation of different hypothalamic lineages through lineage-specific factors. In the figure, bubbles of different colors represent distinct hypothalamic lineages. (Provided by Wu Qing-Feng's team, designed by Xie Rui)

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# Message from the Director



Deputy Director in Charge  
Fu Xiangdong

Over the past year, focusing on the commanding heights of science and technology, the Institute of Genetics and Developmental Biology (IGDB) has steadily pushed forward in-depth reforms and achieved remarkable results in funding applications, scientific outputs, and talent development.

2025 stood as a strategic milestone for wrapping up the 14th Five-Year Plan and mapping out the 15th Five-Year Plan. After five years of unremitting efforts, we have achieved significant progress both in basic research and applied research. Multiple theoretical breakthroughs have been achieved in plant growth and development, disease resistance and stress tolerance, and balancing high yield with efficiency. Key technologies, including the rapid *de novo* domestication strategy, plant gene editing technology, improved varieties and cultivation techniques for the improvement and utilization of severe saline-alkali lands, and *in vitro* tissue and organ manufacturing, have continued to lead the way in innovations. Excellent varieties have been successfully developed, such as the "Zhongkefa" rice series, the high-yield and disease-resistant corn variety "Keyu 2028", the high-yield and Fusarium head blight-resistant wheat variety "Zhongke 166", and gene-edited powdery mildew-resistant wheat MLO-KNRNP. Building on the fruitful past achievements, we have worked diligently to formulate the 15th Five-Year Plan to a high standard.

In 2025, we newly undertook 62 projects with a total contracted funding of 260 million yuan. With the goal of "increasing yield while reducing chemical inputs and water consumption", we successfully completed the Strategic Priority Research Program of the Chinese Academy of Sciences titled "Precision Design and Creation of Seeds", yielding a series of breakthroughs that pave the way for advances in the molecular precision design-based breeding technology. We achieved phased progress in the Major Special Project on Saline-Alkali Land Improvement, developing 31 new varieties (lines) and implementing demonstration planting covering over 400 hectares. The China Crop Phenomics Facility (CCPF) broke ground in Wuhan. Our scientists published 525 SCI papers, including 20 in CNS journals and 107 in CNS sister journals. A total of 154 patents

were granted (including 15 international patents), 6 new plant variety protection rights were secured, 13 varieties were certified (10 at the national level), and 6 software copyrights were registered. The total promoted area of these crop varieties has reached approximately 530,000 hectares.

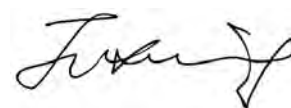
Two achievements, "Epigenetic Variation Drives Plant Stress Adaptation" and "AI-Driven Protein Engineering Enables Breakthroughs in Chromosome Precision Manipulation Technology", were named among the Top 10 Advances in Life Sciences in China 2025. The achievements "De Novo Domestication of Rice" and "Functional Research on Disease Resistance Bodies" were included in the landmark publications of the "Cell Line: 2014–2024" published by Cell Press. "Sesbania-Based Biological Improvement Technology for Saline-Alkali Lands" and the new salt-tolerant soybean variety "Kedou 35" were included in China's 2025 Major New Agricultural Technologies, Products and Scenarios. 12 scientists were selected as "Highly Cited Researchers 2025" by Clarivate.

In 2025, we achieved fruitful outcomes in talent development. We launched the institutional Young Talent Program, recruiting 6 young researchers as scientific and technological backbones. Eight researchers were selected for national or CAS talent programs. Fu Xiangdong was elected a Member of the Chinese Academy of Sciences, and Gao Caixia was named a Beijing Scholar and Associate Member of the European Molecular Biology Organization (EMBO). A total of 124 students graduated from the Institute in 2025.

We have steadily expanded our domestic and international cooperation networks. We teamed up with 4 enterprises and 7 universities to address key challenges in core breeding fields; jointly established a digital twin base network with local governments of Chifeng and Aksu; and collaborated with Alibaba Cloud on Intelligent Breeding. We renewed

the agreement with the China-Spain Center of Excellence for Plant Environment-Interactions (CEPEI), and signed a memorandum of understanding with the Cuban Center for Neuroscience. We also hosted the 7th International Symposium on Frontier Genomics Editing in 2025.

Finally, I would like to take this opportunity to express my sincere gratitude and highest respect to our sponsors and funding agencies for their substantial support, as well as to our staff and students for making this year highly productive and successful.



Fu Xiangdong  
Director of IGDB, CAS  
January 2026

# Leadership



**Fu Xiangdong**  
Deputy Director in Charge



**Xing Xuerong**  
Party Secretary & Deputy  
Director



**Shen Yanjun**  
Deputy Director



**Shen Yimin**  
Deputy Party Secretary &  
Secretary of the Disciplinary  
Inspection Commission



**Shen Yi**  
Deputy Party Secretary

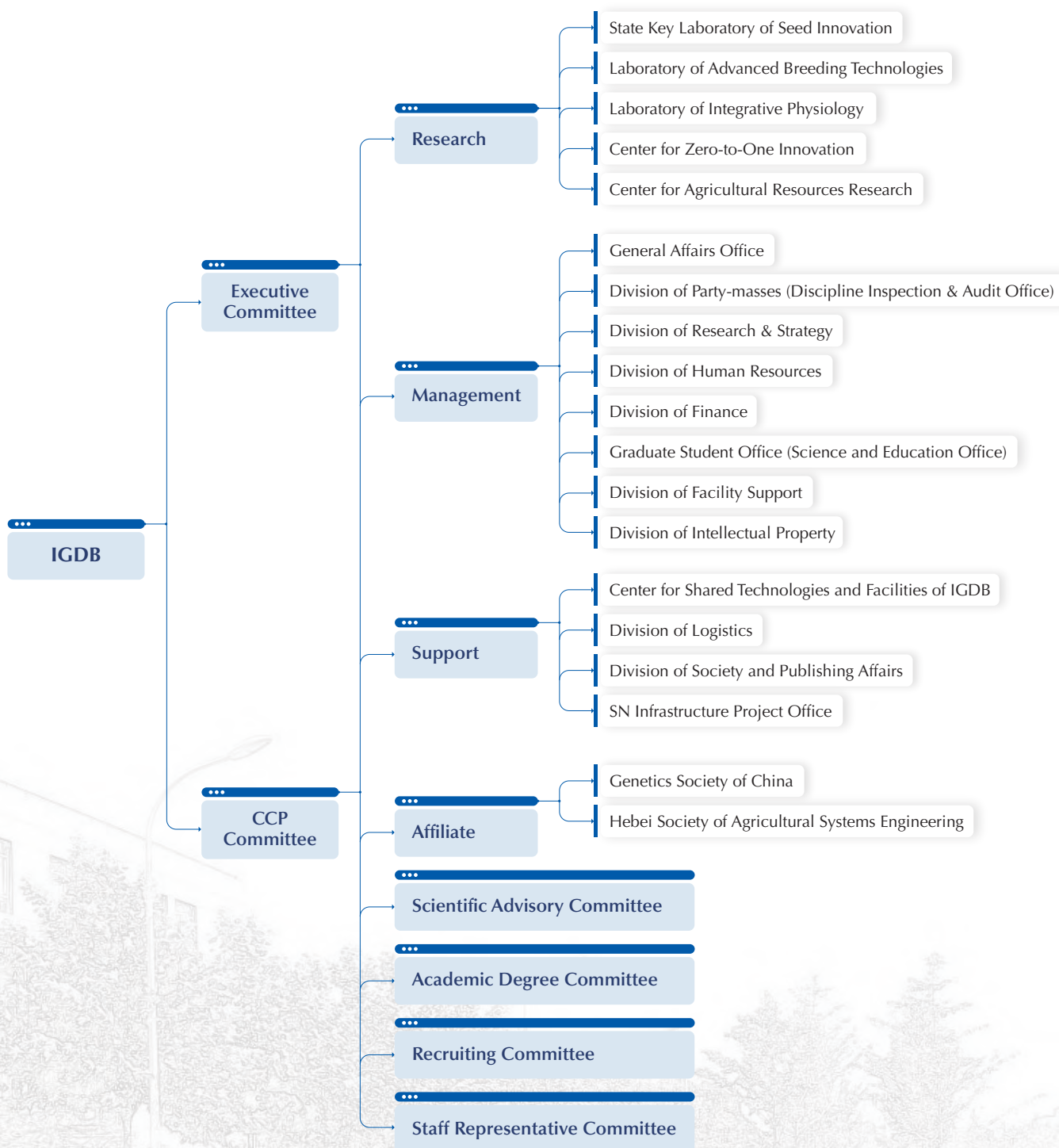


**Wu Qingfeng**  
Deputy Director



**Lu Fei**  
Deputy Director

# Organization



# Research Units

## State Key Laboratory of Seed Innovation



The mission of the laboratory is to systematically carry out research on the original theory and core key technologies of precise seed design and intelligent manufacturing, become an internationally leading seed innovation research organization, so as to ensure national food security and scientific and technological security from the source. The major research directions of the laboratory include precision control theory of crop traits, crop intelligent design breeding system, de novo domestication and future crop design, etc.

## Laboratory of Advanced Breeding Technologies



The mission of the laboratory is to drive the next-generation agricultural revolution and provide support to ensure national food security. Centered on cutting-edge breeding systems, the laboratory is built with three pioneering research pillars: Intelligent Design of Biomolecules, Precision Engineering of Chromosomes, and Digital Phenomics. The laboratory strives to achieve groundbreaking advances in biotechnology, and become a global center of excellence for innovation and talent development of breeding.

## Laboratory of Integrative Physiology



The laboratory is dedicated to systematically investigating the development, structure, and function of organisms at multiple levels—from cells, tissues, and organs to entire systems—under both physiological and pathological conditions, aiming to elucidate the regulatory mechanisms governing the establishment, maintenance, and disruption of homeostasis in the nervous, circulatory, and reproductive systems. Through synergistic innovation in theory and technology, the laboratory develops intervention strategies for major diseases and products for injury repair.

## Center for Zero-to-One Innovation



The Center is dedicated to addressing major scientific challenges in human health and sustainable agriculture by advancing frontier technologies. Driven by artificial intelligence and biotechnology, the Center focuses on four major research directions: developing algorithms for multi-omics analysis and data mining, building computational models to reveal the organizing principles of life processes, pioneering new omics and imaging technologies, and elucidating the mechanisms underlying fundamental processes in living systems. These efforts are underpinned by the integration of expertise in bioinformatics, proteomics, structural biology, evolutionary genetics, and systems biology.

## Center for Agricultural Resources Research



The Center is committed to meeting China's strategic needs for food security, water security, and ecological security by focusing its research on the efficient utilization of agricultural water resources. Specifically, the center works to innovate on the resource ecology theory and the resource-saving modern agricultural technology system, accelerate the application of advances in science and technology, and improve social services, thereby developing the center into an innovation powerhouse that can benefit the whole world.

# Institute of Genetics and Developmental Biology Chinese Academy of Sciences

## 2025 Research Outputs

 **525** SCI Papers

Total Impact Factor

 **5915**

Average Impact Factor

 **11.26**

CNS Papers

 **20**

CNS Papers  
(First/Corresponding Author)

 **15**

CNS Family Journal Papers

 **107**

CNS Family Journal Papers  
(First/Corresponding Author)

 **73**

High-Impact Papers  
(IF>10, First/Corresponding Author)

 **149**

Domestic  
Granted Patents

 **139**

Approved Varieties

 **13**

Plant Variety Rights

 **6**

Software Copyrights

 **6**

International  
Granted Patents

 **15**

Patent  
Commercialization

 **9**

Variety Promotion Area

 **800** million  
mu

Total Transfer and  
Commercialization Revenue

 **3090** million  
yuan

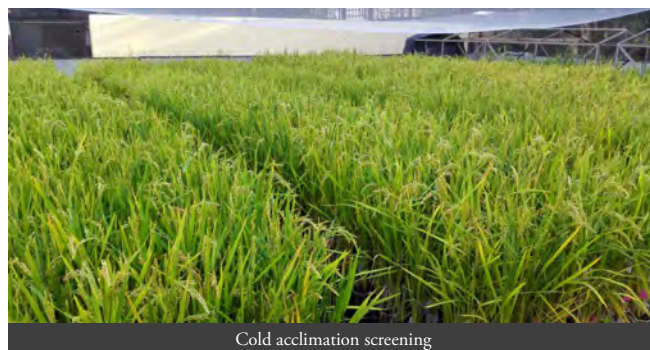
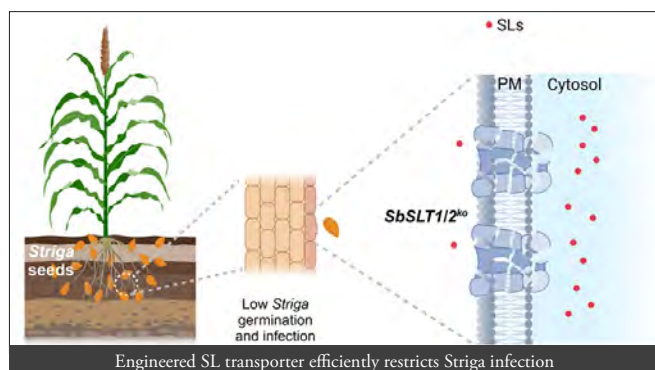
# Science Highlights

## Elucidation of Plant Stress Tolerance Mechanisms

### Key Genes Aid Crop Parasite Resistance

Parasitic plants have long posed severe threats to crops, with the most damaging being *Striga* and *Orobanche* of the Orobanchaceae family. Each year, they infest about 70 million hectares worldwide, threatening the food security of nearly 300 million people and causing direct economic losses of \$10–12 billion. In-depth research on host-parasite interactions is thus vital for crop resistance. Xie Qi and Li Jiayang's teams with collaborators, identified sorghum strigolactone ABCG transporters SbSLT1 and SbSLT2, elucidating their molecular mechanism in mediating root strigolactone exudation and revealing conserved structural features. This study provides a novel parasitic weed control strategy without impeding crop growth, offering key scientific support to address global food security threats from parasitic plants.

☀ *Resistance to Striga parasitism through reduction of strigolactone exudation, Cell. DOI: 10.1016/j.cell.2025.01.022*



### Epigenetic Variation Drives Plant Cold Adaptation

Before Darwin's natural selection theory, Lamarck proposed the "inheritance of acquired characteristics", holding that organisms actively adapt to environments and stably pass advantageous traits to offspring. This theory has long been controversial due to the lack of molecular genetic evidence. Cao Xiaofeng's team found that multigenerational prolonged cold stress induces specific DNA methylation variations at the ACT1 locus in rice, leading to heritable cold-tolerant traits. This study provides solid molecular evidence for Lamarck's theory, challenging the traditional view that adaptive evolution relies solely on random DNA mutations. It also uncovers new pathways for breeding stress-resistant crops, offering innovative strategies to tackle agricultural challenges from global climate change.

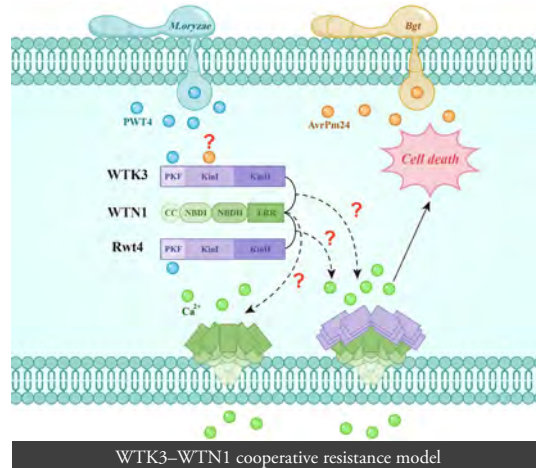
☀ *Inheritance of acquired adaptive cold tolerance in rice through DNA methylation, Cell. DOI: 10.1016/j.cell.2025.04.036*

## Novel Plant Disease Resistance Mechanisms

### A New Mechanism of Plant Disease Resistance

Tandem kinases are a novel class of disease resistance proteins discovered in wheat and barley, which confer resistance to rusts, powdery mildew, wheat blast and smut respectively. Teams led by Liu Zhiyong, Chen Yuhang and Zhou Jianmin, in collaboration with other researchers, identified a new disease resistance gene *Pm24* (WTK3) only present in the Chinese wheat landraces and elucidated a novel immune mechanism mediated by wheat tandem kinases, in which the classic NLR protein WTN1 and the tandem kinase WTK3 cooperate to recognize pathogenic fungi. This work provides new insight of the molecular mechanism of tandem kinases in plant immunity and lays a theoretical and practical foundation for the precise design of crop varieties with broad-spectrum and multiple disease resistance.

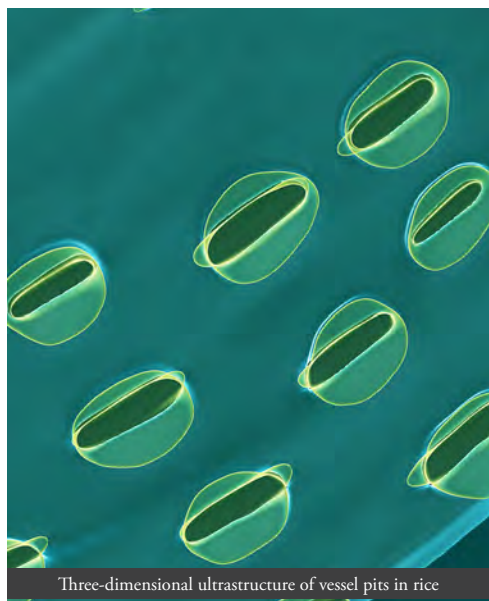
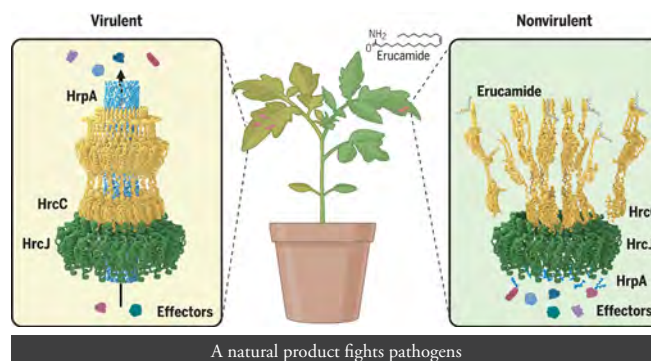
☀ *A wheat tandem kinase and NLR pair confers resistance to multiple fungal pathogens, Science. DOI: 10.1126/science.adp5469*



## A Phytochemical Disarms Bacterial Pathogens

Bacterial pathogens cause severe crop diseases and harm agricultural productivity. Understanding how plants fight pathogens will help control diseases and enhance food security. Zhou Jian-Min's team collaborated with chemists to identify erucamide, a very long-chain fatty acid derivative, as a potent defense metabolite utilized by numerous plant species against bacterial pathogens. Unlike known defense compounds, erucamide does not harm normal bacteria. It specifically disrupts the virulence machinery pathogens use to infect host plants. This discovery may guide the development of eco-friendly biopesticides.

☀️ *A widespread plant defense compound disarms bacterial type III injectisome assembly, Science. DOI: 10.1126/science.ads0377*



## Regulation of Complex Traits

### Shaping Vessel Pits Boosts Xylem Transport and Rice Yield

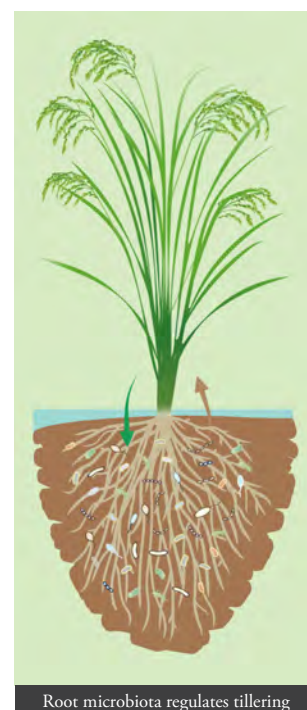
The emergence of plant vascular tissue marks a key milestone in terrestrial life evolution. Vasculature acts as a "life hub" for nutrient long-distance transport and whole-plant growth and physiology regulation. Xylem vessel pits affect plant hydraulics, nitrogen transport and crop yield, but the mechanisms of their 3D ultrastructure formation remain unclear. Zhou Yihua and Zhang Baocai's teams obtained the complete 3D ultrastructure of rice vessel pits using cutting edge FIB-SEM and identified the nitrogen-responsive module MYB61-PS1. They proved that PS1-mediated xylan deacetylation shapes pit 3D geometry, enhancing hydraulic capacity and nitrogen transport to boost yield. This study reveals a multiscale regulatory mechanism underlying xylem vessel plasticity and polysaccharide-guided cell morphogenesis.

☀️ *Shaping pit structure in vessel walls sustains xylem hydraulics and grain yield, Cell. DOI: 10.1016/j.cell.2025.09.018*

## Decoding Microbial Control of Tillering

Rice tiller number is a core agronomic trait determining yield and is regulated by genetics and various environmental factors. Whether and how the root microbiota regulates tiller formation has long been a major unanswered question. By integrating microbiomics, molecular biology, crop genetics, natural product chemistry, and structural biology, the team of Li Jiayang and Wang Bing, together with collaborators, systematically elucidated the function and molecular mechanism of the root microbiota in regulating rice tillering. The study identified core functional bacteria and their key metabolite, cyclo (Leu-Pro), and revealed the molecular mechanism by which they suppress rice tillering through strigolactone signaling pathway. This work establishes a paradigm for studying plant-root microbe interactions. It marks a new era in plant microbiome research, shifting from descriptive science to mechanistic dissection and engineering applications, and provides scientific support for microbial applications and sustainable crop yield improvement.

☀️ *Root microbiota regulates tiller number in rice, Cell. DOI: 10.1016/j.cell.2025.03.033*



## Efficient Nutrient Utilization

### Chromatin Remodeling Confers High Yield and NUE in Rice

Against the global context of increasingly tight resource and environmental constraints, how to ensure a sustained increase in grain yield while reducing fertilizer application has become a core scientific issue urgently to be solved for the development of green and low-carbon agriculture. Fu Xiangdong's team revealed for the first time that precise remodeling of three-dimensional chromatin conformation enables synergistic improvement of high yield and high nitrogen use efficiency in rice. This novel mechanism provides important theoretical support and an innovative breeding strategy for cultivating a new generation of Green Revolution varieties characterized by "less input, more output, and environmental friendliness".

☀ *Precise control of chromatin loop extrusion enhances sustainable green revolution yield in rice, Nature Genetics. DOI: 10.1038/s41588-025-02376-y*



New rice varieties with high yield and high nitrogen use efficiency

### Multi-Omics to Dissect Genetic Basis of Water Use Efficiency in Wheat

The safe and efficient production of wheat is of critical strategic importance for ensuring national food security. Currently, the water use efficiency (WUE) of wheat in China lags significantly behind global leaders, indicating both substantial potential for improvement and valuable opportunities for scientific and technological innovation. Xiao Jun's team studied a diverse 228-accession wheat population, using a phenotype-genotype-transcriptome framework to explore WUE's genetic basis and clarify TaMYB7-A1's drought resilience mechanism. This study builds a macro-micro closed-loop research framework, advancing from statistical association to causal validation, providing a reproducible drought tolerance paradigm and generalizable gene discovery strategy for wheat complex agronomic traits.

☀ *Integrative omics of the genetic basis for wheat WUE and drought resilience reveal the function of TaMYB7-A1, Nature Communications. DOI: 10.1038/s41467-025-63642-5*



Seedling-stage WUE evaluation system in wheat



Nitrate rhythms in the rice field

### Ca<sup>2+</sup> Signaling in Rice N Homeostasis

Nitrogen (N) is a crucial nutrient for crop productivity. How the rapid primary nitrate response connects with long-term N utilization for homeostasis remains elusive. Chu Chengcai's team identified a novel Ca<sup>2+</sup>-dependent signaling pathway in rice. They show the nitrate sensor OsNRT1.1B interacts with cyclic nucleotide-gated channels OsCNGC14 and OsCNGC16 to form a "transceptor-channel" complex. When nitrate perception occurs, this complex triggers intracellular Ca<sup>2+</sup> influx, leading to the phosphorylation of the master transcription factor OsNLP3 at Ser193. This specific phosphorylation accelerates OsNLP3 nuclear translocation and amplifies the transcriptional activation of nitrate-responsive genes. These findings reveal a dual regulatory network in rice, the Ca<sup>2+</sup>-OsNLP3 pathway rapidly amplifies nitrate signals, partnering traditional ubiquitination-mediated pathway to keep homeostasis. This research has created a crucial link from plants "perceiving nitrate" to "enhancing nitrogen use efficiency (NUE)," providing actionable genetic targets to improve NUE for sustainable agriculture.

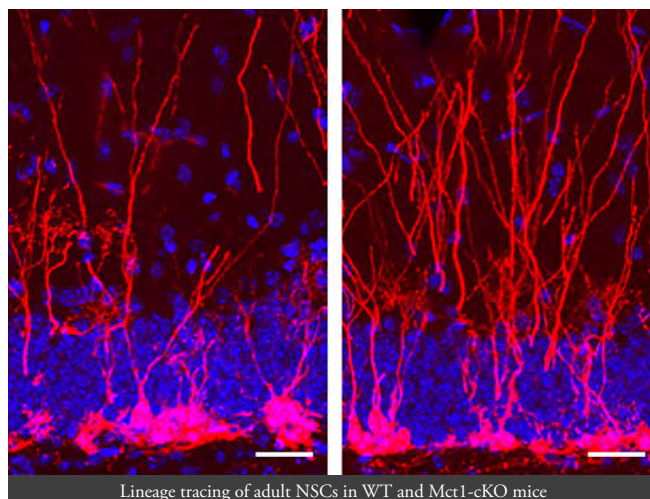
☀ *OsNRT1.1B-OsCNGC14/16-Ca<sup>2+</sup>-OsNLP3 pathway: Phosphorylation-mediated maintenance of nitrogen homeostasis, Advanced Science. DOI: 10.1002/adv.202507919*

## Neural Development and Regeneration

### Lactate Hemostasis and Adult Neurogenesis

Lactate has emerged as a crucial metabolic fuel and signaling molecule. Lactate homeostasis is essential for adult neurogenesis and cognition, but it's unclear how lactate shuttles across NSCs' plasma membranes to control their activity and neurogenic potential. Guo Weixiang's team showed that the lactate shuttle helps maintain the quiescence-activation balance of NSCs. They also systematically explained the molecular mechanism of how the lactate shuttle regulates adult neurogenesis through histone lactylation modification. This research offers a theoretical foundation for understanding NSCs' lactate homeostasis and lactate's impact on neurogenesis and brain function.

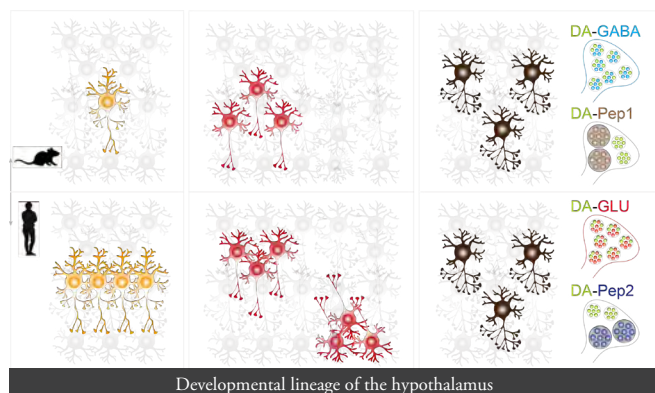
💡 *Lactate shuttling links histone lactylation to adult hippocampal neurogenesis in mice, Developmental Cell. DOI:10.1016/j.devcel.2024.12.021*



### Development and Evolution of the Hypothalamus

The hypothalamus is a central hub for homeostatic regulation, profoundly regulating survival, growth, aging and disease progression. However, its developmental programming and evolutionary patterns remains poorly understood. To address this, Wu Qing-Feng's team integrated single-cell transcriptomic data from humans, macaques, and mice, generating a cross-species atlas of over 350,000 cells and establishing the first comprehensive hypothalamic developmental database (<https://hypoatlas.org/>). This study reveals that the neural patterning of the developing hypothalamus are evolutionarily conserved. Neurogenic lineages are also shared between human and mouse hypothalamus. Notably, human hypothalamic neurons exhibit unique subtypes and enhanced neuromodulatory features. Neuronal distribution and neurochemical traits also display species-specific variations. Together, these findings provide a framework for understanding hypothalamic development, function, disease, and evolution.

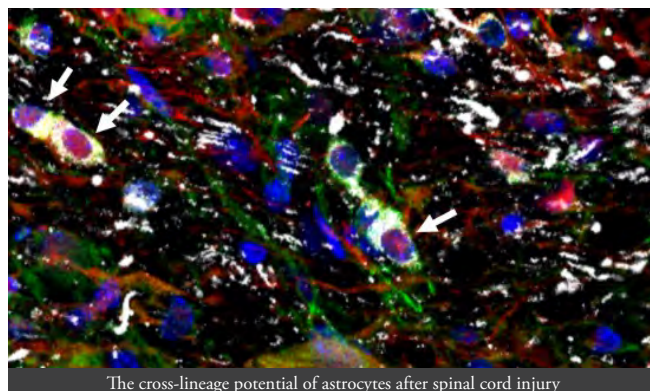
💡 *Transcriptional conservation and evolutionary divergence of cell types across mammalian hypothalamus development, Developmental Cell. DOI: 10.1016/j.devcel.2025.03.009*



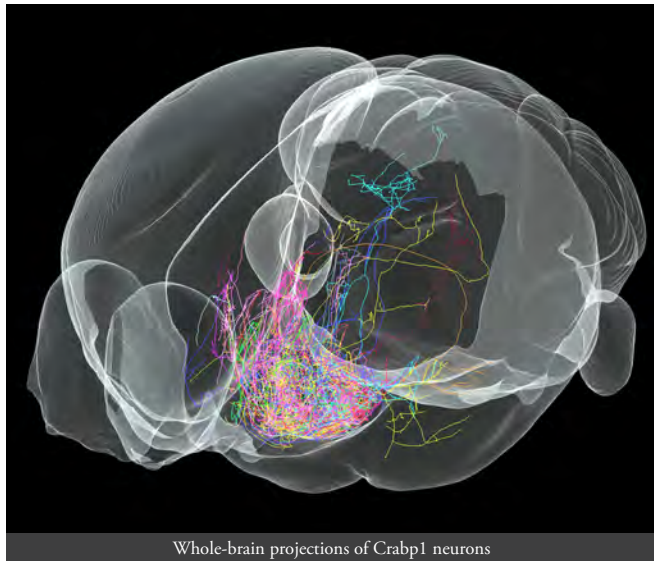
### New Cellular Findings in Primate Spinal Cord Injury

Spinal cord injury is a severe condition often leading to lifelong disability, with treatment largely hindered by the limited regenerative capacity of the central nervous system. Professor Dai Jianwu's team has long been dedicated to SCI repair research. They established scRNA-seq databases for human and rhesus monkey spinal cord development and injury, providing a crucial foundation for systematically analyzing cellular characteristics in primates. Through cross-species analysis, the team systematically investigated the dynamic changes of ependymal cells and astrocytes during development and after injury. Lineage tracing revealed their divergent fates post-injury: primate ependymal cells show limited activation and low plasticity, lacking stem cell potential, whereas astrocytes can be markedly activated, with a subset capable of transdifferentiating into oligodendrocytes and participating in remyelination under injury stimuli. This work offers a novel perspective for understanding SCI mechanisms and promoting regeneration therapy.

💡 *Characterizing progenitor cells in development and injured spinal cord: Insights from single-nucleus transcriptomics and lineage tracing, PNAS. DOI: 10.1073/pnas.2413140122*



## Brain-Body Interaction and Regulation



Whole-brain projections of Crabp1 neurons

### Neural Basis for Energy Expenditure in the Arcuate Hypothalamus

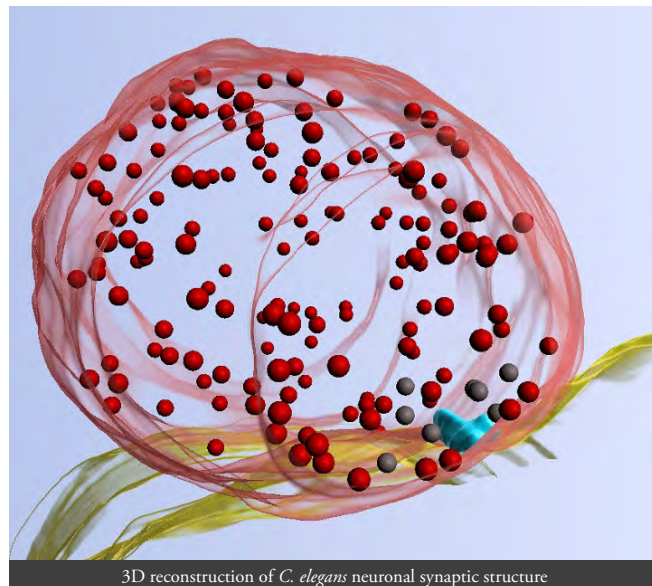
Obesity and related metabolic disorders are major global public health challenges. Elucidating neural mechanisms that enhance energy expenditure without suppressing appetite may provide new strategies beyond dietary restriction. Professor Wu Qing-Feng's team identified Crabp1 neurons in the arcuate hypothalamus as a critical population regulating energy homeostasis. These neurons promote energy expenditure by targeting multiple downstream nuclei. They are activated by cold exposure and exercise but suppressed by long photoperiods, indicating their role in integrating environmental and physiological signals. Genetic manipulation of these neurons prevents against high-fat diet-induced obesity. This work reveals a neural mechanism for energy homeostasis and highlights Crabp1 neurons as potential therapeutic targets for obesity.

☀ *Identification of a neural basis for energy expenditure in the mouse arcuate hypothalamus, Neuron. DOI: 10.1016/j.neuron.2025.08.021*

### Neuronal Calcium Oscillations Orchestrate Inter-Organ Communication and Lifespan via TMBIM-2

Aging is associated with deteriorated neuronal mitochondrial function and prolonged mitochondrial stress regulates systemic metabolism through inter-tissue signaling. Nevertheless, the underlying molecular mechanisms remain elusive. Tian Ye's team revealed that chronic neuronal mitochondrial stress stimulates serotonin release via TMBIM-2-mediated  $Ca^{2+}$  oscillations, which in turn triggers the intestinal UPR<sup>mt</sup>. TMBIM-2 expression declines with age, while its overexpression rescues neuronal function and prolongs the lifespan of *C. elegans*. These findings highlight the critical role of neuronal calcium oscillations in interorgan communication and lifespan regulation, providing new theoretical bases and promising targets for aging intervention and health management.

☀ *TMBIM-2 orchestrates systemic mitochondrial stress response via facilitating  $Ca^{2+}$  oscillations, Journal of Cell Biology. DOI: 10.1083/jcb.202408050*

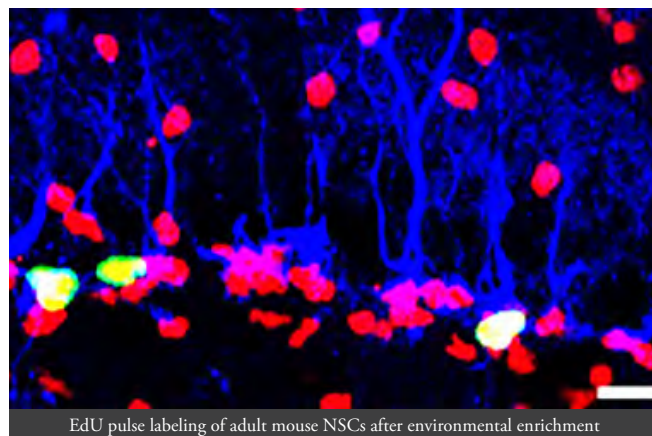


3D reconstruction of *C. elegans* neuronal synaptic structure

### Tactile Processing and Adult Neurogenesis

The tactile system empowers us to act on and interact with the changes of the external environment. In rodents, tactile sensation, a fundamental sense, is largely mediated via the vibrissae and the barrel cortex. However, it remains unclear how tactile perception reshapes the brain when exploring a novel environment. Guo Weixiang's team discovered a neural axis activated by enriched environment, in which mechanotransduction of Merkel cells can promote adult neurogenesis and cognitive function. This study highlighted the important role of intact tactile processing in brain function.

☀ *Merkel cell mechanotransduction facilitates adult neurogenesis and cognition in an enriched environment, PNAS. DOI: 10.1073/pnas.2510374122*



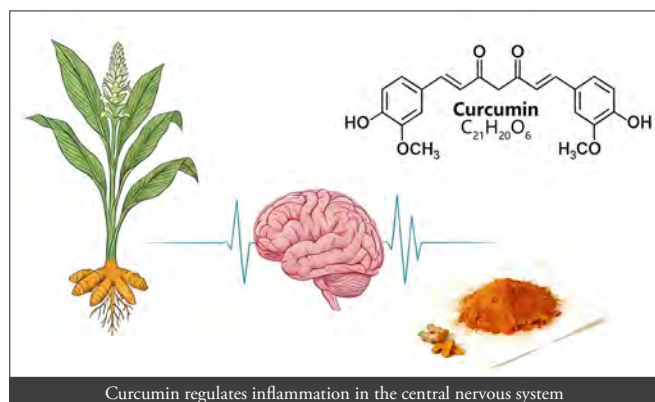
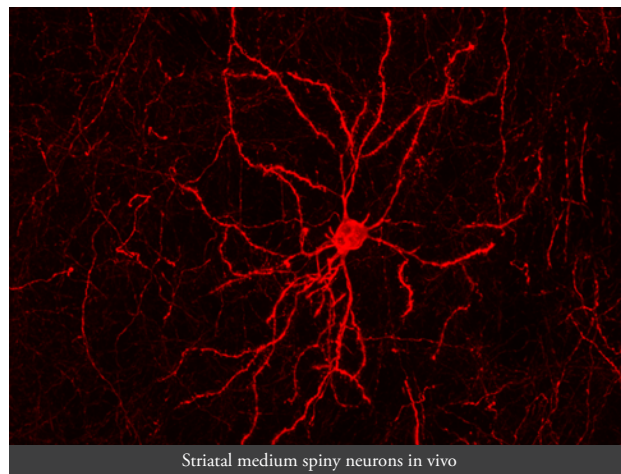
EdU pulse labeling of adult mouse NSCs after environmental enrichment

## Pathogenesis of Autism, Epilepsy and Other Disorders

### A New Mechanism of ASD: Abnormal Brain Lateralization

Brain lateralization, the structural and functional asymmetry between cerebral hemispheres, is a key nervous system feature. Its disruption in the striatum is linked to autism spectrum disorder (ASD), but the molecular mechanisms remain unclear. Through integrated proteomic and phosphoproteomic analyses, Xu Zhiheng's team has, for the first time, identified asymmetric protein phosphorylation patterns between the bilateral striatum. They further reveal that the ASD associated protein SH3RF2 forms a complex with CaMKII and PPP1CC to modulate striatal lateralization. This work elucidates how dysfunction of this complex contributes to ASD-like behaviors, offering new directions for understanding brain lateralization and developing treatments.

💡 *Autism-related proteins form a complex to maintain the striatal asymmetry in mice, Cell Research. DOI: 10.1038/s41422-025-01174-9*



### Role and Mechanism of Curcumin in Post-Epileptic Neuroinflammation

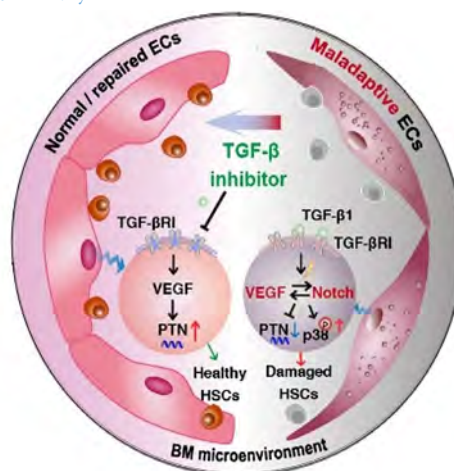
Epilepsy is a severe neurological disorder characterized by recurrent seizures that not only cause neuronal damage but also trigger widespread inflammatory responses in the brain. These responses activate local immune pathways and promote the release of pro-inflammatory factors, thereby exacerbating disease progression in a vicious cycle. The traditional Baijin Pill has long been used to treat epilepsy. Curcumin, the principal bioactive component of *Curcuma longa* (Yujin), exerts neuroprotective effects, potentially by modulating neuroimmune homeostasis within the central nervous system. However, its precise molecular targets and underlying mechanisms remain unclear. Recent work by Meng Wenxiang and colleagues demonstrates that curcumin attenuates excessive neuroinflammation following seizures through the regulation of the receptor-type tyrosine phosphatase PTPRZ1, providing mechanistic insight and potential therapeutic implications for neurological diseases.

💡 *Curcumin modulates PTPRZ1 activity and RNA m<sup>6</sup>A modifications in neuroinflammation-associated microglial response, Advanced Science. DOI: 10.1002/advs.202405263*

### TGF-β1 Regulates Hematopoietic Recovery

Under physiological conditions, TGF-β1 mediates tissue repair, yet persistent stress (chemotherapy, inflammation, transplantation injury) triggers its excessive activation, driving bone marrow vascular endothelial cells into maladaptive repair. This phenotype features reduced hematopoietic factor secretion and hyperactivated pathways associated with fibrosis and epithelial-mesenchymal transition. Wang Yingchun's team and their collaborators delineated the central role of the TGF-β1 pathway in the maladaptive remodeling of the bone marrow microenvironment by integrated multi-omics approaches, including transcriptomics and phosphoproteomics. They demonstrated that hyperactive TGF-β1 disrupts VEGF/Notch crosstalk, sustains p38 MAPK activation, impairs vascular niche function and causes hematopoietic reconstitution failure. This work clarifies the pathogenesis and establishes a novel therapeutic paradigm centered on repairing the bone marrow microenvironment.

💡 *TGF-β1-triggered maladaptive bone marrow endothelium impedes hematopoietic recovery, Signal Transduction and Targeted Therapy. DOI: 10.1038/s41392-025-02429-y*



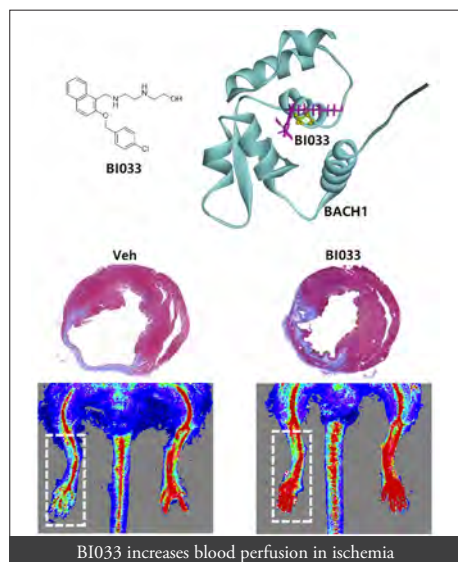
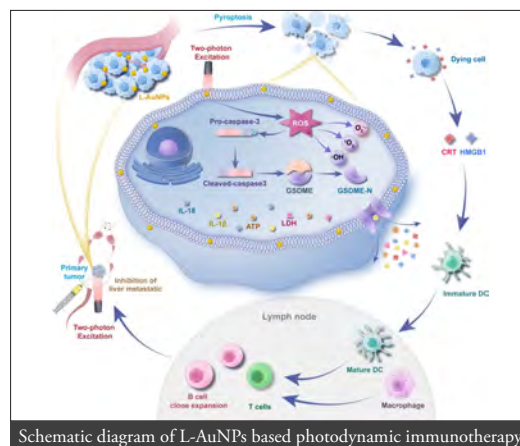
TGF-β1 regulates hematopoietic recovery

## New Treatment Strategies for Tumors, Cardiovascular Diseases, etc.

### New Therapeutic Strategies for Tumors and Cardiovascular Diseases

Luminescent gold nanoparticles (L-AuNPs), distinguished by their physicochemical properties and biological functionalities, have emerged as a promising class of nanoluminescent materials. Jiang Yuqiang's team developed a cell membrane-targeted L-AuNP-based two-photon photodynamic therapy (TP-PDT) nanoplatform. This system induces pyroptosis and immunogenic cell death (ICD), thereby eliciting antitumor efficacy in colorectal cancer models. The treatment suppresses liver metastasis and tumor recurrence, highlighting the tumor microenvironment and antitumor immunity. Collectively, this work establishes a therapeutic paradigm for solid tumors, underscoring the potential of L-AuNP-based photodynamic nanomedicine as a cancer treatment.

☀ *Hybrid near-infrared-activated luminescent gold nanoparticle platform for efficient cancer therapy. Advanced Composites and Hybrid Materials. DOI: 10.1007/s42114-024-01141-9*



### Small-Molecule Inhibitors for Vascular Regeneration in Ischemic Cardiovascular Diseases

Myocardial infarction and peripheral artery disease are characterized by arterial occlusion-induced ischemia, which may cause severe disability or even death. Effective therapeutic agents that restore blood supply and promote angiogenesis remain insufficient. Wang Xiu-Jie's team and collaborators identified BI033, a BACH1-targeting inhibitor, via a small-molecule virtual screening approach. BI033 inhibits BACH1, upregulates NRF2 expression and nuclear localization, increases H3K27ac modification, and activates VEGFA, HMOX1, and other angiogenic genes. In animal experiments, BI033 markedly enhanced vascular density and functional recovery in myocardial infarction and hindlimb ischemia models. This study provides a highly targeted, low-cost and efficient novel therapeutic strategy for ischemic diseases, with important clinical translation value and promising application prospects.

☀ *A BACH1 inhibitor ameliorates myocardial infarction and limb ischemia in mice, Molecular Therapy. DOI: 10.1016/j.ymthe.2025.07.008*

## Intelligent Robotic Automated Breeding Technology

### "GEAIR": An Intelligent Robot Ushers in a New Era of Smart Crop Breeding

To tackle hybrid breeding hurdles—high labor costs, long cycles and low efficiency—Xu Cao's team integrated biotechnology and AI. Using gene editing to reshape floral structure, the team quickly developed "robot-friendly" male-sterile lines with exposed stigmas, realizing crop-robot co-design for the first time. The team further created GEAIR, an intelligent breeding robot for autonomous navigation and precise pollination. Paired with a fully automated facility, this system cuts breeding costs by over 25% and shortens cycles by more than 60%. It establishes the BAR intelligent breeding model: Biotechnology as foundation, AI as enabler, Robotics as labor force. This work pioneers smart breeding core technologies and showcases AI's transformative power for scientific innovation.

☀ *Engineering crop flower morphology facilitates robotization of cross-pollination and speed breeding. Cell. DOI: 10.1016/j.cell.2025.07.028*

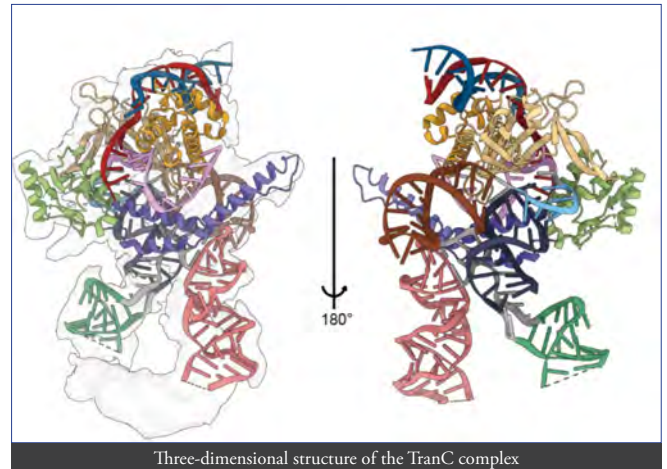


## AI-Enabled Research and Development of Underlying Technologies for Gene Editing

### Deciphering the Evolutionary Mechanism of CRISPR Systems

Gao Caixia's team pioneers genome editing innovation, gaining insights into CRISPR origins, building AI protein design platforms, and engineering scarless large DNA fragment editing methods. After seven years' research, they identified TranC, which bridges the long-missing link between transposons and CRISPR, filling a gap in the CRISPR evolutionary. They found TnpB's evolution into Cas12 relies on guide RNA's "functional splitting", unraveling the mystery of the molecular mechanism behind the origin of Cas12 and providing experimental evidence for how the modular evolution of RNA drives the evolution of complex molecular machines.

🔦 *Functional RNA splitting drove the evolutionary emergence of type V CRISPR-Cas systems from transposons, Cell. DOI: 10.1016/j.cell.2025.09.004*



### AI-Informed Constraints for Protein Engineering

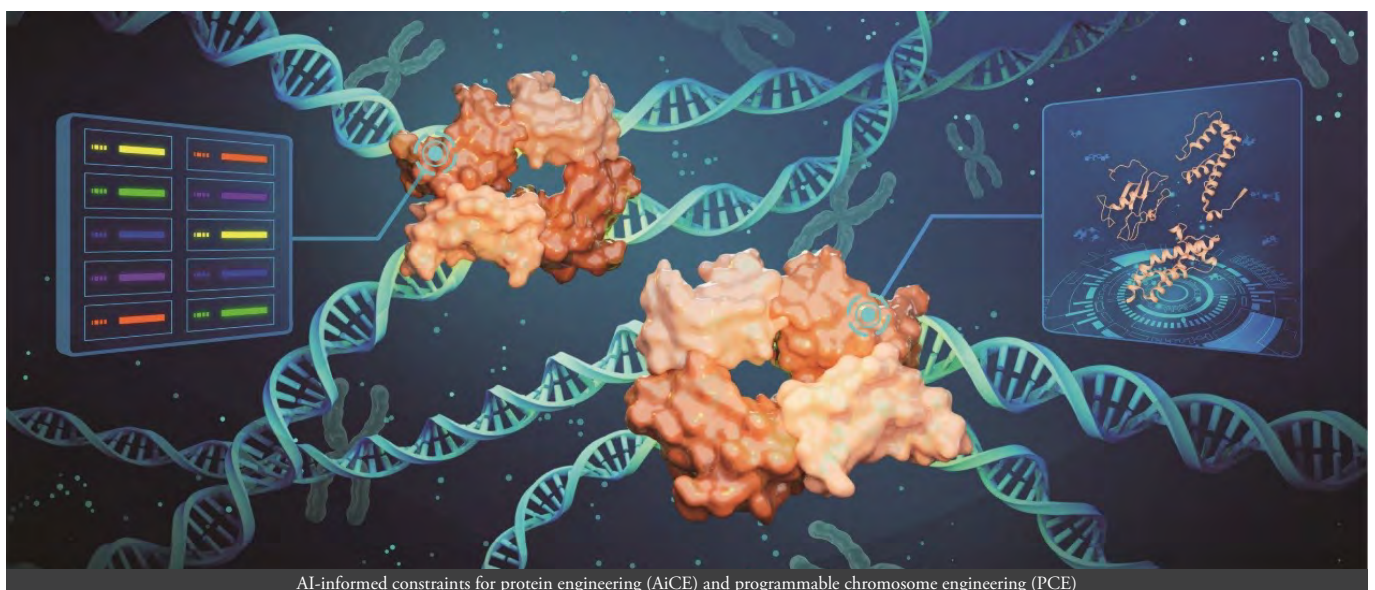
Protein engineering alters amino acid sequences to modify protein structure and function, optimizing protein functions far faster than natural evolution. Gao Caixia's team developed AI-informed constraints for protein engineering (AiCE), an approach that facilitates efficient protein evolution using generic protein inverse folding models, reducing reliance on human heuristics and task-specific models. Compared to traditional methods, it excels in efficiency, scalability and universality. It supplements or replaces wet-lab experiments via computational simulation with minimal load, making AI more accessible to biologists. AiCE elevates AI-based protein evolution to an entirely new level.

🔦 *Advancing protein evolution with inverse folding models integrating structural and evolutionary constraints, Cell. DOI: 10.1016/j.cell.2025.06.014*

### Programmable Chromosome Engineering

Genome editing, a revolutionary life science breakthrough, supports basic research and application development. However, large DNA fragment editing is a major challenge, with precise manipulation of vast base pairs a core field bottleneck. Gao Caixia's team developed programmable chromosome engineering (PCE) and RePCE, programmable systems enabling scarless kilobase-to-megabase DNA manipulations in plants and human cells, including inversions, replacements, deletions, translocations. These tools offer a robust framework for programmable, efficient, scarless large DNA manipulation across species, with great breeding and gene therapy application potential.

🔦 *Iterative recombinase technologies for efficient and precise genome engineering across kilobase to megabase scales, Cell. DOI: 10.1016/j.cell.2025.07.011*

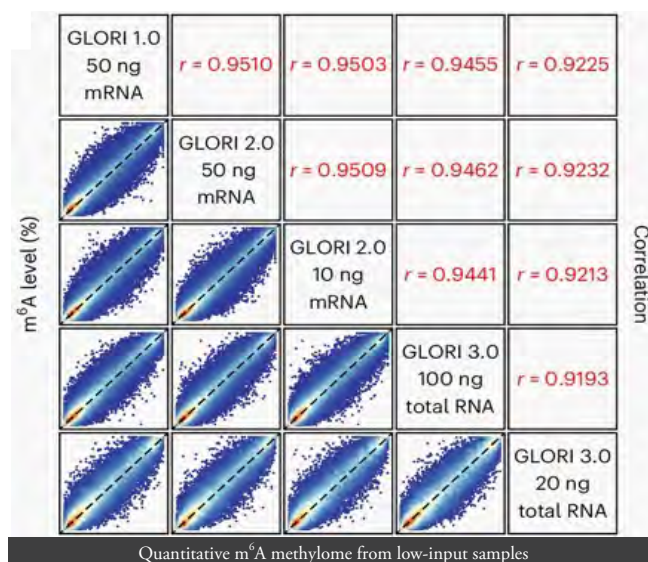


## Development of Sequencing, Probe, and Cloning Technologies

### Absolute Quantification of m<sup>6</sup>A Methylome from Low-input Samples

GLORI is a powerful tool for absolute quantification of N<sup>6</sup>-methyladenosine (m<sup>6</sup>A). However, GLORI 1.0 causes severe RNA degradation, which substantially limits its applicability to samples with low-input RNA amounts. Wang Xiu-Jie's team and collaborators updated GLORI approaches (GLORI 2.0 and 3.0) for quantitative m<sup>6</sup>A profiling in low-input samples. These improved methods significantly enhance the technical performance of GLORI, reduce the required RNA input, enable detection of m<sup>6</sup>A sites on low-abundance mRNAs, and allow accurate locus-specific m<sup>6</sup>A detection, thereby expanding the utility for absolute m<sup>6</sup>A quantification in epitranscriptomic studies.

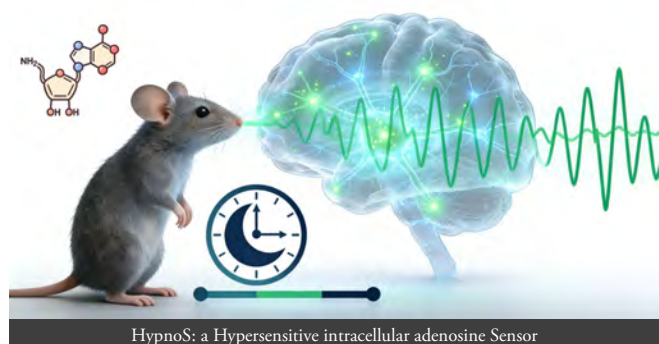
☀ *Mild and ultrafast GLORI enables absolute quantification of m<sup>6</sup>A methylome from low-input samples, Nature Methods. DOI: 10.1038/s41592-025-02680-9*



### Development and Application of Metabolite Fluorescent Probes *in vivo*

Adenosine is a vital energy metabolite that regulates sleep, brain activity, and cellular communication, but its rapid, millisecond-scale fluctuations have long evaded detection. Traditional methods cannot capture its real-time dynamics or cellular origins, leaving fundamental questions unanswered. Wu Zhaofa's team and collaborators have now developed HypnoS, the first genetically-encoded fluorescent probe capable of tracking intracellular adenosine in living animals. By combining this tool with EEG/EMG monitoring, the researchers uncovered how adenosine fluctuates in a cell type-specific manner during sleep-wake cycles and seizures, revealing its precise regulatory patterns. This study fills a critical technological gap and offers a powerful new lens for studying adenosine's roles in health and disease.

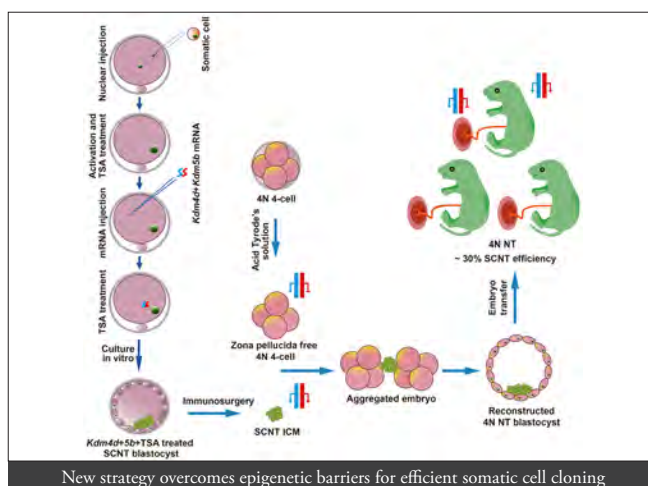
☀ *A high-performance fluorescent sensor spatiotemporally reveals cell-type specific regulation of intracellular adenosine in vivo, Nature Communications. DOI: 10.1038/s41467-025-59530-7*



### New Technology Overcomes Epigenetic Barriers to Achieve Highly Efficient Somatic Cell Cloning

The breeding of high-value livestock and creation of animal disease models require production of genetically identical individuals. While somatic cell cloning can yield these identical individuals, low efficiency has severely limited the application of this technology. Lu Falong's team and their collaborators have developed a highly efficient combined technical strategy that simultaneously overcomes both the pre- and post-implantation epigenetic barriers during cloned embryonic development. This breakthrough achieves a new record of 30% for somatic cell cloning efficiency in mice, providing a novel, cost-effective strategy for efficient mammalian reproduction via somatic cell cloning.

☀ *Efficient somatic cell nuclear transfer by overcoming both pre- and post-implantation epigenetic barriers, Advanced Science. DOI: 10.1002/adv.202504669*



## Approved Varieties

**ZhongkeFa 55** A conventional japonica rice variety. Moderately resistant to rice blast. In regional trials, the average yield was 611.7 kg per *mu*, an 8.3% increase over the control; in production trials, the average yield was 585.7 kg per *mu*, a 7.2% increase over the control.

**ZhongkeFa Early Rice 2** A conventional japonica rice variety. Moderately susceptible to rice blast, susceptible to bacterial leaf blight and white-backed planthoppers. In regional trials, the average yield was 532.9 kg per *mu*, a 4.0% increase over the control; in production trials, the average yield was 562.2 kg per *mu*, a 4.6% increase over the control.

**ZhongkeYou 1** A rapeseed variety suitable for edible oil production, with an oil content of up to 54.32%. It shows low resistance to Sclerotinia stem rot but high resistance to viral diseases, as well as strong resistance to lodging, cold and pod cracking. The average yield was 163.2 kg per *mu* in the first growing cycle and 157.8 kg per *mu* in the second.

**Jiayou Zhongke 211, 221, 215, 225, 2012, 216, 227** A series of japonica hybrid rice varieties with moderate susceptibility to rice blast and stripe virus disease. In regional trials, the average yield was 688-744.1 kg per *mu*, a 10.1%-19.1% increase over the control; in production trials, the average yield was 712.8-754.8 kg per *mu*, a 16.5%-18.4% increase over the control.

## Research Application

IGDB is committed to developing core agricultural technologies, translating scientific research into practical applications, and establishing a collaborative platform that involves the government, enterprises, and institute. In 2025, we have facilitated the commercialization of ten new saline-alkali tolerant varieties, including wheat and rapeseed. We have also explored an innovative forage-livestock integration model in several regions of China. Under this model, the daily feeding costs for beef cattle have been reduced by 1 yuan per day, providing significant economic benefits and improving the efficiency of the production.



# External Recognition

## Two Research Achievements Featured Among "2025 China's Top 10 Life Sciences Advances"<sup>①</sup>

### **Epigenetic Variation Drives Plant Stress Adaptation**

Understanding how species adapt to environmental changes is fundamental to the life sciences. Cao Xiaofeng's team has discovered stable variations in DNA methylation in specific regions of the rice genome under continuous cold stress across generations. This study provides critical molecular evidence for the ongoing 200-year-old debate on the inheritance of acquired characteristics and expands the framework of modern evolutionary theory. It also offers a new approach to achieving sustainable agricultural development in the context of global climate change.

### **AI-Driven Protein Engineering**

The ability to rewrite the genome code using genetic manipulation tools is critical for genetic disease therapy, crop development and the creation of synthetic life. Gao Caixia's team has created AiCE, a novel AI-based protein engineering method, and has developed a PCE system that can achieve precise, large-scale seamless editing at the chromosome level in plants and animals for the first time. This achievement represents a significant paradigm shift in genetic engineering technologies. *Cell* described the achievement as "deeply integrating deep learning applications into biological problems".

## Two Research Achievements Featured Among "*Cell* line: 2014-2024"<sup>②</sup>

### **De Novo Domestication of Rice**

Rapid global population growth, climate warming and frequent extreme weather events pose severe challenges to food security, making improving crop yields an urgent priority. Li Jiayang's team has proposed a strategy for the rapid de novo domestication of highly productive, adaptable allotetraploid wild rice varieties. This offers a new solution to the global food crisis and opens up a new approach to crop breeding. This study was published in *Cell* in February 2021.

### **Functional Study of Resistosomes**

Crop pests and diseases limit the potential for high-yield, high-quality agriculture. Plant disease-resistant proteins detect pathogens and activate defenses, but how they do this has long been a key puzzle. Teams led by Zhou Jianmin, Chen Yuhang, and He Kangmin, in collaboration with others, used interdisciplinary approaches to clarify the biochemical function of the ZAR1 resistosome and reveal the molecular mechanism of immune activation. This work will inform the development of long-lasting, broad-spectrum disease-resistant proteins to promote sustainable green agriculture. The study was published in *Cell* on May 12, 2021.

## Two Research Achievements Featured Among "2025 China's Major New Technologies, New Products, and New Applications in Agriculture"<sup>③</sup>

### ***Sesbania* Planting for Saline-Alkali Land Bioremediation**

A team led by Prof. Cao Xiaofeng and its partners have developed core technologies for the bioremediation of saline-alkali land using *Sesbania*. By integrating elite varieties and the best cultivation practices, they have pioneered a new "matching crops to land" paradigm.

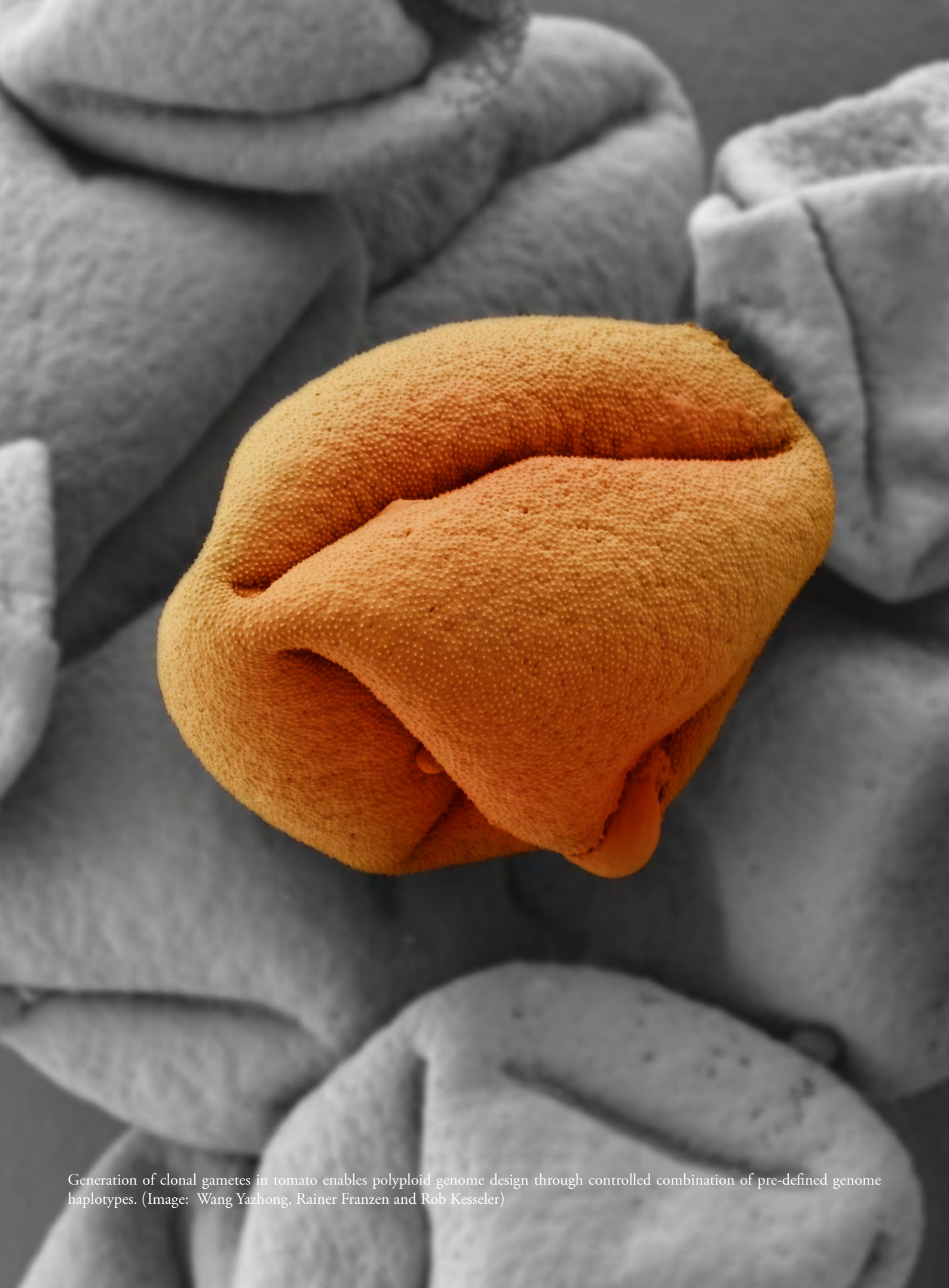
### **The Salt-Tolerant Soybean Variety Kedou 35**

Prof. Tian Zhixi's team developed Kedou 35. It combines outstanding traits such as high yield, salt tolerance, drought tolerance, tolerance to waterlogging, and disease resistance. In Dongying, Shandong province, it has achieved a maximum yield of over 300 kilograms per *mu* on coastal saline-alkali land with a salinity level of between 3‰ to 5‰.

① The Top 10 Advances in Chinese Life Sciences: An annual selection of ten representative major achievements, organized by the Life Sciences Society Alliance of China Association for Science and Technology.

② *Cell* Line: 2014–2024: A special issue launched by *Cell* to mark the journal's 10-year anniversary, highlighting outstanding major scientific achievements published in the journal from 2014 to 2024.

③ China Major New Agricultural Technologies, Products, and Scenarios: Organized by the Chinese Society of Agricultural Sciences acting on behalf of the Department of Science and Technology, Ministry of Agriculture and Rural Affairs.



Generation of clonal gametes in tomato enables polyploid genome design through controlled combination of pre-defined genome haplotypes. (Image: Wang Yazhong, Rainer Franzen and Rob Kessler)

# Cooperation and Exchange

Guided by a philosophy of openness and innovation, IGDB has established an international cooperation network and a domestic collaborative innovation system spanning the entire chain from basic research to technology development and commercialization in plant science and modern agriculture.

## International Cooperation

IGDB maintains close cooperation and academic exchanges with renowned universities and research institutions around the world. In collaboration with the John Innes Centre and The Sainsbury Laboratory in the UK, we have established the CAS-JIC-TSL Centre of Excellence for Plant and Microbial Science (CEPAMS). We have also established the China-Africa Sub-center for Modern Agricultural Research and Demonstration with Jomo Kenyatta University of Agriculture and Technology in Kenya. These collaborations foster cross-continental innovation in plant and agricultural sciences. Memoranda of Understanding have been signed with leading research bodies in Germany, Japan, the United States and Azerbaijan, focusing on key areas including personnel exchanges, joint research initiatives and postgraduate training. This further expands our global collaborative network. IGDB also serves as a governing member of the China-LAC Innovation center for Sustainable Food Systems.

In 2025, IGDB took another step forward in terms of international cooperation by co-founding the China-Spain Centre of Excellence for Plant-Environment Interactions (CEPEI) alongside the Center for Plant Biotechnology and Genomics in Madrid and the Center for Excellence in Molecular Plant Sciences of the Chinese Academy of Sciences (CAS). Focusing on plant stress responses, environmental adaptation and nutrition, CEPEI aims to enhance crop yield and quality through joint research, personnel exchanges, and the sharing of technology platforms and high-level academic activities. We have also signed a cooperation memorandum with Cuba's Center for Neuroscience, paving the way for collaborative efforts in drug screening for Alzheimer's disease and bilateral exchanges in cutting-edge brain science research.



## Domestic Cooperation



By 2025, IGDB had established extensive partnerships with municipal governments, universities, and enterprises, promoting collaboration in areas such as scientific research, project implementation, talent development, and technology transfer. We proactively joined newly formed innovation consortia, establishing an efficient collaboration mechanism characterized by seamless coordination and substantial synergy. We deepened our cooperation with the Henan Institute of Science and Technology in the areas of agricultural innovation, smart breeding, and artificial intelligence, in order to support the development of the "Central Plains Grain Valley" initiative and to foster new productive forces in regional agriculture. In collaboration with Shandong Saline-Alkali Land Modern Agriculture Co., Ltd., we established the Yellow River Delta Saline-Alkali Land Tomato Innovation Research Institute, focusing on researching and developing salt-tolerant crop varieties. In collaboration with Three Gorges University and the People's Government of Zhijiang City, we initiated a project focusing on high-protein forage *Sesbania* and established a government-industry-academia-research-application innovation platform to promote rural revitalisation. In partnership with Alibaba Cloud, we launched the "Shennong Plan" for intelligent breeding, developing a "digital

brain" for plant breeding by integrating artificial intelligence and cloud computing. Furthermore, we have strengthened our cooperation with Xianghu Laboratory, the Hubei Academy of Agricultural Sciences, and other institutions in the areas of seed innovation, bio-breeding, and eco-efficient agriculture. These efforts have continuously enhanced our capacity to serve national strategies and promote high-quality regional development.



## Visits

In 2025, IGDB hosted a number of visits, exchanges and research activities involving foreign delegations, government departments, businesses and universities. Overseas visitors included delegations from Chile's Ministry of Agriculture, the International Maize and Wheat Improvement Center (CIMMYT) and France's National Research Institute for Agriculture, Food and Environment (INRAE). In-depth discussions were held on personnel exchanges, research cooperation, technology platforms, academic visits and international collaboration, with the aim of advancing joint research and nurturing young talent. Officials from the Ministry of Agriculture and Rural Affairs inspected intelligent breeding applications and conducted follow-up research on the proposals from the Chinese People's Political Consultative Conference (CPPCC). The Vice Mayor of Chifeng City in Inner Mongolia discussed the joint development of research bases, the implementation of major national science projects, the application of microbial additives, and the development of green, clean and circular animal husbandry with us. The West Lake Management District in Changde City discussed the establishment of a forage industry innovation pilot zone. We also held a seminar on AI-powered smart agriculture with the experts from Alibaba Cloud. We also welcomed the teachers and students from the Li Zhensheng Experimental Class at the School of Future Technology at Shandong Agricultural University.



## Academic Activities

In 2025, IGDB organized a variety of academic events, both online and offline, to foster a vibrant academic atmosphere. These included the "Symposium on Digital Twins and Crop Breeding Design", the "Symposium on Crop Phenomics and Advanced Breeding Technologies", and the "IGDB Youth Innovation Academic Report". IGDB also hosted the 7th Frontier Symposium on Genome Editing and the 2025 Annual Academic Conference of the Hydrographic Geography. Research units regularly organized summer and winter forums to encourage internal academic exchange among young scholars. More than 60 academic lectures were held, leveraging high-level platforms including the CEPAMS Seminar, the Forum on Plant Genomics and the New Green Revolution, the Summit Forum on Development-Genetics-Diseases, the Future Science Salon, the Forum on Omics and Systems Biology, the First-Author Lecture, the National Science Advanced Agriculture Forum, and the Lecture on the Spirit of Scientists. Renowned scientists and journal editors were invited to speak at these lectures. A total of 38 technical training sessions were conducted to enhance experimental skills and data analysis capabilities. The monthly *JGG Mendel* Online Forum attracted an average of 4,500 participants per session, facilitating extensive scientific communication across the country.





*SbSLT1/2* knockout leads to reduced *Striga* germination, potentially improving yields in regions with impacted crop production. (Provided by Xie Qi's team)

# Institute of Genetics and Developmental Biology Chinese Academy of Sciences

## Staff

### Staff Size

Staff

 **683**

Senior Professionals

 **95**

Associate Senior Professionals

 **159**

Postdoctoral Fellow

 **133**

### Talent Award

CAS Academicians

 **3**

Leading Talents of the  
National Talent Program

 **8**

NSFC Young Scientists Fund  
(Category A) (Category B)

 **27**

 **16**

National Talent  
Recruitment Program

 **23**

CAS Talent  
Recruitment Program

 **48**

### 2025 Talent Award

National & CAS Talent  
Recruitment Program

 **5**

NSFC Young Scientists Fund  
(Category A) (Category B)

 **4**

 **2**

NSFC Youth Project

 **12**

National Support Program  
for Young Top-notch Talents

 **1**

National Postdoctoral  
Fellowship Program

 **8**

NSFC Postdoctoral Science  
Foundation General Program

 **6**

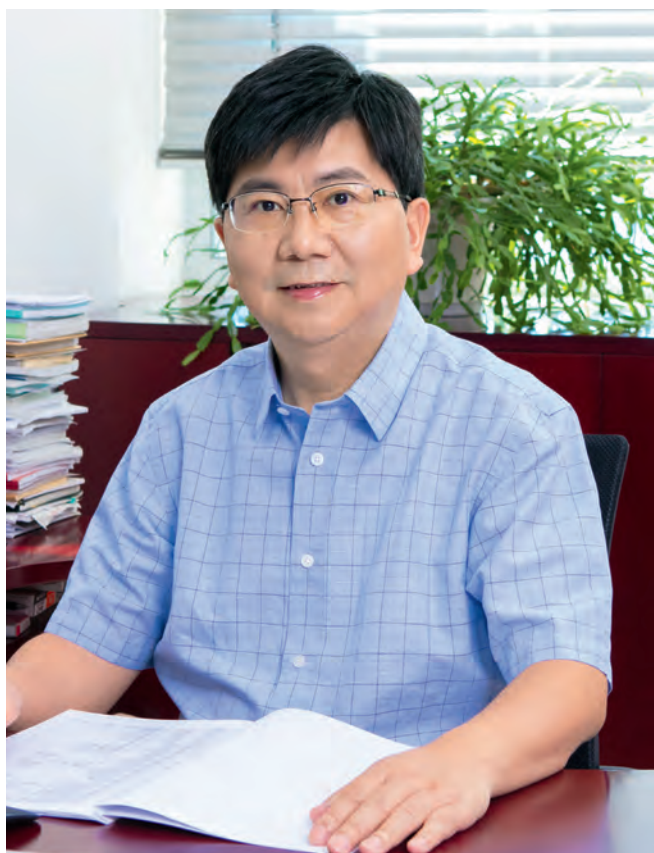
CAS Special Research  
Assistant Program

 **5**

### 2025 Team Development

- A full-chain talent development system was established, along with a Development Strategy Committee, an International Advisory Committee, and a Talent Working Group.
- Three core teams were piloted: Forage Grass Breeding, Nutrient Use Efficiency and Plant Immunity. A pest and disease green control team was introduced, and a team for human brain developmental genetics is in preparation.
- Capacity building for management cadres was strengthened via training in policies, professional skills, and confidentiality. Four cadres were assigned to temporary posts in central ministries, competent departments, and remote mountainous areas. Four management backbones were selected for political inspections.

## Awards and Honors



### Fu Xiangdong Elected as Academician of the Chinese Academy of Sciences

On 21 November 2025, Prof. Fu Xiangdong was elected as a member of the Chinese Academy of Sciences. His research focuses on the hormonal regulation of plant growth, development, and adaptation to stress. He has achieved notable breakthroughs in gibberellin signalling, the carbon-nitrogen balance, and the molecular basis of breeding high-yielding, nitrogen-efficient rice varieties. He has cloned genes that simultaneously improve rice yield, quality and nitrogen use efficiency, and has established a regulatory network for synergistic crop improvement. His discoveries have been widely adopted in breeding programs, resulting in over 150 new rice varieties being cultivated across an area of more than 100 million *mu*. His work has been recognised multiple times as a top national scientific advance. He is a highly cited scientist and a New Cornerstone Investigator, and has received numerous honors, including the State Natural Science Award and the National Innovation Pioneer Award. He is Vice President of the Crop Science Society of China and sits on the editorial boards of several international journals.

### Gao Caixia Elected as EMBO Foreign Member

On 1 July 2025, Gao Caixia was elected as an Associate Member of the European Molecular Biology Organization (EMBO). She has long been committed to innovating plant genome editing technology and has made significant contributions to the development of precise genome editing tools, crop genome editing breeding methods, and germplasm innovation. Her work has received widespread recognition and has been featured in MIT Technology Review's Top 10 Breakthrough Technologies in 2016, China's Top 10 Scientific Advances in 2023 and *Nature's* "Seven Technologies to Watch in 2024". She has also been the subject of exclusive interviews in *Science* and *Nature*. She has been a Clarivate Highly Cited Researcher for seven years and a New Cornerstone Investigator since 2023. She has won the National Innovation Pioneer Award and the Tan Jiazhen Life Science Innovation Award. She sits on the editorial boards of *Science* and *Cell* and is Director of the Genome Editing Branch of the Genetics Society of China.



## Twelve Scholars Named "Clarivate Highly Cited Researchers"<sup>①</sup>

Twelve scientists in IGDB were named "Clarivate Highly Cited Researchers" in 2025. They are: Chen Kunling, Chu Jinfang, Fu Xiangdong, Gao Caixia, Li Jiayang, Li Yunhai, Meng Xiangbing, Tian Zhixi, Yu Hong, Zhou Jianmin and Zong Yuan. Notably, Gao Caixia was recognized in two fields: Plant and Animal Science and Biology and Biochemistry.



## The Saline-Alkali Land Improvement Innovation Team Awarded "Keyuan Master Artisan" of CAS<sup>②</sup>

In April 2025, the saline-alkali land improvement innovation team, led by Prof. Cao Xiaofeng, received the 6th "Keyuan Master Artisan" award from the Chinese Academy of Sciences. The team develops key technologies for salt-tolerant forage breeding and the biological improvement of saline-alkali land, thereby supporting national food security and alleviating shortages of forage. They have established an integrated system of biological improvement, ecological restoration and resource utilization. They have applied a pioneering *Sesbania-Leymus* mixed sowing technique to over 10,000 *mu* of land, effectively restoring salinised grasslands in northern China. They also provide policy recommendations for establishing a green improvement system to promote the green transformation of agriculture and increase grain production.



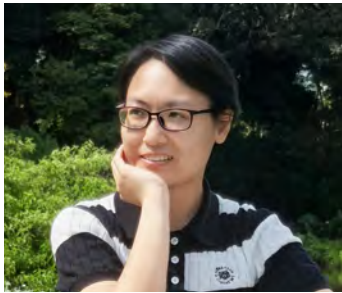
## Cao Xiaofeng Awarded "CAS Advanced Individual"

In January 2026, Academician Cao Xiaofeng was awarded "Advanced Individual" by the Chinese Academy of Sciences for her work in 2025. A leading researcher in plant epigenetics, she has dedicated her career to addressing the global challenge of improving saline-alkali land to ensure national food security. Her team developed new salt-tolerant varieties of *Sesbania cannabina*, as well as key bio-improvement technology recognized as a China's Major New Agricultural Technology in 2025. Having been applied to over 50,000 *mu* in Northeast China and Xinjiang, her work has provided significant support for ecological restoration and food security.



- ① The Highly Cited Researchers list, released by Clarivate, aims to recognize the world's leading researchers who have made a significant impact in their field of research.
- ② The "Keyuan Master Artisan" Award is established by the Trade Union of the Chinese Academy of Sciences (CAS), aims to promote the spirit of model workers, labourers, craftsmen and scientists, and to recognize those who demonstrate exceptional scientific and technological innovation and top-level professional skills in their field.
- ③ The "Advanced Individual" Award is co-awarded by the Ministry of Human Resources and Social Security and the CAS every five years in honor of individuals who have contributed to the development of CAS and China's scientific and technological innovation.

## New Faculties



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**Deng Xian** received her Ph.D. from IGDB, CAS, in 2012. She has been working at the institute since 2012, was appointed as a Youth Researcher in 2022, and was appointed as a Research Fellow at the Breeding Frontier Technology Laboratory in 2025. In 2022, she was selected as an Outstanding Member of the Youth Innovation Promotion Association of the Chinese Academy of Sciences. Her research focuses on the epigenetic regulation mechanisms of higher plants, as well as the genetic and epigenetic mechanisms underlying stress tolerance and environmental adaptation of forage legumes.

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**Gao He** obtained his Ph.D. degree in Agronomy from Nanjing Agricultural University in 2012. He then moved to Germany and became a postdoctoral researcher at the Max Planck Institute for Plant Breeding. He joined State Key Laboratory of Seed Innovation, IGDB, since 2025. He studies the mechanisms that control plant reproductive development in response to seasonal signals in model plants. He focuses on understanding how the "florigen" and "anti-florigen" proteins transport, how they are recruited and function to the "florigen activation" and "florigen repression" complexes to regulate floral transition and inflorescence development.

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**Li Chuan-Yun** obtained his Ph.D. from Peking University in 2009 and worked as a postdoctoral researcher until 2010. He served as a Principal Investigator at Peking University from 2011 to 2025 and joined the Center for Zero-to-One Innovation in 2025. His research uses rhesus macaques to study human-specific brain development and related diseases. His team identified human-specific young genes and regulatory events via an iterative "experiment-computation-experiment" optimization loop, and he currently explores their links to tumor development and translational potential.

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**Liu Yucheng** earned his Ph.D. from IGDB in 2021. He received the National Science Fund for Distinguished Young Scholars in 2024 and was promoted to a Professor of the State Key Laboratory of Seed Innovation in 2025. He focused on soybean germplasm dissection, big data platform construction and soybean de novo domestication. By comparative genomics, pan-genomics and population genetics, he attempts to understand the principle of soybean/crop domestication and evolution, mine node gene or pathway for crop genetic improvement, and explore the de novo domestication and new design breeding system for soybean.

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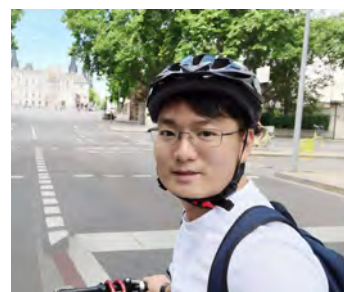
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**Song Xianwei** earned his Ph.D. from IGDB in 2011. He has been working at the institute ever since and was appointed as a Principal Investigator at the Laboratory of Advanced Breeding Technologies in 2025. His research focuses on plant epigenetic regulation and saline-alkali land improvement, including the mechanisms of DNA methylation and small RNAs in shaping important traits, breeding of stress-tolerant forage, as well as the development and mechanistic study of biological improvement technologies for saline-alkali land.

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**Wang Yazhong** is a Principal Investigator at the Laboratory of Advanced Breeding Technologies. He earned his PhD from China Agricultural University (2019) for maize meiosis research. As a postdoc at Max Planck Institute for Plant Breeding Research (2019-2024), he engineered clonal gametes to create tetraploid tomatoes with four-haplotype genomes, a breakthrough featured in *Nature Genetics*. His lab now studies sexual/asexual reproduction and precise polyploid genome design in crops, focusing on meiosis, apomixis, polyploid breeding, and haploid induction.



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**Wang Bing** received a Ph.D. from IGDB in 2011 and has worked at the institute ever since. She was appointed as a Young Investigator in 2021 and as a Principal Investigator of the State Key Laboratory of Seed Innovation in 2025. She received the National Science Fund for Distinguished Young Scholars in 2015 and Excellent Young Scholars in 2021, the National Innovation Award Medal in 2023, and the Rising Stars in Plant Sciences in 2025. She focuses on deciphering how the phytohormone strigolactone regulates plant architecture and environmental adaptability, enabling the precise improvement of high-yield and disease-resistant traits in crops.



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**Wu Kun** is a Professor at the State Key Laboratory of Seed Innovation. He received his Ph.D. in Biology from the University of Science and Technology of China in 2017. He has worked as Research Associate, Postdoctoral Fellow and Junior Investigator at IGDB, and was promoted to Professor in 2025. Dr. Wu's research focuses on dissecting the regulatory networks underlying rice nitrogen use efficiency and molecular design breeding. His work aims to identify key genes and mechanisms underlying grain yield, quality, and nitrogen use efficiency, mine elite allelic variations, and develop high-yielding, high-quality, nitrogen-use-efficient rice varieties for sustainable agricultural development.



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**Yu Zhenyu** received her Ph.D. in 2012 from the Institute of Plant Physiology and Ecology, CAS. She worked at the Institute of Biophysics, CAS from 2012 to 2025, was selected for the CAS Youth Innovation Promotion Association in 2017, and became Professor in 2023. In July 2025, she joined the Laboratory of Advanced Breeding Technologies, IGDB. Her research focuses on plant chromatin architecture, particularly the epigenetic regulation of centromeric chromatin during polyploid formation, as well as chromatin-mediated gene expression and stress responses. She integrates structural biology with deep learning-based protein design to advance mechanism-driven crop improvement.



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**Zhao Xin** earned her Ph.D. degree from the Institute of Geographic Sciences and Natural Resources Research in 2017. From 2017 to 2025, she conducted research as a Postdoctoral Researcher and Research Associate at the National Institute for Environmental Studies (NIES), Japan. In June 2025, she joined the Center for Agricultural Resources Research. Her research focuses on crop phenology and agricultural greenhouse gas emissions, via remote sensing detection and model-based emission estimation with field observations.



# Education

IGDB is committed to the mission of "fostering virtue and talent" and cultivating an environment for top-tier innovators. IGDB offers eight PhD programmes, including Genetics, Developmental Biology, Neurobiology, Cell Biology, Bioinformatics, Biophysics, Crop Science, and Plant Nutrition, as well as a Master's programme in Biological and Pharmaceutical Engineering, featuring a comprehensive academic layout and distinct interdisciplinary characteristics.



**103** Newly Enrolled PhD Students



**51** Newly Enrolled Master's Students



**562** Current PhD Students



**154** Current Master's Students

By December 2025, IGDB has 716 enrolled graduate students, including 562 PhD candidates and 154 Master's candidates. There are 70 Principal Investigators, with 68 qualified for PhD supervision. In 2025, students received nearly 190 awards, including one CAS President's Special Award, 24 National Scholarships, and 6 Zhensheng Scholarships. Student recruitment quality continued to trend upward, with the enrollment of 103 PhD and 51 Master's candidates.

By optimizing enrollment quota allocation, resources were strategically prioritized for major research missions and key laboratories. Diversified online and offline recruitment efforts propelled both applicant numbers and the enrollment of recommended students to record highs. In 2025, IGDB

conferred 124 degrees, including 111 PhDs and 13 Master's. The overall employment rate reached 97%, with approximately 75% of graduates pursuing careers in scientific research, 6% continuing their studies at world-renowned institutions like the University of Cambridge, and 5% entering public service, demonstrating the success of our multifaceted career development pathways.

IGDB prioritised broadening students' international vision by selecting 12 outstanding graduate students to attend the 19th International Student Workshop in Nara, Japan—a prestigious event co-organized by IGDB, NAIST, and UC Davis. Students engaged in cutting-edge academic and cross-cultural exchanges through academic presentations and poster



sessions. This 19-year-old series activities have become a high-level platform for young scholars. The system for ideological and political education, as well as talent cultivation systems advanced in tandem. Over 20 staff training sessions and "Spirit of Scientists" events were held. Regular "Leadership-Student Meetings" strengthened value guidance and care. More than 50 student academic and cultural activities promoted all-round development. Supervisor training, experience-sharing, and thematic seminars were held over ten times to continuously improve mentoring and educational capabilities.

Steady progress has been made in science and education integration. The UCAS College of Advanced Agricultural Sciences, led by IGDB, welcomed 350 enrolled students. Focusing on "fostering virtue and talent", the college has integrated classroom learning with field practice. Students participated in rice transplanting and harvesting, gaining firsthand experience of agriculture at "Doctoral Farms". The "Chunfen Project" outreach team delivered over 100 science lectures to the public, and the *UCAS Agricultural Newsletter* served as an open platform. The stage play *Tilling Dreams in Green Fields*, depicting Academician Li Zhensheng's dedication, won first prize at the "Flowers of May" Art Festival. By November 2025, the Agricultural Science discipline had risen to the 5th place nationwide, solidifying its position in the global top 0.01%.



Class of 2025 Graduation Group Photo

# Journals



## Journal of Genetics and Genomics

*Journal of Genetics and Genomics (JGG)*, founded in 1974 and formerly known as *Acta Genetica Sinica*, is sponsored by IGDB and Genetics Society of China. Currently, the Editor-in-Chief is Prof. Zuo Jianru. *JGG* aims to promote academic communications and foster scientific advancements via publishing peer-reviewed articles of novel and significant discoveries in a broad scope of life sciences. The 2024 JCR Impact Factor is 7.1, ranking Q1 in GENETICS & HEREDITY (Top 10%). In 2025, *JGG* published 153 articles, including 120 full-length and review articles. *JGG* has striven to increase its academic influence through, but not limited to, promoting articles and the latest scientific progress in WeChat, holding the "JGG Mendel Webinar", and organizing four special issues focusing on international cutting-edge research.

## Hereditas (Beijing)

*Hereditas (Beijing)* is sponsored by IGDB and the Genetics Society of China, and published in Chinese monthly by Science Press. Prof. Huang Xun has been the Editor-in-Chief by 2025. As a national academic journal and Chinese core journal, it is indexed in over 20 retrieval systems and databases, including PubMed/MEDLINE, Scopus, and Chemical Abstract (CA). The journal primarily publishes reviews and research articles in the fields of genetics, genomics, developmental biology, and related disciplines. In 2025, two special issues titled "Biological Evolution and Adaptation" and "Frontiers and Challenges in RNA Research" were published. Two new columns named "Tribute to Classic" and "Guideline" were successively set up. These initiatives help the journal to continue enhancing its academic and social impact.

## Chinese Journal of Eco-Agriculture

*Chinese Journal of Eco-Agriculture (CJEA)*, founded in 1993, is a monthly peer-reviewed academic journal sponsored by the Center for Agricultural Resources Research of IGDB, and is published by Science Press. It publishes in both Chinese and English. *CJEA* focuses on agroecosystems and their regulation, crop cultivation and physiological ecology, agricultural resources and the environment, as well as agricultural ecological economics and eco-agriculture. It is indexed in major databases including Peking University Core Journals, CSCD, CNKI, Scopus, and DOAJ. As a leading Chinese journal under the Excellence Action Plan, *CJEA* was awarded the title of "2025 China's Most Internationally Influential Academic Journal". Its core impact factor has ranked first in the discipline of comprehensive agriculture discipline for four consecutive years.

# Facilities



(Rendering)

## China Crop Phenomics Facility

The China Crop Phenomics Facility (hereafter referred to as the CCPF) is a major national science and technology infrastructure project, with the IGDB acting as the legal entity. The facility is located in Wuhan, Hubei Province, with a construction area of 104,000 square meters and a construction period of five years.

The engineering objective is to construct a crop phenomics research facility based on multi-modal imaging and intelligent big data analytics. The facility will enable intelligent and controllable regulation of environmental factors, including light, temperature, water, soil, disease, and pests. The facility will be capable of high-throughput phenotyping for over 20 important agronomic traits and will have the capacity

to support efficient association analysis between complex agronomic traits and genes.

The construction content of the CCPF includes the Genome Engineering System, Controlled Environment System, Automated Plant Phenotyping System, Multi-Omics Analysis System, Intelligent Data Analytics System and the 24/7 Control Platform. Supporting civil and utility facilities will also be built, including the main research laboratory building, auxiliary buildings, and field phenotyping cultivation areas.

Steady progress was made on the project in terms of planning, technological design, team organization and management in 2025. Construction is set to start in 2026.

# Facilities and Platforms

IGDB has established a Proteomics Core Facility, a Metabolomics Facility, a Plant Hormone Analysis Platform, a Lipidomics Platform, a Bio-Imaging Facility, a Cryo-Electron Microscopy Platform, a Phenomics Facility, and a Scientific Data Center. These facilities enable comprehensive testing and analysis in the fields of proteomics, metabolomics, plant hormones, lipidomics, imagingomics, phenomics, and genomics.

## Proteomics Core Facility

The Proteomics Core Facility is dedicated to the development of leading-edge proteomics technologies. It is equipped with comprehensive facilities, including high-resolution liquid chromatography-mass spectrometry (LC-MS) systems such as the Orbitrap Fusion™ Lumos™ Tribrid™, LTQ–Orbitrap Elite, and TripleTOF 5600, as well as sample processing auxiliary equipment. It enables high-throughput quantitative and qualitative proteomic analysis of plant and animal samples, as well as the analysis of post-translational modifications.

In 2025, the facility's efforts resulted in 13 publications in prestigious journals. Utilizing phosphoproteomics technology, the facility revealed a novel mechanism triggered by TGF-β1 and driven by dysfunctional bone marrow vascular endothelial cells, leading to poor hematopoietic recovery. By IP-MS, the composition of the NuRD complex in *Caenorhabditis elegans* under stress conditions and the regulatory mechanisms of its core components were analyzed. This technology also assisted SUG1 in screening several interacting transcription factors, uncovering its role in regulating seed size through GA, BR and growth signaling pathways.



## Metabolomics Facility

The Metabolomics Facility integrates various chromatography-mass spectrometry technologies, and supports the comprehensive qualitative and quantitative analyses of small-molecule metabolites in biological systems. Combined with advanced

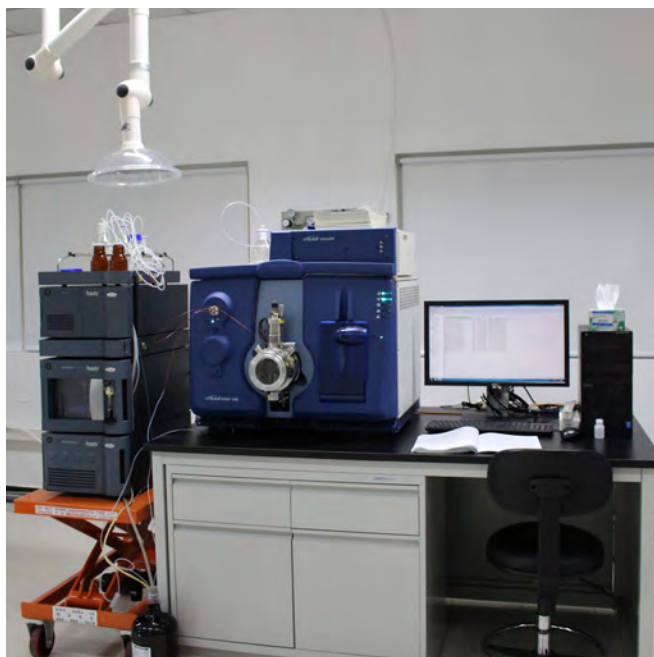
bioinformatics approaches, these technologies enable facilitate the identification of biomarker clusters, the discovery of previously unknown metabolic pathways, deeper insights into established pathways, and the elucidation of organismal metabolic network states. Equipped with high-resolution LC/MS-QTOF, GC/MS-QTOF, and sensitive LC/MS-QQQ, GC/MS instruments, the facility provides comprehensive metabolomics services, including untargeted (global) metabolomics profiling and targeted metabolomics analyses. To date, it has served over one hundred users from both within and outside IGDB, and has contributed as a co-author to over 60 high impact publications, including in *Nature Plants*, *Genome Biology* and *PNAS*.

In 2025 alone, the platform supported over 20 research groups, analyzed more than 2,000 samples, and published four independent and five collaborative papers. Customized UPLC/MS-QQQ methods enable accurate quantitation of metabolites in the Calvin cycle, TCA cycle, as well as more than 60 flavonoids, chiral compounds, and neurotransmitters. A GC/MS method for analyzing suberin in soybean roots was developed, providing reliable technical support for research projects.

## Plant Hormone Analysis Platform

The Plant Hormone Analysis Platform is the first domestic specialized research facility dedicated to plant hormone analysis. Equipped with comprehensive chromatography-mass spectrometry instruments and various analytical devices, it has long been committed to developing highly efficient and sensitive analytical methods for plant hormones. It has established highly efficient methods for simultaneously quantifying all known classes of plant hormones. This has delivered critical technical support for studies in plant physiology, crop breeding, and related fields, earning high recognition from botanists for its technical proficiency.

In terms of technical services, by 2025, the platform had provided high-level technical support to over 30 research institutions, analyzing nearly 3,000 samples, resulting in 17 co-authored papers in high-impact journals, including three



papers in *Cell*. In technological development, the platform has constructed efficient quantitative analysis methods for plant growth regulators such as tomentosin. Furthermore, it has established an accurate analytical technique for organic acid metabolites in the tricarboxylic acid cycle, offering reliable technical support for studies such as high-photosynthetic-efficiency crop design. Going forward, the platform will collaborate with biologists to develop new technical methods that align with national priorities and the institute's core research directions. It will continuously provide comprehensive technical support for plant scientists.

## Lipidomics Platform

The Lipidomics Platform was initially established in 2014 to meet the demands of disciplinary development. Currently, the platform mainly provides lipidomics analysis services for LC/GC-MS and ion chromatography, enabling the quantification of thousands of lipids. The services of the platform are used by many domestic research units, including IGDB, as well as many renowned universities and institutes, such as Peking University, Tsinghua University, and Fudan University. The subjects of lipidomics tests include humans, mice, *Drosophila melanogaster*, *Arabidopsis thaliana*, and many other species.

In terms of technical services, in 2025, high-level technical services were provided to over 20 scientific research institutions, with nearly 2,000 samples analyzed. A total of 15 papers were published in 2025. In terms of technological research and development, the potential functions of MASLD fibrosis lipid biomarkers and sulfatides have been revealed. Integrating multi-omics data with clinical phenomena revealed that sulfatides are functional lipids and their reduced levels may be involved in the pathogenesis of fibrosis in MASLD.

## Phenomics Facility

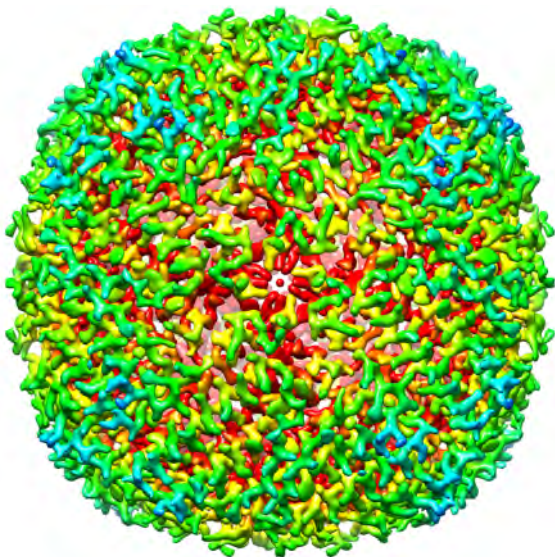
Established in 2021, the Phenomics Facility is an innovative research facility specializing in image analysis and AI technologies for comprehensive crop phenotyping. The Facility has successfully established diverse systems spanning UAV-based field platforms, mobile ground systems, autonomous wheeled sugarcane vehicles, mobile robotic arms for 3D phenotyping, dynamic seed germination vigor monitors, and hyperspectral imagers, which cover applications from the field to the laboratory and from the macroscopic to the microscopic scale. Independently developed algorithms and software solutions achieve efficient and precise phenotypic data analysis, serving as powerful tools for elucidating genotype-phenotype relationships.

In 2025, the Facility filed 7 patent applications, with 2 patents granted, registered 2 software copyrights, and published 10 papers. It engineered an autonomous sugarcane phenotyping vehicle capable of autonomous navigation, real-time video acquisition, and instantaneous stem counting. For soybean phenotyping, the Facility developed portable field image acquisition systems and smartphone-based video analysis tools. Additionally, the UAV flight planning and image-based phenotyping extraction algorithms enable full-season analysis of soybeans, wheat, and corn throughout their entire growth cycles. Moving forward, the Facility will continue advancing technological innovation, expanding our service portfolio, and enhancing domestic and international collaborations to contribute significantly to crop phenomics research and agricultural progress.



## Cryo-Electron Microscopy Platform

The Cryo-Electron Microscopy Platform was established in 2021, supported by the IGDB and the State Key Laboratory of Plant Cell and Chromosome Engineering (PCCE). It houses a 120 kV TEM (FEI Talos L120C), a 200 kV cryo-electron microscope (FEI Glacios) equipped with a Gatan K3 direct electron detector, and supporting sample-preparation instruments. The platform focuses on near-atomic structural



analysis of proteins and complexes to reveal molecular mechanisms, identify drug targets and advance crop molecular breeding. It provides cell ultrastructure imaging, negative staining, single-particle screening and data collection, as well as structural characterization of liquid samples.

In 2025, the Talos L120C and Glacios logged 1,350 and 3,126 operating hours, respectively. The platform has served nearly 20 research institutions and supported high-impact studies published in journals including *Science*, *Nature Materials*, *PNAS*, *hLife* and *PLoS Pathogens*, underpinning key projects and major scientific breakthroughs during the 14th Five-Year Plan period.

## Bio-Imaging Facility

Established in 2012, the Bio-Imaging Facility is equipped with three CT scanners, five advanced fluorescence microscopes, and a range of high-end biological imaging instruments. It enables microscopic imaging and observation at the tissue, cellular, organelle levels. In 2025, the facility provided data support for the publication of eight high-impact papers, achieved seven patent commercialization, and was granted six patents. The platform recorded a total of 7,943 service hours, serving more than 20 institutions, including over 35 research groups from the IGDB.

Key technical developments of the facility in 2025 include: (1) development of a Novel Temperature-Sensitive Probe; (2) development of a photodynamic immunotherapy approach, enabling efficient in situ tumor treatment; and (3) development of a Cascade Mask R-CNN-based deep learning model, enabling non-invasive, high-precision automatic identification of human round sperm cells.

## Scientific Data Center

Established in 2020, the Scientific Data Center is dedicated to the collection, storage and sharing of multi-omics data from research on plants, animals, humans and microorganisms. It has developed a sharing platform for data query and download, and provides professional support related to scientific data and bioinformatics. It also ensures interoperability with the Scientific Data Center of CAS, delivering 24/7 service with an annual uptime rate of  $\geq 99.9\%$ . It manages a high-performance computing cluster (HPC) with over 1,800 CPU cores, 11 GPUs and 5.0 PB of storage. To date, it has collected over 1,200 TB of multi-omics data, of which over 900 TB is shareable. It has served over 70 research groups and contributed to 31 publications. In addition, it has provided support for a number of major projects.

In 2025, the center made the following achievements: (1) It developed a BioAI online visualization tool integrating AlphaFold and DeepSeek, and deployed an institutional management knowledge base to facilitate the secure local application of AI. (2) The HPC ran for over 2.22 million hours, supporting 92 users from 47 groups. The center upgraded its infrastructure by incorporating new GPUs and fat nodes, and enhanced file backup systems to ensure 24-hour data recoverability, thereby maintaining a record of zero security incidents. (3) 328 TB of scientific data has been added to the database. The center fulfilled 65 data submission tasks, collected 4 million germplasm records and 10 million phenotypic entries, and established storage standards. (4) Twenty-two technical workshops were organized for over 400 participants. (5) One software copyright was granted. Additionally, three articles were published, including two co-authored ones.



## Plant Greenhouse

The Institute's greenhouse is divided into two sections: an eastern section and a western section. With a total floor area of 8,706 m<sup>2</sup>, it comprises 276 rooms. The eastern section covers 6,859 m<sup>2</sup> and the western section covers 1,847 m<sup>2</sup>. These sections provide an environment that simulates natural conditions for plant growth. They enable the year-round cultivation of various plants, including *Arabidopsis*, rice, wheat, corn, soybeans and tomatoes. The greenhouse houses a wheat rust identification platform featuring a robust system for infecting, subculturing and preserving stripe rust pathogens. This platform facilitates the inoculation and grading evaluation of wheat and its wild relatives at seedling and adult stages, as well as VIGS-treated plants.

In 2025, the greenhouse was used by over 700 researchers from more than 60 research groups to cultivate over 20 plant species.



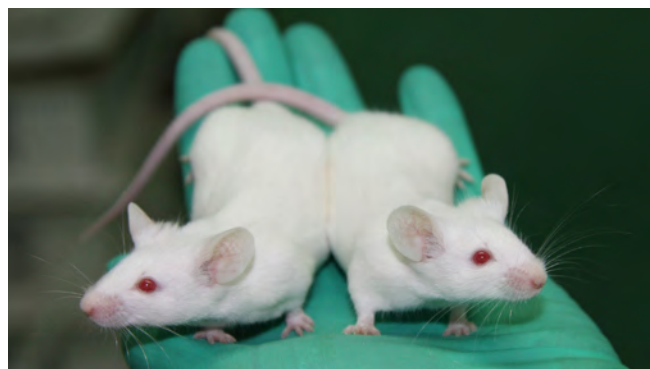
## Animal Facility

Animal Facility is a professional technical platform for animal feeding, resource conservation, and experimentation. Spanning 6,299 m<sup>2</sup>, it provides specialized services including breeding, behavioral testing, electrophysiology, antibody preparation, and genetic resource preservation. In February 2025, it successfully passed the on-site supervision assessment conducted by the CNAS expert panel and obtained a new Accreditation Decision. In June, it received the highest 5-star rating in the Laboratory Animal Welfare and Ethics Evaluation organized by the CALAS.

The West Building facility spans a total area of 3,865 m<sup>2</sup>, with a barrier facility of 1,230 m<sup>2</sup>. It has been granted a dual certification for the production and use of "Laboratory Animal Production License" and "Laboratory Animal Use License" for rats and mice. The 24 m<sup>2</sup> ABSL-2 laboratory has completed online registration and passed multiple biosafety special inspections. The East Building facility has a total area of 2,434 m<sup>2</sup> and approximately 800 m<sup>2</sup> of barrier facilities. It contains a barrier facility for rats, mice, and guinea pigs, a conventional

facility for rabbits and guinea pigs, and a breeding facility for aquatic animals such as zebrafish, medaka, and *Xenopus*. In July 2025, dual certificates of "Laboratory Animal Production License" and "Laboratory Animal Use License" were obtained for barrier environmental rats, mice, and guinea pigs, as well as a "Laboratory Animal Use License" for conventional environmental rabbits, guinea pigs, and experimental fish.

In 2025, Animal Facility served 33 internal research teams and over 80 external teams. Service offerings included housing 9,100 cages of rats and mice, as well as 1,500 tanks of experimental fish, 805 animals used for polyclonal antibody preparations, 7,920 hours of behavioral testing, and 1,583 hours of electrophysiology, rederived 46 mouse strains and cryopreserved 87 strains. It supported the publication of 18 academic research papers for the institute. Its staff were listed as authors on 5 papers, including 2 as co-first authors. It held 3 science popularization activities, receiving a total of 127 visitors. Through guided tours of standardized facilities, it promoted public understanding of experimental animals and life science.



# Breeding Bases

The breeding base is an indispensable and important support for the agricultural scientific research, IGDB has established breeding bases in various ecological regions, including Changping District of Beijing, Chifeng City of Inner Mongolia Autonomous Region, Dongying City of Shandong Province, Potianyang and Lingshui in Sanya City, Hainan Province. These bases provide research groups with full-process plant cultivation services and standardized field management, including land preparation, weeding, fertilization, irrigation, pest and disease control, and straw cleaning.

## Chifeng Base

Construction of the Chifeng Base began in 2025 with the support of the People's Government of Chifeng City and the Chifeng Academy of Agriculture and Animal Husbandry. It covers 440 *mu* of land designated for research. Its flat terrain and fertile soil make it ideal for cultivating crops such as corn, soybeans, spring wheat, coarse cereals and forage grasses. With an annual effective accumulated temperature of 3,000°C, the site provides ideal conditions for agricultural experimentation. The supporting facilities are well equipped with shared

accommodation, offices, and living spaces, providing strong support for research.

Taking into account the resources and development needs of the Chifeng district, the base will establish a long-term observation platform and conduct research into digital breeding, optimizing livestock and green agriculture, and improving saline-alkali land. The ultimate goal is to develop an AI-enabled intelligent breeding system that will drive technological innovation and applications.





## Yellow River Delta Saline-Alkali Land Agricultural Experimental Station

The Yellow River Delta Saline-Alkali Land Agricultural Experiment Station, established in 2018, is located in the Modern Agricultural Demonstration Zone of Huanghekou Town in the Kenli District of Dongying City in Shandong Province. The station features soil salinity ranging from low to high levels, which supports research into salt-tolerant crop breeding and the improvement of saline-alkali land. It also includes a transgenic rice trial isolation zone for transgenic rice research.

Spanning 1,000 *mu*, the station comprises a comprehensive research building, greenhouses, a high-throughput plant phenotyping platform, a drying ground, an agricultural machinery warehouse and an exhibition hall. The 2,000 m<sup>2</sup> solar greenhouses are fitted with meteorological instrument to

support generation-adding and winter crop experiments. The 1,600 m<sup>2</sup> phenotyping platform is equipped with visible and hyperspectral cameras to enable automatic plant phenotyping and the accurate evaluation of salt tolerance. The station can accommodate 40 researchers simultaneously.

In 2025, 18 research teams conducted trials on major crops, including wheat, maize, sorghum, millet, rice, soybeans, rapeseed, *Sesbania cannabina* and *Elymus elongatus*. Additionally, nine research teams completed variety validation for key saline-alkali land projects.

Located adjacent to the Yellow River Estuary, the station is home to hundreds of migratory bird species, including swans and oriental cranes, in the surrounding wetlands.

## Hainan Base

The Hainan Base comprises two parts: the Lingshui Base and the Potianyang Base. The base supports the experimental cultivation of various crops, including rice, corn, sorghum, soybeans, cotton, wheat, *Sesbania cannabina* and foxtail

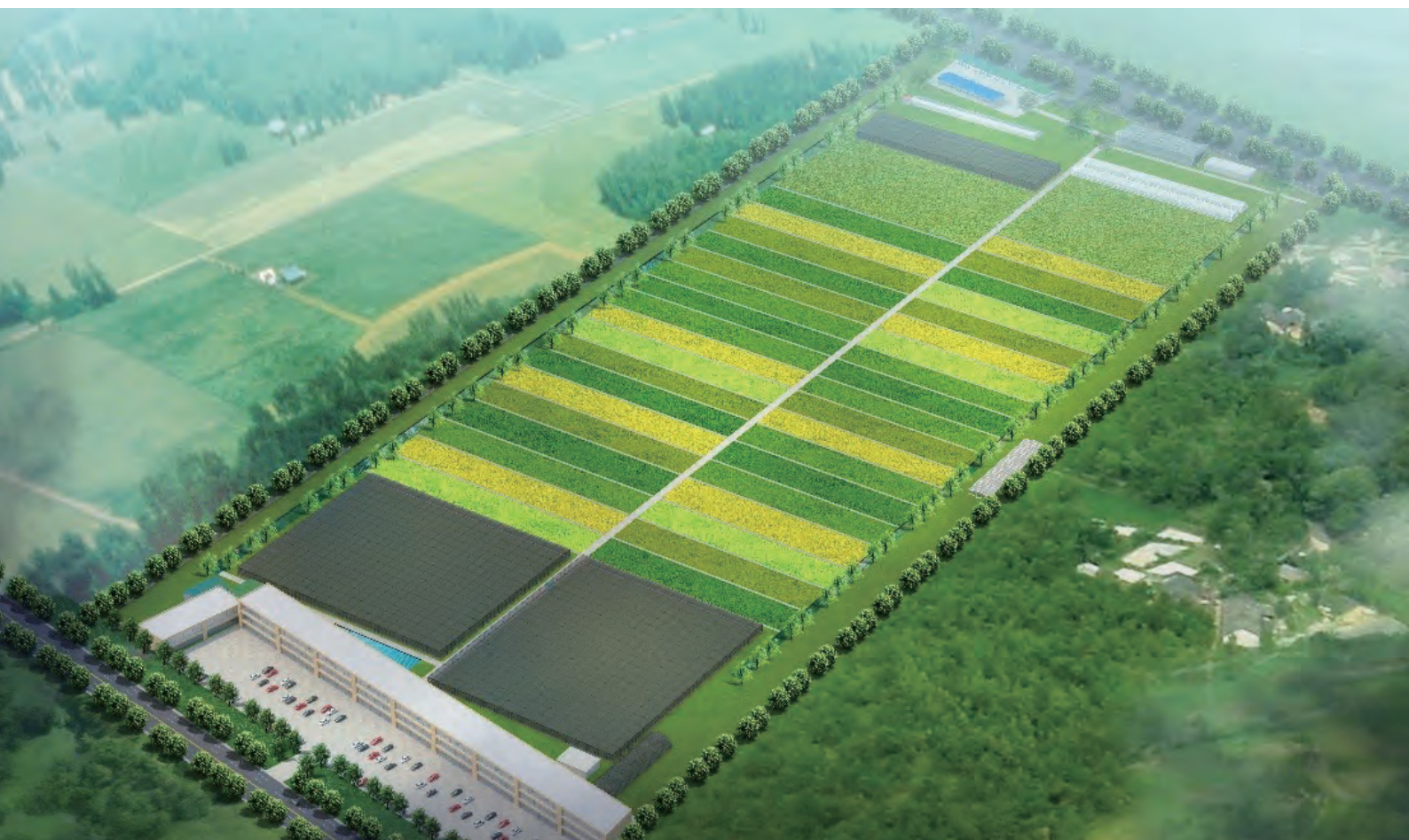
millet. Over 30 research groups conduct crop propagation and breeding activities at the base each year, making 60–80 visits annually. In 2025, the Lingshui Nanfan Base covered 104.91 *mu*, while the Potianyang Base covered 294.14 *mu*.

## Changping Base

Established in 1994, the Changping Experimental Base covers a total area of 13.3 hectares. This includes 150 *mu* of dry land, 30 *mu* of paddy fields, and 19.5 *mu* of supporting facilities. The site is equipped with greenhouses for tomatoes, rice nurseries, facilities for drought resistance, a high-throughput field phenotyping platform, and ponds for identifying salt

tolerance and wheat nutrition. These features provide ideal conditions for breeding high-yielding, high-quality, disease-resistant crops. In 2025, the base supported field experiments for 41 research groups, both within and outside the institute, and cultivated over ten crops, including rice, wheat, corn, proso millet, soybeans and rapeseed.

(Rendering)





*Curcuma longa* (Yujin) (Provided by Meng Wenxiang's team)

# Major Events

## January

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- Jan 3 • IGDB held Annual Work Summary and Commendation Meeting.
- Jan 17 • Teachers and students from the "Li Zhensheng Experimental Class" of Shandong Agricultural University visited IGDB.
- Jan 20 • The new leadership of IGDB was announced.

## February

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- Feb 18 • IGDB held a strategic cooperation exchange meeting with the People's Government of Chifeng City, Inner Mongolia Autonomous Region.
- Feb 22 • IGDB signed a strategic cooperation agreement on science and technology collaboration with the Xianghu Laboratory.

## March

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- Mar 7 • IGDB signed a strategic cooperation agreement with Henan Institute of Science and Technology.
- Mar 14 • The Academic Committee Meeting of the National Key Laboratory of Seed Innovation was held.
- Mar 14 • A delegation led by Vice President Yao Bing of Hebei University of Architecture and Civil Engineering visited the Agricultural Resources Research Center.

## April

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- Apr 8 • Professor Timothy Clough from Lincoln University, UK, visited the Center for Agro-resources Research as a PIFI Distinguished Scientist.
- Apr 15 • A delegation led by Xin Guochang, Deputy Director of the Bureau of Animal Husbandry and Veterinary Services of the Ministry of Agriculture and Rural Affairs, conducted an inspection at IGDB.
- Apr 27 • The Saline-Alkali Land Improvement Innovation Team led by Prof. Cao Xiaofeng was awarded 'Keyuan Master Artisan' of CAS.

## May

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- May 15 • A delegation led by Esteban Valenzuela, Minister of Agriculture of Chile, visited IGDB.
- May 15-18 • The 2025 Academic Annual Meeting of the Hydrological Geography Professional Committee of the Geographical Society of China, hosted by the Agricultural Resources Research Center, was held in Shijiazhuang.
- May 17-18 • IGDB successfully held the 21st Public Science Day both in Beijing and Shijiazhuang City.
- May 17 • Dr. Wang Enli, Chief Scientist of the Commonwealth Scientific and Industrial Research Organization (CSIRO) of Australia, visited the Agricultural Resources Research Center.
- The 2025 Editorial Board Meeting of *Journal of Genetics and Genomics* was held in Fuzhou.
- May 19 • The National Meeting on Wheat Powdery Mildew Resistance was held at the Gaoyi Base.
- May 22 • A delegation from the Beijing Municipal Bureau of Agriculture and Rural Affairs visited the National Key Laboratory of Seed Innovation.

## June

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- Jun 1-2 • The Agricultural Resources Research Center held a seminar on the development strategy of Beijing-Tianjin-Hebei Field Station.

- Jun 5 • A delegation led by Hu Xiaoming, Party Secretary of Xihu District, Changde City, Hunan Province, visited IGDB.
- Jun 17 • The Agricultural Resources Research Center signed a strategic cooperation agreement with the Langfang Center of China Geological Survey.
- Jun 20 • The 2025 graduation ceremony and degree awarding ceremony was held.

## July

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- Jul 1 • Prof. Gao Caixia was elected as an Associate Member of the European Molecular Biology Organization (EMBO).
- Jul 11 • A delegation from the International Maize and Wheat Improvement Center (CIMMYT) visited IGDB.
- Jul 24 • A delegation from the French National Research Institute for Agriculture, Food and the Environment (INRAE) visited IGDB.

## August

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- Aug 4 • A delegation from Alibaba Cloud Computing Co. Ltd visited IGDB to discuss potential cooperation in intelligent breeding.
- Aug 9 • The 6th Editorial Board Meeting of the Chinese Journal of Eco-Agriculture was held.

## September

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- Sep 26 • IGDB held a Forum on Crop Phenomics and Advanced Breeding Technologies.
- Sep 15-20 • The 2025 China-Japan-US International Student Workshop was held in Japan.
- Sep 19 • IGDB held an opening ceremony for the freshmen of the class of 2025.
- Sep 26 • IGDB hosted Symposium on Cutting-Edge Technologies in Crop Phenomics and Breeding.

## October

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- Oct 17 • A delegation from Miyun District Science and Technology Commission visited IGDB.

## November

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- Nov 1 • IGDB hosted events for the "8th Science Festival of the Chinese Academy of Sciences".
- The Department of Science, Technology and Education of the Ministry of Agriculture and Rural Affairs conducted a survey on the application scenarios of intelligent breeding robots.
- Nov 16 • IGDB, together with China Three Gorges University and Zhijiang City, jointly promoted the development of the *Sesbania cannabina* industry and signed a tripartite framework cooperation agreement.
- Nov 18-20 • IGDB signed a cooperation agreement with Aksu City Agriculture and Animal Husbandry Investment and Development Co., Ltd.
- Nov 20 • IGDB organized the onboarding training for new employees in 2025.
- Nov 21 • Prof. Fu Xiangdong was elected as a Member of the Chinese Academy of Sciences.
- Nov 21 • The Chifeng Base of IGDB was inaugurated.
- Nov 28-29 • IGDB held the 2025 Strategic Seminar.

## December

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- Dec 8-10 • The workshop on Digital Twin and Crop Breeding Design was held in Beijing.
- Dec 28 • IGDB and Alibaba Cloud Computing Co. Ltd, jointly launched the "Shennong Plan" for Intelligent Breeding.

# Appendix: Faculty List

## State Key Laboratory of Seed Innovation



**Fu Xiangdong**

Director, Academician  
Hormonal regulation of plant development and stress responses



**Xu Cao**

Executive Deputy Director  
Plant development and stress resilience



**He Yan**

Deputy Director  
Molecular genetic breeding of maize



**Zhang Youjun**

Deputy Director  
Plant metabolism and synthetic biology



**Li Zhensheng**

Academician  
Wide hybridization between wheat and *Thinopyrum Ponticum*



**Li Jiayang**

Academician  
Developmental biology and metabolic pathways of higher plants



**Chen Huabang**

Maize genetics & breeding



**Chu Jinfang**

Analysis method for quantification of plant hormones



**Feng Jian**

Legume-rhizobial symbiosis signaling



**Gao He**

Plant-environment interactions, floral transition "decision-making" and developmental plasticity



**Han Fangpu**

Plant chromosome biology



**Hu Zanmin**

Plant molecular breeding and production of functional peptides by bioreactor



**Li Hongju**

Plant reproduction and environmental response



**Li Hui**

Molecular plant-pathogen interactions



**Li Lei**

Plant and microbe interaction



**Li Yunhai**

Plant molecular and developmental biology



**Liang Chengzhi**

Genomic big data analysis



**Liu Cuimin**

Structure and function of photosynthetic complexes



**Liu Yucheng**

Functional genomics of soybean



**Liu Zhiyong**

Wheat genomics, genetics and breeding



**Tang Sanyuan**

Molecular breeding of sorghum and its efficiency application



**Tong Yiping**

Genetics of plant nutrition



**Wang Bing**

Molecular mechanisms of phytohormones



**Wang Guodong**

Plant metabolism



**Wang Yuan**

RNA biology and plant development



**Wu Kun**

Rice genetics and molecular breeding



**Yao Shanguo**

Rice genetics and molecular breeding



**Zhang Baocai**

Plant glycobiology



**Zhang Jinsong**

Ethylene signaling and stress response



**Zheng Qi**

Wheat wild hybridization



**Zhu Zhen**

Plant functional genomics and genetic engineering technology



**Zuo Jianru**

Cytokinin signal transduction and programmed cell death

## Laboratory of Advanced Breeding Technologies



**Lu Fei**

Director  
Genomics and quantitative genetics



**Ren Bo**

Deputy Director  
Soybean nodulation and nutrient use efficiency



**Xiao Jun**

Deputy Director  
Genetic analysis of wheat agronomic traits related to high yield and efficiency



**Yang Baojun**

Deputy Director  
Root biology



**Cao Xiaofeng**

Academician  
Plant epigenetics



**Chen Mingsheng**

Plant comparative genomics



**Deng Xian**

Plant epigenetic regulation



**Gao Caixia**

Genome editing and plant synthetic biology



**He Fei**

Wheat genomics and bioinformatics



**Jiang Ni**

Crop phenomics



**Li Xiang**

Single cell biology in plant photosynthesis



**Shen Qianhua**

Molecular plant-microbe interactions



**Song Xianwei**

Plant epigenetics and stress resistance



**Wang Yazhong**

Plant sexual reproduction and asexual reproduction, polyploid breeding



**Wang Yanpeng**

Plant genome editing and new traits creating



**Xie Qi**

Protein ubiquitination and plant stress biology



**Xue Yongbiao**

Plant molecular and reproductive biology



**Yu Zhenyu**

Dynamic regulatory mechanisms of chromatin structural plasticity in plants



**Zhao Yusheng**

Molecular mechanisms of temperature-sensing signals in plants



**Zhou Yihua**

Molecular mechanism in plant cell wall metabolism and formation

## Laboratory of Integrative Physiology



**Tian Ye**

Director  
Mitochondrial stress response  
and aging



**Lu Falong**

Deputy Director  
Epigenetics and cell fate  
determination



**He Kangmin**

Deputy Director  
Dynamics and regulation of  
membrane trafficking and  
phospholipid signaling



**Jia Shunji**

Deputy Director  
Embryonic development and  
organogenesis



**John Speakman**

Academician  
Energy balance in animals and  
humans



**Yang Weicai**

Academician  
Molecular genetics of sexual  
plant reproduction



**Ai Youwei**

Biochemical mechanisms of cell  
death



**Bao Shilai**

Epigenetics and golgi apparatus  
biogenesis



**Dai Jianwu**

Stem cells and regenerative  
medicine



**Duan Lihui**

Development and function of  
brain fibroblasts



**Guo WeiXiang**

Neural stem cells and  
neurogenesis



**Huang Xun**

The cellular and developmental  
biology of lipid metabolism



**Jiang Yuqiang**

Optical micro-manipulation and  
its application in dynamics of  
biomacromolecules



**Liu Jiajia**

Molecular and cellular  
mechanisms of membrane traffic



**Meng Wenxiang**

Dynamic coordination of  
cytoskeleton network



**Wang Zhaohui**

Gametogenesis



**Wu Qingfeng**

Hypothalamus development,  
function and disease



**Wu Zhaofa**

Neuronal communication and  
brain function



**Xu Zhiheng**

Signal transduction in neuronal  
apoptosis

## Center for Zero-to-One Innovation



**Wang Xiujie**

Director  
Bioinformatics and systems  
biology



**Du Zhuo**

Deputy Director  
4D digital development



**Chen Yuhang**

Structural biology, membrane  
protein, ion channels and  
transporters



**Li Chuanyun**

Genetic decoding and translation  
of human-specific brain  
development



**Qian Wenfeng**

From decoding evolution to  
designing genetic elements



**Tu Qiang**

Systems biology, developmental biology, gene networks, medaka fish, zebrafish



**Wang Yingchun**

Functional proteomics



**Zhang Chunxia**

Mechanisms of cell fate regulation

## Center for Agricultural Resources Research



**Shen Yanjun**

Director  
Agricultural hydrology and water resources



**Liu Xiaojing**

Deputy Director  
Sustainable development of agriculture in saline soil areas



**Wang Shiqin**

Deputy Director  
Water and matter cycle and groundwater environment



**An Diaoguo**

Wheat genetic improvement and germplasm enhancement



**Bai Zhaohai**

Crop-livestock system



**Cao Jiansheng**

Mountain eco-hydrological process and regulation mechanism



**Dong Baodi**

Plant physiology and ecology



**Dong Wenxu**

Nutrients cycling in farming ecosystems



**Hu Chunsheng**

Nutrients cycling of farming ecosystems



**Han Lipu**

Ecological processes of marginal land



**Liu Binbin**

Microbial ecology



**Liu Jintong**

Management for agricultural resources and ecosystems



**Liu Xiuwei**

Root phenomics



**Li Xiaofang**

Environmental biotechnology for sustainable agriculture



**Min Leilei**

Water cycle and related processes in Earth Critical Zone



**Qin Shuping**

C & N processes in soil-plant system and their environmental effects



**Shen Yanjun**

Ecohydrological modeling and water environment management in watersheds



**Sun Hongyong**

Water and salt transport process and regulation in farmland ecosystem



**Wang Lei**

Plant molecular genetics



**Yang Yonghui**

Sustainable agricultural water management in regional scale



**Zhang Yucui**

Agricultural ecological hydrology and water conservation



**Zhang Xiyang**

Mechanisms and techniques of farmland water use efficiency



**Zhao Xin**

Crop phenology and farmland greenhouse gas research



**Zhu Feng**

Terrestrial ecology and plant sciences

# 2025 Annual Report

Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

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Address: No. 1 West Beichen Road, Chaoyang District, Beijing 100101, P.R. China

Tel: +86-10-64803652

Email: [info@genetics.ac.cn](mailto:info@genetics.ac.cn)

Website: <http://www.genetics.ac.cn>