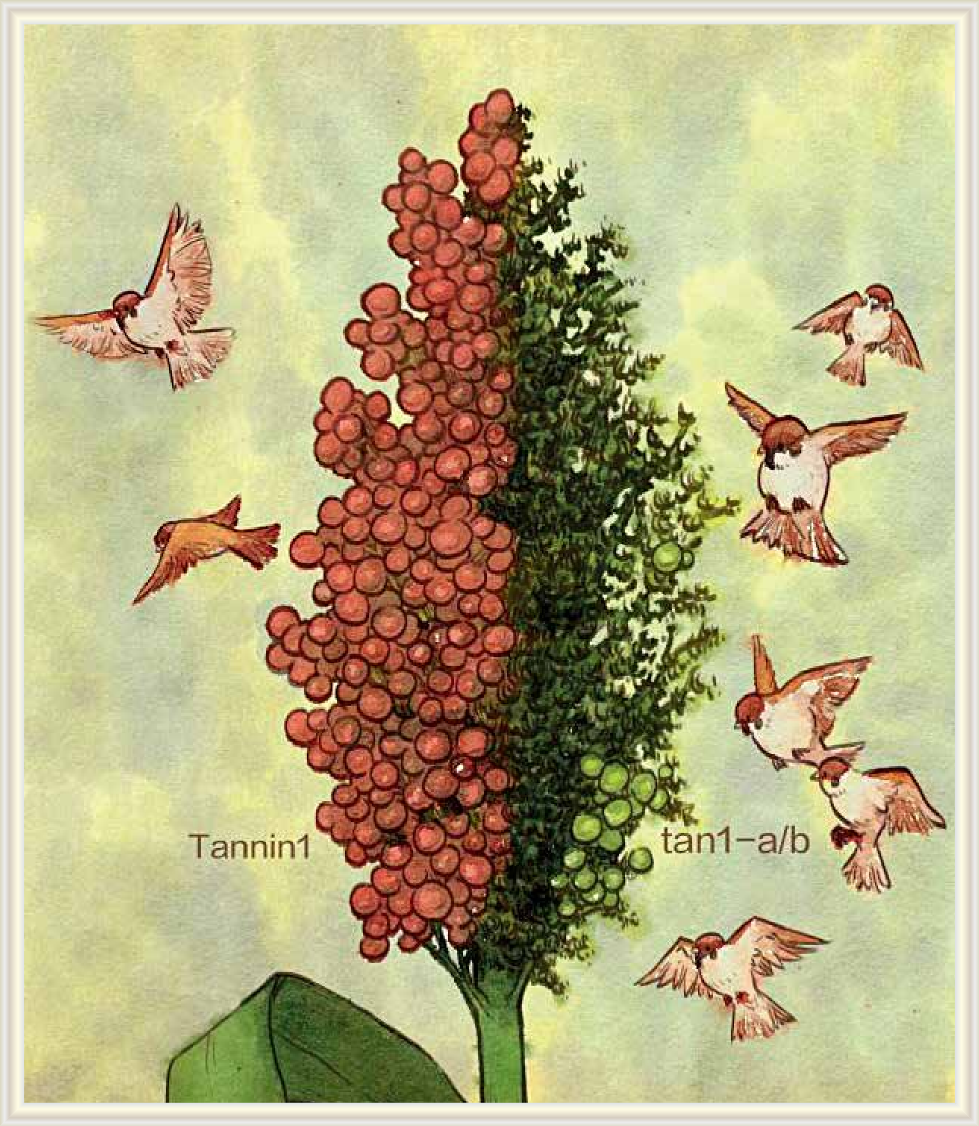
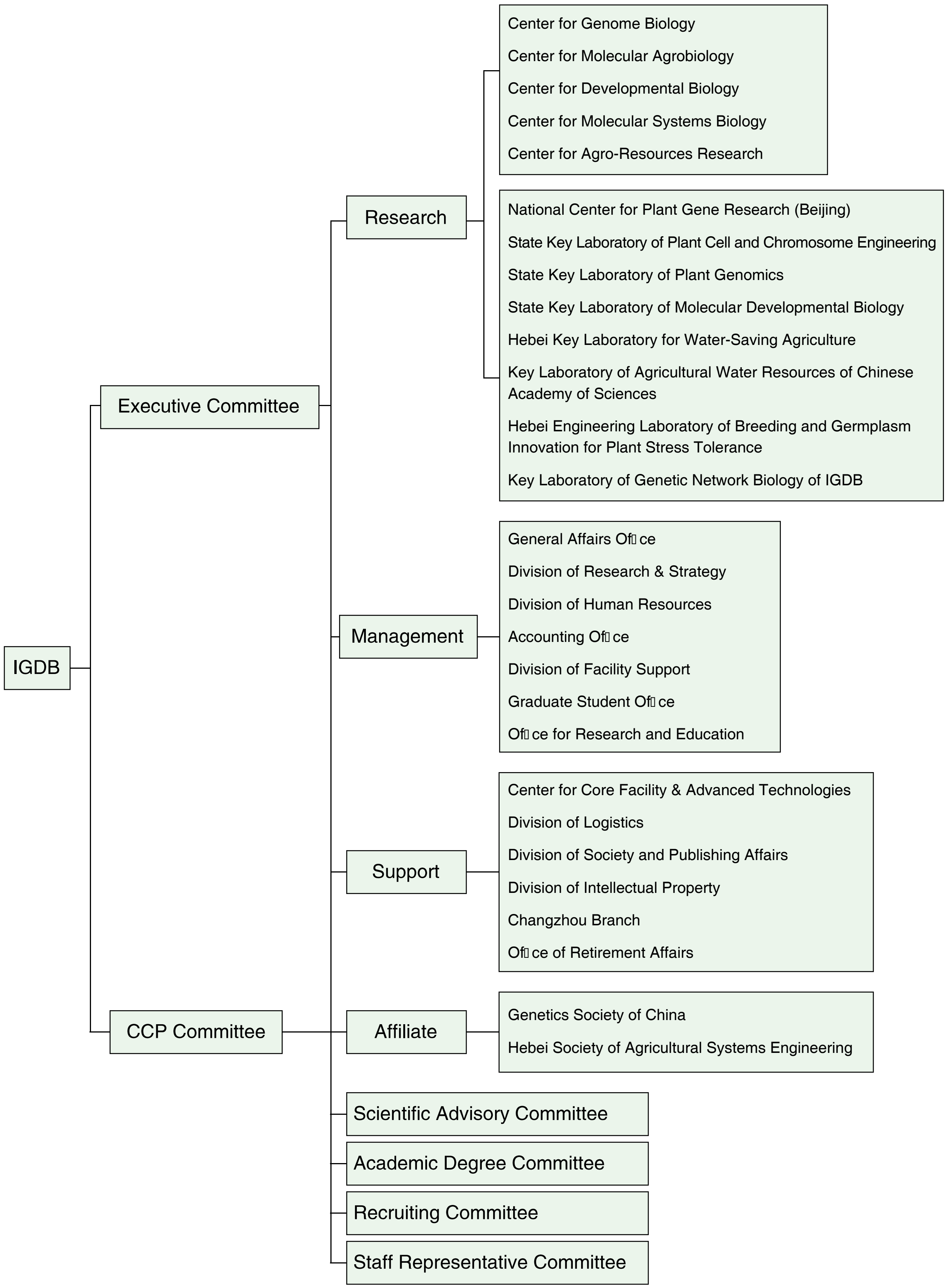
2019 Annual Report

Institute of Genetics and Developmental Biology
Chinese Academy of Sciences



Institute Organization



- IGDB
  - Executive Committee
  - CCP Committee
    - Research
      - Center for Genome Biology
      - Center for Molecular Agrobiology
      - Center for Developmental Biology
      - Center for Molecular Systems Biology
      - Center for Agro-Resources Research
      - National Center for Plant Gene Research (Beijing)
      - State Key Laboratory of Plant Cell and Chromosome Engineering
      - State Key Laboratory of Plant Genomics
      - State Key Laboratory of Molecular Developmental Biology
      - Hebei Key Laboratory for Water-Saving Agriculture
      - Key Laboratory of Agricultural Water Resources of Chinese Academy of Sciences
      - Hebei Engineering Laboratory of Breeding and Germplasm Innovation for Plant Stress Tolerance
      - Key Laboratory of Genetic Network Biology of IGDB
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      - General Affairs Office
      - Division of Research & Strategy
      - Division of Human Resources
      - Accounting Office
      - Division of Facility Support
      - Graduate Student Office
      - Office for Research and Education
    - Support
      - Center for Core Facility & Advanced Technologies
      - Division of Logistics
      - Division of Society and Publishing Affairs
      - Division of Intellectual Property
      - Changzhou Branch
      - Office of Retirement Affairs
    - Affiliate
      - Genetics Society of China
      - Hebei Society of Agricultural Systems Engineering
    - Scientific Advisory Committee
    - Academic Degree Committee
    - Recruiting Committee
    - Staff Representative Committee

Director's Report

The year 2019 is the 70th anniversary of the founding of the People's Republic of China and also the 60th anniversary of the establishment of the Institute of Genetics and Developmental Biology (IGDB), Chinese Academy of Sciences (CAS). Focused on the "13th Five-year Plan" and the CAS Strategic Priority Research Program, we have witnessed a continued rapid development of IDGB in the past year.

The establishment of the CAS Innovative Academy for Seed Design was accelerated in 2019. A new CAS Priority Research Program on seed precision design and creation was initiated by the Academy. Collaborated with Hainan Provincial Department of Agriculture and the government of Sanya City, Hainan Branch of the CAS Innovative Academy for Seed Design was jointly established based on Hainan free trade zone and Yazhouwan Science and Technology City. The construction of the national research facilities of crop phenotype, called Shen Nong, was promoted jointly with more than 50 other collaborative partners at home and abroad. In 2019, the College of Modern Agricultural Sciences of University of Chinese Academy of Sciences, led by IGDB, continued to optimize its curriculum system and 311 new graduates were recruited in 2019.

In 2019, the Institute made gratifying progress in scientific research too. The Institute published 428 SCI-indexed papers, and 65 patents, 15 new plant variety rights, and 13 new crop varieties were granted. Research on "the mechanisms of histone methylation and small RNAs in regulating plant development and transposons jumping" won the second prize of National Natural Science in 2019. Drs. Jiayang Li, Jianmin Zhou, Chengcai Chu and Caixia Gao were recognized by Clarivate Analytics Hightly-Cited Researchers 2019.

Dr. John Speakman was selected as a CAS Foreign Member. The innovation team on national facility of crop phenotypic research was selected as an Innovation Team of Key Fields in the Innovation Talent Promotion Program, while the team on stem cell regulation mechanism of the plasticity of plant growth won the LU Jiaxi Award for International Cooperation. Drs. Wenfeng Qian, Bin Hu and Baocai Zhang were supported by the National Science Fund for Excellent Young Scholars.

The Institute continued to do great efforts to strengthen the application and commercialization of the research outputs. The poverty alleviation through science and technology in Kulun Qi of Inner Mongolia led by IGDB has been highly affirmed by the CAS headquarters. China Hu-sheep Industry Research Institute & Yancheng Joint Innovation Center of IGDB, and Dongying Center on Molecular Design and Breeding both started running in 2019. IGDB signed an agreement with Ningxia Academy of Agricultural and Forestry Sciences to build a demonstration base for new rice varieties in the irrigation area in the west of the Yellow River. We also signed an agreement with Tianjin Food Company Group to jointly promote the Xiaozhan Rice Redevelopment Initiative in Tianjin. Moreover, the Institute signed a strategic agreement with Shenzhen Huada Institute of Life Sciences to build a joint research center of cell and multidimensional omics.

In 2019, the Institute followed the national strategy, constantly broadened its international partners, and further improved its ability to deal with the global scientific challenges by international collaborations. The CAS-JIC Center of Excellence for Plant and Microbial Science (CEPAMS) has successfully complete the first five-year collaboration with a series of progress in talents recruitment, academic exchange and cooperation, and the joint center will proceed its mission to maximize the synergy of CAS and JIC research to work together for excellent science and global public good. In 2019, the Centre of Excellence for Plant-Environment Interactions was established jointly by Centre for Plant Biotechnology and Genomics (CBGP) in Spain, the Shanghai Centre for Plant Stress Biology (PSC) and IGDB. To meet the national Belt and Road strategy, we signed a memorandum of understanding with the Brazilian Agricultural Research Corporation (EMBRAPA) to carry out cooperative research on soybean. Also, a research project led by Dr. John Speakman on the economic and demographic health of the countries along Belt and Road was launched in 2019.

All these achievements and progresses are not possible without the efforts of IGDB staff and students. Finally, I would like to express my sincere thanks to our sponsors and funding agencies for their enormous support. I am pleased to present this annual report and wish you a prosperous 2020.

Weicai Yang

Weicai Yang, Director, IGDB, CAS
January 2020

CONTENTS

Center for Genome Biology

The mission of the Center for Genome Biology (the Center, thereafter) is to develop and apply genomic tools to understand how plant growth and development are regulated. In 2019, scientists in the Center have made important advances in multiple fronts, including gene function studies, plant genomic studies, plant hormone biology, plant health, plant biotechnology and molecular breeding.

In the area of gene function, Jiayang Li's group revealed a molecular mechanism for the coordinated control of plant height and tiller number in rice by gibberellins, two genes *SLR1* and *MOC1* (Liao et al., *Nat Commun*, 2019). The Li group found a crosstalk between strigolactones and cytokinin in rice, in which strigolactones could induce the expression of *OsCKX9* to down regulate cytokinin contents (Duan et al., *PNAS*, 2019). The Li group additionally revealed that two transcription factors, MOC1 and MOC3, jointly promote rice tiller bud formation and outgrowth (Shao et al., *Mol Plant*, 2019). Yonghong Wang's group and Jiayang Li's group identified OsBRXL4 as a regulatory component of the rice tiller angle, providing new insights into genetic regulation of rice shoot architecture (Li et al., *Mol Plant*, 2019). Chengcai Chu's group uncovered a signaling pathway by which nitrate activates both phosphate and nitrate responses, in which the nitrate sensor NRT1.1B promotes the ubiquitination and degradation of a repressor protein SPX4 (Hu et al., *Nat Plants*, 2019). The Chu group also demonstrated that shortening rice maturity duration had no yield penalty using the quantitative trait locus *Early flowering-completely dominant* (*Ef-cd*) (Fang et al., *PNAS*, 2019).

In the area of plant genomics, Xiaofeng Cao's group and collaborators showed that gene translational efficiency could be regulated through the G-content-dependent PAB binding (Zhao et al., *Genome Biol*, 2019). The Cao group uncovered distinct mechanisms regulating accumulation of a monocot-specific miRNA in rice (*Oryza sativa*) and revealed a potential role of transcription factor OsSPL9 in this process (Yang et al., *Mol Plant*, 2019). The Cao group also found that H3K27me3 demethylase REF6 preferentially binds to hypo-methylated CTCTGYTY-motifs, revealing a mechanism that a histone modifying enzyme avoids heterochromatic binding through its intrinsic DNA methylation unfavorable binding activity (Qiu et al., *Nat Commun*, 2019). The Cao group and collaborators revealed the structure of *Arabidopsis* JMJ13 catalytic domain and its function in photoperiod and temperature-dependent flowering responses, which showed that JMJ13-mediated H3K27me3 demethylation is a new mechanism regulating temperature- and photoperiod-dependent flowering regulation (Zheng et al., *Nat Commun*, 2019). The Cao group and collaborators uncovered a mechanism by which an H3K4 demethylase JMJ16 regulates the transcriptional reprogramming of SAGs during senescence by modulating H3K4me3 levels in an age-dependent manner (Liu et al., *Plant Cell*, 2019). Chengzhi Liang's group reported HERA, a novel genome assembly method that resolves repeats efficiently and assembles most of the previously unassembled regions (Du et al., *Nat Commun*, 2019). The Liang group and collaborators investigated the off-target mutations resulting from CRISPR/Cas9-based base editing tools in rice (Jin et al., *Science*, 2019). The Liang group and collaborators also completed a near-complete genome assembly of snapdragon (*Antirrhinum majus*) cultivar JI7, providing a reference genome for the Plantaginaceae (Li et al., *Nat Plants*, 2019). Zhukuan Cheng's group demonstrated that the meiotic bipolar spindle in rice forms via conversion of multiple poles into two poles, supporting OsMTOPVIB as an initiation factor of homologous recombination conserved among various species (Xue et al., *PNAS*, 2019). Yuling Jiao's group released a domain-specific gene expression map covering key shoot apex and leaf domains, allowing direct comparison among them (Tian et al., *Nat Commun*, 2019).

In the area of plant health, Jian-Min Zhou's group and collaborators showed that the *Arabidopsis* immune receptor ZAR1 forms an oligomeric resistosome upon activation. They solved structures of the ZAR1 complex in inactive, intermediate and active forms to uncover the mechanism by which this immune receptor is activated during pathogen attack. The activated ZAR1 resistosome structure additionally revealed a molecular switch for immune activation in plants. The findings provide a structural template for understanding of NLR superfamily immune receptors and represent a milestone in the field of plant immunity (Wang et al., *Science*, 2019a, b). Yang Bai's group and Chengcai Chu's group revealed a link between root microbiome and nitrogen use efficiency in rice subspecies and demonstrated a role of the nitrate sensor gene NRT1.1B in the establishment of root microbiota (Zhang et al., *Nat Biotechnol*, 2019). The Bai group and collaborators dissected a triterpene biosynthetic network in *Arabidopsis* thaliana and demonstrated that triterpene plays a crucial role in shaping root microbiome structure (Huang et al., *Science*, 2019). Xiaofeng Cao's group and collaborators discovered that HSFA2 and H3K27me3 demethylase REF6 form a positive feedback loop to transmit long-term epigenetic memory of heat, which revealed that the thermos-memory machinery promotes plant reproduction and fitness by accelerating flowering and attenuating disease resistance through the ta-siRNA target *HTT5* (Liu et al., *Cell Res*, 2019).

In the area of plant hormone biology, Guodong Wang's group identified CYP72A as a new player controlling plant gibberellins metabolism, showing that members of the CYP72A subfamily encode *bona fide* gibberellin 13-oxidase, which catalyzes the conversion of 13-H gibberellins to the corresponding 13-OH gibberellins (He et al., *Nat Plants*, 2019). Chuanyou Li's group and collaborators identified enhancers specifically involved in jasmonate signaling through profiling the occupancy pattern of MYC2 and MED25 (Wang et al., *Nat Plants*, 2019). The Li group and collaborators further identified the *Aft* and *atv* genes to uncover regulatory mechanism underlying anthocyanin biosynthesis in tomato fruit, and generated purple-fleshed tomato plants which accumulate anthocyanins in both peel and flesh (Sun et al., *Mol Plant*, 2019). The Li group identified a mechanism by which the *Arabidopsis* Gro/Tup1 family member LUH activates MYC2-regulated transcription of jasmonate-responsive genes (You et al., *Plant Cell*, 2019). The same group described an additional and unexpected function of MYC2 in forming an autoregulatory negative feedback circuit that regulates the termination of jasmonate-signaling in tomato (Liu et al., *Plant Cell*, 2019). Qi Xie's group pinpointed genetic polymorphisms at a single locus, *Tannin1*, that confers major metabolic regulatory impacted on multiple pathways of plant polyphenol and fatty-acid metabolism, ultimately determining birds feeding preference (Xie et al., *Mol Plant*, 2019). Yihua Zhou's group identified a rice GDSL esterase DARX1, providing insight into how the arabinoxylan acetylation pattern, as well as its conformations, are established. The findings promises a new strategy to breed robust elite crops with improved mechanical strength and plant yield (Zhang et al., *Plant Cell*, 2019). Cao Xu's group and collaborators revealed the CLV compensation mechanisms, and found that compensation among ligand and receptor paralogs is critical for stem cell homeostasis (Rodriguez-Leal et al., *Nat Genet*, 2019).

In the area of plant biotechnology and molecular breeding, Jiayang Li's group and collaborators generated herbicide tolerant wheat germplasms using base editing to facilitate weed control (Zhang et al., *Nat Plants*, 2019). The Li group and collaborators bred and released new rice elite cultivars "Zhongkefa 928", "Qianxiangyou 220", "Quanyou 220", "Jiaheyou 5" and "Zhonglongjing 100".

In recognition of their contributions to related fields, Profs. Jiayang Li, Xiaofeng Cao, Qi Xie, Chengcai Chu, Chuanyou Li and Yuling Jiao were invited to contribute 12 review articles and commentaries for *Annu Rev Plant Biol*, *Trends Plant Sci*, *Mol Plant*, *New Phytol*, *Plant Cell*, and *J Exp Bot*.

AWARDS AND RECOGNITIONS

Prof. Jiayang Li was elected a Vice-President of the China Science Center of the International Eurasian Academy of Sciences, and was honored with the CSCB Lifetime Service Award by Chinese Society for Cell Biology. Prof. Xiaofeng Cao was elected a member of the International Eurasian Academy of Sciences, and was honored for the 2019 CSPB Outstanding Achievement Award by the Chinese Society for Plant Biology. Prof. Yuling Jiao received the 2019 CSPB Outstanding Young Investigator Award, and Dr. Caihuan Tian received the 2019 CSPB Outstanding Young Women Award. Profs. Jiayang Li, Chengcai Chu and Jian-Min Zhou were recognized as Clarivate Analytics Highly-Cited Researchers 2019. Dr. Bin Hu and Dr. Baocai Zhang received a grant for the Excellent Young Scientists Fund from the National Natural Science Foundation of China.

Interaction Between Plant and Root Microbiome

Yang Bai, Principal Investigator, Ph.D. (2010, University of Cologne, Germany).

Research Interests: The role of root microbiome in plant nutrition, disease resistance and yield, and related research methods.

Email: ybai@genetics.ac.cn

Publications

Zhang, J., Liu, Y.-X., Zhang, N., Hu, B., Jin, T., Xu, H., Qin, Y., Yan, P., Zhang, X., Guo, X., Hui, J., Cao, S., Wang, X., Wang, C., Wang, H., Qu, B., Fan, G., Yuan, L., Garrido-Oter, R., Chu, C. and Bai, Y. (2019). *NRT1.1B* is associated with root microbiota composition and nitrogen use in field-grown rice. Nature Biotechnology 37(6): 676-684.

Huang, A. C., Jiang, T., Liu, Y.-X., Bai, Y.-C., Reed, J., Qu, B., Goossens, A., Nützmann, H.-W., Bai, Y. and Osbourn, A. (2019). A specialized metabolic network selectively modulates *Arabidopsis* root microbiota. Science 364(6440): eaau6389.

Liu, Y.-X., Qin, Y. and Bai, Y. (2019). Reductionist synthetic community approaches in root microbiome research. Current Opinion in Microbiology 49: 97-102.

Chen, Q., Jiang, T., Liu, Y.-X., Liu, H., Zhao, T., Liu, Z., Gan, X., Hallab, A., Wang, X., He, J., Ma, Y., Zhang, F., Jin, T., Schranz, M. E., Wang, Y., Bai, Y. and Wang, G. (2019). Recently duplicated sesterterpene (C25) gene clusters in *Arabidopsis thaliana* modulate root microbiota. Science China Life Sciences 62(7): 947-958.

A specialized metabolic network selectively modulates *Arabidopsis* root microbiota

Plant specialized metabolites have ecological functions, yet the presence of numerous uncharacterized biosynthetic genes in plant genomes suggests that many molecules remain unknown. We discovered a triterpene biosynthetic network in the roots of the small mustard plant *Arabidopsis thaliana*. Collectively, we have elucidated and reconstituted three divergent pathways for the biosynthesis of root triterpenes, namely thalianin (seven steps), thalianyl medium-chain fatty acid esters (three steps), and arabidin (five steps). *A. thaliana* mutants disrupted in the biosynthesis of these compounds have altered root microbiota (Figrue A/B). In vitro bioassays with purified compounds reveal selective growth modulation activities of pathway metabolites toward root microbiota members and their biochemical transformation and utilization by bacteria, supporting a role for this biosynthetic network in shaping an *Arabidopsis*-specific root microbial community.

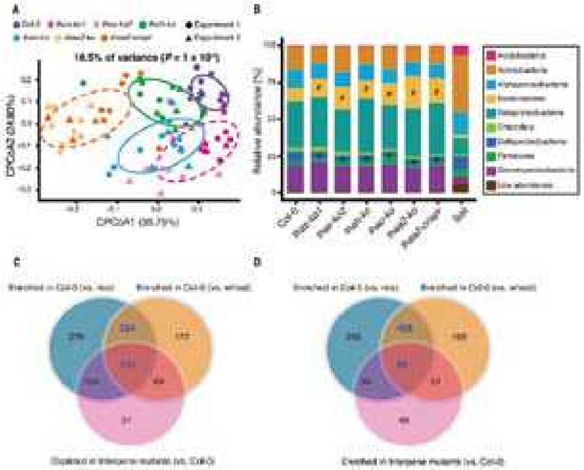

Figure: Modulation of specific root bacterial taxa in triterpene pathway mutants. (A) Constrained principal coordinate analysis (CPCoA) of Bray-Curtis dissimilarity showing triterpene mutant effects.(B) Phylum distribution of the root microbiota compositions of the tested *A. thaliana* genotypes. (C/D) Venn diagrams showing substantial overlap of OTUs (C) depleted or (D) enriched in the root microbiota of *A. thaliana* triterpene mutant lines as compared with the wild type (Col-0) (pink circles), compared with those depleted in the root microbiota of rice (blue circles) and wheat (orange circles) versus the *A. thaliana* Col-0 wild type.

Epigenetics in Higher Plants

Xiaofeng Cao, Principal Investigator, Member of Chinese Academy of Sciences, Academician of The third World Academy of Sciences.

Research Interests: The laboratory mainly focuses on investigating the epigenetic regulation in higher plants, including histone methylation in plant development and genome stability, regulatory mechanism of protein arginine methylation in Arabidopsis and RNA metabolism in response to ambient temperature in rice.

Email: xfcao@genetics.ac.cn

DNA methylation repels targeting of *Arabidopsis* histone demethylase REF6

Polycomb-mediated trimethylation of histone H3 lysine 27 (H3K27me3), a conserved epigenetic mark associated with chromatin compaction and gene repression, plays a key role in cell identity and developmental regulation in both plants and metazoans. Dynamic regulation of H3K27me3 at specific targets is achieved by both the histone methyltransferase, PRC2 complex, and the JmjC-domain containing demethylases of H3K27me3. *Arabidopsis* histone demethylase REF6 specifically demethylates H3K27me3 at thousands of genes by directly recognizing the CTCTGYTY motif via its zinc-finger (ZnF) domains (Lu, *et al*., *Nature Genetics*, 2011; Cui, *et al*., *Nature Genetics*, 2016). REF6 tends to bind CTCTGYTY-motifs located in active chromatin states and depleted in heterochromatic regions. However, the underlying mechanism remains unknown. In collaboration with Prof. MA Jinbiao's team from Fudan University, we revealed H3K27me3 demethylase REF6 preferentially binds to hypo-methylated CTCTGYTY-motifs via its zincfinger domains, suggesting that DNA methylation might deter REF6 binding in heterochromatin. We found that REF6 prefers to bind hypo-methylated genomic regions *in vivo*, and that CHG methylation in CTCTGYTY-motif decreases REF6 DNA binding affinity *in vitro*. In addition, crystal structure of REF6 ZnF-clusters in complex with DNA oligonucleotides reveals that 5-methylcytosine is unfavorable for REF6 binding. To further study the effect of DNA methylation on REF6-binding, we profiled REF6-binding sites in *drm1 drm2 cmt2 cmt3* (ddcc) quadruple mutants, in which non-CG methylation is significantly reduced. Interestingly, REF6 ectopically bind to a small number of new target loci, most of which are located in or neighbored with short TEs in euchromatic regions.These results reveal a mechanism that a histone modifying enzyme avoids heterochromatic binding through its intrinsic DNA methylation unfavorable binding activity. It will be interesting to further explore how recruitment of a chromatin-modifying enzyme is tightly regulated to achieve the appropriate level of chromatin modification and maintain proper chromatin status at the right place in the genome. The article entitled "DNA methylation repels targeting of *Arabidopsis* REF6" has been published online in *Nature Communications* (DOI: 10.1038/s41467-019-10026-1).

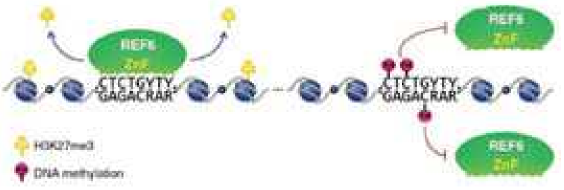

Figure: Model of how DNA methylation prevents REF6 binding to the CTCTGYTY motif

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Song, X., Li, Y., Cao, X., and Qi, Y. (2019). MicroRNAs and their regulatory roles in plant-environment interactions. Annual Review of Plant Biology 70: 489-525.

Qiu, Q., Mei, H., Deng, X., He, K., Wu, B., Yao, Q., Zhang, J., Lu, F., Ma, J. and Cao, X. (2019). DNA methylation repels targeting of *Arabidopsis* REF6. Nature Communications 10(1): 2063.

Yang, R., Li, P., Mei, H., Wang, D., Sun, J., Yang, C., Hao, L., Cao, S., Chu, C., Hu, S., Song, X. and Cao, X. (2019). Fine-tuning of MiR528 accumulation modulates flowering time in rice. Molecular Plant 12(8): 1103-1113.

Zheng, S., Hu, H., Ren, H., Yang, Z., Qiu, Q., Qi, W., Liu, X., Chen, X., Cui, X., Li, S., Zhou, B., Sun, D., Cao, X. and Du, J. (2019). The Arabidopsis H3K27me3 demethylase JUMONJI 13 is a temperature and photoperiod dependent flowering repressor. Nature Communications 10: 1303.

Liu, J., Feng, L., Gu, X., Deng, X., Qiu, Q., Li, Q., Zhang, Y., Wang, M., Deng, Y., Wang, E., He, Y., Baurle, I., Li, J., Cao, X. and He, Z. (2019). An H3K27me3 demethylase-HSFA2 regulatory loop orchestrates transgenerational thermomemory in *Arabidopsis*. Cell Research 29(5): 379-390.

Plant Comparative Genomics

Mingsheng Chen, Principal Investigator, Ph.D. (1998, Purdue University, USA).

Research Interests: Comparative genomics and genome evolution of Oryza and grasses

Email: mschen@genetics.ac.cn

Comparative evolutionary analysis of two subgenomes of broomcorn millet

Broomcorn millet (*Panicum miliaceum* L.) is an allotetraploid. To understand the allotetraploid evolution, we *de novo* assembled a high-quality chromosome-scale genome sequence of *P. miliaceum*. By phylogenetic analysis, we sort the *P. miliaceum* genome into subgenomes - A and B. We date the divergence of these two subgenomes at ~5 million years ago. The sizes of A and B subgenomes are estimated to be ~350 Mb and ~454 Mb, respectively. We found the main cause of the size variation was due to the differences in Gypsy-type LTR-retrotransposon contents. Further analysis of the LTR-retrotransposons showed a random insertion/deletion pattern. The comparative analysis of the syntenic genes between A and B subgenomes of *P. miliaceum* showed that the coding genes between subgenomes have very conserved synteny, while the intergenic regions are variable due to different repeat element insertions. The comparative analysis of the segments on chromosome one showed that the gene loss between A and B subgenomes were rare.

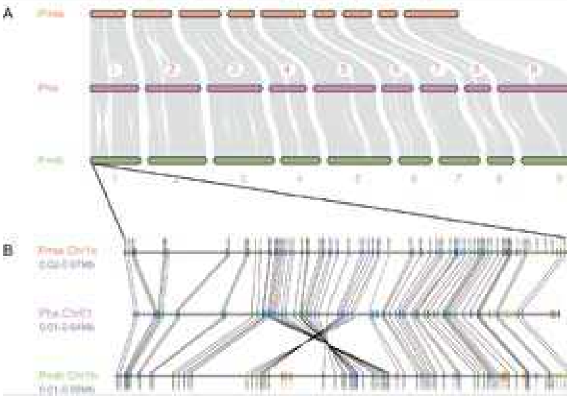

Figure: Synteny analysis of (sub) genomes of *Panicum*. (A) Macrosynteny between genomic regions in Panicum. (B) Microsynteny between genomic regions in *Panicum* as an example. Blocks represent genes with orientation on the same strand (blue) or reverse strand (green); the syntenic gene pairs are connected by straight lines.

Molecular Mechanisms of Abiotic Stress Response in Higher Plants and Soybean Seed Trait Regulation

Shouyi Chen, Principal Investigator Emeritus. She graduated from the Department of Biology of Peking University in 1963. She worked at the Institute of Biophysics, CAS, from 1963 to 1989, and worked at the Columbia University and Public Health Research Institute of City of New York from 1981 to 1984.

Research Interests: 1) Identification of new gene and new mechanisms related to plant abiotic stress tolerance; 2) Identification of genes for regulating seed traits by QTL mapping and genomic analysis.

Email: sychen@genetics.ac.cn

A class B heat shock factor selected for during soybean domestication contributes to salt tolerance by promoting flavonoid biosynthesis

Soybean (*Glycine max*) production is severely affected in unfavorable environments. Identification of regulatory factors conferring stress tolerance would facilitate soybean breeding. In this study, through coexpression network analysis of salt-tolerant wild soybeans, together with molecular and genetic approaches, we unraveled a previously unidentified function of a class B heat shock factor, HSFB2b, in soybean salt stress response. We showed that HSFB2b improves salt tolerance through the promotion of flavonoid accumulation by activating one subset of flavonoid biosynthesis-related genes and by inhibiting the repressor gene *GmNAC2* to release another subset of genes in the flavonoid biosynthesis pathway. Moreover, four promoter haplotypes of *HSFB2b* were identified from wild and cultivated soybeans. Promoter haplotype II from salt-tolerant wild soybean Y20, with high promoter activity under salt stress, is likely selected for during domestication. Another promoter haplotype, haplotype III, from salt-tolerant wild soybean Y55, had the highest promoter activity under salt stress, had a low distribution frequency and may be subjected to the next wave of selection. Together, our results revealed the mechanism of *HSFB2b* in soybean salt stress tolerance. Its promoter variations were identified, and the haplotype with high activity may be adopted for breeding better soybean cultivars that are adapted to stress conditions.

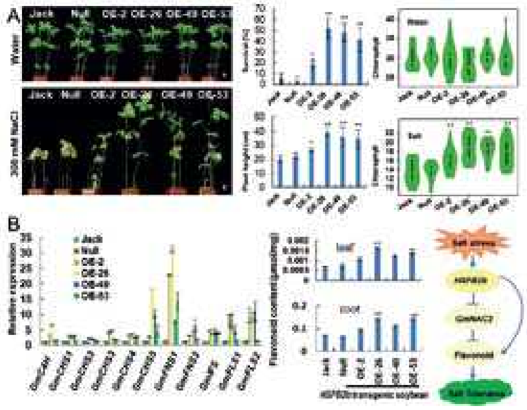

Figure: Overexpressed *HSFB2b* enhances salt tolerance in soybean A.The phenotype of *HSFB2b* transgenic soybean in water and after salt treatment (left); Survival rate and plant height of *HSFB2b* transgenic soybean seedlings after salt treatment (middle); Chlorophyll content of the first trifoliate leaves of soybean seedlings in water and after salt treatment (right). B. The expression of flavonoid related genes in *HSFB2b* transgenic soybeans (left); Flavonoid content in the leaves and roots of *HSFB2b* transgenic soybeans (middle); Working model of HSFB2b in response to salt stress in soybean (right).

Publications

Wei, W., Liang, D., Bian, X., Shen, M., Xiao, J., Zhang, W., Ma, B., Lin, Q., Lv, J., Chen, X., Chen, S. and Zhang, J. (2019). GmWRKY54 improves drought tolerance through activating genes in abscisic acid and Ca^{2+} signaling pathways in transgenic soybean. The Plant Journal 100: 384-398.

Bian, X., Li, W., Niu, C., Wei, W., Hu, Y., Han, J., Lu, X., Tao, J., Jin, M., Qin, H., Zhou, B., Zhang, W., Ma B., Wang, G., Lai, Y., Chen, S. and Zhang, J. (2019). A class B heat shock factor selected for during soybean domestication contributes to salt tolerance by promoting flavonoid biosynthesis. New Phytologist. Doi: 10.1111/nph.16104.

Zhou, Y., Xiong, Q., Yin, C., Ma, B., Chen, S. and Zhang, J. (2019). Ethylene biosynthesis, signaling and crosstalk with other hormones in rice. Small Methods. Doi: 10.1002/smtd.201900278.

Plant Molecular Cytogenetics

Zhukuan Cheng, Principal Investigator, Ph.D. (1999, Institute of Genetics, CAS, China).

Research Interests: Regulatory mechanism of plant meiosis.

Email: zkcheng@genetics.ac.cn

Publications

- Xue, Z. H., Liu, C. Z., Shi, W. Q., Miao, Y. J., Shen, Y., Tang, D., Li, Y. F., You, A. Q., Xu, Y. Y., Chong, K. and Cheng, Z. K. (2019). OsMTOPVIB is required for meiotic bipolar spindle assembly. Proceedings of the National Academy of Sciences of the United States of America 116(32): 15967-15972.
- Shi, W. Q., Tang, D., Shen, Y., Xue, Z. H., Zhang, F. F., Zhang, C., Ren, L. J., Liu, C. Z., Du, G. J., Li, Y. F., Yan, C. J. and Cheng, Z. K. (2019). OsHOP2 regulates the maturation of crossovers by promoting homologous pairing and synapsis in rice meiosis. New Phytologist 222(2): 805-819.
- Xie, E., Li, Y. F., Tang, D., Lv, Y. L., Shen, Y. and Cheng, Z. K. (2019). A strategy for generating rice apomixis by gene editing. Journal of Integrative Plant Biology 61(8): 911-916.
- Cheng, X. J., Yu, H. X. and Cheng, Z. K. (2019). Protocols for analyzing rice meiotic chromosomes. Chinese Bulletin of Botany 54(4): 503-508.
- Tang, D. and Cheng, Z. K. (2018). From basic research to molecular breeding - Chinese scientists play a central role in boosting world rice production. Genomics Proteomics Bioinformatics 16(6): 389-392.

OsMTOPVIB is required for meiotic bipolar spindle assembly in rice

The organization of microtubules into a bipolar spindle is essential for chromosome segregation. Both centrosome and chromatin-dependent spindle assembly mechanisms are well studied in mouse, *Drosophila melanogaster*, and *Xenopus oocytes*; however, the mechanism of bipolar spindle assembly in plant meiosis remains elusive. According to our observations of meiotic microtubule assembly in *Oryza sativa*, *Zea mays*, *Arabidopsis thaliana*, and *Solanum lycopersicum*, we propose that a key step of plant bipolar spindle assembly is the correction of the multipolar spindle into a bipolar spindle at metaphase I. The multipolar spindles failed to transition into bipolar ones in *OsmtopVIB* with the defect in double-strand break (DSB) formation. However, bipolar spindles were normally assembled in several other mutants lacking DSB formation, such as *Osspo11-1*, *pair2*, and *crc1*, indicating that bipolar spindle assembly is independent of DSB formation. We further revealed that the mono-orientation of sister kinetochores was prevalent in *OsmtopVIB*, whereas biorientation of sister kinetochores was frequently observed in *Osspo11-1*, *pair2*, and *crc1*. In addition, mutations of the cohesion subunit OsREC8 resulted in biorientation of sister kinetochores as well as bipolar spindles even in the background of *OsmtopVIB*. Therefore, we propose that OsMTOPVIB plays a crucial role in meiotic spindle assembly.

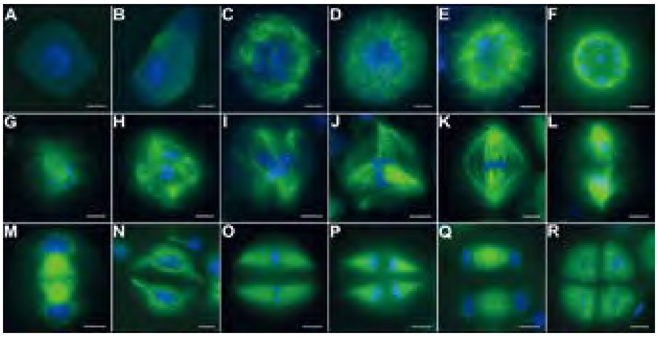

Figure: The process of meiotic spindle assembly in rice. (A) Leptotene. (B) Early zygotene. (C) Late zygotene. (D) Pachytene, reticular microtubule arrays are shown. (E-F) Early diakinesis, radial microtubules (E), and bright 'peri-nuclear ring' (F). (G) Diakinesis, microtubules penetrate the nucleus after NEB. (H-J) Early metaphase I, showing multipolar spindles. (K) Metaphase I, showing bipolar spindles. (L) Anaphase I. (M) Telophase I. (N) Dyad. (O) Metaphase II. (P) Anaphase II. (Q) Telophase II. (R) Tetrad. Meiotic chromosomes were stained with DAPI (blue), and microtubules were immunodetected with α-tubulin antibody (green). Scale Bars: 5 µm.

Rice Functional Genomics and Agrobiotechnology

Chengcai Chu, Principal Investigator, Ph.D. (1996, Martin-Luther University, Germany).

Research Interests: The laboratory mainly focuses on the dissecting the molecular basis of nutrient use efficiency and source-sink interaction using a combination of genetic, biochemical, physiological, and molecular tools. We are also interested in molecular design of super green rice based on the knowledge, resources and tools obtained from our studies.

Email: ccchu@genetics.ac.cn

Nitrate-NRT1.1B-SPX4 cascade integrates nitrogen and phosphorus signaling networks in plants

To ensure high crop yields in a sustainable manner, a comprehensive understanding of the control of nutrient acquisition is required. Particularly the signaling networks controlling coordinated utilization of the two most highly demanded mineral nutrients, nitrogen (N) and phosphorus (P), are of utmost importance. Here we reveal a mechanism by which nitrate activates phosphate and nitrate utilization in rice (*Oryza sativa* L.). We show that the nitrate sensor NRT1.1B interacts with a phosphate signaling repressor SPX4. Nitrate perception strengthens the NRT1.1B-SPX4 interaction and promotes ubiquitination and degradation of SPX4 by recruiting NBIP1 (NRT1.1B Interacting Protein 1), an E3 ubiquitin-ligase. This in turn allows the key transcription factor of phosphate signaling, PHR2, to translocate to the nucleus and initiate transcription of P utilization genes. Interestingly, the central transcription factor of nitrate signaling, NLP3, is also under the control of SPX4. Thus, nitrate-triggered degradation of SPX4 activates both phosphate and nitrate responsive genes, implementing the coordinated utilization of N and P.

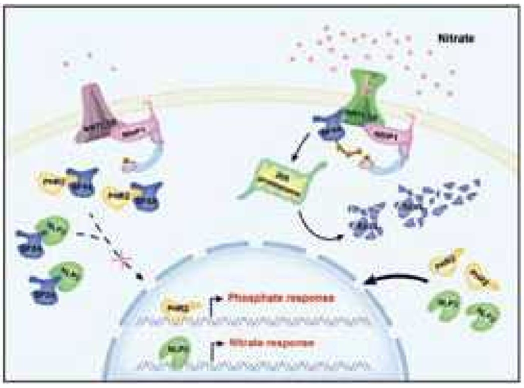

Figure: A proposed model of N-P coordinated response. In the absence or at low levels of nitrate, SPX4 is stable and binds to PHR2 and NLP3, and represses the downstream phosphate and nitrate responses. In high levels of nitrate, perception of nitrate leads to NRT1.1B-NBIP1 mediated SPX4 ubiquitination and degradation, which in turn releases PHR2 and NLP3, and coordinately activates downstream phosphate and nitrate responses.

Publications

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Environmental Epigenetics

Danhua Jiang, Principal Investigator, Ph.D. (2012, National University of Singapore, Singapore).

Research Interests: Epigenetic mechanisms of plant environmental response and memory. The function of histone variants and their incorporation mechanisms.

Email: dhjiang@genetics.ac.cn

Functional analysis of histone variant H3.3 in plant development and environmental response

Epigenetic mechanisms regulate and maintain gene expression patterns without altering the nucleotide sequence of DNA. Our group mainly focuses on the function of histone variants in epigenetic regulation and the epigenetic mechanisms of plant environmental responses. Through genetics, biochemistry, and epigenetic approaches, we found that histone H3 variant H3.3 plays an important role in plant development and environmental response. Mutations of H3.3 strongly delay seed germination. Transcriptome analysis indicated that a large number of genes related to seed germination are mis-regulated in the *h*3.3*ko* mutant during the germination process. Exogenous application of GA or ABA inhibitor Fluridone could promote germination rate of *h3.3ko*, suggesting that H3.3 regulates the expression of GA synthesis pathway and ABA degradation pathway genes. We propose that H3.3 is involved in epigenetic reprogramming during seed germination. In addition, by using the *h3.3* knockdown (*h3.3kd*) mutant, we found that H3.3 is required for plant response to ambient temperatures. ASF1a/b, the deposition chaperone of H3.3, interact with ELF7, the subunit of transcription elongation complex, and ELF7 is also required for plant response to ambient temperatures. Therefore, the assembly of H3.3 coordinates with transcriptional elongation to regulate the plant response to the environment. Our results suggest the pivotal function of H3.3 in plant development and environmental responses.

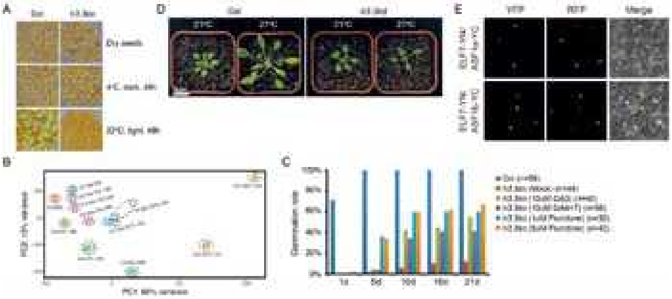

Figure: H3.3 regulates plant development and environmental responses. (A) Germination is delayed in *h*3.3*ko* mutant. (B) PCA analysis of Col and *h*3.3*ko* transcriptome during seed germination. (C) *h*3.3*ko* see germination is promoted by GA and ABA inhibitor fluridone. (D) *h*3.3*kd* mutant is hyposensitive to high ambient temperatures. (E) ASF1a/b directly interact with ELF7 in BiFC analysis.

Systems Biology of Plant Organogenesis

Yuling Jiao, Principal Investigator, Ph.D. (2006, Yale University, USA).

Research Interests: We combines transcriptome analysis, imaging, molecular genetics, and modeling to understand shoot lateral appendage formation and patterning, and its application in molecular design of wheat spike architecture.

Email: yljiao@genetics.ac.cn

A microtubule mediated mechanical feedback controls leaf blade flattening

Many plant species have flattened leaf-like organs (like leaf, sepal, *etc*.) and axisymmetric cylindrical organs (like root, stem, *etc*.). How plants regulate the morphogenesis of different organ shapes is a fundamental question in biology. Combining experimental analysis and mathematical modeling, we have uncovered a microtubule-mediated mechanism in sensing and amplifying mechanical stress, which can account for the formation of different organ shapes in plant species. Using high-resolution imaging, we find a differential arrangement of cortical microtubule (CMT) organization in periclinal and anticlinal cell walls. Disruption of this regular microtubule patterns affects anisotropic cell growth/division and organ flattening. Mathematical simulations indicate that CMTs align along predicted mechanical stress patterns in internal walls and amplify the local heterogeneity of mechanical stress, which generates a positive feedback mechanism in promoting organ growth. In addition, through mutant analysis and microsurgical experiments, we further demonstrate that the final organ shapes rely on both initial shapes and CMT-mediated mechanical feedback. This mechanism can either amplify an initial degree of flatness in leaf-like organs or promote the formation of axisymmetric organs, and therefore can be a general explanation in morphogenesis of different organ shapes.

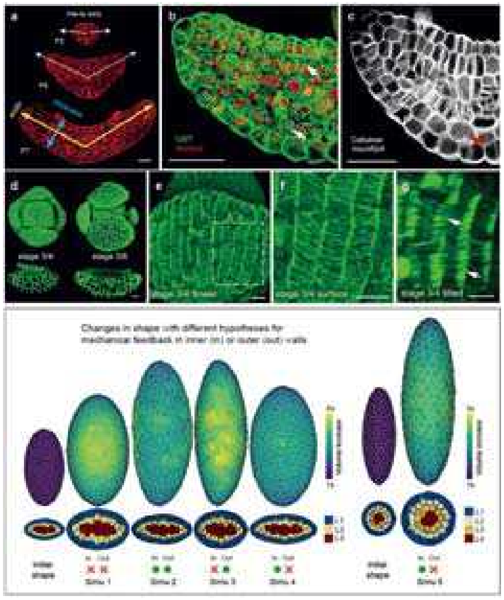

Figure: Anisotropic growth and cortical microtubule organization in leaf-like organs. (a) Anisotropic growth in Arabidopsis leaf primordium (P) along the medio-lateral (me-la) axis. (b) Immunolocalization of cortical microtubule arrays in anticlinal cell walls of Arabidopsis leaf primordium. (c) Arrangement of cellulose microfibrils in anticlinal cell walls of Arabidopsis leaf primordium. (d) Anisotropic growth in Arabidopsis sepal primordia. (e) Cortical microtubule arrays in periclinal cell walls of Arabidopsis sepal primordium. (f) Magnification of the inset in (e). (g) Cortical microtubule arrays in anticlinal cell walls of the same Arabidopsis sepal primordium in (e). Scale bars, 20 μm in (a-d) and 10 μm in (e-g) Figure 2. Computational modeling of organ shape formation. Starting from a flattened ellipsoid (simulations 1-4) different levels of flatness amplification can be achieved depending on whether the feedback is active (green dot) or inactive (red cross) on outer and/or inner walls. A spheroid (Simulation 5) remains axisymmetric with the feedback on inner walls only. Colors in cross sections of simulated organs represent cells in different layers.

Publications

Tian, C., Wang, Y., Yu, H., He, J., Wang, J., Shi, B., Du, Q., Provart, N. J., Meyerowitz, E. M. and Jiao, Y. (2019). A gene expression map of shoot domains reveals regulatory mechanisms. Nature Communications 10(1): 141.

Jiao, Y. (2019). Designing plants: modeling ideal shapes. Molecular Plant 12(2): 130-132.

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Regulation of Plant Immunity and Tomato Quality Formation

Chuanyou Li, Principal Investigator, Ph.D. (1999, Institute of Genetics, CAS, China).

Research Interests: Tomato as a model to investigate systemin/jasmonate-signaled systemic plant immunity and the molecular mechanism of tomato quality formation.

Email: cyli@genetics.ac.cn

Publications

Wang, H., Li, S., Li, Y., Xu, Y., Wang, Y., Zhang, R., Sun, W., Chen, Q., Wang, X. J., Li, C. and Zhao, J. (2019). MED25 connects enhancer-promoter looping and MYC2-dependent activation of jasmonate signalling. Nature Plants 5(6): 616-625.

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Zhou, W., Lozano-Torres, J. L., Blilou, I., Zhang, X., Zhai, Q., Smant, G., Li, C. and Scheres, B. (2019). A jasmonate signaling network activates root stem cells and promotes regeneration. Cell 177(4): 942-956 e914.

Molecular mechanism of enhancers in regulating jasmonate signaling

Enhancers are promoter-distal cis-regulatory DNA elements that control gene expression independently of their orientation to and distance from target promoters. Enhancers communicate with target promoters by recruiting transcription factors and their cofactors, which establish enhancer–promoter chromatin looping. Signal-dependent chromatin looping dynamically brings remote enhancers into close spatial proximity to their target promoters, allowing accurate spatiotemporal gene expression. In this study, we performed chromatin immunoprecipitation followed by sequencing (ChIP-seq) to investigate the genomewide co-occupancy pattern of MYC2 and MED25 during JA signalling. A set of 461 co-occupied sites, which are distal to any promoters of MYC2 and MED25 co-targeted genes, were predicted to be putative JA enhancers (JAEs). Chromosome conformation capture assays revealed that JA regulates the dynamic chromatin looping between JAEs and their promoters in a MYC2- and MED25-dependent manner. We demonstrated that an intergenic JAE of ME2 could exert distinct effects on MYC2 expression during short- or long-term JA responses, revealing the exquisite precision of JAEs in regulation of JA signalling. We demonstrate that new gene editing tools open up new avenues to elucidate the in vivo function of enhancers. Our work provides a paradigm for functional study of plant enhancers in the regulation of specific physiological processes.

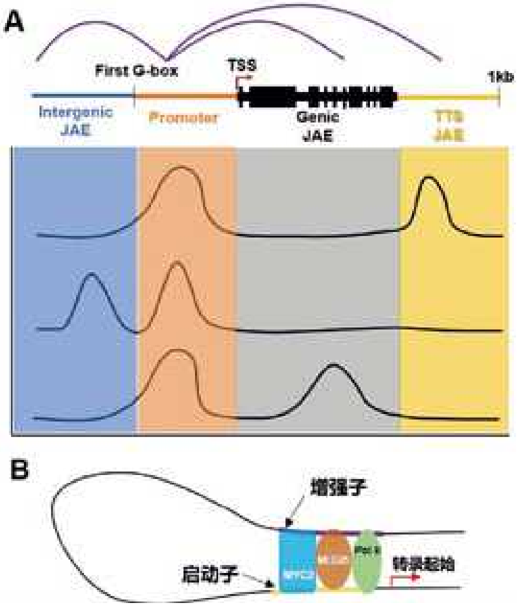

Figure: MED25 mediates enhancer-promoter looping during jasmonate signaling. (A) Schematic diagram showing three JAE categories. (B) A work model showing that MED25 mediates enhancer-promoter looping during jasmonate signaling.

Developmental Biology and Metabolic Pathways of Higher Plants

Jiayang Li, Principal Investigator, Member of Chinese Academy of Sciences, Fellow of TWAS, Member of the German National Academy of Sciences, Foreign Associate of USA National Academy of Sciences and Foreign Fellow of the Royal Society of London for Improving Natural Knowledge.

Research Interests: Molecular genetics of plant development and metabolism, focusing on the understanding of molecular bases of plant architecture features and key metabolic pathways that define major agronomic traits and devoting on the breeding of high-yield, superiorquality, stress-resistant, and resource-use-efficiency new varieties of rice and natural rubber crops.

Email: jyli@genetics.ac.cn

SLR1 inhibits MOC1 degradation to coordinate tiller number and plant height in rice

The breeding of cereals with altered gibberellin (GA) signaling propelled the 'Green Revolution' by generating semidwarf plants with increased tiller number. The mechanism by which GAs promote shoot height has been studied extensively, but it is not known what causes the inverse relationship between plant height and tiller number. Here we show that rice tiller number regulator MONOCULM 1 (MOC1) is protected from degradation by binding to the DELLA protein SLENDER RICE 1 (SLR1). GAs trigger the degradation of SLR1, leading to stem elongation and also to the degradation of MOC1 and hence a decrease in tiller number. This discovery provides a molecular explanation for the coordinated control of plant height and tiller number in rice by GAs, SLR1 and MOC1.

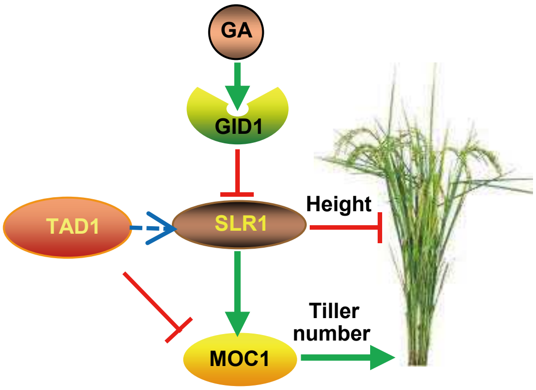

Figure: A model of GA signaling and MOC1 regulation of plant height and tiller number in rice.

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Genomic Big Data Analysis and Software Development

Chengzhi Liang, Principal Investigator, Ph.D. (1995, Institute of Genetics, CAS). M.Math. (2001, Computer Science, University of Waterloo, Canada).

Research Interests: Comparative and population genomic analysis in plants. The whole genome duplication events occurred in several plants. Amplification of gene families led to strong environmental adaptation and evolution of key traits. Population genomic analysis of a large collection of Chinese rice accessions and GWAS. Assembly of high-quality, near complete genomes using single-molecule sequencing and mapping data and Hi-C data. We developed a software tool HERA for assembling high-quality genomes by efficiently resolving repetitive sequences. HERA can dramatically improve the contiguity of the assembled sequences on the basis of existing tools. We have assembled many genomes of rice, wheat, maize, soybean and several heterozygous plants. Database development. We developed an integrated omics knowledgebase (MBKbase, www.mbkbase.org) to support functional genomics and molecular breeding. MBKbase aims to integrate pan-genome and genotype to phenotype information, includes multiple reference genomes and population level genetic variants.

Email: cliang@genetics.ac.cn

MBKbase for rice: an integrated omics knowledgebase for molecular breeding in rice

To date, large amounts of genomic and phenotypic data have been accumulated in the fields of crop genetics and genomic research, and the data are increasing very quickly. However, the bottleneck to using big data in breeding is integrating the data and developing tools for revealing the relationship between genotypes and phenotypes. Here, we report a rice sub-database of an integrated omics knowledgebase (MBKbase-rice,www.mbkbase.org/rice), which integrates rice germplasm information, multiple reference genomes with a united set of gene loci as a pan-genome, population sequencing data, phenotypic data, known alleles and gene expression data. In addition to basic data search functions, MBKbase provides advanced web tools for genotype searches at the population level and for visually displaying the relationship between genotypes and phenotypes. Furthermore, the database also provides online tools for comparing two samples by their genotypes and finding target germplasms by genotype or phenotype information, as well as for analyzing the user submitted SNP or sequence data to find important alleles in the germplasm. A soybean sub-database and wheat and maize data will be added in 1–2 years. The data and tools integrated in MBKbase will facilitate research in crop functional genomics and molecular breeding.

Figure: An example of a locus page showing multiple types of information associated with the locus OsG00067204 on rice gene *GS5*.

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- Yu, H., Lu, L., Jiao, B. and Liang, C. (2019). Systematic discovery of novel and valuable plant gene modules by large-scale RNA-seq samples. Bioinformatics 35: 361-364.

Rice Genome Design and Molecular Breeding

Shaoyang Lin, Principal Investigator, Ph.D. (1993, Chiba University, Japan).

Research Interests: We focus on building a new model of genomic updating and design breeding for crops. We replace the 'bug' loci of rice variety Kongyu131 with other favorable alleles by the results of QTL analysis and re-sequencing. Our projects involve rice blast resistance, eating quality, high yield, regional adaptation and other agronomic traits.

Email: sylin@genetics.ac.cn

Improving the elite rice variety Kongyu131 by updating *badh2* and *Spk* loci of the genome

Achieving precise and targeted improving is an important part of molecular breeding in rice. Inspired by App upgrade, our group focuses on finding out the 'bugs' and updating the genome of the elite rice variety Kongyu131 to the SPSL (Single Point Substitution Line), which is replaced only a small chromosome segment carrying a favorable allele by genetic recombination. Kongyu131 is a nonfragrant *japonica* rice variety which displays a compact plant architecture with erect tillers. Recently, two new SPSLs are obtained by replacing the tiller angle locus *Spk* and the fragrant recessive allele *badh2-E7* of Kongyu131 (Fig.a-d). Using 4-5 SNP markers designed against the sequence within and around allele, the introgressed segments of two SPSLs were shortened to nearly 800Kb (*badh2-E7*) and 1Mb (*Spk*) to minimize the linkage drag. Finally, the recovery ratio of the recurrent parent genome (RRPG) were 99.82% (*badh2-E7*) and 99.58% (Spk) (Fig.e-f). The SPSL(*+badh2-E7*) had the distinctive fragrance as GKKZ and exhibited no statistical difference in yield and other agronomic performance to Kongyu131. The SPSL(+*Spk*) exhibited a spread-out plant architecture by increase the tiller angle nearly 20°compared to Kongyu131 and showed 2-4 g yield increase per plant at three different cultivated density.

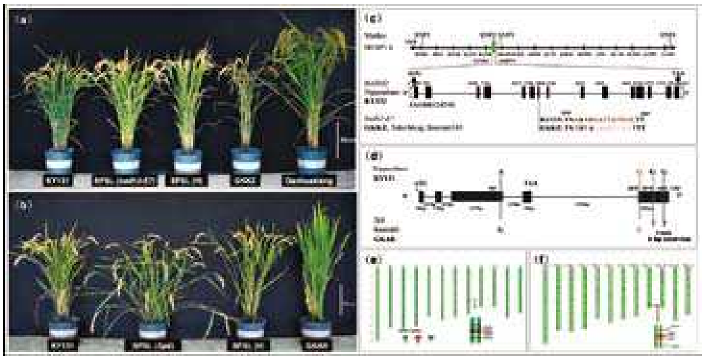

Figure: Two new SPSLs of Kongyu131 and the alleles of *BADH2* and *Spk*. (a-b) Plant architecture of Kongyu131 and its SPSLs at Jiamusi. Scale bar, 30cm. (c-d) The gene structure and the alleles of *BADH2* and *Spk*. (e-f) Graphical genotype of the SPSLs. e: SPSL(+*badh2-E7*); f: SPSL(+*Spk*). The green bars represent the chromosome fragments derived from Kongyu131, and the red ones are from Donors.

Publications

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Plant Functional Metabolomics

Guodong Wang, Principal Investigator, Ph.D. (2003, Shanghai Institute of Plant Physiology and Ecology, CAS, China).

Research Interests: Plants collectively produce huge diverse specialized metabolites, many of which have beneficial effect to human health. The overall interest within my laboratory is to study how plant synthesizes these healthy specialized metabolites, the key enzymes potentially involved in these biosynthesis pathways and the mechanism of the enzymatic reactions.

Email: gdwang@genetics.ac.cn

Publications

He, J., Chen, Q. W., Xin, P. Y., Yuan, J., Ma, Y. H., Wang, X. M., Xu, M. M., Chu, J. F., Peters, R. J. and Wang, G. D. (2019). CYP72A enzymes catalyse 13-hydrolyzation of gibberellins. Nature Plants 5(10): 1057-1065.

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CYP72A9, a new player controlling plant gibberellins metabolism

Bioactive gibberellins (GAs, diterpenes) are essential hormones in land plants, controlling many aspects of plant growth and developments. Recently, we discovered that members of the CYP72A subfamily, rather than above-mentioned CYP714 subfamily, encode *bona fide* gibberellin 13-oxidase, which catalyzes the conversion of 13-H GAs (GA_{12}, GA_9 and GA_4) to the corresponding13-OH GAs (GA_{53}, GA_{20} and GA_1). CYP72A9 in Arabidopsis is predominantly expressed in developing seeds. *cyp72a9* mutants show a deficiency in GA_1 and an increase in the concentration of GA_4, suggesting that CYP72A9 plays a key role in controlling GA metabolism in Arabidopsis. Comprehensive gibberellin profiling revealed the difference of GA metabolism between rice and Arabidopsis: GA_1 was biosynthesized from far upstream precursor GA_{53} in rice, which GA_1 was directly biosynthesized from GA_4 in Arabidopsis. We further demonstrated that the conversion of GA_4 to GA_1 is an indispensable and conserved factor for primary seed dormancy in Brassicaceae plants.

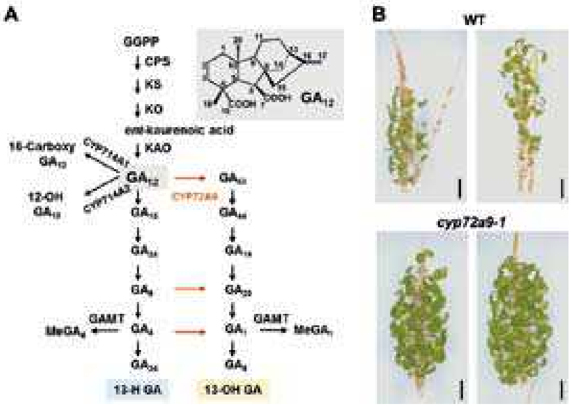

Figure: CYP72A9 enzyme catalyzes 13-hydroxylzation of gibberellins, indicated with red arrows (A), and controlling seeds primary dormancy in plants (B).

Molecular Basis of Shoot Branching

Yonghong Wang, Principal Investigator, Ph.D. (2004, Institute of Genetics and Developmental Biology CAS, China).

Research Interests: Using *Arabidopsis* and rice as model systems, we mainly focus on dissecting the molecular networks involved in formation and development of the shoot axillary meristems, including the initiation, dormancy and activation of axillary buds and the determination of axillary shoot angle, trying to identify genes applicable to improving crop yields.

Email: yhwang@genetics.ac.cn

Towards molecular mechanism underlying rice tiller angle

Tiller angle is one of the most important agronomic traits for rice (*Oryza sativa* L.) plant architecture and grain yield. LAZY1 (LA1) was previously reported to control tiller angle via affecting shoot gravitropism, but the underlying molecular mechanism remains largely unknown. In this study, we identified an LA1-interacting protein Brevis Radix Like 4 (OsBRXL4) through yeast two hybrid system. We showed that the interaction between OsBRXL4 and LA1 occurs at the plasma membrane and their interaction determines nuclear localization of LA1(Fig. A-E). Further analysis demonstrated that nuclear localization of LA1 is essential for its function (Fig. F), which is different from the Arabidopsis *LA1* gene. Overexpression of *OsBRXL4* leads to a prostrate growth phenotype, whereas the *OsBRXLs* RNAi plants, in which the expression levels of *OsBRXL1*, *OsBRXL4*, and *OsBRXL5* were decreased, display a compact phenotype(Fig. G). Genetic analysis further supported that OsBRXL4 controls rice tiller angle by affecting nuclear localization of LA1. Taken together, our study not only identifies OsBRXL4 as a regulatory component of rice tiller angle but also provides new insights into genetic regulation of rice plant architecture.

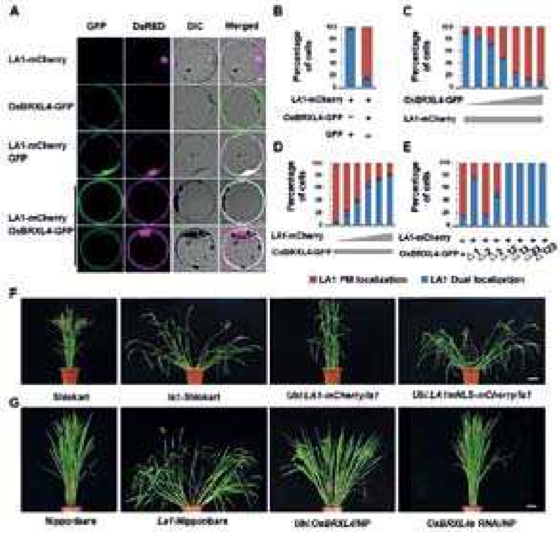

Figure: OsBRXL4 regulates rice tiller angle through affecting LAZY1 nuclear localization. (A-E) OsBRXL4 significantly affects nuclear localization of LA1. Scale bars, 5 μm.(F) Nuclear localization of LA1 is required for its function. Scale bar, 10 cm.(G) OsBRXL4 regulates rice tiller angle. Scale bar, 10 cm.

Publications

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Ubiquitination Modification and Plant Stress Signal Transduction

Qi Xie, Principal Investigator, Ph.D. (1994, Universidad de Madrid, Spain).

Research Interests: Breed crops (mainly focus on sorghum and maize) with high biomass and stress tolerance through the molecular genetics, bioinformatics and traditional breeding methods. Uncover the functional mechanism on ubiquitination modification of proteins in response to biotic and abiotic stresses with the biochemical and genetic approaches in the model plant Arabidopsis.

Email: qxie@genetics.ac.cn

Control of bird feeding behavior by *Tannin1*

Bird predation during seed maturation causes great loss to agricultural production. Through GWAS analysis of a large-scale sorghum germplasm diversity panel, we identified that *Tannin1*, encoding a WD40 protein functioning in the WD40/MYB/bHLH complex, controls bird feeding behavior in sorghum. Metabolic profiling analysis showed that a group of sorghum accessions preferred by birds contain mutated *tan1-a/b* alleles and accumulate significantly lower levels of anthocyanins and condensed tannin compounds. In contrast, a variety of aromatic and fatty acid-derived volatiles accumulate at significantly higher levels in these bird-preference accessions. Both sparrow feeding and sparrow volatile attractant assays, which confirmed, respectively, the antifeedant and attractant functions of these differentially accumulated metabolites. In addition, the connection between the biosynthesis pathway of anthocyanin and proanthocyanidin and the pathway of fatty acid–derived volatile biosynthesis was demonstrated by discovering that Tannin1 complex modulates fatty acid biosynthesis by regulating the expression of *SbGL2*, thus affecting the accumulation of fatty acid-derived volatiles. Taken together, our study identified *Tannin1* as the gene underlying the major locus controlling bird feeding behavior in sorghum, illustrating an example of the identification of an ecologically impactful molecular mechanism from field observation and providing significant insights into the chemistry of bird–plant ecological interactions.

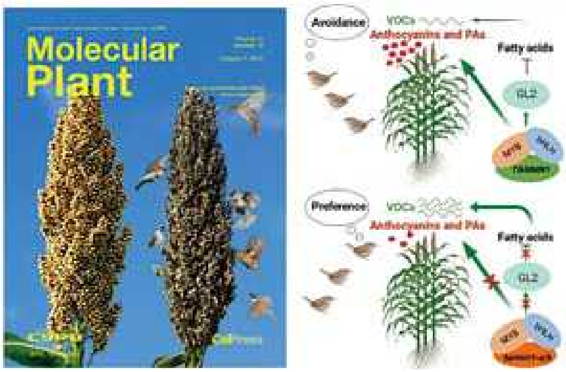

Figure: A working model for the ecological impact of the *Tannin1* locus

Publications

Xie, P., Shi, J. Y., Tang, S. Y., Chen, C. X., Khan, A., Zhang, F. X., Xiong, Y., Li, C., He, W., Wang, G. D., Lei, F. M., Wu, Y. R. and Xie, Q. (2019). Control of bird feeding behavior by Tannin1 through modulating the biosynthesis of polyphenols and fatty acid-derived volatiles in sorghum. Molecular Plant 12(10): 1315-1324.

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Yu, F. and Xie, Q. (2019). Approaches to identify protein ubiquitination sites in plants. Methods in Molecular Biology 2026: 85-93.

Plant Cell Communications and Biological Robustness

Cao Xu, Principal Investigator, Ph.D. (2012, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences), Postdoctoral Fellow (2013-2017, Cold Spring Harbor Laboratory).

Research Interests: Small signaling peptides and plant cell-to-cell communications. Plant robustness and rational design of smart crops

Email: caoxu@genetics.ac.cn

Protein allostery determines cell fate of plant shoot apical meristem

Shoot apical meristem (SAM) maintenance and maturation determine plant architecture and flowering time, which set up the developmental basis for crop design. The molecular machinery composed of peptide ligand CLAVATA3 (CLV3) and its receptor CLAVATA1 (CLV1) controls tomato SAM proliferation, while TERMINATING FLOWERING (TMF), an *Arabidopsis* LSH1 and *Oryza* G1 (ALOG) family transcription suppressor, and its related transcriptional complex regulate the programed maturation of the SAM. We found that transcriptional compensation between ligand paralogs, *SlCLV3* and *SlCLE9*, operates in tomato to achieve the robustness of SAM maintenance. Loss of *SlCLV3* triggers a dramatic up-regulation of *SlCLE9*, which functions through SlCLV1 to control stem cell proliferation. To ensure a precise transition from proliferation into differentiation of tomato SAM, TMF senses the spatio-temporal altered cellular redox conditions to undergo protein phase separation that directly turns on/off the expression of a flowering promoting gene *ANANTHA* (*AN*). Together, our study reveals that protein allostery achieved by ligand-receptor binding and phase separation of transcription factors control the activity of plant shoot apical stem cells.

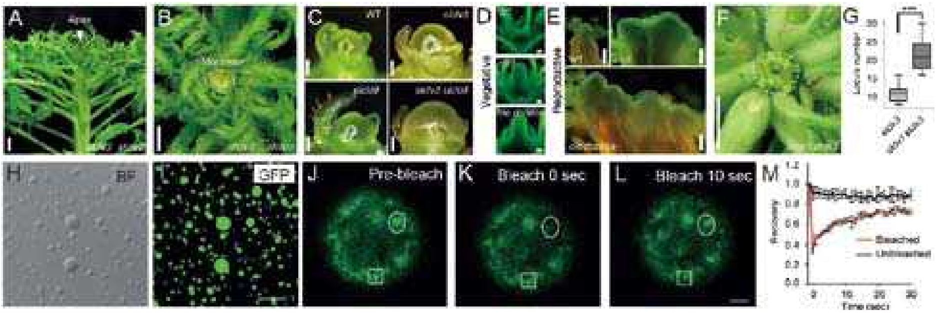

Figure: (A-B) Side and top-down view of *slclv3 slcle9*. White arrowhead, apex; white dotted circle, meristem. Scale bars, 1 cm. (C) Primary meristems from WT, *slclv3*, *slcle9* and *slclv3 slcle9*. Scale bars, 100 μm. (D-E) Confocal micrographs of *Arabidopsis* vegetative and inflorescence meristems from WT, *clv3* and *dodeca-cle*. Scale bars, 50 μm in (D) and 100 μm in (E). (F) Top-down view of *slclv1 slclv3* showing an enlarged meristem flanked by multiple fasciated floral buds (dashed circle). Scale bar, 2 cm. (G) Quantification of locule number from *slclv3* (n = 43) and *slclv1 slclv3* (n = 24). $***P = 5 \times 10^{-22}$, two-tailed, two-sample t-test. (H-I) Representative DIC and fluorescence images showing the liquid-like droplets formed by eGFP-TMF protein. Scale bar, 10 μm. (J-M) FRAP assay showing the dynamic property of TMF-eGFP condensates in *35S:TMF-eGFP* transgenic plants represented by images (JL) and quantification data (M). Quantitative data are representative of three independent photobleaching events. Scale bar, 2 μm. The bleached (red line) event occurred at time = 0 s. The unbleached (black line) was used as control.

Publications

Rodriguez-Leal, D., Xu, C., Kwon, C. T., Soyars, C., Demesa-Arevalo, E., Man, J., Liu, L., Lemmon, Z. H., Jones, D. S., Van Eck, J., Jackson, D. P., Bartlett, M. E., Nimchuk, Z. L. and Lippman, Z. B. (2019). Evolution of buffering in a genetic circuit controlling plant stem cell proliferation. Nature Genetics 51(5): 786-792.

Rice Genetics and Molecular Breeing

Shanguo Yao, Principal Investigator, Ph.D. (2004, Ehime University, Japan).

Research Interests: Molecular design of new rice varieties in northeast China.

Email: sgyao@genetics.ac.cn

Developed a new version of Zhongke902 with improved grain length and lodging resistance

By introducing the superior alleles of blast resistance and fragrance under the background of Kongyu 131, we developed a new variety of Zhongke 902 which is suitable for extension in the third accumulative temperature zone of Heilongjiang Province.Zhongke 902 is a multi-panicle variety with strong tillering ability, and its high yield relies on the number of effective panicles per unit. However, in the current planting system, the excessive application of nitrogen fertilizer, coupled with the longterm low temperature and rainy in 2019, made the lodging problem of Zhongke 902 more prominent and hinder the further extension.In addition, the domestic rice market's preference for long grain also urgently needs to improve the round grain appearance of Zhongke 902.Therefore, we focused on introducing the lodging resistance and long grain alleles into the background of Zhongke 902 in this year.Combined with the evaluation of other agronomic traits including yield, we developed a new line of Zhongke 633 with longer grain and stronger lodging resistance (Figure), which will be tested in the experiment of "Long Grain Tackling Program" in the third accumulative temperature zone of Heilongjiang Province in 2020.

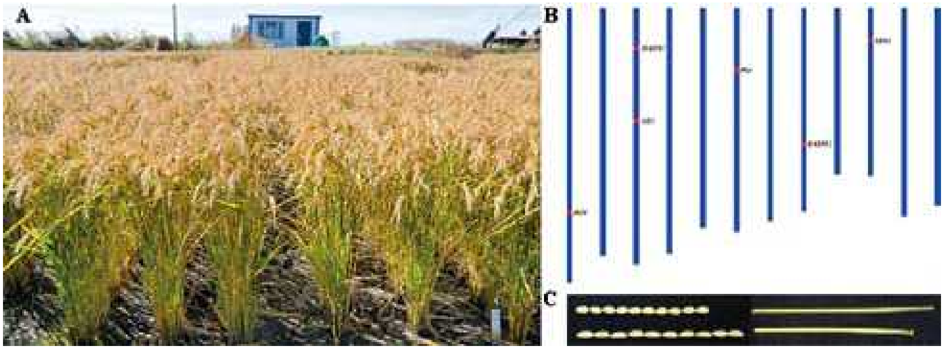

Figure: Development of a new version of ZK902 with improved grain length and lodging resistance. A: Population morphology of the modified version ZK633. B: Diagram of the introduced alleles in the new version of ZK633. C: Morphology comparison of grain length and the upper most internode betweenZH902 and the modified version of ZK633. Top: ZK902; Bottom: ZK633.

Ethylene Signaling and Seed Trait Regulation

Jinsong Zhang, Principal Investigator, Ph.D. (1991, Peking University, China).

Research Interests: We identified novel components and mechanisms in rice ethylene signaling, and discovered molecular networks involved in regualtion of seed size and oil accumulation in soybean. Genes in stress tolerance were also investigated.

Email: jszhang@genetics.ac.cn

A GDSL lipase regulates ethylene signaling in rice

We characterized the rice *mhz11* mutant whose roots are insensitive to ethylene. *MHZ11* encodes a GDSL lipase, and its PLA2 activity is required for ethylene response. Overexpression of the MHZ11 caused short root of constitutive ethylene response. *MHZ11* can hydrolyze phospholipids to generate fatty acids, which can be transfered to sterol to form sterol esters. MHZ11 acts at ethylene receptor level upstream of OsEIN2 and OsEIL1. OsCTR2 has two forms, the phosphorylated and non-phosphorylated. *MHZ11* mediates fast inhibition of OsCTR2 phosphorylation by ethylene, while in mhz11 mutant, the OsCTR2 phosphorylation remains at high levels. An inhibitor of sterol biosynthesis, FEN, can partially rescue the ethylene response of the *mhz11* mutant. We propose that, *MHZ11* acts to reduce sterol level, and conformation change of receptors would block its association with OsCTR2, leading to OsCTR2 dephosphoryaltion and activation of downstream events.

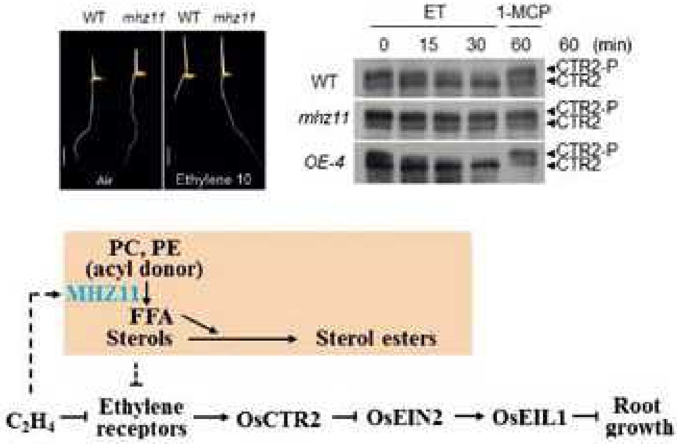

Figure: MHZ11 working model in regulation of ethylene response in rice. Upper left panel: root of *mhz11* is insensitive to ethylene. Upper right panel: Effects of ethylene treatment on OsCTR2 phosphorylation in *mhz11* and *MHZ11*-overexpressing plants. Ethylene gradually inhibits OsCTR2 phosphorylation in WT plants, but does not affect OsCTR2 phosphorylation status in *mhz11* mutant. In MHZ11-overexpressing plants, ethylene treatment quickly and drastically suppressed OsCTR2 phosphorylation. Lower panel: Possible mechanism of MHZ11 regulation on rice ethylene signaling. Upon ethylene treatment, MHZ11 hydrolyzes phospholipids to produce fatty acids, which can form sterol esters with sterols. This function blocks association of ethylene receptors with OsCTR2, leading to dephosphorylation of OsCTR2 and downstream ethylene response.

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Zheng, H., Dong, L., Han, X., Jin, H., Yin, C., Han, Y., Li, B., Qin, H., Zhang, J., Shen, Q., Zhang, K. and Wang, D. (2019). The TuMYB46L-TuACO3 module regulates ethylene biosynthesis in einkorn wheat defense to powdery mildew. New Phytologist. Doi: 10.1111/nph.16305.

Molecular Basis of Plant-microbe Interaction

Jian-Min Zhou, Principal Investigator, Ph.D. (1994, Purdue University, USA), Assistant Professor and Associate Professor (1997-2004, Kansas State University, USA), Associate Investigator and Investigator (2004-2012, National Institute of Biological Sciences, China).

Research Interests: Plants use numerous immune receptors, pattern-recognition receptors (PRRs) and NB-LRR proteins, to detect invading pathogens and resistance against pathogen infection. Our work aims at understanding how plant immune receptors work at the molecular level and how downstream signaling is activated.

Email: jmzhou@genetics.ac.cn

Publications

Wang, J., Hu, M., Qi, J., Han, Z., Wang, G., Qi, Y., Wang, H. W., Zhou, J. M. and Chai, J. (2019). Ligand-triggered allosteric ADP release primes a plant NLR complex. Science 364(6435).

Wang, J., Hu, M., Wu, S., Qi, J., Wang, G., Han, Z., Qi, Y., Gao, N., Wang, H. W., Zhou, J. M. and Chai, J. (2019). Reconstitution and structure of a plant NLR resistosome conferring immunity. Science 364(6435).

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Wang, J., Liu, X., Zhang, A., Ren, Y., Wu, F., Wang, G., Xu, Y., Lei, C., Zhu, S., Pan, T., Wang, Y., Zhang, H., Wang, F., Tan, Y. Q., Jin, X., Luo, S., Zhou, C., Zhang, X., Liu, J., Wang, S., Meng, L., Chen, X., Lin, Q., Guo, X., Cheng, Z., Tian, Y., Liu, S., Jiang, L., Wu, C., Wang, E., Zhou, J. M., Wang, Y. F., Wang, H. and Wan, J. (2019). A cyclic nucleotide-gated channel mediates cytoplasmic calcium elevation and disease resistance in rice. Cell Research 29(10): 820-831.

Reconstitution and structure of a plant NLR resistosome conferring immunity

Effector triggered immunity (ETI) is an essential layer of plant innate immune system that uses nucleotide-binding leucine-rich repeat receptors (NLRs) to recognize pathogen effector proteins in a highly specific manner. We found that PBL2, a paralogs of BIK1, functions as a decoy protein that enables pathogen perception. PBL2 is similarly modified by AvrAC through uridylation and this modification activates a NLR receptor ZAR1, leading to immune activation. To further understand how a plant NLR is activated upon recognition of its ligand, we collaborated with structure biologists and solved the structure of an ADP bound preformed ZAR1-RKS1 complex representing the resting state of the NLR, the ZAR1-RKS1-PBL2^{UMP} complex representing an intermediate state, and an dATP/ATP bound ZAR1-RKS1-PBL2^{UMP} complex representing an activated state which we term “resistosome”. The formation of resistosome is essential for immune activation and disease resistance. The first α--helix of pentamer forms a funnel structure to associate with plasma membrane, suggesting that the resistosome acts as an ion channel or pore for immune activation. The discovery of resistosome represents a major milestone in plant immunity research and opens up new avenues for better design of disease/pest resistant crop plants.

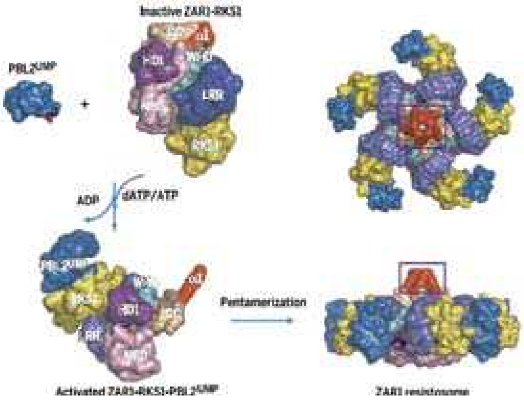

Figure: PBL2^{UMP}-induced assembly of the ZAR1 resistosome. Interaction of PBL2^{UMP} with the preformed ZAR1-RKS1 complex triggers conformational changes in ZAR1NBD and adenosine diphosphate (ADP) release, allowing the complex to bind dATP or ATP. dATP or ATP binding induces structural remodeling and fold switching of ZAR1, resulting in full activation of ZAR1 and formation of the pentameric ZAR1 resistosome, that is required for cell death triggering and disease resistance.

Molecular Genetics and Cell Wall Biology

Yihua Zhou, Principal Investigator, Ph.D. (1998, Institute of Genetics, CAS, China).

Research Interests: Dissecting mechanisms for secondary wall biosynthesis and functions on plant growth, which may be helpful for improving agronomic traits, eg. lodge resistance in crops.

Email: yhzhou@genetics.ac.cn

Identification of a cell growth coordinator in rice

Cell growth includes two fundamental events: cell expansion and wall reinforcement. Plants have evolved complex mechanisms to coordinate the two cellular events during cell morphogenesis. However, the combinatorial mechanism that integrates different regulatory pathways to orchestrate cell expansion and wall strengthening remains elusive. Here, we report that rice homeobox protein KNAT7 interacts with a growth master regulator, GRF4, and a secondary wall regulator, NAC31, to coordinate cell expansion and wall thickening in fiber cells. Mutation in KNAT7 resulted in enhanced secondary wall biosynthesis and cell expansion in the internodes and grain glumes; overexpression of *KNAT7* gave rise to the opposite effects. Biochemical and molecular analyses revealed that KNAT7 interacts with the secondary wall key regulator NAC31 and the master cell growth factor GRF4 to repress their downstream regulatory pathways. Moreover, performing anatomical analysis and examining the expression of *KNAT7* and its interacting partners *NAC31* and *GRF4* in the developing internodes and panicles corroborated the spatiotemporal actions of the KNAT7-GRF4 and KNAT7-NAC31 modules. Therefore, KNAT7 is an integrative regulator to control cell morphogenesis, offers a mechanistic view for combinatorial modulation of plant cell growth. This finding may provide a tool for synergistic improvement of lodging resistance and grain yield in crops.

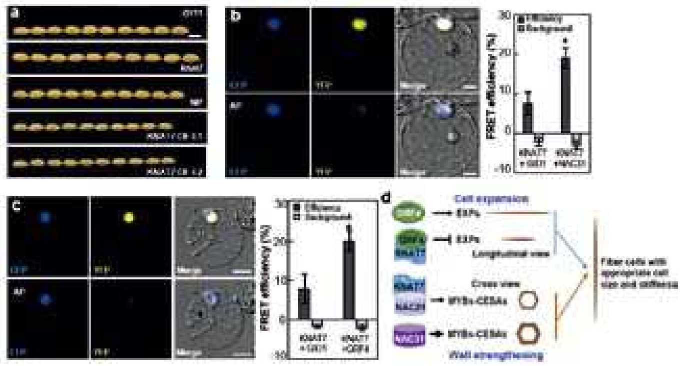

Figure: RiceHomeobox protein KNAT7 coordinates cell expansion and wall stiffness.(a) Rice grains of wild type, the *knat7* mutant and the overexpression plants. Bar = 5 mm. (b and c) FRET analysis in rice protoplasts, verifying the interactions between KNAT7 and NAC31/GRF4. The bottom panel shows fluorescence in the cell after photobleaching YFP (AP). Bars = 10 μm. The right panelsshowquantification of the FRET efficiency observed in left. FRET efficiency represents the fluorescence change of the donor fluorophore (CFP) after photobleaching YFP. The background indicates the stability of CFP fluorescence before photobleaching. Error bars represent the mean ± SD (n = 10 cells). *P < 0.01by Welch's unpaired t-test. Rice GID1 was used as a negative control. (d) The working model of rice KNAT7, showing that it coordinates cell expansion and cell wall stiffness via interacting with distinct regulators.

Publications

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Zhang, L., Zhang, B. and Zhou, Y. (2019). Cell wall compositional analysis of rice culms. Bio-protocol 9(20): e3398.

Wei, K., Zhao, Y., Zhou, H., Jiang, C., Zhang, B., Zhou, Y., Song, X. and Lu, M. (2019). PagMYB216 is involved in the regulation of cellulose synthesis in *Populus*. Molecular Breeding 39(5): 65.

Plant Functional Genomics and Breeding by Biotechnologies

Zhen Zhu, Principal Investigator, Ph.D. (1988, Institute of Genetics, CAS, China).

Research Interests: Study on no-homologous gene inducing post-transcriptional gene silencing Study the heterosis mechanism by large-scale comparative transcriptomeand molecular biology analysis of the super-hybrid rice Development of transgenic insect resistant rice, including the Lepidoptera pests resistant rice, and the novel anti-Brown planthopper rice.

Email: zzhu@genetics.ac.cn

Publications

Liu, Z., Wang, X., Dai, Y., Wei, X., Ni, M., Zhang, L. and Zhu, Z. (2019). Expressing double-stranded RNAs of insect hormone-related genes enhances baculovirus insecticidal activity. International Journal of Molecular Sciences 20(2):419.

Expressing double-stranded RNAs of insect hormone-related genes enhances baculovirus insecticidal activity

Baculoviruses have already been used for insect pest control, but the slow killing speed limits their further promotion and application. Here we develop a strategy for improving baculovirus insecticidal activity using Helicoverpa armigera nucleopolyhedrovirus (HearNPV) to express double-stranded RNAs (dsRNAs) targeting cotton bollworm (*Helicoverpa armigera*) juvenile hormone (JH)-related genes, JH acid methyl transferase gene (*HaJHAMT*) and JH acid binding protein gene (*HaJHBP*). Droplet-feeding bioassays show that the 50% lethal concentration (LC_{50}) values of recombinant baculoviruses expressing dsJHAMT and dsJHBP were 1.24 × 10^4 polyhedral inclusion bodies (PIB)/mL and 2.26 × 10^4 PIB/mL, respectively. Both were much lower than the control value (8.12 × 10^4 PIB/mL). Meanwhile, the LT_{50} of recombinant baculovirus expressing dsRNA of *HaJHBP* was only 54.2% of the control value, which means that larval death was accelerated. This study establishes a new strategy for pest management by interfering with insect hormone-related gene expression via baculoviruses, and the engineered baculoviruses have great potential application in cotton production.

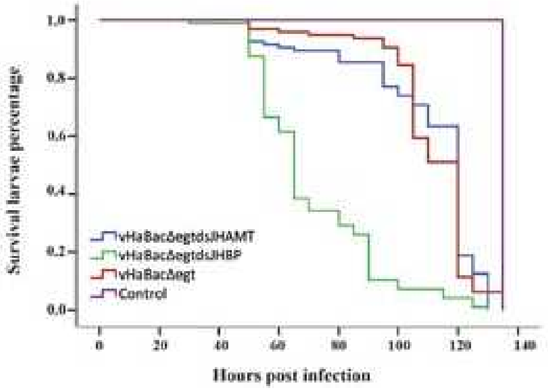
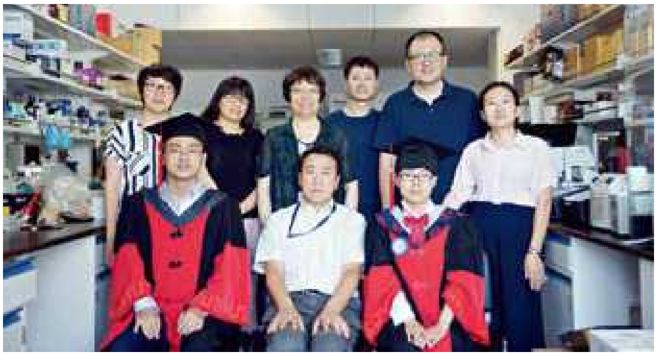


Figure: Survival analysis of third instar *H. armigera* larvae feeding with OBs of baculoviruses. The concentration of OBs was 100 times the LC_{50} value. The observation continued until all larvae died or pupated. Larvae feeding without baculovirus were used as controls; a total of 96 larvae were tested for each virus. Survival analysis were performed using the Kaplan–Meier estimator by SPSS 22.0.



Molecular Mechanisms on Plant Disease Resistance

Lihuang Zhu, Principal Investigator Emeritus.

Research Interests:Components essential in the processes of plant disease resistance are studied, with aims to elucidate the signalling pathway of Resistance proteins-mediated resistance. Rice blast defense-related genes are cloned, especially of those Resistance genes. This study aims to improve the blast resistance of the parent varieties of hybrid rice.

Email: lhzhu@genetics.ac.cn

Important signalling molecules for NLR protein-mediated resistance to rice blast disease

NLR-type Resistance(R) proteins serve as important immune receptors in the response to rice blast, a troubling fungal disease of world-wild rice farming, however, the molecular mechanisms underlying the processes are largely unknown, and the search for immediate or downstream targets of R proteins remains a challenge. We set out to solve this problem with PID3, a rice NLR gene cloned earlier by our research group. Firstly, we proved that PID3-mediated blast resistance also relies on OsRac1, a small GTPase, which has been shown to involve in Pit-mediated blast resistance. We showed that the NBS domain of PID3 physically interacts with OsRac1, and this interaction may induce immune responses in rice protoplasts. In addition, we identified RAI1, an earlier known transcription factor, as a PID3 interactor. RAI1 specifically interacts with the CC domain of PID3 and importantly, RAI1 was shown to positively regulate PID3-mediated blast resistance. Evidence suggested that OsRac1 works upstream of RAI1, and positively regulates *RAI1's* transcription. Therefore, we suggest that PID3, once activated, relays its defense signals by way of the OsRac1-RAI1 chain. As far as known, the majority of rice *R* genes that confer blast resistance are of NLR type. Our findings may thus provide an important reference for elucidating the molecular mechanisms of NLR immune receptors.

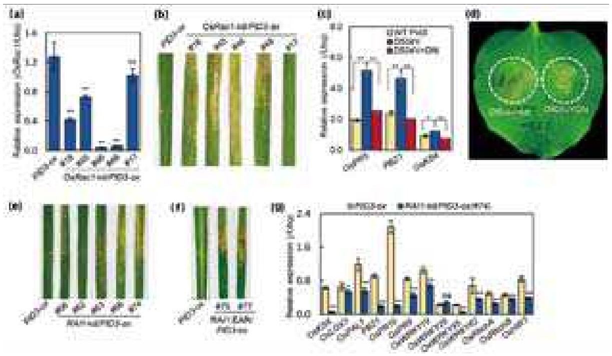


Figure: ID3 depends on OsRac1 and RAI1 to induce immune responses. (a) Knocking down of *OsRac1* transcripts in *PID3-ox* plants. (b) The RNAi compromises PID3's blast resistance. (c) Dominant-negative form of OsRac1 (DN) arrests the induction of defense-related genes by the auto-active form of PID3 (D504V). (d) DN-OsRac1 attenuates HR-like cell death caused by the autoactive form of PID3 (D504V). (e) Knocking down of *OsRac1* transcripts in *PID3-ox* plants compromises PID3's blast resistance. (f) Fusing RAI1 with a a repressive EAR motif also compromises PID3's blast resistance. (g) RAI1 is shown to regulate the transcription of many defense-related genes in rice.

Publications

Zhou, Z. Z., Pang, Z. A., Zhao, S. L., Zhang, L. L., Lv, Q. M., Yin, D. D., Li, D. Y., Liu, X., Zhao, X. F., Li, X. B., Wang, W. M. and Zhu, L. H. (2019). Importance of OsRac1 and RAI1 in signalling of nucleotide-binding site leucine-rich repeat protein-mediated resistance to rice blast disease. New Phytologist 223(2): 828-838.

Plant Molecular Genetics

Jianru Zuo, Principal Investigator. Ph.D. (1994, Miami University, USA), Postdoctoral fellow (1995-2001, Rockefeller University, USA).

Research Interests: Nitric Oxide Signaling and Nitrogen Nutrition in Plants.

Email: jrzuo@genetics.ac.cn

Publications

Feng, J., Chen, L. and Zuo, J. (2019). Protein S-Nitrosylation in plants: Current progresses and challenges. Journal Of Integrative Plant Biology 61: 1206-1223.

Rice *ARE2* encodes a ppgpp hydrolase regulating nitrogen starvation responses

Nitrogen is an essential macronutrient for all living organisms. Mutations in the rice ferredoxin-dependent glutamine: 2-oxoglutarate amidotransferase (Fd-GOGAT) gene (also known as *ABC1*) cause various defects. The *abc1 repressor 2* (*are2*) mutations partially rescue the *abc1* phenotype (Figure A). The *are2* mutants show reduction in the plant height, the tillering number and the chlorophyll contents (Figure B-C). *ARE2* encodes a protein sharing homology with bacteria enzymes involved in metabolism of (p)ppGpp (Figure D), a class of second messengers regulating nitrogen starvation and stress responses. Genetic rescue experiments and liquid chromatography-mass spectrometry revealed that ARE2 is a (p)ppGpp hydrolase (Figure E-F). Moreover, *are2* reduced the high ppGpp level induced by nitrogen deficiency in *abc1* (Figure G). These results suggest that the ppGpp regulated nitrogen starvation response is a highly conserved mechanism.

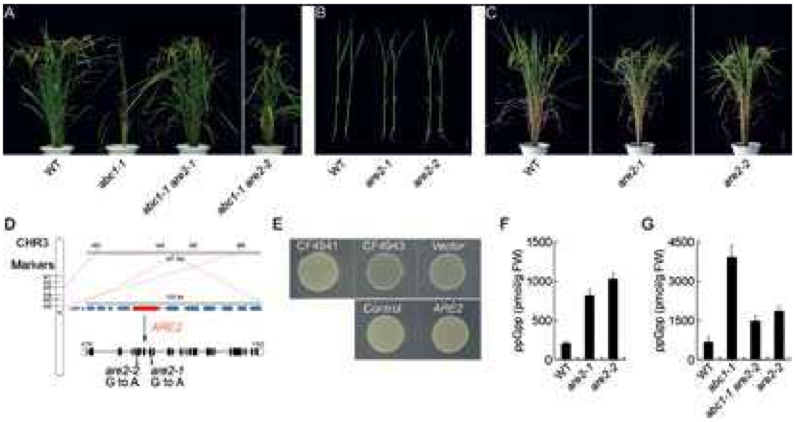


Figure: Identification and functional characterization of *ARE2* (A) The phenotype of wild type (WT), *abc1-1*, *abc1-1 are2-1*, and *abc1-1 are2-2* at the filling stage. (B-C) The phenotype of WT, *are2-1* and *are2-2* plants at the seedling stage (B) and the filling stage (C). (D) A schematic flow of map-based cloning of *ARE2*. (E) Genetic complementation of the bacterial CF4943 strain (CF4941 with mutations in the (p)ppGpp hydrolase gene). (F) Quantification of ppGpp in the leaves of WT, *are2-1*, and *are2-2*. (G) Quantification of ppGpp in the leaves of WT, *abc1-1*, *abc1-1 are2-2*, and *are2-2*.

Center for Molecular Agrobiology

The main mission of the Center for Molecular Agrobiology (CMA) is oriented to the national strategic needs of food security and sustainable agricultural development, and is geared to international frontier of plant science and focused on the key scientific issues of the genetics and breeding research in the major crops, to conduct basic and applied basic research.

In 2019, CMA scientists have published fifty-five papers in leading peer-reviewed academic journals such as *Science, Plant Cell,* and *Nature Plants.* CMA scientists made important progress in projects such as performing complex genomic analysis, understanding the architecture of complex agronomic traits, improving efficiency of nutritional use, as well as advancing genome editing techniques, chromosomal engineering, and breeding.

Genetic Architecture of Complex Agronomic Traits: Xiangdong Fu's lab obtained the *NAL1* gene. Pyramiding of the *dep1-1* and $NAL1^{NJ6}$ alleles achieves sustainable improvements in nitrogen-use efficiency and grain yield in *japonica* rice breeding (Xu et al. *J Genet Genomics*, 2019). *NGR5* was cloned and characterized and the expression level and protein level of *NGR5* were induced by nitrogen. NGR5 can interact with the subunit LC2 of PRC2 complex to regulate the growth and the nitrogen utilization efficiency. Yunhai Li's group discovered the crucial role of the endocycle in determining organ size (Liu et al., *Plant Cell*, 2019). Group members were invited to write a review about seed size control, which summarizes current findings in seed size regulation and discusses the future research directions and the main challenge we now face (Li et al., *Annu Rev Plant Biol*, 2019). Aimin Zhang's Lab completed the fine mapping and genetic effect analysis of Rht12, an important dwarf gene in wheat (Sun et al., *Plant J*, 2019); Another project unraveled the genetic architecture of grain size in einkorn wheat (Yu et al., *J Exp Bot*, 2019).

Genome editing Technology: Caixia Gao's Lab used whole-genome sequencing to analyze specificity for base editors, including BE3, high-fidelity BE3 (HF1-BE3) and ABE, and found that BE3 and HF1-BE3, induced substantial unpredictable genome-wide off-target mutations in rice plant (Jin et al., *Science* 2019). They used the base editing technology to modify the wheat acetolactate synthase (ALS) and acetyl-coenzyme A carboxylase (ACC) genes, and generated transgene-free wheat germplasms bearing herbicide tolerance mutations, which would facilitate better weed control. Furthermore, they developed a protocol for manipulating gene translation efficiency in plants by genome editing, and this method can achieve fine-tuning of gene translation in transgene-free derivatives, which accelerates the analysis of gene function and the improvement of crops.

Complex Genomic Analysis: Zhixi Tian's Lab updated soybean Zhonghuang 13 genome to a golden reference (Shen et al., *Science China Life Science*, 2019). Another project participated in the sequencing and *de novo* assembly of a wild pear (*Pyrus betuleafolia*) genome (Dong et al., *Plant Biotechnol J*, 2019). The decrease of gene expression diversity during domestication of animals and plants was revealed at the genome-wide level (Liu et al., *BMC Evol Biol*, 2019). Participated in writing the review of the genomics of *Oryza* species provides insights into rice domestication and heterosis. Fei Lu 's lab constructed a high-quality genetic variation map of wheat (VMap I) and found that alien introgression contributed 13%~36% of the bread wheat genome. The lab also developed an efficient gene expression profiling approach, Simplified Poly(A) Anchored Sequencing (SiPAS), to boost population transcriptomic studies in plants. Jun Xiao's lab uncovered the SUMOylation converted two-step histone modification switch during photo-morphogenesis in *Arabidopsis*. Meanwhile, they developed new strategy for identifying key factors regulating important agronomic traits in wheat.

Improving Efficiency of Nutrient Use: Yiping Tong's Lab constructed the gene regulatory network of TaNAC2, and identified that the TaNAC2-NRT2.5 module has a key role in regulating grain nitrate accumulation and seed vigour (Li et al., *New Phytol*, 2019); Another project uncovered that TabZIP60 and TaNADH-GOGAT interaction plays important roles in mediating N use and wheat growth (Yang et al., *Plant Biotechnol J*, 2019). Daowen Wang's lab carried out a RNAi cassette for suppressing lipoxygenase (LOX) gene expression in wheat grains and developed marker-free and transgene insertion site-defined transgenic wheat with improved grain storability and fatty acid content (Cao et al., *Plant Biotechnol J*, 2019). Hong-Qing Ling's lab summarized the regulation mechanisms of FIT and its binding proteins in the plant iron absorption (Wu et al., *Front Plant Sci*, 2019, 10: 844).

Resistance mechanism: Qian-Hua Shen's lab investigated the functions of multiple CSEPs of *Blumeria graminis* f. sp. hordei and analyzed the variation of the *Pm60* locus in *Triticum urartu* accesstions. Two molecular markers were developed for screening functional Pm60 alleles that can confer disease resistance to *Blumeria graminis* f.sp. tritici E09 (Zhao et al., *Crop J*, 2019). Zhiyong Liu's lab cloned a powdery mildew resistance gene Pm24 which encoded a tandem kinase protein WTK3 with putative kinase-pseudokinase domains. And revealed that a rare 6-bp natural deletion of lysine-glycine codons is critical for the gain of powdery mildew resistance function. Wenxue Zhai's Lab obtained the two granted patents about the genes *lmm5.1* and *lmm5.4* which exhibit broad-spectrum resistance to *Magnaporthe grisea* and *Xanthomonas oryzae* pv. *oryza* in rice. Zhensheng Li's lab suggested that PUFAs could contribute to salt tolerance in common wheat by enhancing the photosynthetic system and JA-related pathways (Luo et al., *Crop J*, 2019)

Chromosome Engineering and Breeding: Fangpu Han's Lab identified two functional centromeric satellites and highlighted role of rearrangement of centromere organization in asymmetry found in polyploid wheat, which may function in homologous chromosome pairing during meiosis, ultimately leading to speciation (Su et al., *Plant Cell*, 2019). Another project characterized the deposition of CENH3 in maize by over-expression and mutational analysis (Feng et al., *Plant J*, 2019). Zhang Xiangqi Lab reported that development and identification of new common wheat-*Elytrigia* intermedia blue-grained substitution lines, which could be used for blue-grained cultivars breeding and genetics study (Ye et al., *Triticeae Crops*, 2019). Huabang Chen's Lab bred maize varieties 'Keyu 153' (National Reg. 20190298) and 'Keyu 175' (National Reg. 20190097). 'Keyu 153' is authorized Plant Variety Protection right (CNA20181994.2). Baoge Zhu's Lab selected soybean variety Kedou 13 with wide adaptability and high yield and soybean variety Kedou 10 with high quality and high yield.

Others: Yongbiao Xue's Lab found that the *Antirrhinum* genome sequence brings this classic model plant into the genomic age and opens up increased avenues for plant biology research. Cuimin Liu's Lab employed cryo-elecron microscopy single particle reconstruction to determine the sturctures of *Chlamydomonas* chloroplast chaperonin system in two conformational states, offering a structural insight of how exactly this hetero-oligomeric chaperonin system conduct its protein folding function. Zanmin Hu's Lab found TMP-to-regular feed ratio of 1 per thousand can promote the growth of broiler chickens by increasing weight. mNP-1 can improve duodenum morphology by promoting long and thin villi and affect the microbial community of the duodenum by increasing the diversity and abundance of beneficial microbes.

Maize Genetics and Breeding

Huabang Chen, Principal Investigator, Ph.D. (1999, Purdue University, USA).

Research Interests: My lab is focused on corn genetics and breeding. Three areas are of particular interests: 1) Maize germplasm enhancement. 2) Mapping, cloning, functional molecular marker development, and utilization of genes of agronomic importance. 3) Integration of corn genomics, proteomics, and bioinformatics into corn breeding program to maximize corn improvement efficiency and efficacy.

Email: hbchen@genetics.ac.cn

Genetic analysis and functional study of maize ear apical degeneration gene, *EAD1*

Maize yield is a complicated quantitative trait. Kernel number per ear is an important yield determinant. It is determined by ear length and kernel row number. Although a lot of studies and QTLs were reported on these, few functional genes were cloned. In our study, a maize short ear length mutant was used. Comparing to wild type, the kernel number of the mutant is less. During the immature ear development, the ear tip of the mutant becomes growth retardation. So we named the mutant *ear apical degeneration1*, *ead1*. Genetic analysis showed that the short ear phenotype of *ead1* segregated as a single recessive trait. The candidate gene, *ZmG21*, was cloned by map-based cloning and verified by CRISPR/Cas9 knockout experiment. This gene encodes a plasma membrane localized anion transporter. It is mainly expressed in ear vascular tissue. These indicated that *ZmG21* might function on nutrient and energy supply during immature ear development.

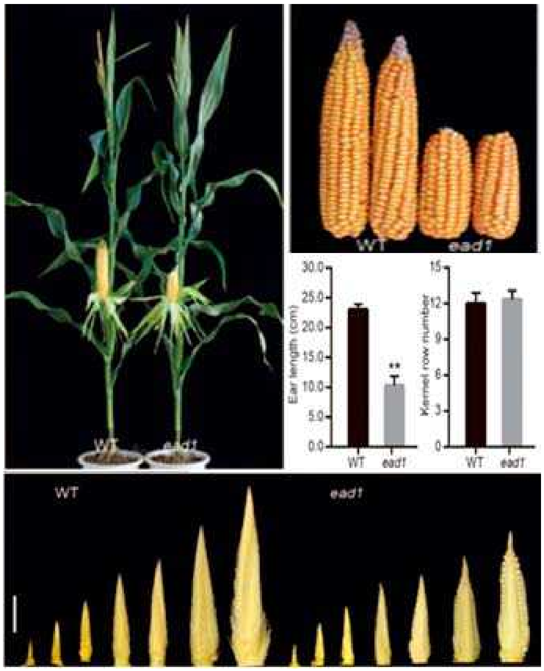


Figure: The phenotype comparison between wild type and *ead1* mutant.

Plant Molecular and Genetic Biology

Xiangdong Fu, Principal Investigator, Ph.D. (2001, Zhejiang University, China & John Innes Centre, UK).

Research Interests: The research interests include determining GA action in the coordinated regulation of plant growth and metabolism, and investigating the genetic basis of the improvement of panicle branching and grain yield in crops.

Email: xdfu@genetics.ac.cn

Novel insights to the synergy improvement of NUE and yield in rice

Rice is one of the most important cereal crops in the world, and a substantial increase in grain yield is necessary for food security. There is an urgent need to develop new rice green revolution varieties (GRVs), which increase N-use efficiency (NUE) while maintaining their high yields. The *NAL1* gene was obtained by QTL analysis and map-based cloning. Pyramiding of the *dep1-1* and *NAL1*^{NJ6} alleles achieves sustainable improvements in nitrogen-use efficiency and grain yield in *japonica* rice breeding. *NGR5* was cloned and characterized. The expression level and protein level of NGR5 were induced by nitrogen. *NGR5* can interact with the subunit LC2 of PRC2 complex to regulate the growth and the nitrogen utilization efficiency. These research provide important gene resources for breeding "resource-saving and environment-friendly" rice varieties.

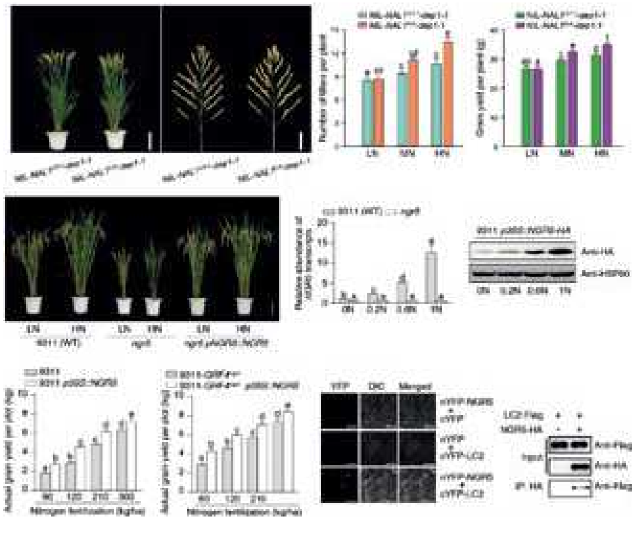


Figure: New genes improving NUE and yield in rice.

Publications

Xu, X., Wu, K., Xu, R., Yu, J., Wang, J., Zhao, Y., Wang, Y., Song, W., Wang, S., Gao, Z., Zhong, Y., Li, X., Liao, H. and Fu, X. (2019). Pyramiding of the dep1-1 and NAL1(NJ6) alleles achieves sustainable improvements in nitrogen-use efficiency and grain yield in japonica rice breeding. Journal Of Genetics and Genomics 46(6): 325-328.

Zhong, Y., Yang, Y., Liu, P., Xu, R., Rensing, C., Fu, X. and Liao, H. (2019). Genotype and rhizobium inoculation modulate the assembly of soybean rhizobacterial communities. Plant Cell and Environment 42(6): 2028-2044.

Guo, X., Zhang, X., Qin, Y., Liu, Y., Zhang, J., Zhang, N., Wu, K., Qu, B., He, Z., Wang, X., Zhang, X., Hacquard, S., Fu, X. and Bai, Y. (2019). Host-Associated Quantitative Abundance Profiling Reveals the Microbial Load Variation of Root Microbiome. Plant Communications. Doi:10.1016/j.xplc.2019.100003.

Chen, H., Yang, Y., Ye, Y., Tao, L., Fu, X., Liu, B. and Wu, Y. (2019). Differences in cadmium accumulation between indica and japonica rice cultivars in the reproductive stage. Ecotoxicology and Environmental Safety 186: 109795.

Plant Genome Editing

Caixia Gao, Principal Investigator, Ph.D. (1997, China Agricultural University, China).

Research Interests: Developing novel technologies to achieve efficient and specific genome engineering, and applying them to study the function of genes and modify plant traits for high-quality, disease resistance and stress tolerance in crop species.

Email: cxgao@genetics.ac.cn

Publications

Ji, X., Wang, D. and Gao, C. (2019). CRISPR editing-mediated antiviral immunity: a versatile source of resistance to combat plant virus infections. Science China Life Sciences 62(9): 1246-1249.

Gao, C. (2019). Precision plant breeding using genome editing technologies. Transgenic Research 28(2): 53-55.

Hickey, L. T., N. Hafeez, A., Robinson, H., Jackson, S. A., Leal-Bertioli, S. C. M., Tester, M., Gao, C., Godwin, I. D., Hayes, B. J. and Wulff, B. B. H. (2019). Breeding crops to feed 10 billion. Nature Biotechnology 37(7): 744-754.

Zhang, R., Liu, J., Chai, Z., Chen, S., Bai, Y., Zong, Y., Chen, K., Li, J., Jiang, L. and Gao, C. (2019). Generation of herbicide tolerance traits and a new selectable marker in wheat using base editing. Nature Plants 5(5): 480-485.

Jin, S., Zong, Y., Gao, Q., Zhu, Z., Wang, Y., Qin, P., Liang, C., Wang, D., Qiu, J.-L., Zhang, F. and Gao, C. (2019). Cytosine, but not adenine, base editors induce genome-wide off-target mutations in rice. Science 364(6437): 292.

Cytosine, but not adenine, base editors induce genome-wide off-target mutations in rice

Cytosine and adenine base editors (CBEs and ABEs) are promising new tools for achieving the precise genetic changes required for disease treatment and trait improvement. However, genome-wide and unbiased analyses of their off-target effects in vivo are still lacking. Our whole-genome sequencing analysis of rice plants treated with the third-generation base editor (BE3), high-fidelity BE3 (HF1-BE3), or ABE revealed that BE3 and HF1-BE3, but not ABE, induce substantial genome-wide off-target mutations, which are mostly the C→T type of single-nucleotide variants (SNVs) and appear to be enriched in genic regions. Notably, treatment of rice with BE3 or HF1-BE3 in the absence of single-guide RNA also results in the rise of genome-wide SNVs. Thus, the base-editing unit of BE3 or HF1-BE3 needs to be optimized in order to attain high fidelity.

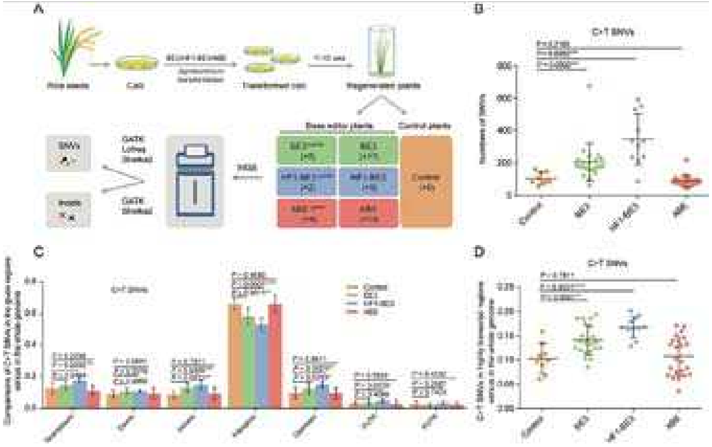


Figure: Analysis of genome-wide off-target mutations for base editors. (A) Experimental design and workflow.(B) Numbers of total SNVs identified in the BE3, HF1-BE3, and ABE plants. (C) Comparisons of C>T SNVs in the given regions versus in the whole genome among BE3, HF1-BE3, ABE, and control groups. (D) C>T SNVs in highly transcribed regions versus in the whole genome among BE3, HF1-BE3, ABE, and control groups.

Plant Chromosome Biology

Fangpu Han, Principal Investigator, Ph.D. (1998, Northeast Normal University, China).

Research Interests: The laboratory is mainly focused on wheat chromosome engineering and genome evolution of polyploidy, structure and function of plant centromere, molecular mechanism of plant meiosis, plant artificial chromosome and specific genome modification.

Email: fphan@genetics.ac.cn

Analysis of centromeric satellite repeats in wheat subgenomes reveals rapid changes in polyploid wheat

One challenge polyploids face is correct pairing of homologous chromosomes during meiosis. Centromeres mediate this pairing, but centromere sequence composition, functional centromeric satellites, and evolutionary history in polyploid wheat (*Triticum aestivum*) and other wheat lines with different ploidy levels, are largely unknown. Here, we performed centromere mapping of common wheat via chromatin immunoprecipitation sequencing using antibodies to CENH3 and identified two functional centromeric satellites that are abundant in the wheat subgenomes. Unlike typical centromeric satellites, which have a unit size of 150–180 bp, wheat centromeric satellites had unit sizes of 567 and 581 bp and contained specific sites with highly phased binding to CENH3-containing nucleosomes. Satellite signals decreased from diploid to hexaploid wheat, and several satellite-free centromeres were detected in common wheat. We identified a 223-bp fragment of the centromeric satellite in a wheat centromeric Ty3/gypsy retrotransposon. Rearrangements of centromere organization, including local expansion and satellite variations, gene loss and inversions, and changes in gene expression occurred during the evolution from diploid progenitors to tetraploid and hexaploid wheat. These results highlight role of rearrangement of centromere organization in asymmetry found in polyploid wheat, which may function in homologous chromosome pairing during meiosis, ultimately leading to speciation.

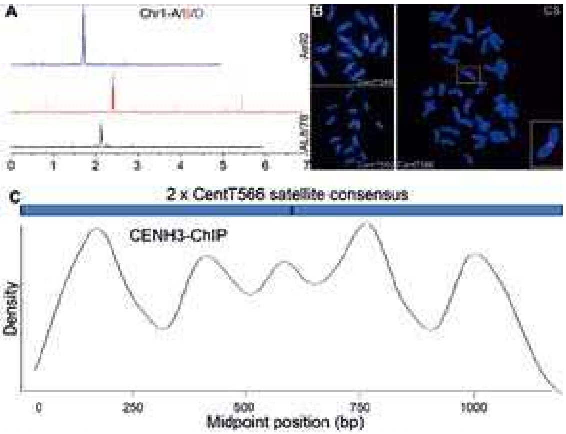


Figure: Distribution of centromeric satellite repeats in wheat subgenomes.(A) Genome-wide mapping of CENH3 ChIP-seq reads from CS to the IWGSC reference genome. (B) FISH confirms the centromere location of satellite repeats in different wheat lines. (C)CENH3 nucleosomes are highly phased with specific sites on monomers of the wheat centromeric satellite.

Publications

Su, H., Liu, Y., Liu, C., Shi, Q., Huang, Y. and Han, F. (2019). Centromere satellite repeats have undergone rapid changes in polyploid wheat subgenomes. The Plant Cell 31(9): 2035-2051.

Feng, C., Yuan, J., Bai, H., Liu, Y., Su, H., Liu, Y., Shi, L., Gao, Z., Birchler, J. A. and Han, F. (2019). The deposition of CENH3 in maize is stringently regulated. Plant Journal. Doi: 10.1111/tpj.14606.

Wang, J., Shi, Q., Guo, X. and Han, F. (2019). Establishment and characterization of a complete set of *Triticum Durum-Thinopyrum* elongatum monosomic addition lines with resistance to wheat fusarium head blight. Journal of Genetics and Genomics. Doi: 10.1016/j.jgg.2019.09.006.

Plant Biotechnology

Zanmin Hu, Principal Investigator, Ph.D. (1995, Peking University, China).

Research Interests: Improment of oil seed rape in yield and quality; The theoretical and applied research on biosynthesis of polypeptides and lipopeptid using Chlorella and Bacillus subtilis as bioreactors; Research on plant chromosome repetitive sequences and chromosome engineering.

Email: zmhu@genetics.ac.cn

Publication

Fan, C., Wu, J., Xu, L., Bai, L., Yang, H., Yan, C., Wu, Q., Chen, Y. and Hu, Z. (2019). A mutated rabbit defensin NP-1 produced by *Chlorella ellipsoidea* can improve the growth performance of broiler chickens. Scientific Reports 9(1): 12778.

A mutated rabbit defensin NP-1 produced by *Chlorella* ellipsoidea can improve the growth performance of broiler chickens

The demand for alternatives to antibiotics to improve the growth performance of food animals is increasing. Defensins constitute the first line of defence against pathogens in the innate immune system of animals and humans. A transgenic *Chlorella ellipsoidea* strain producing mNP-1 was previously obtained. Now, a process for producing the transgenic strain on a large scale was developed, and *C. ellipsoidea* strain producing mNP-1 was used as a feed additive to improve the health and growth performance of chickens. The volume of *C. ellipsoidea* producing mNP-1 can be scaled up to 10,000 L with approximately 100 g/L dry biomass, and the mNP-1 content of transgenic microalgal powder (TMP) was 90-105 mg/L. A TMP-to-regular feed ratio of 1 per thousand, as the optimal effective dose, can promote the growth of broiler chickens by increasing weight by 9.27-12.95%. mNP-1 can improve duodenum morphology by promoting long and thin villi and affect the microbial community of the duodenum by increasing the diversity and abundance of beneficial microbes. These results suggested transgenic *Chlorella* producing mNP-1 can be industrially produced and used as an effective feed additive and an alternative to antibiotics for improving the health and growth performance of food animals.

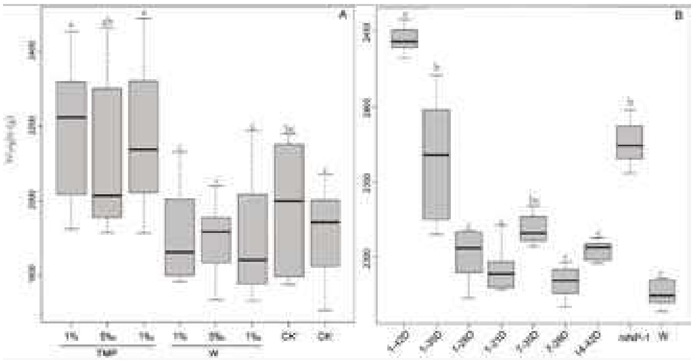


Figure: mNP-1 improved thegrowth performance of broiler chickens. A, Identification ofthe optimal effective dose of TMP. The concentrations of 1‰, 5‰ and 1% TMP or W in the feed were tested. CK^-, base diet; CK^+, base diet with 15 mg/kg virginiamycin. B, Screeningthe suitable feeding model. TMP(1‰)was added to the feed at differenttime points in the experiment: 1-42D, 1-35D, 1-28D, 1-21D, 7-35D, 7-28D, 14-42D, in which the first number is the starting day and the second number is the ending day. W, wild-type microalgal powder. mNP-1, the treatment with crude mNP-1 peptides added to the water at a concentration of 0.5 mg/L. Data are shown as the mean +/- SD, n=5. The letters on the bar indicate the significance of the difference at p<0.05.

Control of Seed and Organ Size in Plants

Yunhai Li, Principal Investigator, Ph.D. (2003, Institute of Genetics and Developmental Biology, China). Postdoc fellow (2003-2008, John Inners Center, UK).

Research Interests: To elucidate the molecular mechanisms that control the final size of seeds and organs, and to identify ways of rationally engineering seed and biomass yield in key crops.

Email: yhli@genetics.ac.cn

The mechanism of endoreduplication in plant cell and organ growth control

Endoreduplication is often associated with cell growth and differentiation in plants and animals, but molecular mechanisms of plant endoreduplication have not been fully understood. Here, we describe that the Mediator complex subunit *MED16* acts as a negative regulator of endoreduplication to influence cell growth in Arabidopsis. The med16 mutations cause larger and more cells, resulting in large organs. The large cells in *med16* are associated with high DNA ploidy levels. MED16 associates with the promoters of the Anaphase Promoting Complex/Cyclosome (APC/C) activators *CCS52A1* and *CCS52A2*, which are the important factors for endoreduplication and cell growth in Arabidopsis, and represses their expression. MED16 interacts physically with the transcription repressor DEL1 to repress expression of *CCS52A2*. Genetic analyses suggest that *MED16* is partially dependent on *CCS52A1/A2* to control endoreduplication and cell growth. Thus, our results reveal that the transcriptional repression of *CCS52A1/A2* by MED16 regulates endoreduplication and cell growth in Arabidopsis.

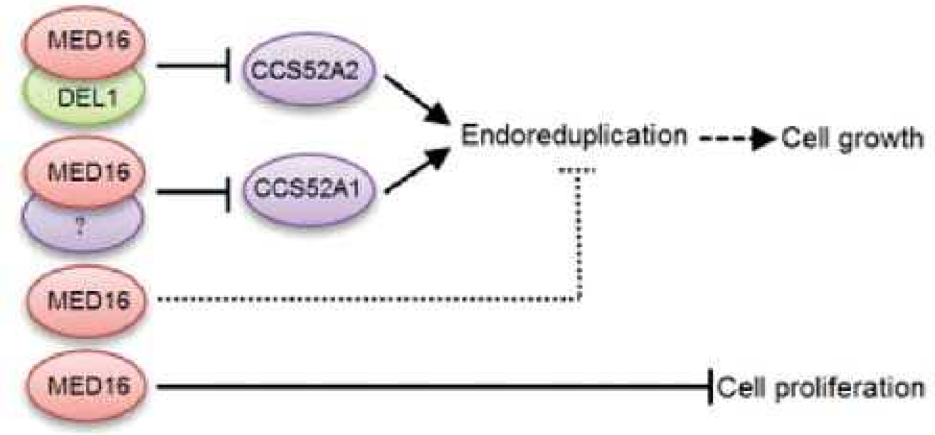


Figure: Working Model of the Role of MED16 in Controlling Cell Growth and Proliferation.

Publications

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Xu, R., Li, N. and Li, Y. (2019). Control of grain size by G protein signaling in rice. Journal of Integrative Plant Biology 61(5):533-540.

Wheat Genetics and Breeding

Prof. Zhensheng Li, Academician, Chinese Academy of Sciences. Principal investigator. Winner of National Supreme Award of Science and Technology of China in 2006, Award of Outstanding Contribution to China Agriculture in 2005.

Research Interests: The laboratory is mainly interested in: (1) development of new wheat germplasms via wheat distant hybridization, chromosome engineering, and molecular markers; (2) breeding new wheat varieties with tolerance to saline land and improved photosynthetic efficiency.

Email: zsli@genetics.ac.cn

Transcriptome analysis of salt-stress response in three seedling tissues of common wheat

Xiaoyan 60 is a new wheat variety bred in the laboratory of Zhensheng Li. After salt treatment, seedlings of XY60 maintain green leaves and produce longer roots than the high yielding cultivar Zhongmai 175. To explain these different phenotypes we carried out an RNA-Seq analysis using 12 samples from three tissues of both varieties subjected to salt and control treatments.By comparing data from the salt treated plants with the control, 703, 979, and 1197 differentially expressed genes were detected in new leaves, old leaves, and roots of XY60, respectively. The corresponding numbers for ZM175 were 613, 1401, and 1301. The most significantly enriched Gene Ontology terms and KEGG pathways were associated with polyunsaturated fatty acid metabolism inboth new and old leavesfrom XY60. They were associated with photosynthesis and energy metabolism in ZM175. The most significantly enriched KEGG pathway in roots of both varieties was “glucosinolate biosynthesis”. In addition, jasmonic acid concentration in XY60 was higher than in ZM175, although it increased significantly in both varieties following salt treatment. Trends in relative expression levels of *AOS*, *MYC2*, and *JAZ* revealed by qRT-PCR were concordant with those from RNA-Seq. Our results suggest that PUFAs may contribute to salt tolerance in common wheat by enhancing the photosynthetic system and JArelated pathways.

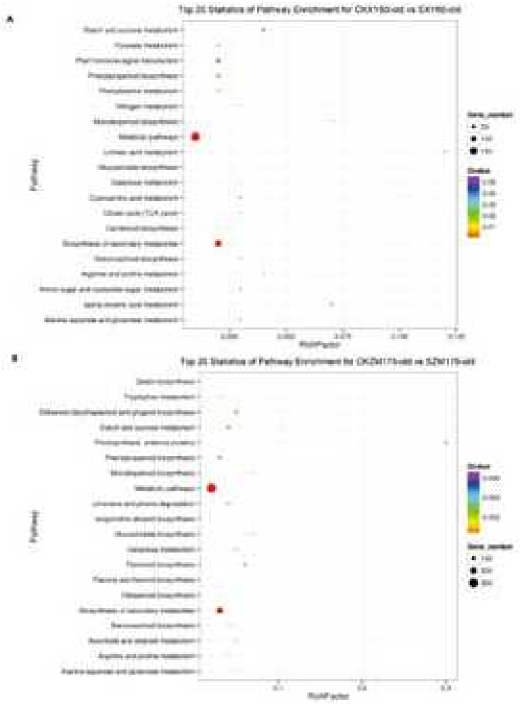

Figure: The top 20 significantly enriched KEGG pathways for old leaf tissue.

Publications

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Liu, Y., Xu, Q., Li, W., Yang, X., Zheng, Q., Li, B., Li, Z. and Li, H. (2019). Long-term high light stress induces leaf senescence in wheat (*Triticum aestivum* L.). Photosynthetica 57(3): 830-840.

Li, H., Boshoff, W. H. P., Pretorius, Z. A., Zheng, Q., Li, B. and Li, Z. (2019). Establishment of wheat-*Thinopyrum ponticum* translocation lines with resistance to *Puccinia graminis* f. sp. *tritici* Ug99. Journal of Genetics and Genomics 46(8): 405-407.

Molecular Biology of Plant Nutrition and Wheat Genomics

Hong-Qing Ling, Principal Investigator, Director of the State Key Laboratory of Plant Cell and Chromosome Engineering, Ph.D. (1993, Christian-Albrechts University of Kiel, Germany), Postdoctoral fellow (1993-1998, Leibniz Institute of Plant Genetics and Crop Plant Research, Germany), Senior Scientist (1998-2001, Institute of Plant Biology, University of Zurich, Switzerland).

Research Interests: The research directions of our group are molecular biology of plant nutrition and wheat genomics. In the molecular biology of plant nutrition, our research mainly focuses on the molecular regulation mechanism of phosphorus and iron uptake with Arabidopsis and tomato; In wheat genomics, the studies focus on illustrating genome structures of Triticum urartu and common wheat by genome sequencing and their comparative genomic analysis.

Email: hqling@genetics.ac.cn

FIT-Binding proteins and their functions in the regulation of Fe homeostasis

Iron is an essential micronutrient in plants, its deficiency and excess will impair plant growth. Therefore, the Fe homeostasis in plant is tightly controlled. FIT is a key regulator of the iron deficiency response and homeostasis in Arabidopsis. During past several years, we identified and cloned ten regulatory genes (*bHLH38/39/100/101, bHLH18/19/20/25, MED16, FBP*), which encode proteins interacting with FIT. Combined with results from other laboratories, we systematically reviewed the regulation network of FIT. As shown in Figure, in root epidermal cells, bHLH38/39/100/101, MED16, MED25, EIN3/EIL1, and CIPK11 as positive modulators interact with FIT, functioning in activation of the expression of iron acquisition genes such as *FRO2* and *IRT1* under iron limitation condition, whereas DELLA, ZAT12, and bHLH18/19/20/25 as negative modulators compete with bHLH38/39/100/101 to bind FIT for negative regulation of FIT activity for avoidance of excessive iron uptake. In stele cells, FBP as a negative regulator sequestered FIT to obstruct the heterodimer formation of FIT with bHLH38/39/100/101 to down-regulate the expression of *NAS1*, *NAS2*, and *NAS4* for balancing Fe and Zn homeostasis in Arabidopsis.

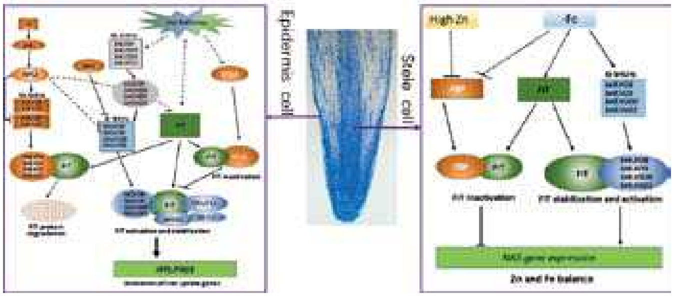

Figure: Outline of the regulation networks and functions of FIT-binding proteins in iron deficiency responses and homeostasis in rootepidermis cells (left part) and stele cells (right part).

Publications

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Wu, H. and Ling, H. Q. (2019). FIT-binding proteins and their functions in the regulation of fe homeostasis. Frontiers in Plant Science 10: 844.

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Structure and Function of Photosynthetic Complexes

Cuimin Liu, Principal Investigator, Ph.D. (2006, University of Freiburg, Germany), Postdoc fellow (2006-2010, Max Planck Institute of Biochemistry, Germany).

Research Interests: Investigation of structure, function and biogenesis of Rubisco, try to elucidate the mechanisms of Rubisco folding and assembly. Study of composition and function regulation of chloroplast chaperonin Cpn60, try to decipher its function as a housekeeping protein and its regulation roles on stress response. Study on the function and activity of enzymes in Calvin-Benson Cycle, try to reveal the mechanisms and synergistic effects of these enzymes which lead to the improvement of plant photosynthetic efficiency.

Email: cmliu@genetics.ac.cn

Publication

Zhao, Q., Zhang, X., Sommer, F., Ta, N., Wang, N., Schroda, M., Cong, Y. and Liu, C. (2019). Hetero-oligomeric CPN60 resembles highly symmetric group-I chaperonin structure revealed by Cryo-EM. The Plant Journal 98(5): 798-812.

Folding and assembly of *Arabidopsis* Rubisco *in vitro*

Photosynthesis is the major source of biomass and oxygen on earth.Ribose-1,5-bisphosphate carboxylase/oxygenase (Rubisco)- mediated CO_2 fixation is the most critical rate-limiting enzyme in this process.Therefore, Rubisco has beenone of the most outstanding target for improving and increasing crop productivity. In eukaryotes (plants, algae, etc.), Rubisco is a hexadecameric complex composed of eight large (RbcL) and eight small subunits (RbcS). The folding of RbcL are strictly rely on chaperonin system and the assembly of holo-enzyme are depend on mutiple assmbly factors. This complex requirement of Rubisco biogenesis has limited the recombinant expression and the large scale mutagenesis, hindering the bioengineering of Rubisco. Therefore, it is vital to elucidate the biogenesis of eukaryotic Rubisco. In this study, we expressed and purified all the components required for reconstitution of *Arabidopsis* Rubisco (*At*Rubisco) *in vitro*, and successfully achieved the positive *At*Rubisco for the first time, which will provide a theoretical basis for improving and screening high efficient Rubisco.

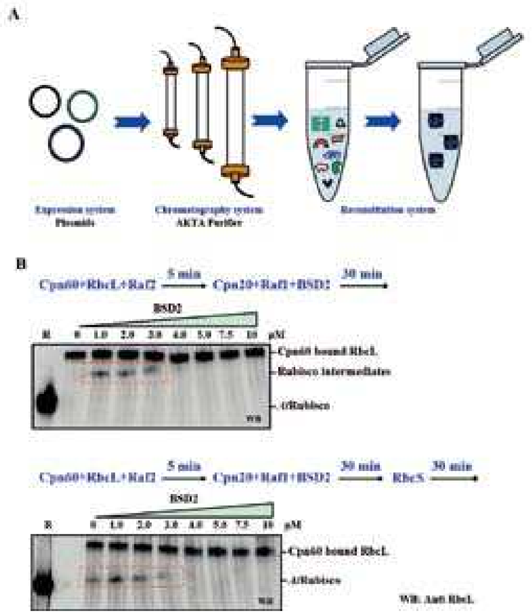

Figure: (A) Overall Cryo-EM structures of chloroplast chaperonin system CPN60αβ1β2, CPN112023-CPN60αβ1β2. (B) ADP binding pocket in cis-ring of CPN60αβ1β2-ADP and CPN112023-CPN60αβ1β2-ADP complex.

Wheat Genomics, Genetics and Breeding

Zhiyong Liu, Principal Investigator, Ph.D. (1999, China Agricultural University, China). Postdoctural researcher, (1999-2001, ETH Zurich, Swiss; 2001-2004, Hawaii Agriculture Research Center, USA), Professor (2004-2015, China Agricultural University, China).

Research Interests: My lab is doing wheat genetics & genomics research focused on identification, mapping and map-based cloning of important genes for disease resistance (powdery mildew, stripe rust, leaf rust, spot blotch, etc.) and agronomic traits (yield, plant architecture, etc.). We are trying to use the genes identified for developing wheat breeder friendly germplasms and wide adapted high-yielding new cultivars.

Email: zyliu@genetics.ac.cn

Map-based cloning and haplotype variation of powdery mildew resistance gene *Pm24* in wheat

Powdery mildew, caused by *Blumeria graminis f. sp. tritici* (*Bgt*), is one of the most destructive diseases that pose a great threat to wheat production worldwide. Isolation of powdery mildew resistance genes is crucial to understand the molecular mechanism of wheat-*Bgt* interaction and to manipulate them in breeding via molecular marker-assisted selection and genome editing. Here, we report the map-based cloning of powdery mildew resistance gene *Pm24* from Chinese wheat landrace Hulutou. It encodes a tandem kinase protein (TKP) with putative kinase-pseudokinase domains, designated WHEAT TANDEM KINASE 3 (WTK3). The resistance function of *Pm24* was validated by transgenic assay, independent mutants, and allelic association analyses. Haplotype analysis revealed that a rare 6-bp natural deletion of lysine-glycine codons, endemic to wheat landraces of Shaanxi Province, China, in the kinase I domain (Kin I) of WTK3 is critical for the gain of powdery mildew resistance function. Transgenic assay of WTK3 chimeric variants revealed that only the specific two amino acid deletion, rather than any of the single or more amino acid deletions, in the Kin I of WTK3 is responsible for gaining the resistance function of WTK3 against the *Bgt* fungus.

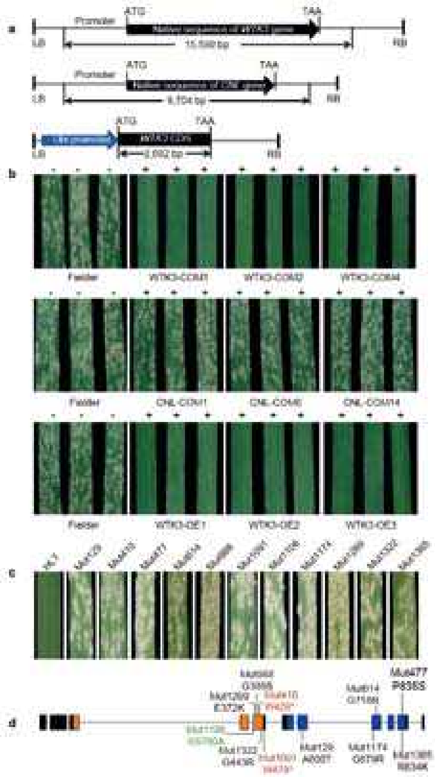

Figure: Validation of *Pm24* candidates using transgenic assay and EMS mutants

Publications

Yang, J., Zhou, Y., Wu, Q., Chen, Y., Zhang, P., Zhang, Y., Hu, W., Wang, X., Zhao, H., Dong, L., Han, J., Liu, Z. and Cao, T. (2019). Molecular characterization of a novel *TaGL3-5A* allele and its association with grain length in wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 132(6): 1799-1814.

Zhang, D., Zhu, K., Dong, L., Liang, Y., Li, G., Fang, T., Guo, G., Wu, Q., Xie, J., Yongxing, C., Lu, P., Li, M., Zhang, H., Wang, Z., Zhang, Y., Sun, Q. and Liu, Z. (2019). Wheat powdery mildew resistance gene *Pm64* derived from wild emmer (*Triticum turgdium* var. *dicoccoides*) is tightly linked in repulsion with stripe rust resistance gene *Yr5*. The Crop Journal. Doi:10.1016/j.cj.2019.03.003.

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Wu, P., Hu, J., Zou, J., Qiu, D., Qu, Y., Li, Y., Li, T., Zhang, H., Yang, L., Liu, H., Zhou, Y., Zhang, Z., Li, J., Liu, Z. and Li, H. (2019). Fine mapping of the wheat powdery mildew resistance gene *Pm52* using comparative genomics analysis and the Chinese Spring reference genomic sequence. Theoretical and Applied Genetics 132(5): 1451-1461.

Quantitative Genetics and Statistical Genomics in Plant

Fei Lu, Principal Investigator, Ph.D. (2010, Institute of Genetics and Developmental Biology, CAS, China), Postdoc Fellow and Research Associate (2010-2017, Institute for Genomic Diversity, Cornell University, USA). He is also a group leader at CAS-JIC Centre of Excellence for Plant and Microbial Science.

Research Interests: To speed up breeding cycle and further improve crop varieties, we are trying to understand the genetics of agronomic traits, especially the complex traits (e.g. yield, heterosis, drought tolerance, resistance, etc.) by using quantitative genetic and statistical genomic approaches. We use wheat and maize as research models. Our research goal is to enhance the genomic selection and/or develop a new system for breeding by efficiently using genomic editing technologies.

Email: flu@genetics.ac.cn

Publications

Zhang, C., Wang, P., Tang, D., Yang, Z., Lu, F., Qi, J., Tawari, N. R., Shang, Y., Li, C. and Huang, S. (2019). The genetic basis of inbreeding depression in potato. Nature Genetics 51(3): 374-378.

Chen, H., Jiao, C., Wang, Y., Wang, Y., Tian, C., Yu, H., Wang, J., Wang, X., Lu, F., Fu, X., Xue, Y., Jiang, W., Ling, H., Lu, H. and Jiao, Y. (2019). Comparative population genomics of bread wheat (*Triticum aestivum*) reveals its cultivation and breeding history in China. BioRxiv. Doi: 10.1101/519587.

Kremling, K. A. G., Chen, S., Su, M., Lepak, N. K., Romay, M. C., Swarts, K. L., Lu, F., Lorant, A., Bradbury, P. J. and Buckler, E. S. (2018). Dysregulation of expression correlates with rare-allele burden and fitness loss in maize. Nature 555(7697): 520-523.

Springer, N. M., Anderson, S. N., Andorf, C. M., Ahern, K. R., … Xiong, W. and Brutnell, T. P. (2018). The maize W22 genome provides a foundation for functional genomics and transposon biology. Nature Genetics 50(9): 1282-1288.

Alien introgression: insights of wheat adaptation from *Triticum* population sequencing

Bread wheat expanded its habitats from the Fertile Crescent to global environments within ~10,000 years. Genetic mechanisms of this evolutionary success are not well understood. By whole-genome sequencing of populations from 25 subspecies within genera *Triticum* and *Aegilops*, we identified a single domestication of bread wheat and that free-threshing tetraploid wheats directly contributed to bread wheat emergence. Meanwhile, we found that 13%~36% of the bread wheat genome was contributed by alien introgression, which tremendously increased the genetic diversity of bread wheat and allowed its divergent adaptation worldwide. These results showed the genetic necessities of wheat as a global crop and conduce to wheat genetics and breeding research.

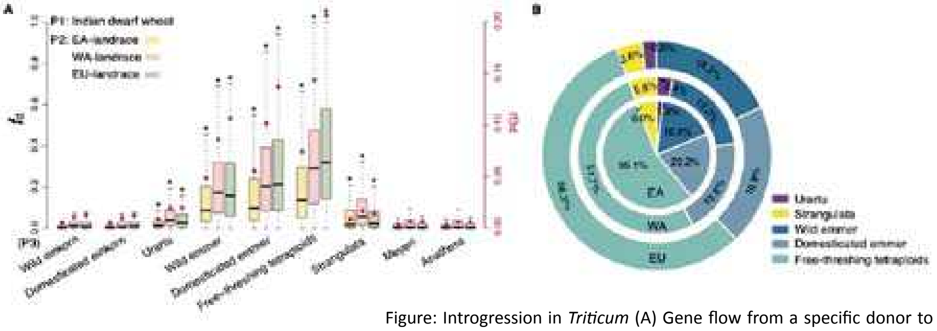

Figure: Introgression in *Triticum* (A) Gene flow from a specific donor to bread wheat using Indian dwarf wheat as P1. Star means gene flow (as indicated by f_d) from a certain donor was significantly higher than from wild einkorn ($P < 0.01$). (B) The relative proportion of introgression from different donors to landraces. The inner, middle, and outer layers are landraces from East Asia, West Asia, and Europe.

Molecular Plant and Microbe Interactions

Qianhua Shen, Principal Investigator, Ph.D. (2004, Max Planck Institute for Plant Breeding Research, Germany).

Research Interests: Mechanism of NLR receptor-mediated disease resistance in plants Cross-kindom signaling and regulation in plant and fungal pathogen interactions Disease resistance genetics and gene cloning from barley and wheat.

Email: qhshen@genetics.ac.cn

Powdery mildew disease resistance and marker-assisted screening at the *Pm60* locus in wild diploid wheat *Triticum urartu*

Triticum urartu, a diploid wild wheat and progenitor of the A genome of bread wheat, is an important resource for resistance to powdery mildew fungus caused by *Blumeria graminis* f. sp. *tritici* (*Bgt*). In the present study we systematically characterized the interaction between the *Bgt* fungus and *T. urartu* at the microscopic level. We also tested 227 *T. urartu* accessions for reaction to *Bgt* isolate E09 and discovered previously uncategorized powdery mildew resistance in this collection. *Pm60* is an CC-NB-LRR type powdery mildew resistance gene that has at least three functional alleles, *Pm60*, *Pm60a* and *Pm60b*. A marker-assisted screen targeting the *Pm60* locus identified a non-functional allele of *Pm60a*, designated as *Pm60a'*. A sequence comparison of *Pm60a'* and *Pm60a* revealed that they differed by 58 SNPs and one 3-nucleotide deletion. Based on the sequence variations two molecular markers were developed to differentiate the functional *Pm60a* allele from the non-functional *Pm60a'*. Our screen revealed the presence of a previously uncharacterized powdery mildew resistance in *T. urartu* and provides new insights into the *Pm60* locus. We believe that the two molecular markers developed here and new *T. urartu* resistant accessions will facilitate further identification of novel powdery mildew resistance genes and benefit breeding for powdery mildew resistance.

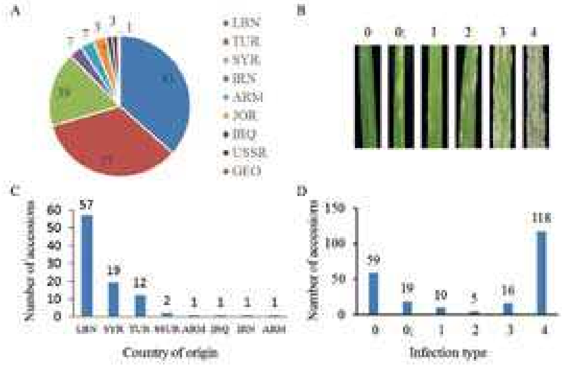

Figure: The country of origin and infection type of *T. urartu* accessions. (A) The country of origin of 227 *T. urartu* accessions. (B) Infection type (IT) of *T. urartu* accessions with *Bgt* E09. (C) The distribution of country of origins of resistant accessions (IT 0-2). (D) Distribution of *T. urartu* accessions in each IT scale.

Publications

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Zheng, H., Dong, L., Han, X., Jin, H., Yin, C., Han, Y., Li, B., Qin, H., Zhang, J., Shen, Q., Zhang, K. and Wang, D. (2019). The TuMYB46L-TuACO3 module regulates ethylene biosynthesis in einkorn wheat defense to powdery mildew. New Phytologyist. Doi:10.1111/NPH.16305.

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Functional Genomics and Genetics of Soybean

Zhixi Tian, Principal Investigator, Ph.D. (2007, Institute of Genetics and Developmental Biology, CAS, China), Postdoc Fellow and Rsearch Geneticist (2007-2010, Purdue University, USA).

Research Interests: Our group will combine association mapping, QTL mapping, map-based cloning along with comparative genomic approach, as well as construction and utilization of mutant database to identify genes controlling important agronomical traits and to apply them into the soybean breeding, which will facilitate soybean germplasm enhancement and benefit soybean production.

Email: zxtian@genetics.ac.cn

Update soybean Zhonghuang 13 genome to a golden reference

Zhixi Tian's Lab updated soybean Zhonghuang 13 genome to a golden reference (Shen et al., *Science China Life Science*, 2019), collaborating with Dr. Yufen Cao's group *de novo* assembled a wild pear (*Pyrus betuleafolia*) genome (Dong et al., *Plant Biotechnology Journal*, 2019), and collaborating with Dr. Wen Wang's group disclosed the rule of gene expression diversities were decreased during the domestication of animals and plants (Liu et al., *BMC Evolutionary Biology*, 2019). Zhixi Tian also participated in the writing of a review of the genomics of *Oryza* species provides insights into rice domestication and heterosis (Chen et al., *Annual Review of Plant Biology*, 2019).

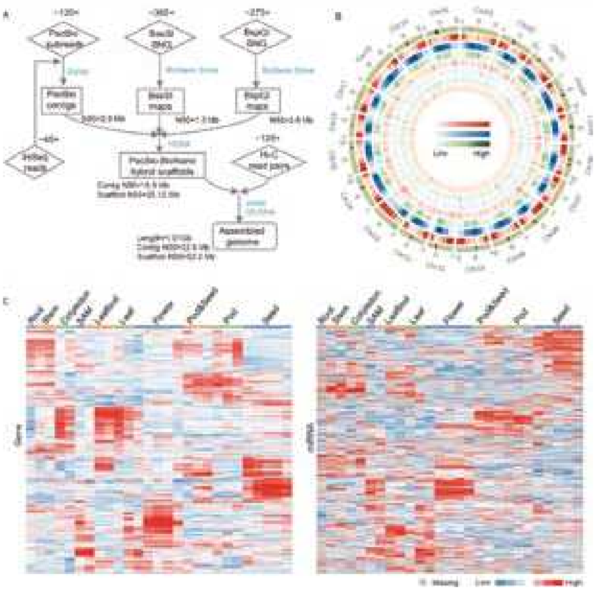

Figure: Update of Gmax_ZH13_v2.0 genome. (A) Pipeline for genome assembly. (B) Distribution of genome features. Tracks from outer to inner circles indicate chromosomes, and density of protein coding genes, repeat sequence, snoRNA, tRNA, miRNA, snRNA and rRNA, respectively. (C) Expression profiling of protein coding genes (left panel) and miRNAs (right panel).

Publications

Shen, Y., Du, H., Liu, Y., Ni, L., Wang, Z., Liang, C. and Tian, Z. (2019). Update soybean Zhonghuang 13 genome to a golden reference. Science China Life Sciences 62(9): 1257-1260.

Dong, X., Wang, Z., Tian, L., Zhang, Y., Qi, D., Huo, H., Xu, J., Li, Z., Liao, R., Shi, M., Wahocho, S. A., Liu, C., Zhang, S., Tian, Z. and Cao, Y. (2019). *De novo* assembly of a wild pear (*Pyrus betuleafolia*) genome. Plant Biotechnology Journal 1:1-15.

Liu, W., Chen, L., Zhang, S., Hu, F., Wang, Z., Lyu, J., Wang, B., Xiang, H., Zhao, R., Tian, Z., Ge, S. and Wang, W. (2019). Decrease of gene expression diversity during domestication of animals and plants. BMC Evolutionary Biology 19(1): 19-29.

Chen, E., Huang, X., Tian, Z., Wing, R. A. and Han, B. (2019). The genomics of *Oryza* species provides insights into rice domestication and heterosis. Annual Review of Plant Biology 70: 639-665.

Genetics of Plant Nutrition

Yiping Tong, Principal Investigator, Ph.D. (1999, Institute of Genetics, CAS, China).

Research Interests: 1) Identifying QTL/genes regulating nitrogen and phosphorus use in wheat; 2) Molecular breeding of wheat varieties withimproved nitrogen and phosphorus use efficiency.

Email: yptong@genetics.ac.cn

A wheat transcription factor positively sets seed vigour by regulating the grain nitrate signal

Seed vigour and early establishment are important factors determining the yield of crops. A wheat nitrate-inducible NAC transcription factor, *TaNAC2*, plays a critical role in promoting crop growth and nitrogen use efficiency (NUE), and now its role in seed vigour is revealed. A TaNAC2 regulated gene was identified that is a NRT2-type nitrate transporter *TaNRT2.5* with a key role in seed vigour. Overexpressing *TaNAC2-5A* increases grain nitrate concentration and seed vigour by directly binding to the promoter of TaNRT2.5-3B and positively regulating its expression. TaNRT2.5 is expressed in developing grain, particularly the embryo and husk. In Xenopus oocyte assays *TaNRT2.5* requires a partner protein TaNAR2.1 to give nitrate transport activity, and the transporter locates to the tonoplast in a tobacco leaf transient expression system. Furthermore, in the root *TaNRT2.5* and *TaNRT2.1* function in post-anthesis acquisition of soil nitrate. Overexpression of *TaNRT2.5-3B* increases seed vigour, grain nitrate concentration and yield, whereas RNA interference of *TaNRT2.5* has the opposite effects. The TaNAC2-NRT2.5 module has a key role in regulating grain nitrate accumulation and seed vigour (Figure). Both genes can potentially be used to improve grain yield and NUE in wheat.

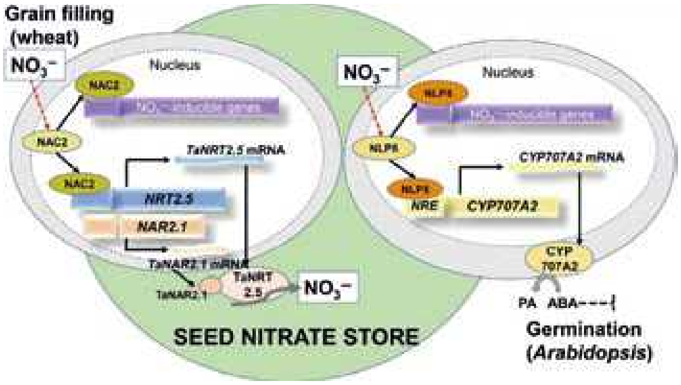

Figure: Proposed schematic model for NAC2/TaNRT2.5/TaNAR2.1 activity in nitrate grain filling and subsequent germination integrating data from Arabidopsis and wheat. Nitrate promotes TaNAC2 expression to activate the *TaNRT2.5*/*TaNAR2.1* nitrate grain-filling activity. Nitrate stored in the grain helps provide the signal promoting germination mediated by the abscisic acid (ABA) content controlled by NIN-like protein 8 (*NLP8*) and *CYP707A*.

Publications

Li, W., He, X., Chen, Y., Jing, Y., Shen, C., Yang, J., Teng, W., Zhao, X., Hu, W., Hu, M., Li, H., Miller, A. and Tong, Y. (2019). A wheat transcription factor positively sets seed vigour by regulating the grain nitrate signal. New Phytologist 10.1111/nph.16234.

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Xu, Y., Ren, Y., Li, J., Li, L., Chen, S., Wang, Z., Xin, Z., Chen, F., Lin, T., Cui, D. and Tong, Y. (2019). Comparative proteomic analysis provides insights into the regulatory mechanisms of wheat primary root growth. Scientific Reports 9: 11741.

Molecular Studies of Agronomic Traits and Genetic Improvement of Wheat

Daowen Wang, Principal Investigator, Ph.D. (1993, University of East Anglia and John Innes Center, UK).

Research Interests: Understanding and improving the quality, yield, and disease and stress tolerance traits of wheat through comparative studies of the genes functioning in important biological processes in common wheat and model plant species.

Email: dwwang@genetics.ac.cn

Marker-free and transgene insertion site-defined transgenic wheat with improved grain storability and fatty acid content

Development of marker-free and transgene insertion site-defined (MFTID) transgenic plants is essential for safe application of transgenic crops. We have prepared a RNAi cassette for suppressing lipoxygenase (LOX) gene expression in wheat grains using a double right border T-DNA vector with the aim to improve seed storability. The resultant construct was introduced into wheat genome via *Agrobacterium*-mediated transformation, with four homozygous marker-free transgenic lines (namely GLRW-1, -3, -5 and -8) developed. The T-DNA insertion sites in GLRW-3 and GLRW-8 were elucidated at base pair resolution. While the T-DNA in GLRW-3 inserted in an intergenic region, that of GLRW-8 inactivated an endogenous gene. Compared to wild type (WT) control, GLRW-1, -3 and -5 showed decreased *LOX* gene expression, lower LOX activity, and less lipid peroxidation in the grains; they also exhibited significantly higher germination rates and better seedling growth after artificial aging treatment. Interestingly, the three GLRW lines also had substantially increased contents of several fatty acids (e. g., linoleic acid and linolenic acid) in their grain and flour samples than WT control. Collectively, our data suggest that suppression of grain LOX activity can be employed to improve the storability and fatty acid content of wheat seeds, and that the MFTID line GLRW-3 is likely of commercial value. Our approach may also be useful for developing the MFTID transgenic lines of other crops with enhanced grain storability and fatty acid content.

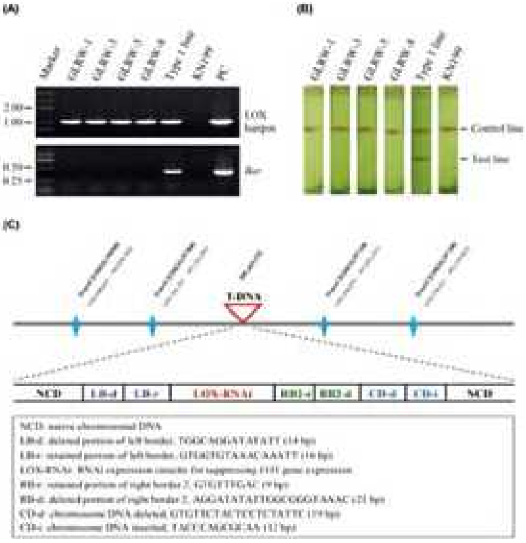

Figure: Identification of marker-free transgenic plants and analysis of T-DNA integration site in GLRW-3(A)Four markerfree transgenic lines were identified by PCR, designated as GLRW-1, -3, -5 and -8, respectively. (B) The lack of Bar protein in GLRW-1, -3, -5 and -8marker-free transgenic plantswas validated using the QuickStix strip test. (C) The T-DNA in GLRW-3 was located in an intergenic region on chromosome 1D. The upstream and downstream flanking genes of the insertion are *TraesCS1D02G297000* and *TraesCS1D02G297100*, respectively.

Publications

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Epigenetic Regulation of Plant Development and Adaptation to Changeable Environments

Jun Xiao, Principal Investigator, Ph.D. (2012, Institute of Botany, CAS, China).

Research Interests: Integration of epigome and forward population genetics to identify and functional study the key factors involved in environmental adaptation of wheat, build up transcriptional regulation network of particular developmental stages and environmental response, screen for elite allele to improve the adaptation of major wheat cultivars to harsh environments. We are also studying the epigenetic regulation of plant adaptation to different environmental conditions such as ambient temperature, dark-to-light switching and drought in Arabidopsis, utilizing chromatin regulator mutants.

Email: jxiao@genetics.ac.cn

SUMOylation converted two-step histone modification switch during photomorphogenesis in *Arabidopsis*

Chromatin modification has been suggested to play role in light-mediated hypocotyls growth, but the underlying mechanism is still elusive. Here we found that mutation of both ‘writer’ and ‘eraser’ of H3K27me3 exhibited altered hypocotyls elongation from dark to light shift. Numerous genes showed correlated H3K27me3 enrichment alteration and expression change, such as *IAA19*, *XTH17*, *SAUR10*. PRC2, the writer of H3K27me3, generally occupied more regions at genome-wide and selectively bound to genes involved in cell elongation during the D-L switch. We found several transcription factors specifically interact with PRC2 during the switch. Among them, NF-YC was reported to inhibit hypocotyls elongation at light through recruiting histone deacetylase (HDAC) and directly inhibiting the expression of *IAA19* and *XTH17*. Further, we found a two-step histone modification switch from high acetylation (active) to abundant H3K27me3 (repressive) at those light-repressed genes during different time window. This is likely achieved by different SUMOylation status of NF-YC during D-L switch. Low/no SUMOylated NF-YC interacts and recruits HDAC at early stage, while SUMOylated NF-YC attracts PRC2 at later stage during D-L switch. Further analysis is still undergoing on how the light signaling could trigger quantitative SUMOylation of NF-YC to precisely recruit HDAC and PRC2 sequentially during D-L.

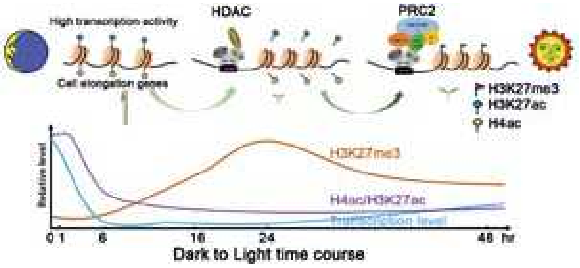

Figure: Histone modification dynamics mediates the elongation of hypocotols during dark to light transition.

Publications

Sun, B., Zhou, Y., Cai, J., Shang, E., Yamaguchi, N., Xiao, J., Looi, L. S., Wee, W. Y., Gao, X., Wagner, D. and Ito, T. (2019). Integration of transcriptional repression and polycomb-mediated silencing of WUSCHEL in floral meristems. The Plant Cell 31(7): 1488-1505.

Xu, S., Xiao, J., Yin, F., Guo, X., Xing, L., Xu, Y. and Chong, K. (2019). The protein modifications of *O*-GlcNAcylation and phosphorylation mediate vernalization response for flowering in winter wheat. Plant Physiology 180(3): 1436-1449.

Plant Molecular and Reproductive Biology

Yongbiao Xue, Principal Investigator, Ph.D. (1989, University of East Anglia and John Innes Centre, Norwich, UK).

Research Interests: The laboratory is mainly interested in the molecular control of reproductive barriers in flowering plant, focusing on self-incompatibility (SI) in *Antirrhinum* and *Petunia*. We are also investigating the molecular genetic mechanism of rice response to environmental temperature.

Email: ybxue@genetics.ac.cn

Genome structure and evolution of *Antirrhinum majus* L

Snapdragon (*Antirrhinum majus* L.), a member of the Plantaginaceae family, is an important model for plant genetics and molecular studies on plant growth and development, transposon biology and self-incompatibility. Here we report a nearcomplete genome assembly of *A. majus* cultivar JI7 (*A. majus* cv.JI7) comprising 510 Megabases (Mb) of genomic sequence and containing 37,714 annotated protein-coding genes. Scaffolds covering 97.12% of the assembled genome were anchored on eight chromosomes. Comparative and evolutionary analyses revealed that a whole-genome duplication event occurred in the Plantaginaceae around 46–49 million years ago (Ma). We also uncovered the genetic architectures associated with complex traits such as flower asymmetry and self-incompatibility, identifying a unique duplication of TCP family genes dated to around 46–49 Ma and reconstructing a near-complete *ψ S*-locus of roughly 2 Mb (Figure). The genome sequence obtained in this study not only provides a representative genome sequenced from the Plantaginaceae but also brings the popular plant model system of Antirrhinum into the genomic age.

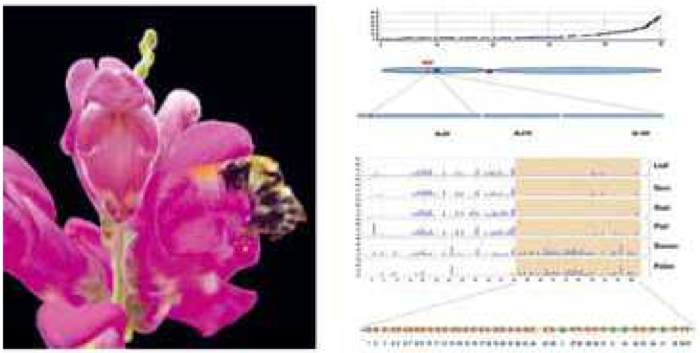

Figure: Genomic features of the *ψ S*-locus of *A. majus*

Publications

Li, M., Zhang, D., Gao, Q., Luo, Y., Zhang, H., Ma, B., Chen, C., Whibley, A., Zhang, Y., Cao, Y., Li, Q., Guo, H., Li, J., Song, Y., Copsey, L., Li, Y., Li, X., Qi, M., Wang, J., Chen, Y., Wang, D., Zhao, J., Liu, G., Wu, B., Yu, L., Xu, C., Zhao, S., Hu, S., Liang, C., Yin, Y., Coen, E. and Xue, Y. (2019). Genome structure and evolution of *Antirrhinum majus* L. Nature Plants 5(2): 174-183.

Pervaiz, N., Shakeel, N., Qasim, A., Zehra, R., Anwar, S., Rana, N., Xue, Y., Zhang, Z., Bao, Y. and Abbasi, A. A. (2019). Evolutionary history of the human multigene families reveals widespread gene duplications throughout the history of animals. BMC Evolutionary Biology 19(1): 128.

Li, Z., Wang, M., Lin, K., Xie, Y., Guo, J., Ye, L., Zhuang, Y., Teng, W., Ran, X., Tong, Y., Xue, Y., Zhang, W. and Zhang, Y. (2019). The bread wheat epigenomic map reveals distinct chromatin architectural and evolutionary features of functional genetic elements. Genome Biology 20(1): 139.

Plant Molecular Genetics and Molecular Breeding

Wenxue Zhai, Principal Investigator, Ph.D. (1999, Institute of Genetics, CAS, China).

Research Interests: The laboratory mainly focuses on molecular cloning and molecular breeding of rice functional genes, particularly those with important agronomic traits. The present work includes positional cloning of rice bacterial blight resistance genes, breeding bacterial blight resistant hybrid rice with the cloned genes, as well as rice and maize molecular breeding.

Email: wxzhai@genetics.ac.cn

Characteristic dissection of *Xanthomonas oryzaepv*. oryzae responsive microRNAs in rice

MicroRNAs (miRNAs) are crucial player in plant-pathogen interaction. Herein, we emphatically monitored the responsive changes of rice miRNAs at 0, 8, 24 hours across *Xoo* strain PXO86 infection in its compatible rice variety IR24 and incompatible variety IRBB5 by small RNA sequencing, and the genes targeted by miRNAs were also detected via degradome technology. The faithfulness of sequencing data was validated through quantitative real-time stem-loop reverse transcription-polymerase chain reaction assay. Bioinformatic analysis showed that the differentially expressed miRNAs could be divided into 3 immunity-related clusters, and 80 regulatory units, comprising 43 differentially expressed known miRNAs and 42 cleaved targets, were emerged in infection process. Further, the miRNA presumptive function of separate immunity cluster in rice-Xoo interplay was confirmed through overexpressing miR164a, miR167d and miR159b, and the disruption of regulatory units, miR164a/*OsNAC60*, miR167d-5p/*OsWD40-174* and miR159b/*OsMYBGA*, *OsLRR-RLK2*, *OsMPK20-4*, may reset rice defense response to *Xoo* infestation in a controllable manner.

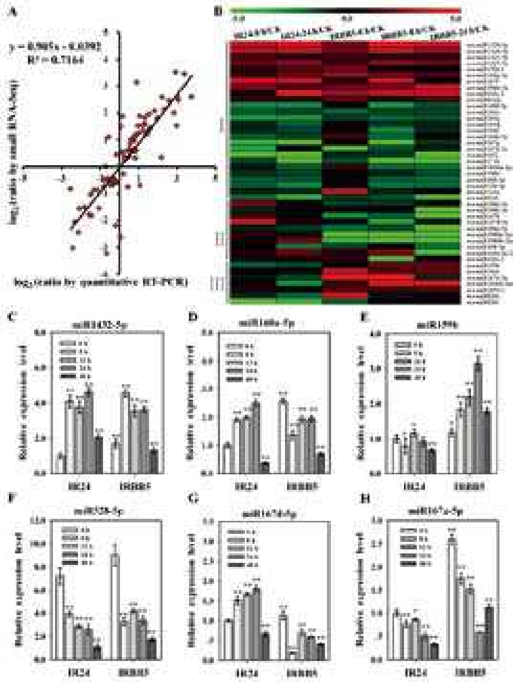

Figure: The responsive expression changes of miRNAs after *Xoo* infection (A) The correlation analysis of miRNA expression level between small RNA sequencing and qRT-PCR experiments. (B) Heat map of the documented miRNAs with |log2 (fold change ratio)| ⩾ 1.5 across Xoo infection. Red and green colors represent up-regulated and down-regulated expression level, respectively. CK represents IR24-0 h. (C and F) The expression profile of basal immunity regulators, miR1432-5p and miR528-5p, in response to *Xoo* strain.(D and G) The expression profile of negative immunity regulators, miR160a-5p and miR167d-5p, in response to *Xoo* strain. (E and H) The expression profile of positive immunity regulators, miR159b and miR167a-5p, in response to *Xoo* strain. Bars represent mean ± standard deviation (n = 3 independent biological replicates). Asterisks indicate a statistically significant difference (student t-test, $^{**}P < 0.01$, $^{*}P < 0.05$).

Publication

Li, T., Fang, Z., Peng, H., Zhou, J., Liu, P., Wang, Y., Zhu, W., Li, L., Zhang, Q., Chen, L., Li, L., Liu, Z., Zhang, W., Zhai, W., Lu, L. and Gao, L. (2019). Application of high-throughput amplicon sequencing-based SSR genotyping in genetic background screening. BMC Genomics 20(1): 444-455.

Wheat Molecular Breeding

Aimin Zhang, Principal Investigator, Ph.D. (1989, Beijing Agricutural Universtiy, China).

Research Interests: Marker-assisted selection of important agronomic traits in wheat and molecular design breeding of wheat varieties.

Email: amzhang@genetics.ac.cn

Publications

Yu, K., Liu, D., Chen, Y., Wang, D., Yang, W., Yang, W., Yin, L., Zhang, C., Zhao, S., Sun, J., Liu, C. and Zhang, A. (2019). Unraveling the genetic architecture of grain size in einkorn wheat through linkage and homology mapping and transcriptomic profiling. Journal of Experimental Botany 70(18): 4671-4687.

Xu, Y., Liu, X., Fu, J., Wang, H., Wang, J., Huang, C., Prasanna, B. M., Olsen, M. S., Wang, G. and Zhang, A. (2019). Enhancing genetic gain through genomic selection: from livestock to plants. Plant Communications: 100005.

Sun, L., Yang, W., Li, Y., Shan, Q., Ye, X., Wang, D., Yu, K., Lu, W., Xin, P., Pei, Z., Guo, X., Liu, D., Sun, J., Zhan, K., Chu, J. and Zhang, A. (2019). A wheat dominant dwarfing line with *Rht12*, which reduces stem cell length and affects gibberellic acid synthesis, is a 5AL terminal deletion line. The Plant Journal 97(5): 887-900.

Shoaib, M., Yang, W., Shan, Q., Sajjad, M. and Zhang, A. (2019). Genome-wide identification and expression analysis of new cytokinin metabolic genes in bread wheat (*Triticum aestivum* L.). PeerJ 7:e6300.

Fine mapping of an important dwarf gene *Rht12* and analysis of its genetic effects in wheat

Dwarfing and semi-dwarfing are important agronomic traits that have great potential for the improvement of wheat yields. *Rht12*, a dominant gibberellic acid (GA)-responsive dwarfing gene from the gamma-rayinduced wheat mutant Karcagi 522M7K, is located in the long arm of chromosome 5A, which is closely linked with the locus Xwmc410. *Rht12* is likely an ideal gene for GA biosynthesis and deactivation research in common wheat. However, information on the *Rht12* locus and sequence is lacking. In this study, *Rht12* significantly shortened stem cell length and decreased GA biosynthetic components. Using bulked segregant RNA-Seq, wheat 660k single nucleotide polymorphism chip detection, and newly developed simple sequence repeat markers, *Rht12* was mapped to a 11.21-Mb region at the terminal end of chromosome 5AL, and was found to be closely linked with the Xw5ac207 SSR marker with a 10.73-Mb fragment deletion in all of the homologous dwarfing plants. Transcriptome analyses of the remaining 483-kb region showed significantly higher expression of the *TraesCS5A01G543100* gene encoding the GA metabolic enzyme GA 2-b-dioxygenase in dwarfing plants than in high stalk plants, suggesting that *Rht12* reduces plant height by activating *TaGA2ox-A14*. Taken together, our findings will promote cloning and functional studies of *Rht12* in common wheat

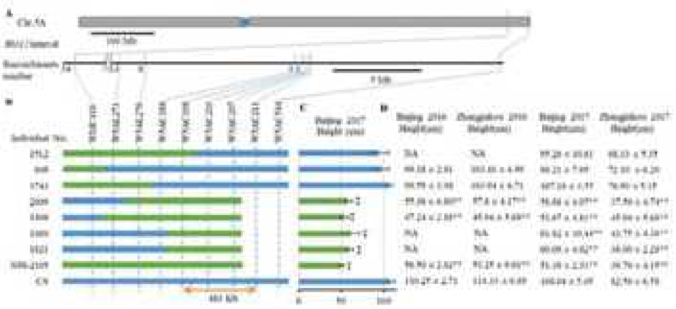

Figure: Graphical illustrations of the recombinant genotypes in the *Rht12* interval and their phenotypes. A. Physical distance between molecular markers and the recombinant's number left in each region. B. Graphical illustrations of the recombinant genotypes in the *Rht12* interval. C. The plant height phenotype of the recombinants in Beijing 2017. D. The plant height phenotype of the recombinants among different environments in 2016 and 2017.

Molecular Genetics of Resistance and Processing Quality of Wheat

Xiangqi Zhang, Principal Investigator, Ph.D. (1990, Northeast Normal University, China).

Research Interests: 1) Development of wheat germplasms with disease resistance and other excellent characters by molecular chromosome engineering and application to molecular breeding. 2) Genetic basis and regulatory mechanism of fungal diseases resistance and processing quality of wheat, mainly include stripe rust resistance and high-molecular-weight glutanin subunit genes cloning, function verification and regulatory mechanism dissection.

Email: xqzhang@genetics.ac.cn

Development and identification of new common wheat-*elytrigia intermedia* blue-grained substitution lines

The blue grain trait of wheat can be used as a phenotypic marker in wheat breeding and genetics research. Blue-grained germplasm derived from *Elytrigia intermedia* have rarely reported. In the present study, two blue-grained lines, Zh5-a2-1 and Zh5- c13-2, were selected from the progenies of Zhong5×N4BT4A and Zhong5×N7BT7D cross combinations. The chromosome constitutions of the two blue-grained lines were analyzed by cytogenetics and molecular marker methods. The GISH analysis using genomic DNA of *Et. intermedia* as probe showed that the chromosome numbers of the two blue-grained lines were all 2n = 42, including 40 wheat chromosomes and 2 *Et. intermedia* chromosomes. The FISH analysis with repetitive sequence probes pSc119.2 and pAs1 indicated that both Zh5-a2-1 and Zh5-c13-2 were disomic substitution lines, the 4B and 4D wheat chromosome pairs were substituted by a pair of *Et. intermedia* chromosomes, respectively. By using St, E^e and E^b genomic DNA as probes, FISH analysis demonstrated that the chromosomes of *Et. intermediain* the two blue-grained substitution lines derived from St genome. However, compared with the Et. intermedia chromosomes in Zhong 5, it was found that the short arm ends of the St chromosomes in the two substitution lines were deleted. The Ee genome specific SNP marker analysis further proved that the *Et. intermedia* chromosomes in the two blue-grained substitution lines were homologous to the $4E^e$ chromosome of diploid *Et. elongata*, i.e. Zh5-a2-1 and Zh5-c13-2 were 4St(4B) and 4St(4D) substitution lines, and named SubZh5-4St(4B) and SubZh5-4St(4D), respectively. Meanwhile, it also proved that the 4St chromosome of *Et. intermedia* possessed blue grain gene. In order to identify and trace blue grain traits by molecular markers more easily, the SSR markers of wheat were screened. As result, the 4 pairs of specific SSR primers distinguishing 4St chromosomes in the blue-grained substitution lines were selected from 450 SSR primers of wheat. The results could be used for breeding of blue-grained wheat varieties and genetic study of blue grain gene of *Et. intermedia*. Key words: Triticum aestivum; *Elytrigia intermedia*; Blue-grained substitution line; Chromosome constitution; Molecular marker

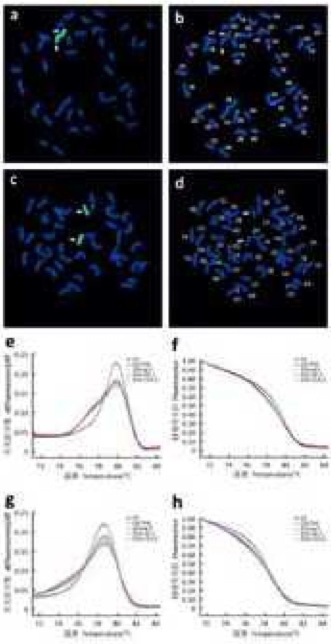

Figure: Identification of blue-grained substitution lines by SNP markers a: The melting peaks of the SNP marker 4E05 from 4EeS; b: The melting curves of the SNP marker 4E05 from 4EeS; c: The melting peaks of the SNP marker 4E16 from 4EeL; d: The melting curves of the SNP marker 4E16 from 4EeL. CS: Common wheat Chinese Spring; CS/THE: Chinese Spring-diploid Et. elongata amphidiploid.

Molecular Design Breeding of Soybean

Baoge Zhu, Principal Investigator, Ph.D. (2005, Chinese Academy of Sciences).

Research Interests: Investigating and mapping genes controlling agronomically important traits; breeding for soybean cultivars attributed for human nutrients; designing, selecting and deploying technologies for breeding soybean cultivars with high yield, good quality and resistance to biotic and abiotic stresses.

Email: bgzhu@genetics.ac.cn

Breeding for soybean cultivars Kedou 13 attributed wide adaptability and high yield

The lack of high-yield varieties with wide adaptability in soybean production makes it difficult to develop large varieties with large extension area in China. It is one of our main breeding goals to select wide adaptability varieties. In 2012, a hybridization was carried out between Youbian 30 and Wansu2156 and its female parent Wansu2156 was selected from the Cross Zhonghuang13 × Zhengjiao 8739-47. Zhonghuang 13 is a wide-adaptability and high-yielding soybean variety. The male parent Youbian 30 is also a high yield and wide adaptability soybean variety bred by institute of Genetics and Developmental Biology, Chinese Academy of Sciences. A superior F_6 generation line Kedou 13 with high yield was selected in 2015. The yield trial were carried out in Beijing, Henan and Anhui province. The yield per mu reached over 200 kg, which was 8.00% higher than that of the control variety. It has the characteristics of wide adaptability, moderate maturity, multiple pods of main stem, high yield and lodging resistance, and can be planted in all huanghuai- hai ecological region, spanning 8 latitudes. In 2016 and 2017, kedou 13 took part in the yield test of the North group of Huanghuaihai region, and the average yield per mu was 208.07 kg and 222.63 kg, respectively, which increased 5.6% and 17.84%, respectively, compared with the control variety Jidou 12. In 2018, we took part in the national regional test of the North group of Huanghuaihai region. The average yield per mu was 188.8 kg, which was 5.70% higher than that of Jidou 12. The yield trial of kedou 13 was continued in 2019. The variety has wide adaptability, high yield potential and good application prospect.

Figure: the photo of kedou 13 in bearing pod and mature stage.

Center for Developmental Biology

The Center for Developmental Biology (CDB) focuses on addressing fundamental questions of developmental biology using model organisms such as *C. elegans, Drosophila, Xenopus,* zebrafish, mouse, monkey, *Arabidopsis* and rice. The mission is to develop innovative technology to meet our national needs in agriculture and human health. Currently CDB has 21 research groups. Among them, 8 principal investigators were awarded the National Science Fund for Distinguished Young Scholars Dr. John Speakman and was elected as CAS foreign member in 2019. During 2019, CDB has made substantial progress in the following areas.

Cell Differentiation and Organ Formation: RNA poly (a) tail is an essential component of mature mRNA and lncRNA, important for RNA stability and translation regulation. Dr. Falong Lu's lab established a new accurate and sensitive method to analyze RNA poly (A) tails. This method is able to read the full-length RNA isoforms with the entire poly (A) tail sequences using the PacBio sequencing platform. They found more than 17% of the mRNAs harbor non-A (U, G and C) residues within the body of poly (A) tails in mouse GV oocytes, besides those known non-A residues at the 3' ends. These findings along with the PAIso-seq method may open the door to a new layer of RNA post-transcriptional regulations (Liu et al., *Nat Commun*, 2019). Little is known about the function of histone arginine methylation in acute lymphoblastic leukemia (ALL). Dr. Shilai Bao's group and Dr. Huyong Zheng's lab of Beijing Children's Hospital found that enhanced protein arginine methyltransferase 5 (PRMT5) promotes pediatric B-cell precursor acute lymphoblastic leukemia (BCP-ALL) leukemogenesis partially by the dysregulation of B-cell lineage differentiation. The symmetric dimethylation of H4R3 (H4R3sme2) and PRMT5 may serve as potential sensitive biomarkers of pediatric BCP-ALL. Suppression of the activation of PRMT5 may offer a promising therapeutic strategy against pediatric BCP-ALL (Mei et al., *Clin Cancer Res*, 2019). Dr. Yuqiang Jiang's group developed an efficient *in vivo* photodynamic therapy system based on a nanomaterial, dihydrolipoic acid-coated gold nanocluster (AuNC@DHLA), that combined the advantages of large penetration depth in tissue, extremely high two-photon (TP) absorption cross-section (σ_2~10^6 GM), efficient ROS generation, a Type I photochemical mechanism, and negligible *in vivo* toxicity. This system has very important clinical application value (Han et al., *ACS Nano*, 2019). Dr. Weicai Yang's group discovered that BICE1 interacts with MCM4 and MCM7 of the pre-replication complex and suggested that BICE1 plays a role in modulating DNA replication via interaction with MCM4 and MCM7 (Long et al., *New Phytol*, 2019).

Neurodevelopment and Regeneration: Adult neurogenesis exhibits distinct characteristics from the embryonic counterpart. However, the intrinsic mechanism underlying the differential regulation of neurogenesis between these two stages remains unclear. Dr. Weixiang Guo's lab found that RNA-binding protein HuR is predominantly expressed in the cytoplasm of embryonic neural stem cells (NSCs) but translocates into the nucleus of adult NSCs. Transcriptomic analysis of HuR-deficient adult NSCs revealed that HuR primarily regulates alternative splicing of numerous premRNA transcripts, including focal adhesion kinase (FAK). These findings provide mechanistic insights into the differential regulation of embryonic and adult neurogenesis through developmental cytoplasmic to nuclear translocation of HuR (Wang et al., *Cell Rep*, 2019). Coronary arteries occlusion results in ischemic myocardial tissue and progressively negative ventricular remodeling. At or after the initial period of myocardial infarction (MI), matrix metalloproteinases (MMPs) are upregulated and cause degradation of the extracellular matrix (ECM) and further decrease of tissue mechanical properties, which contributes to progressive thinning and global dilatation of the ventricular wall in the infarcted area, leading to a deterioration in cardiac function. Dr. Jianwu Dai's group developed a dual-function MI-responsive on-demand growth factor delivery system to promote angiogenesis and inhibit cardiac remodeling by targeting the upregulated MMP-2/9 after MI. The new system increases the local protein concentration and reduces unnecessary diffusion, which results in significantly improved cardiac function, increased vascularization, and ameliorates adverse myocardial remodeling (Fan et al., *Adv Mater*, 2019).

Tissue Metabolism and Aging: Comprehensive assessment of serum lipidomic aberrations before type 2 diabetes (T2DM) onset has remained lacking in Han Chinese. Dr. Guanghou Shui's lab evaluated changes in lipid coregulation antecedent to T2DM and identified novel lipid predictors for T2DM in individuals with normal glucose regulation (NGR). Through the analysis large amounts of data, they further improved prediction of incident diabetes over conventional clinical indices (Lu et al., *Diabetes Care*, 2019). The gut microbiome has been shown to have diverse impacts on human and animal physiology and health. During cold exposure it is well established that animals maintain their body temperature by activating heat production from a specialized tissue known as Brown Adipose Tissue (BAT) and promoting "browning" of white adipose tissue. Dr. John Speakman's lab used different antibiotic recipes to eradicate gut microbiota. They subsequently found that animals lacking gut microbiota had impaired thermoregulation. Therefore, the results reveal that the function of gut microbiota plays an important role in the activation of BAT (Li et al., *Cell Rep*, 2019)

Role of Histone Modifications on Cell Fate Determination During the Lung Development

Shilai Bao, Principal Investigator, Ph.D. (1999, The University of Science and Technology of China); Visiting scholar (1999, Purdue University, USA); Postdoctoral fellow (1999-2003, MD Anderson Cancer Center, USA).

Research Interests: Cell fate determination is very important for organgenesis.Epigenetics is the key during cell fate determiation. We are intersted in the role of epigenetics in cell fate determination during lung developpment. The role of the interactions between Golgi apparatus and other organelles in neurodegenerative diseases.

Email: slbao@genetics.ac.cn

PRMT5-mediated H4R3sme2 confers cell differentiation in pediatric B-cell precursor acute lymphoblastic leukemia

Little is known about the function of histone arginine methylation in acute lymphoblastic leukemia (ALL). The objective was to evaluate whether protein arginine methyltransferase 5 (PRMT5) plays a role in pediatric ALL and to determine the possible mechanism of epigenetic regulation. We used bone marrow samples from patients with pediatric ALL, the Nalm6 cell line, mature B-cell lines, and mouse xenograft models to evaluate the function of PRMT5 in ALL tumorigenesis. Our study showed that PRMT5 and the symmetric dimethylation of H4R3 (H4R3sme2) were upregulated in most initially diagnosed (n=15; 100%) and relapsed (n=4; 75%) bone marrow leukemia cells from patients with pediatric B-cell precursor ALL (BCP-ALL) and were decreased when the disease was in remission (n$^{1}/_{4}$15; 6.7%). Down regulation of H4R3sme2 by PRMT5 silencing induced BCP ALL cell differentiation from the pre-B to immature B stage, whereas overexpressed PRMT5 with enhanced H4R3sme2 promoted human mature B cells to dedifferentiate back to the pre-B II/immature B stagesin vitro. High PRMT5 expression enhanced the proportion of CD43^{+}/B220^{+}/sIgM^{+}B leukocytes in recipient mice. CLC and CTSB were identified as potential target genes of PRMT5 in BCP-ALL cells and were inhibited by H4R3sme2 in gene promoters. Conclusions: We demonstrate that enhanced PRMT5 promotes BCP-ALL leukemogenesis partially by the dysregulation of B-cell lineage differentiation. H4R3sme2 and PRMT5 may serve as potential sensitive biomarkers of pediatric BCP-ALL. Suppression of the activation of PRMT5 may offer a promising therapeutic strategy against pediatric BCP-ALL.

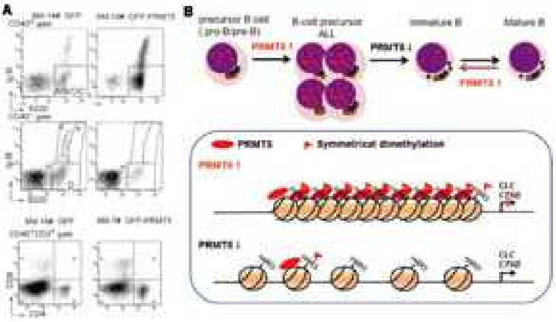

Figure: (A) Upregulation of PRMT5 enhanced the CD43^{+}/B220^{+}/sIg^{+} subpopulation fraction in B lineage cells from irradiated mice. (B) Modal figure for the role of PRMT5 and H4R3sme2 in the BCP-ALL.

Publications

Mei, M., Zhang, R., Zhou, Z. W., Ying, Z., Wang, J., Zhang, H., Zheng, H. and Bao, S. (2019). PRMT5-mediated H4R3sme2 confers cell differentiation in pediatric B-cell precursor acute lymphoblastic leukemia. Clinical Cancer Research 25(8): 2633-2643.

Dong, C., Li, F., Yang, T., Feng, L., Zhang, S., Li, F., Li, W., Xu, G., Bao, S., Wan, X., Lucas, W. J. and Zhang, Z. (2019). Theanine transporters identified in tea plants (Camellia sinensis L.). Plant Journal. Doi: 10.1111/tpj.14517.

Ding, X., Jiang, X., Tian, R., Zhao, P., Li, L., Wang, X., Chen, S., Zhu, Y., Mei, M., Bao, S., Liu, W., Tang, Z. and Sun, Q. (2019). RAB2 regulates the formation of autophagosome and autolysosome in mammalian cells. Autophagy 15(10): 1774-1786.

Plant Molecular Response and Control Mechanism

Fan Chen, Principal Investigator, Ph.D. (1997, Ehime University, Japan).

Research Interests: The laboratory mainly focuses on plant molecular response and control mechanism. The signal transduction during plantdevelopment are concerned. The high-through omics and genetics analysis were used to construct the network of gene expression and regulation in higher plant.

Email: fchen@genetics.ac.cn

Molecular genetics analysis of a high altitude ecotype of *Arabidopsis thaliana* from the Himalayas

Arabidopsis thaliana illuminates the plant world for us. Studies on *A. thaliana* have unraveled the mystery of plant genetics, physiology, and adaptive evolution. After more than ten years of exploration, we discovered five wild *A. thaliana* populations 3770-4340 m above sea level in the Qinghai-Tibet Plateau (QTP) and named it Tibet-0. Phylogenetic analysis and coalescent methods based on genome-wide re-sequencing both showed that Tibet-0 is the most primitive *A. thaliana* ecotype. Using fossil calibrations and Bayesian coalescent models, we estimated that the divergence time between Tibet-0 and other ecotypes was 0.152 – 0.160 million years ago, which is the time of the last uplift of the QTP, indicating that the uplift of QTP promoted the formation of Tibet-0. Ancestor reconstruction of 5741 orthologous genes also updated our knowledge of the *A. thaliana* ancestor. In common garden experiments, Tibet-0 and Can-0 were characterized by more rosette-like leaves and later flowering times, after the long exposure to the extreme environments encountered at high altitude. Accordingly, a number of genes of Tibet-0 in the MAX pathway and the flowering pathway showed positive selection, which may explain this plant's low height and increased shoot branching. As a rare experimental material and potential genetic resource, Tibet-0 from QTP opens a new window through which we can not only know more about the *A. thaliana* ancestor, but also better understand the long-term adaptation of plants to extreme environments.

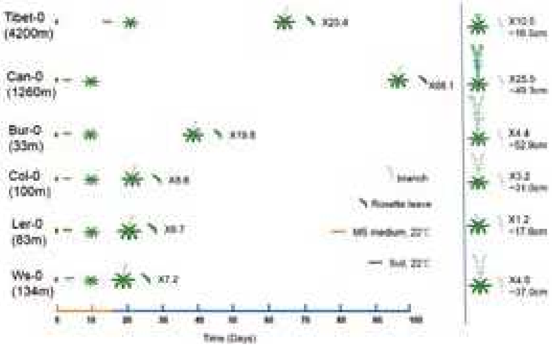

Figure: Common garden experiment design. Tibet-0 and other *A. thaliana* ecotypes were applied to the same treatments. The brown ellipse means the seed. Four picture types showed different stages of plant growth. The altitude of each ecotype is listed under the name.

Publications

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Fang, J., Zhang, F., Wang, H., Wang, W., Zhao, F., Li, Z., Sun, C., Chen, F., Xu, F., Chang, S., Wu, L., Bu, Q., Wang, P., Xie, J., Chen, F., Huang, X., Zhang, Y., Zhu, X., Han, B., Deng, X. and Chu, C. (2019). *Ef-cd* locus shortens rice maturity duration without yield penalty. Proceedings of the National Academy of Sciences of the United States of America 116(37): 18717-18722.

Regenerative Medicine and Tissue/Organ Construction

Jianwu Dai, Principal Investigator, Ph.D. (1998, Duke University, USA).

Research Interests: 1) Development of products to promote tissue and organ regeneration or repair; 2) Mechanisms of tissue and organ regeneration; 3) Tissue and organ fabrication
Email: jwdai@genetics.ac.cn

Publications

Fan, C., Shi, J., Zhuang, Y., Zhang, L., Huang, L., Yang, W., Chen, B., Chen, Y., Xiao, Z., Shen, H., Zhao, Y., Dai, J. (2019). Myocardial-infarction-responsive smart hydrogels targeting matrix metalloproteinase for on-demand growth factor delivery. Advanced Materials 31(40):e1902900

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Han S., Yin W., Li X., Wu S., Cao Y., Tan J., Zhao Y., Hou X., Wang L., Ren C., Li J., Hu X., Mao Y., Li G., Li B., Zhang H., Han J., Chen B., Xiao Z., Jiang X., Dai, J. (2019). Pre-clinical evaluation of CBD-NT3 modified collagen scaffolds in completely spinal cord transected non-human primates. Journal of Neurotrauma 36 (15): 2316-2324.

Myocardial-infarction-responsive smart hydrogels targeting matrix metalloproteinase for on-demand growth factor delivery

Coronary arteries occlusion results in ischemic myocardial tissue and progressively negative ventricular remodeling. At or after the initial period of myocardial infarction (MI), matrix metalloproteinases (MMPs) are upregulated and cause degradation of the extracellular matrix (ECM) and further decrease of tissue mechanical properties, which contributes to progressive thinning and global dilatation of the ventricular wall in the infarcted area, leading to a deterioration in cardiac function. Therefore, *in situ* restoration of the blood supply to the infarction region and attenuation of pre-existing ECM degradation have emerged as potential therapeutic approaches for treating MI. We developed a dual-function MI-responsive on-demand growth factor delivery system to promote angiogenesis and inhibit cardiac remodeling by targeting the upregulated MMP-2/9 after MI. A glutathione (GSH)-modified collagen hydrogel (collagen-GSH) is prepared by conjugating collagen amine groups with GSH sulfhydryl groups and the recombinant protein GST-TIMP-bFGF (bFGF: basic fibroblast growth factor) by fusing bFGF with glutathione-S-transferase (GST) and MMP-2/9 cleavable peptide PLGLAG (TIMP). GST-TIMP-bFGF/collagen-GSH achieved on-demand bFGF release at the infarcted site, increasing the local protein concentration and reducing unnecessary diffusion, which resulted in significantly improved cardiac function, increased vascularization, and ameliorated adverse myocardial remodeling.

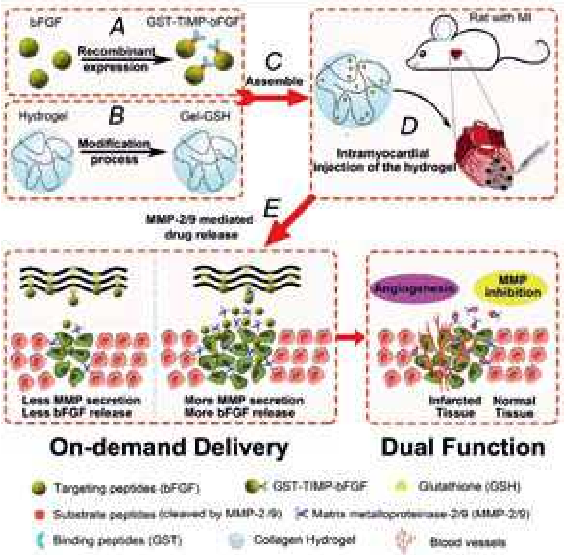


Figure: Schematic representations of MMP-responsive hydrogel preparation and the process of drug release in the wound bed of MI model rats. A) Preparation of GST-TIMP-bFGF via a recombinant protein expression method; B) GSH was loaded into the hydrogel by a chemical crosslinking process to obtain Gel-GSH; C) GST-TIMP-bFGF was mixed with Gel-GSH, and the two components were linked with a bond between GST and GSH; D) Intramyocardial injection of the mixed hydrogel to the wound of a rat after MI; E) In the wound microenvironment, substrate peptides were degraded by MMP-2/9, and specific targeting peptides were released, achieving the dual functions of angiogenesis and MMP inhibition.

The Molecular Mechanisms of Neural Development

Mei Ding, Principal Investigator, Ph.D. (2004, University of California, Santa Cruz, USA).

Research Interests: The simple nervous system of the nematode C. elegans is well suited for studying neural development. The complete synaptic connectivity of the nervous system is known from reconstructions of serial sections of electron micrographs, allowing the analysis to be carried out at the level of a single cell and single synapse. Furthermore, the use of fluorescent protein facilitates the visualization of neuronal processes and synapses in vivo and in living animals. We are studying the development of ne.

Email: mding@genetics.ac.cn

Alleviating chronic ER stress by autophagy activation independent of the *p38-Ire1-Xbp1*-mediated unfolded protein response

The accumulation of unfolded proteins in the endoplasmic reticulum (ER) triggers the ER stress response, which allows cells to fight against fluctuations in protein expression under both physiological and pathological conditions. Severe acute ER stress responses can be induced by drug treatment. However, such intense ER stress rarely occurs ubiquitously *in vivo*. Here, we showed that overexpressing the gap junction protein UNC-9 (Uncoordinated) in *C. elegans* GABAergic neurons specifically triggers the *p38- Ire1-Xbp1*-mediated stress response in an age-dependent and cell-autonomous manner. In the absence of the *p38-Ire1-Xbp1* pathway, UNC-9 protein expressed at the endogenous level is processed normally, while overexpressed UNC-9 accumulates in the ER. UNC-9 overexpression also activates autophagy and the insulin-like receptor DAF-2 inhibits autophagy, but not the transcription of genes encoding ER chaperones, to counteract the *p38-Ire1-Xbp1*-mediated stress response. Together, our results show that chronic ER stress in specific cells *in vivo* can be alleviated independently of the unfolded protein response by enhancing autophagy.

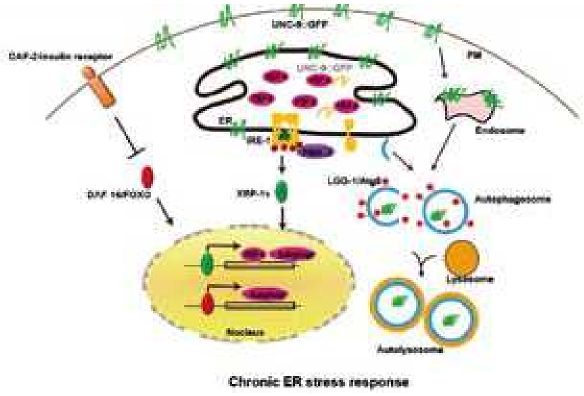


Figure: Autophagy and the PMK-3-IRE-1-XBP-mediated UPR act in parallel to alleviate chronic stress induced by excess UNC-9::GFP proteins.

Publication

Ji, J., Yuan, J., Guo, X., Ji, R., Quan, Q., Ding, M., Li, X. and Liu, Y. (2019). Harmine suppresses hyper-activated Ras-MAPK pathway by selectively targeting oncogenic mutated Ras/Raf in *Caenorhabditis elegans*. Cancer Cell International 19: 159.

Neural Stem Cells and Neurogenesis

Weixiang Guo, Principal Investigator, Ph.D. (2008, Institute of Zoology, CAS, China).

Research Interests: The research in our laboratory focuses on understanding the cellular and molecular mechanisms that regulate neural stem cells and neural development, with the goal to develop better treatment for human neurological disorders.

Email: wxguo@genetics.ac.cn

Publications

Wang, J., Cui, Y., Yu, Z., Wang, W., Cheng, X., Ji, W., Guo, S., Zhou, Q., Wu, N., Chen, Y., Chen, Y., Song, X., Jiang, H., Wang, Y., Lan, Y., Zhou, B., Mao, L., Li, J., Yang, H., Guo, W. and Yang, X. (2019). Brain endothelial cells maintain lactate homeostasis and control adult hippocampal neurogenesis. Cell Stem Cell 25(6): 754-767 e759.

Wang, Y., Guo, Y., Tang, C., Han, X., Xu, M., Sun, J., Zhao, Y., Zhang, Y., Wang, M., Cao, X., Zhu, X. and Guo, W. (2019). Developmental cytoplasmic-to-nuclear translocation of RNA-binding protein HuR is required for adult neurogenesis. Cell Reports 29(10): 3101-3117 e3107.

Developmental cytoplasmic-to-nuclear translocation of RNA-binding protein HuR is required for adult neurogenesis

Although adult neurogenesis recapitulates processes that occur during embryonic development, it exhibits distinct characteristics from the embryonic counterpart. However, the intrinsic mechanism underlying the differential regulation of neurogenesis between these two stages remains unclear. Herein, we show that the ablation of RNA binding protein HuR in NSCs impairs adult, but not embryonic, neurogenesis. HuR is predominantly expressed in the cytoplasm of embryonic NSCs but translocates into the nucleus of adult NSCs. Transcriptomic analysis of HuR-deficient adult NSCs revealed that HuR primarily regulates alternative splicing of numerous premRNA transcripts, including focal adhesion kinase (FAK). HuR-deficient adult NSCs generate increased FAK mRNA isoforms with shorter 5’-UTRs, leading to enhanced FAK mRNA translation and hyperactivated FAK signaling, and inhibition of FAK ameliorates defective adult neurogenesis and impaired hippocampus-dependent learning in HuR-deficient mice. Taken together, these findings provide mechanistic insights into the differential regulation of embryonic and adult neurogenesis through developmental cytoplasmic-to nuclear translocation of HuR.

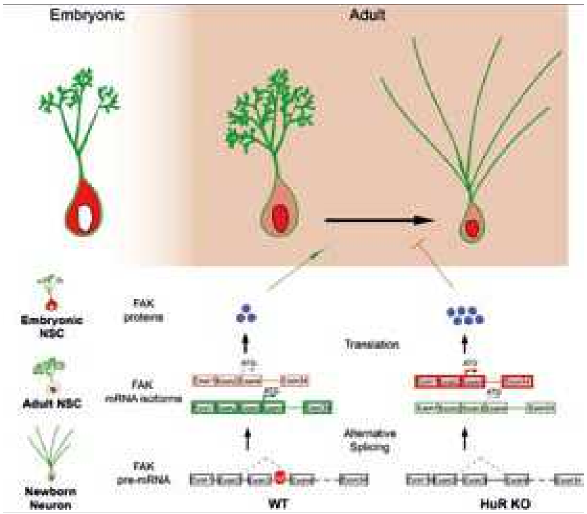


Figure: Developmental cytoplasmic-to-nuclear translocation of hur is required for adult neurogenesis.

Signaling Transduction and Lipid Conversion During Membrane Trafficking

Kangmin He, Principal Investigator, Ph.D. (2013, Academy for Advanced Interdisciplinary Studies, Peking University); Postdoctoral fellow/Instructor/Research Associate (2013-2019, Harvard Medical School/Boston Children's Hospital, USA)

Research Interests: Using live-cell single-molecule quantitative imaging, genome editing, sensor design and other tools to study the molecular mechanism of endocytosis and intracellular trafficking, and the dynamic signaling transduction and phospholipid trafficking/conversion during membrane trafficking.

Email: kmhe@genetics.ac.cn

Single-molecule live-cell imaging of signaling transduction and lipid conversion during membrane trafficking

Since mid-March this year, we have made some progress in the studying of endocytosis and the accompanying signaling transduction and phospholipid trafficking/conversion using tools such as live-cell single-molecule imaging and genome editing. By creating and imaging genome-edited cell lines expressing fluorescent protein tags, our preliminary results have suggested a novel mechanism of early endosome formation from clathrin-mediated endocytic vesicles. By creating human cancer cell lines with endogenous EGFR and its different downstream signaling molecules tagged with different fluorescent proteins and tags, we have developed a system to follow the dynamics of EGFR and its signaling molecules during signal transduction by 3-color singlemolecule live-cell imaging and tracking. By designing novel clathrin-specific phosphoinositide sensors, we have found the specific recruitment of different phosphoinositide species during clathrin-mediated endocytosis.

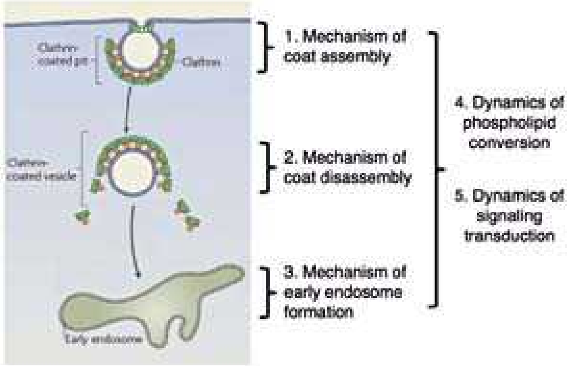


Figure: Research topics in the lab: we use live-cell single-molecule quantitative imaging, genome editing, sensor design and other tools to investigate the molecular mechanisms of endocytosis and intracellular trafficking, the dynamic phospholipid trafficking/conversion as well as the dynamic signaling transduction and regulation during membrane trafficking.

Lipid Metabolism, Development and Disease

Xun Huang, Principal Investigator, Ph.D. (2003, University of California, Santa Cruz, USA).

Research Interests: The long-term goal of our laboratory is to understand the regulating mechanisms of lipid metabolism and disease. Currently the main interest of our lab is to understand the cell biology and developmental biology of lipid metabolism in adipose tissue, neuron and reproduction system under normal physiological conditions and under disease conditions.

Email: xhuang@genetics.ac.cn

Publications

Chen, L. G., Chen, X. W., Huang, X., Song,B. L., Wang, Y. and Wang, Y. G. (2019).Regulation of glucose and lipidmetabolism in health and disease.Science China-Life Sciences 62(11): 1420-1458

Liu, Y., Ji, Y., Li, X., Shui, G. H. and Huang, X. (2019). Lipid storage regulator CdsA is essential for *Drosophila* metamorphosis. Journal of Genetics and Genomics 46(4): 231-234.

Wang, W., Xin, J. X., Yang, X., Lam, S. M., Shui, G. H., Wang, Y. and Huang, X. (2019). Lipid-gene regulatory network reveals coregulations of triacylglycerol with phosphatidylinositol/ lysophosphatidylinositol and with hexosyl-ceramide. Biochimica Et Biophysica Acta-Molecular and Cell Biology of Lipids 1864(2): 168-180.

Yang, X., Liang, J. J., Ding L., Li X., Lam, S. M., Shui, G. H., Ding, M., Huang, X. (2019). Phosphatidylserine synthase regulates cellular homeostasis through distinct metabolic mechanisms. PLoS Genetics Doi: 10.1371/journal.pgen.1008548.

Phosphatidylserine synthetase regulates cellular homeostasis through distinct metabolic mechanisms

Phosphatidylserine (PS), synthesized in the endoplasmic reticulum (ER) by phosphatidylserine synthetase (PSS), is transported to the plasma membrane (PM) and mitochondria through distinct routes. The *in vivo* functions of PS at different subcellular locations and the coordination between different PS transport routes are not fully understood. Here, we report that *Drosophila* PSS regulates cell growth, lipid storage and mitochondrial function. In *pss RNAi*, reduced PS depletes plasma membrane Akt, contributing to cell growth defects; the metabolic shift from phospholipid synthesis to neutral lipid synthesis results in ectopic lipid accumulation; and the reduction of mitochondrial PS impairs mitochondrial protein import and mitochondrial integrity. Importantly, reducing PS transport from the ER to PM by loss of *PI4KIIIa* partially rescues the mitochondrial defects of *pss RNAi*. Together, our results uncover a balance between different PS transport routes and reveal that PSS regulates cellular homeostasis through distinct metabolic mechanisms.

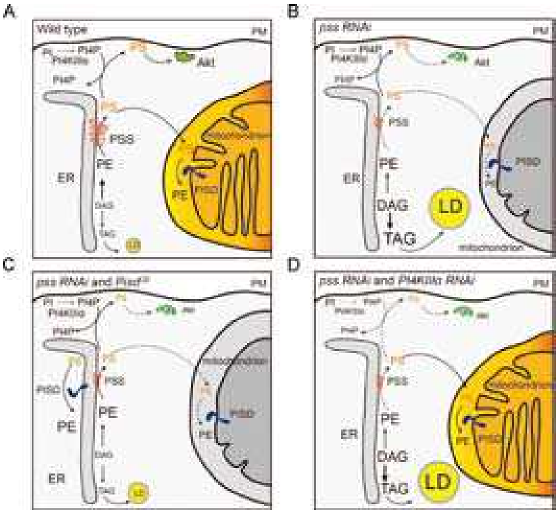


Figure: Proposed models of the mechanisms underlying the different pss RNAi phenotypes. (A-B) Loss of pss function leads to reduced Akt, increased DAG and TAG, and impaired mitochondrial structure and function. (C) The overexpression of *Pisd in pss RNAi* may lead to increased engagement of phospholipids in the PS-PE-PS cycle locally, probably at the ER or mitochondria. Therefore, *Pisd* overexpression reduces the level of PS at the PM and the amount of DAG available for TAG synthesis, leading to smaller cells and decreased lipid storage compared to *pss RNAi* alone (B). (D) *RNAi* of *PI4KIIIα* rescues the defective mitochondrial import of mitoEYFP in *pss RNAi* by increasing the transport of PS to the mitochondria.

Development and Application of Micro Nano Optics and Biological Image Technology

Yuqiang Jiang, Principal Investigator, Ph.D. (2004, Shanxi University, China).

Research Interests: 1) Laser tweezers and its biological application; 2) Nano functional materials and their biological applications; 3) Nonlinear effects in femtosecond acquisition; 4) Phenotypic study of crops.

Email: yqjiang@genetics.ac.cn

Two photon photodynamic therapy has made new progress in tumor treatment

Using gold nanoclusters (AuNC@DHLA) with dihydrolipoic acid as ligand as photosensitizer, combined with near-infrared pulse light source with deep tissue penetration, the killing effect of tumor in vivo was effectively improved. Under the laser irradiation, AuNC@DHLA can produce a large number of superoxide anion $O_2^{-\bullet}$, and realize photodynamic therapy based on type I mechanism (the traditional photodynamic therapy produces reactive oxygen radicals mainly in singlet oxygen $^1O_2$, which is type II mechanism). The experimental results of tumor bearing mice showed that AuNC@DHLA can effectively inhibit the growth of tumor, and its therapeutic effect was significantly better than that of 5-aminolevulinic acid (5-ALA) photosensitizer in clinical use. Our development of AuNC@DHLA two-photon photodynamic therapy has the advantages of high biosafety, good photodynamic effect, large tissue penetration depth and so on, which has very important clinical application value.

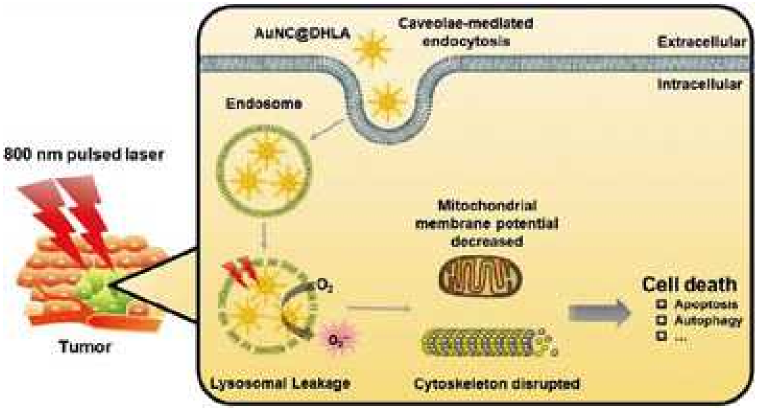


Figure: AuNC@DHLA based on two photon photodynamic therapy and its mechanism. Gold nanoclusters enter cells through receptor-mediated endocytosis and are enriched in lysosome. Under the light condition, gold nanoclusters induce superoxide anion radicals, which cause the change of lysosomal membrane permeability, then lead to the damage of mitochondrial function (the decrease of membrane potential, the change of mitochondrial morphology, etc.) and the breakage of cytoskeleton, finally induce cell death.

Publications

Han, R., Zhao, M., Wang, Z., Liu, H., Zhu, S., Huang, L., Wang, Y., Wang, L., Hong, Y., Sha, Y. and Jiang, Y. (2019). Super-efficient *in vivo* two-photon photodynamic therapy with a gold nanocluster as a type I photosensitizer. ACS Nano. Doi: 10.1021/acsnano.9b05169.

Yan, Y., Yu, J., Gao, Y., Kumar, G., Guo, M., Zhao, Y., Fang, Q., Zhang, H., Yu, J., Jiang, Y., Zhang, H.-T. and Ma, C.-G (2019). Therapeutic potentials of the Rho kinase inhibitor Fasudil in experimental autoimmune encephalomyelitis and the related mechanisms. Metabolic Brain Disease 34(2): 377-384.

Molecular Mechanisms and Functions of Vesicular Transport

Jia-Jia Liu, Principal Investigator, Ph.D. (2000, University of Chicago, USA).

Research Interests: The laboratory is mainly interested in membrane trafficking, focusing on molecular mechanisms of dynein-dynactin-driven vesicular transport in mammalian cells and role(s) of vesicular transport and cytoskeleton dynamics in synaptic development and plasticity.

Email: jjliu@genetics.ac.cn

Endophilin A1 promotes actin polymerization in dendritic spines to initiate structural plasticity

Dendritic spines of excitatory neurons undergo activity-dependent structural and functional plasticity, which are cellular correlates of learning and memory. However, mechanisms underlying the rapid morphological changes immediately after NMDAR-mediated Ca^{2+} influx into spines remain poorly defined. Our study demonstrates that endophilin A1, a neuronal N-BAR protein, functions in the initial phase of long-term potentiation (LTP). Ca^{2+}/calmodulin enhance its binding to its effector p140Cap and the plasma membrane. Upon LTP induction, endophilin A1 rapidly localizes to plasma membrane and promotes actin polymerization via p140Cap. Moreover, both the p140Cap-binding and membrane-binding capacities of endophilin A1 are required for LTP and longterm memory. These data indicate that endophilin A1 functions immediately downstream of calmodulin to promote spine enlargement in response to Ca^{2+} influx in the initial phase of structural plasticity.

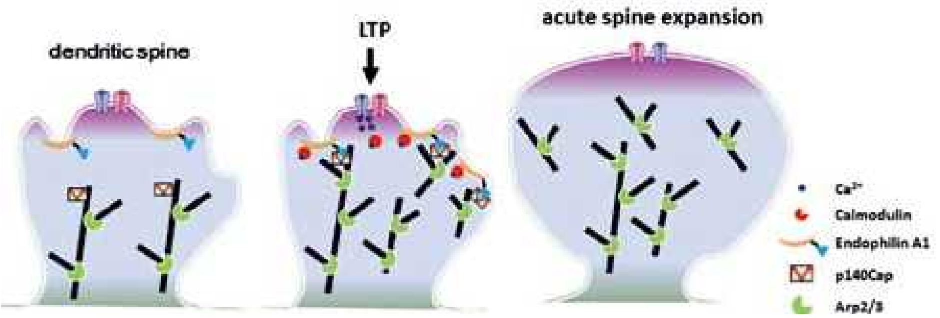


Figure: endophilin A1 promotes actin polymerization to initiate structural palsticity of dendritic spines.

Epigenetics and Cell Fate Determination

Falong Lu, Principal Investigator, Ph.D. (2011, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences); Postdoctoral fellow (2012-2017, UNC-Chapel Hill / Howard Hughes Medical Institute and Boston children's Hospital/ Harvard Medical School / Howard Hughes Medical Institute, USA).

Research Interests: Mechanism of epigenetic regulation, such as the biochemical basis for genome wide DNA methylome establishment; Mechanism of zygotic genome activation in mammals; Heritable chromatin basis of cell fate determination.

Email: fllu@genetics.ac.cn

Poly(A) inclusive RNA isoform sequencing (PAIso−seq) reveals wide-spread non-adenosine residues within RNA poly(A) tails

Message RNA poly(A) tails are vital for their function and regulation. However, the full-length sequence of mRNA isoforms with their poly(A) tails remains undetermined. Here, we develop a method at single-cell level sensitivity that enables quantification of poly(A) tails along with the full-length cDNA while reading non-adenosine residues within poly(A) tails precisely, which we name poly(A) inclusive RNA isoform sequencing (PAIso−seq). Using this method, we can quantify isoform specific poly(A) tail length. More interestingly, we find that 17% of the mRNAs harbor non-A residues within the body of poly(A) tails in mouse GV oocytes. We show that PAIso−seq is sensitive enough to analyze single GV oocytes. These findings will not only provide an accurate and sensitive tool in studying poly(A) tails, but also open a door for the function and regulation of non-adenosine modifications within the body of poly(A) tails.

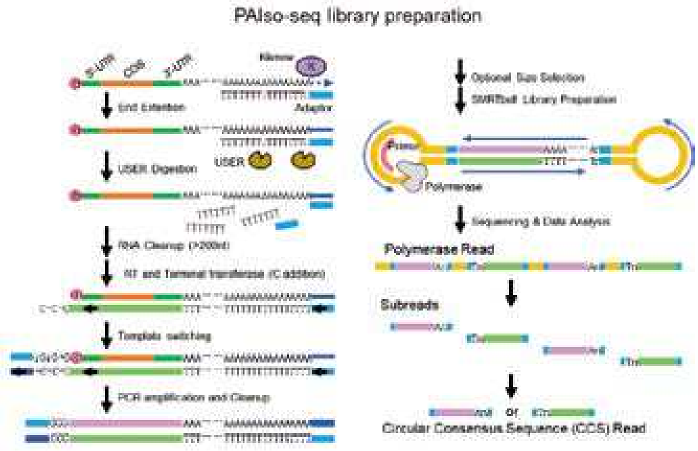


Figure: Flowchart for PAIso-seq method design.

Publications

Liu, Y., Nie, H., Liu, H. and Lu, F. (2019). Poly(A) inclusive RNA isoform sequencing (PAIso-seq) reveals wide-spread non-adenosine residues within RNA poly(A) tails. Nature Communications 10(1): 5292.

Tuesta, L. M., Djekidel, M. N., Chen, R., Lu, F., Wang, W., Sabatini, B. L. and Zhang, Y. (2019). In vivo nuclear capture and molecular profiling identifies *Gmeb1* as a transcriptional regulator essential for dopamine neuron function. Nature Communications 10(1): 2508.

Qiu, Q., Mei, H., Deng, X., He, K., Wu, B., Yao, Q., Zhang, J., Lu, F., Ma, J. and Cao, X. (2019). DNA methylation repels targeting of *Arabidopsis* REF6. Nature Communications 10(1): 2063.

Human and Animal Functional Genomics

Runlin Z. Ma, Principal Investigator. Ph.D. (1991, the Kansas State University, USA); Postdoctoral fellow (1992-1996, University of Illinois, USA); Research Assistant Professor (1997-2001, University of Illinois, USA).

Research Interests: Genomic organization and evolution of the MHC region in the addax.

Email: rlma@genetics.ac.cn

Publications

Guo, Y., Zhang, X., Xu, Q., Gong, F., Shi, X., Li, C., Huang, R., Nie, F., Zhu, W., Li, J., Tang, J., Li, R., Zhang, L., Chen, L. and Ma, R. Z. (2019). Human Papillomavirus 16 oncoprotein E7 retards mitotic progression by blocking Mps1-MAP4 signaling cascade. Oncogene 38(31): 5959-5970.

Li, C., Chen, L., Liu, X., Shi, X., Guo, Y., Huang, R., Nie, F., Zheng, C., Zhang, C. and Ma, R. Z. (2019). A high-density BAC physical map covering the entire MHC region of addax antelope genome. BMC Genomics 20(1): 479.

Nie, F. Y., Tian, J. H., Lin, X. D., Yu, B., Xing, J. G., Cao, J. H., Holmes, E. C., Ma, R. Z. and Zhang, Y. Z. (2019). Discovery of a highly divergent hepadnavirus in shrews from China. Virology 531: 162-170.

A high-density BAC physical map covering the entire MHC region of addax antelope genome

The mammalian major histocompatibility complex (MHC) harbours clusters of genes associated with the immunological defence of animals against infectious pathogens. At present, no complete MHC physical map is available for any of the wild ruminant species in the world. The high-density physical map is composed of two contigs of 47 overlapping bacterial artificial chromosome (BAC) clones, with an average of 115 Kb for each BAC, covering the entire addax MHC genome. The first contig has 40 overlapping BAC clones covering an approximately 2.9 Mb region of MHC Class I, Class III, and Class IIa, and the second contig has 7 BAC clones covering an approximately 500 Kb genomic region that harbours MHC Class IIb. The relative position of each BAC corresponding to the MHC sequence was determined by comparative mapping using PCR screening and the order of BACs was determined by DNA fingerprinting and sequence-specific PCR. The addax MHC physical map showed one gap of approximately 18 Mb formed by an ancient autosomal inversion that divided the MHC Class II into IIa and IIb. The autosomal inversion provides compelling evidence that the MHC organizations in all of the ruminant species are relatively conserved.

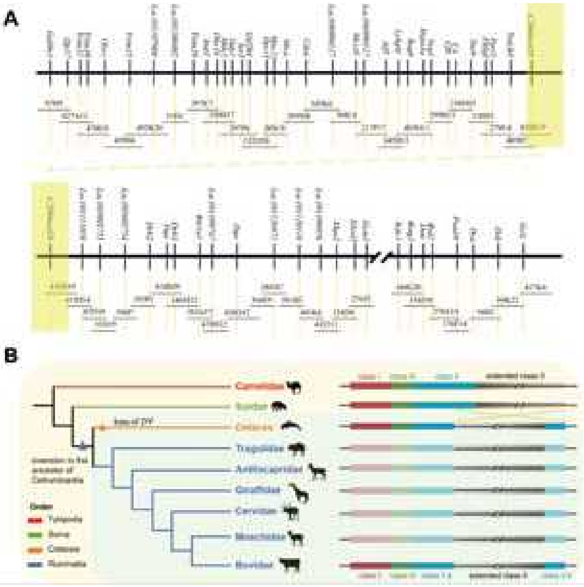
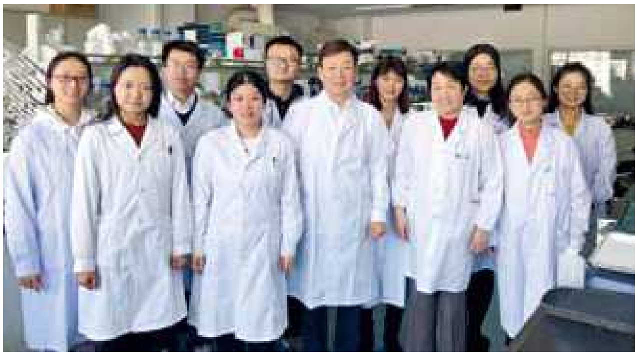


Figure: (A) Physical map covering the entire MHC region of the addax. The genes identified by BAC-end sequencing are marked by vertical bars along the horizontal line, with the locus names listed above. The continuous BAC map is represented by two panels with the overlapping regions marked with the same colored shadows at the ends. (B) The hypothesis of ancient chromosome inversion in the ancestor of Cetruminantia. Genomic organization in the MHC region of Artiodactyla was compared with their phylogenetic relationships listed on the left. This ancient inversion in the MHC region of the other five Ruminantia families remained to be determined due to the lack of genome information or poor genome assemblies.



The Dynamic Coordination of Cytoskeleton Network

Wenxiang Meng, Principal Investigator, Ph.D. (2002, Osaka University, Japan), Postdoctoral fellow (2002-2004, Mie University, Japan). Research Scientist (2004-2010, Riken Center for Developmental Biology, Japan).

Research Interests: The functions and regulation mechanisms of dynamic coordinated microtubule- actin filaments network.

Email: wxmeng@genetics.ac.cn

Altered mating behavior in *Camsap2* knockout mice

CAMSAP2, a microtubule minus-end associated protein, is required for the proper organization and stabilization of interphase microtubules and directional cell migration in cultured cells. However, it's in vivo functions are still poorly understood. To investigate the roles of CAMSAP2, we generated a line of *Camsap2* null allele mice by a gene knockout method and found that *Camsap2* knockout (-/-) male mice showed a disorder of mating behavior. The mating behavior is dependent on the detection of pheromones, and *Camsap2* (-/-) males showed normal olfactory sensitivity during the buried food test, bedding preference assay, and volatile odor test. However, tracing functional circuits using c-FOS activation showed that the medial part of anterior olfactory nucleus (AOM), piriform cortex (Pir), and medial amygdala (MeA) failed to respond to the female scent. These results indicated that neural circuits from the olfactory bulb (OB) to MeA were impaired in *Camsap2* (-/-) mice.

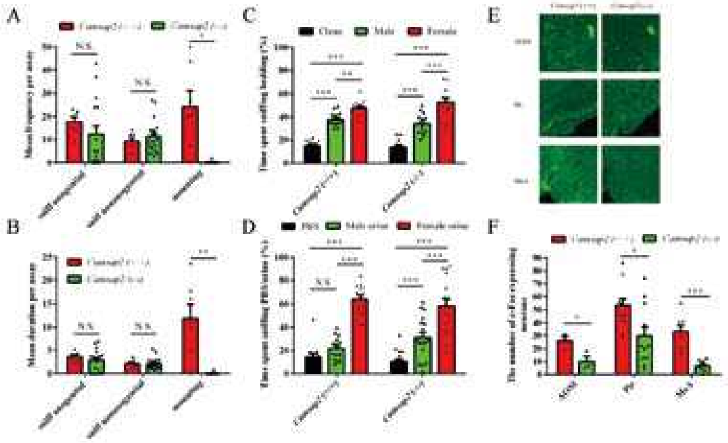


Figure: (A-B) The frequency (A) and duration (B) of mounting were significantly diminished in *Camsap2* (-/-) mice compared to *Camsap2* (+/+) mice. While there were no difference between *Camsap2* (+/+) and *Camsap2* (-/-) males in the total number and duration of female-directed anogenital and non-anogential sniffing. (C-D) The function of odor detection was not affected in *Camsap2* (-/-) mice, *Camsap2* (-/-) mice had the ability to detect pheromone cues in female soiled bedding (C), *Camsap2* (-/-) mice had the ability to detect volatile odor in female urine (D). (E-F) Tracing functional circuits using c-FOS activation showed that medial part of anterior olfactory nucleus (AOM), piriform cortex (Pir) and medial amygdala (MeA) failed to respond to the female scent in *Camsap2* (-/-) mice.

Lipidomics, Lipid Metabolism, Metabolic Disorders

Guanghou Shui, Principal Investigator, Ph.D. (2004, National University of Singapore, Singapore).

Research Interests: Dr Shui's laboratory is mainly interested in lipidomics and lipid metabolism, with particular focus on the role of dysregulated lipid metabolism in development and/or diseases using model organisms such as Caenorhabditis elegans; and employing lipidomic approaches to elucidate potential biomarkers for major diseases.

Email: ghshui@genetics.ac.cn

Publications

- Lu, J., Lam, S. M., Wan, Q., Shi, L., Huo, Y., Chen, L., Tang, X., Li, B., Wu, X., Peng, K., Li, M., Wang, S., Xu, Y., Xu, M., Bi, Y., Ning, G. and Wang, W. (2019). High-coverage targeted lipidomics reveals novel serum lipid predictors and lipid pathway dysregulation antecedent to type 2 diabetes onset in normoglycemic Chinese adults. Diabetes Care 42(11): 2117-2126.
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- Pan, S., Lin, Y., Liu, Q., Duan, J., Lin, Z., Wang, Y., Wang, X., Lam, S. M. and Zou, Z. (2019). Convergent genomic signatures of flight loss in birds suggest a switch of main fuel. Nature Communications 10(1): 2756.
- Li, B., Li, L., Li, M., Lam, S. M., Wang, G., Wu, Y., Zhang, H., Niu, C., Zhang, X., Liu, X., Hambly, C., Jin, W., Shui, G. and Speakman, J. R. (2019). Microbiota depletion impairs thermogenesis of brown adipose tissue and browning of white adipose tissue. Cell Reports 26(10): 2720-2737.

High-coverage targeted lipidomics reveals novel serum lipid predictors and lipid pathway dysregulation antecedent to type 2 diabetes onset in normoglycemic Chinese adults

Our foregoing data underscore the potential importance of lipid metabolism early in the pathogenesis of diabetes and suggest that lipids profiles could effectively improve diabetes risk assessment in normoglycemic Chinese populations beyond that achieved by conventional clinic indices. Furthermore, we put forth a conceptual framework that perturbed peroxisomal oxidation of VLCFAs and BRCFAs associated with a reduction in PUFA-plasmalogens PEs may possibly give rise to an altered composition of TAGs essentially underlying the pathogenesis of dyslipidemia that precedes the development of overt diabetes.

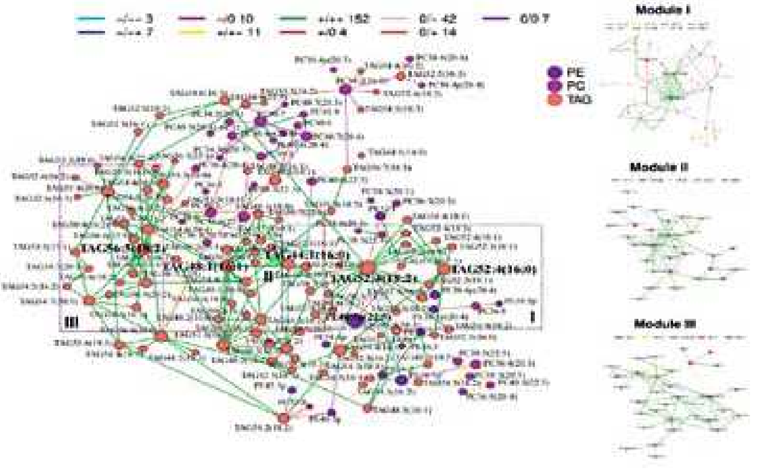

Figure: Multiscale embedded correlation network analysis illustrates the differential correlation between various PCs, PEs, and TAGs in control and incident diabetes. Only lipid pairs with significant differential correlations (empirical P , 0.05) are included. Sign/sign indicates the direction and strength of the correlation in control/incident diabetes, and the number that follows indicates the number of lipid pairs in the global networks exhibiting this pattern of change. For instance, the bright green line +/++ 152 in the upper legend of the global networks indicates that correlation between two connected lipid pairs was positive (+) in controls, and the correlation became even more strongly positive (++) in incident diabetes. A total of 152 lipid pairs connected by bright green lines in the global network displayed this pattern of change (+/++). Three modules identified from multiscale clustering analysisd(I) PUFA-PEps and TAGs, (II) PUFA-PEps and non–PUFA-TAGs, and (III) PUFA-PEps and PUFA-TAGsdare separately illustrated in the lower panel.

Molecular Energetics

John R. Speakman, Principal Investigator, Ph.D. (1984, University of Stirling, UK); Fellow of the Royal Society of Edinburgh (2004); Fellow of the Academy of Medical Sciences (2008); Fellow of the Academy of Europe (2012). Fellow of the Koyal Society (2018); CAS foreign member (2019).

Research Interests: The molecular basis of the regulation of food intake, energy expenditure and body composition. In particular we aim to understand the causes and consequences of the phenomenon of obesity. Our work includes studies of humans, model animals in captivity and wild animals.

Email: j.speakman@genetics.ac.cn

Microbiota depletion impairs thermogenesis of brown adipose tissue and browning of white adipose tissue

The relation between gut microbiota and the host has been suggested to benefit metabolic homeostasis. Brown adipose tissue (BAT) and beige adipocytes facilitate thermogenesis to maintain host core body temperature during cold exposure. However, the potential impact of gut microbiota on the thermogenic process is confused. Here, we evaluated how BAT and white adipose tissue (WAT) responded to temperature challenges in mice lacking gut microbiota. We found that microbiota depletion via treatment with different cocktails of antibiotics (ABX) or in germfree (GF) mice impaired the thermogenic capacity of BAT by blunting the increase in the expression of uncoupling protein 1 (UCP1) and reducing the browning process of WAT. Gavage of the bacterial metabolite butyrate increased the thermogenic capacity of ABX-treated mice, reversing the deficit. Our results indicate that gut microbiota contributes to upregulated thermogenesis in the cold environment and that this may be partially mediated via butyrate.

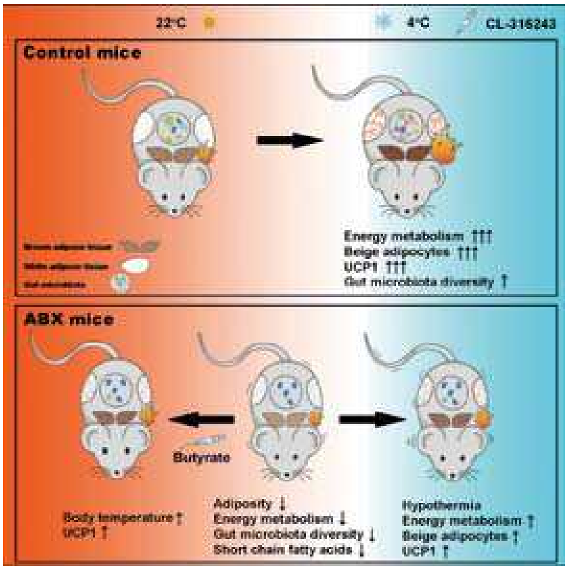

Figure: Mammals can shiver to produce heat and tend to do so as an immediate response to unanticipated acute cold exposure. The source of non-shivering heat involves brown adipose tissue (BAT). Gut microbiota depletion by different antibiotic cocktail protocols (ABX) damages thermoregulation and reduces the energy metabolism of the host under room temperature and cold stimulation. Gavage of ABX mice with butyrate partially rescues the effects on BAT recruitment.

Publications

Hu, S., Wang, L., Togo, J., Yang, D., Xu, Y., Wu, Y., Douglas, A. and Speakman, J. R. (2019). The carbohydrate-insulin model does not explain the impact of varying dietary macronutrients on body weight and adiposity of mice. Molecular Metabolism.Doi:10.1016/j.molmet.2019.11.010.

Li, B., Li, L., Li, M., Lam, S. M., Wang, G., Wu, Y., Zhang, H., Niu, C., Zhang, X., Liu, X., Hambly, C., Jin, W., Shui, G. and Speakman, J. R. (2019). Microbiota depletion impairs thermogenesis of brown adipose tissue and browning of white adipose tissue. Cell Reports 26(10): 2720-2737.

Speakman, J. R. (2019). Fifty shades of brown: The functions, diverse regulation and evolution of brown adipose tissue. Molecular Aspects of Medicine 68: 1-5.

Thurber, C., Dugas, L. R., Ocobock, C., Carlson, B., Speakman, J. R. and Pontzer, H. (2019). Extreme events reveal an alimentary limit on sustained maximal human energy expenditure. Science Advances 5(6).

Togo, J., Hu, S., Li, M., Niu, C. Q. and Speakman, J. R. (2019). Impact of dietary sucrose on adiposity and glucose homeostasis in C57BL/6J mice depends on mode of ingestion: liquid or solid. Molecular Metabolism 27: 22-32.

Mitochondrial Stress Signaling and Aging

Ye Tian, Principal Investigator, Ph.D. (2010, National Institute of Biological Sciences, China); Postdoctoral Fellow, (2010-2016, Salk Institute; University of California, Berkeley).

Research Interests: Dr. Tian's laboratory is mainly interested in molecular mechanism of mitochondrial stress response, focusing on the mitochondrial unfolded protein response (UPR^{mt}), epigenetic regulation of mitochondrial stress and transgeneration inheritance.

Email: ytian@genetics.ac.cn

The NURD complex mediates mitochondrial unfolded protein response and longevity in *C. elegans*

Mitochondrial stress during development causes widespread changes in chromatin structure to promote mitochondrial unfolded protein response (UPR^{mt}), perpetuating an early response across a lifetime results in lifespan extension. We found that the nucleosome remodeling and deacetylase (NURD) complex interact with the UPR^{mt} transcription factor DVE-1 to initiate the global chromatin condensation and induce the UPR^{mt} in animals experienced with mild mitochondrial dysfunction. The condensed chromatin structure can be well maintained into later life that is beneficial for lifespan extension. Moreover, overexpression of the core component of the NURD complex is sufficient to induce the UPR^{mt} response and longevity in *C. elegans*.

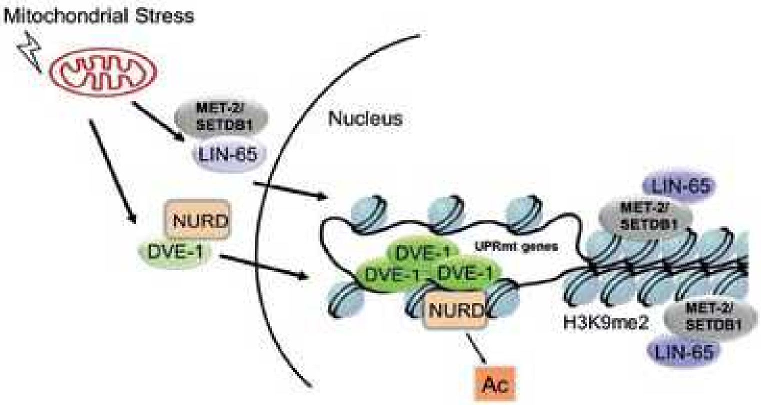

Figure: During the mitochondrial stress, NURD is not only required for the DVE-1 nuclear accumulation, but is also essential for chromatin reorganization via its histone deacetylation function. Furthermore, NURD is required for mitochondrial stress-induced longevity and sufficient to promote lifespan extension.

The Genetic Network of Germline Development

Zhaohui Wang, Principal Investigator, Ph.D. (1998, University of Chicago, USA).

Research Interests: Using fruit fly and mouse models to study: 1) the microenvironment of germline stem cells; 2) the regulation of mitosis-to-meiosis switch.

Email: zhwang@genetics.ac.cn

Notch signaling governs the expression of glypican Dally to define the stem cell niche

Extracellular glypicans play pivotal roles in organogenesis, stem cell maintenance, and cancer development. However, the growth phenotypes associated with different levels of glypican are not consistent in development or tumorigenesis. This requires the clarification on how the spatial patterns of glypican relate to the distribution of signaling molecules in different cellular context, and how glypican expression is regulated. We have previously reported that Dally, one of the glypican members in Drosophila, is required in the niche for the maintenance of germline stem cells (GSCs) via short-range BMP signaling in ovary. However, the regulatory mechanism of glypican pattern in the ovarian stem cell niche remains elusive. Our current data demonstrate that Notch pathway is genetically upstream of Dally and its function to maintain GSC relies on Dally expression. Combining yeast and fruit fly genetics, we illustrate that Dally is under the transcriptional control of Notch signaling via the transcription factor Su(H). Further, we assayed human glypicans and disease-associated variants in Drosophila ovary, which can serve as an effective system to evaluate the structure-function relationship of the human homologs.

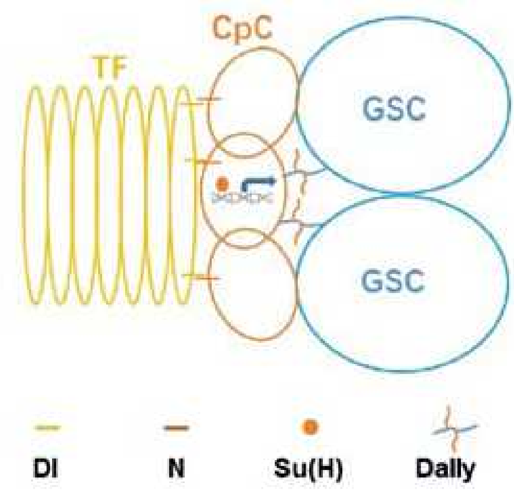

Figure: Schematic model of Notch signaling and glypican Dally expression in the ovarian stem cell niche. TF, terminal filament; CpC, cap cell; GSC, germline stem cell.

Stem Cell Lineage Tracing and Neural Regeneration

Qingfeng Wu, Principal Investigator, Ph.D. (2015, Institute of Neuroscience, Chinese Academy of Sciences, Shanghai, China); Postdoctoral Fellow, (2012-2016, Johns Hopkins University, USA).

Research Interests: 1) Development of nuclear brain structure. 2) Neural control of metabolic disorders. 3) Homeostatic regulation of neural stem cells.

Email: wu_qingfeng@genetics.ac.cn

Publications

Berg, D. A., Su, Y., Jimenez-Cyrus, D., Patel, A., Huang, N., Morizet, D., Lee, S., Shah, R., Ringeling, F. R., Jain, R., Epstein, J. A., Wu, Q. F., Canzar, S., Ming, G. L., Song, H. and Bond, A. M. (2019). A Common Embryonic Origin of Stem Cells Drives Developmental and Adult Neurogenesis. Cell 177(3): 654-668.e615.

Tang, C., Wang, M., Wang, P., Wang, L., Wu, Q. and Guo, W. (2019). Neural stem cells behave as a functional niche for the maturation of newborn neurons through the secretion of PTN. Neuron 101(1): 32-44.e36.

Tbx3 defines a progenitor domain specifying multiple hypothalamic nuclei and neuronal subtype

The hypothalamus plays a central role in diverse native behaviors such as food intake, stress responses and mating. Heterogeneous populations of peptidergic neurons in the hypothalamus orchestrate these behaviors via the secretion of neuronpeptides. However, how specific intracellular machinery controls peptidergic identities and function of individual hypothalamic neurons remains largely unknown. Here, we found that Tbx3^{+} progenitors in the ventral posterior hypothalamus generated multiple functional peptidergic neurons related to metabolism, growth and endocrine. Tbx3-dereived cells occupy multiple nucleus in the tuberal and posterior hypothalamus. Inducible fate-mapping reveals Tbx3-derived cells were restricted to arcuate nucleus in late stage of hypothalamus development. We identify 10 distinct Tbx3-derived cell population with expression of multiple neuropeptides by single-cell RNA seq. Together, Tbx3 may be important for the development of hypothalamic neuroendocrine system.

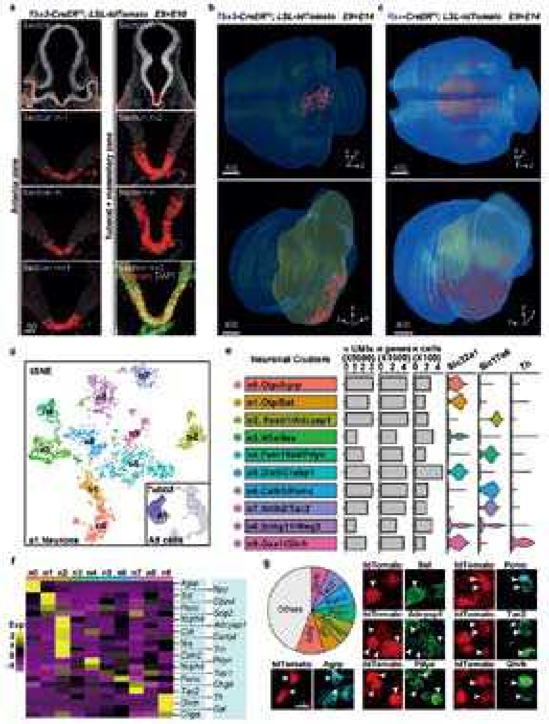

Figure: (a) Flourescent immunoreactivity of coronal sectionins in Tbx3-CreERT2; Ai14 mice. (b) and (c) 3D reconstruction of Tbx3-CreERT2; Ai14 and Rax-CreERT2; Ai14 mice.dTSNE plot for Tbx3-derived neurons. (e) Cluster identification numbers; UMIs per cluster; genes detected per culster; cells per cluster. (f) Expression distributions for notable neuropeptides in all neuronal clusters. g single molecular FISH of Tbx3^{+} derived peptidergic neurons.

Signal Transduction Diseases & Development

Zhiheng Xu, Principal Investigator, Ph.D. (1999, Rutgers University, USA); Postdoc and Research Associate (1999-2005, Columbia University, USA).

Research Interests: The laboratory is mainly interested in studying the underlying mechanisms involved in brain development, and in different diseases including microcephaly, schizophrenia, autism, and neurodegenerative diseases.

Email: zhxu@genetics.ac.cn

MEKK3 coordinates with FBW7 to regulate WDR62 stability and neurogenesis during brain development

WDR62 was identified as the second most causative gene of microcephaly. Our previous study showed WDR62 plays an essential role in the proliferation and differentiation of NPCs in the developing brain. However, how WDR62 is regulated and hence controls neurogenesis and brain size remains elusive.Our recently study reveals the mechanisms that regulate the stability of microcephaly associated protein WDR62 and NPC proliferation and differentiation during brain development. We found knockout of MEKK3 or JNK1 phenocopies WDR62 knockout in the dysregulation of NPC development. Specifically, we demonstrate that MEKK3 interacts with WDR62 to stabilize WDR62 and regulates JNK activity in a synergic way. On the other hand, JNK activity also regulates the phosphorylation of WDR62 at T1053 in a feedback loop which facilities the recruitment of FBW7 degradation of WDR62. Taken together, our results support a model in which the scaffold protein WDR62 organizes a protein complex which includes MEKK3, MKKs and JNK1 to control the proliferation and differentiation of NPCs during corticogenesis.

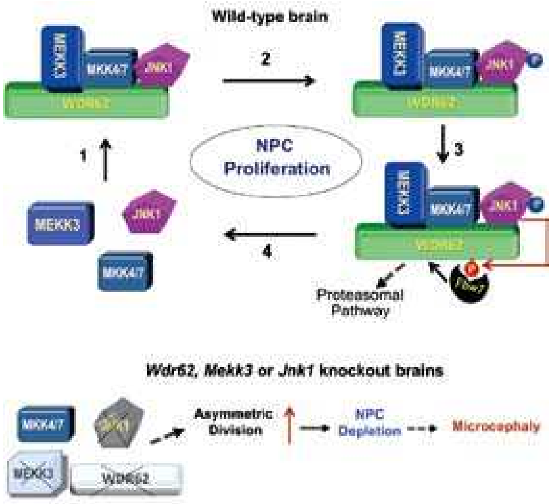

Figure: MEKK3 coordinates with FBW7 to regulate WDR62 stability and neurogenesis during brain development.

Molecular Genetics of Sexual Plant Reproduction

Weicai Yang, Principal Investigator, Director of the Institute, Ph.D. (1994, Wageningen University, The Netherlands); Postdoctoral Fellow (1994-2000, Wageningen University, USA; Cold Spring Harbor Laboratory, USA; The Institute of Molecular Agrobiology, Singapore); Senior Scientist and Principal Investigator (2000-2003, Temasek Life Sciences Laboratory, Singapore).

Research Interests: Our researches are focused on molecular genetics of sexual plant reproduction, including the developmental mechanism of male and female gametophytes; the molecular genetic mechanism of cell polarity, cell fate and cell differentiation during embryonic development; the molecular genetic mechanism of male-female gametophytic interaction, sperm delivery, and fertilization. In addition, we are focused on the molecular mechanism of nitrogen-fixing rhizobium symbioses.

Email: wcyang@genetics.ac.cn

BICELLULAR POLLEN 1 is a modulator of DNA replication and pollen development in *Arabidopsis*

During male gametogenesis in *Arabidopsis*, the haploid microspore undergoes an asymmetric division to produce a vegetative and a generative cell, the latter of which continues to divide symmetrically to form two sperms. This simple system couples cell cycle with cell fate specification. Here we addressed the role of DNA replication in male gametogenesis using a mutant *bicellular pollen* 1 (*bice1*), which produces bicellular, rather than tricellular, pollen grains as in the wild-type plant at anthesis. The mutation prolonged DNA synthesis of the generative cell, which resulted in figure c. 40% of pollen grains arrested at the two-nucleate stage. The extended S phase did not impact the cell fate of the generative cell as shown by cell-specific markers. BICE1 encodes a plant homolog of human D123 protein that is required for G1 progression, but the underlying mechanism is unknown. Here we showed that BICE1 interacts with MCM4 and MCM7 of the pre-replication complex. Consistently, double mutations in BICE1 and MCM4, or MCM7, also led to bicellular pollen and condensed chromosomes. These suggest that BICE1 plays a role in modulating DNA replication via interaction with MCM4 and MCM7.

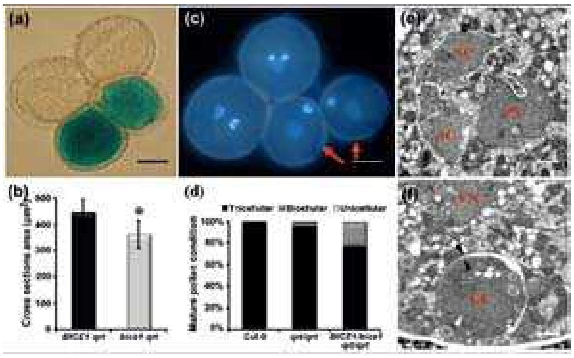

Figure: Phenotype of *bice1* pollen. (a) b-Glucuronidase (GUS) signal is present in the pollen grains with a T-DNA insert (mutants) in *BICE1*/*bice1* *qrt*/*qrt* heterozygous plants. (b) Cross-sectional area was measured and statistically analyzed; pollen of *bice1 qrt* is smaller than that of *BICE1 qrt* (c) Tetrads from *bice1* heterozygous plants. Pollen grains were stained with DAPI and photographed under a microscope. Some pollen (red arrowhead) had only two nuclei (one big vegetative nucleus and one small generative-like nucleus). (d) Percentage of unicellular, bicellular and tricellular pollen grains from wildtype Col-0, *qrt*/*qrt*, and *BICE1*/*bice1* *qrt*/*qrt* heterozygous plants. (e, f) The ultrastructure of mature wild-type pollen (e) and *bice1* binucleate pollen (f).The black arrowheads indicate an abnormal cell wall, and the white arrowhead shows the nuclear membrane of *bice1* pollen grains. GC, generative cell; SC, sperm cell; VN, vegetative nucleus.

Publications

Long, Y. P., Xie, D. J., Zhao, Y. Y., Shi, D. Q. and Yang, W. C. (2019). BICELLULAR POLLEN 1 is a modulator of DNA replication and pollen development in *Arabidopsis*. New Phytologist 222(1): 588-603.

JIa, P. F. X., Y.; Li,H.J.; Yang,W.C. (2019). LOT regulates TGN biogenesis and golgi structure in plants. Plant Signaling & Behavior. Doi:10.1080/15592324.2019.1573100

Li, Y., Li, H. J., Morgan, C., Bomblies, K., Yang, W. and Qi, B. (2019). Both male and female gametogenesis require a fully functional protein S-acyl transferase 21 in *Arabidopsis thaliana*. Plant Journal 100(4): 754-767.

Meng, J. G., Zhang, M. X., Yang, W. C. and Li, H. J. (2019). TICKET attracts pollen tubes and mediates reproductive isolation between relative species in Brassicaceae. Science China Life Sciences 62(11): 1413-1419.

Molecular Mechanisms of Major Neurodevelopmental Diseases

Yongqing Zhang, Principal Investigator, Ph.D. (1991, China Agricultural University, China).

Research Interests: 1) Study the molecular and cellular bases of major neurological diseases including intellectual disability and autism in order to develop an intervention and/or a cure for the diseases, using non-human primate, domestic dog and Drosophila melanogaster as model organisms. 2) Taking an interdisciplinary approach including molecular, cell, developmental and genetic methods to study brain development, structure and function, using Drosophila as a model system.

Email: yqzhang@genetics.ac.cn

CRISPR/Cas9-mediated disruption of SHANK3 in monkey leads to drug-treatable autism-like symptoms

Mutations in *SHANK3* remain one of the top replicated genetic defects in autism spectrum disorders (ASD) in humans. Although a number of mouse models with *Shank3* mutations have been valuable for investigating the pathogenesis of ASD, speciesdependent differences in brain structures and behaviors post considerable challenges to use small animals to model ASD and to translate experimental results to the clinic. We have used CRISPR/Cas9 to generate cynomolgus monkey models by disrupting *SHANK3*. Systematic analyses including molecular, biochemical, and histological revealed apparent brain developmental defects in *SHANK3* mutants, offering previously unappreciated neuropathology defects associated with autism. Behavioral analysis of the live *SHANK3* mutant monkey revealed core abnormalities of ASD, including impaired social interaction and repetitive behaviors. Importantly, these abnormal behaviors in *SHANK3* mutant were alleviated by the antidepressant fluoxetine treatment. Our findings provide the first demonstration that the genetically modified non-human primate can be effectively used for translational research of therapeutics for ASD.

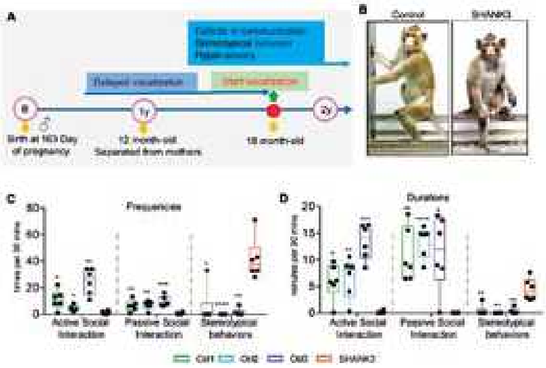

Figure: (A) Synaptic levels of GluRIIA but not IIB were increased in both calpain mutants and postsynaptic RNAi knockdown larvae. (B) Calpain A enriches at postsynaptic NMJ. Confocal imaging of synaptic boutons at the third instar larval NMJ demonstrates that calpain A immunoreactivity is located underneath the postsynaptic GluRIIA clusters. (C) Red arrow indicates the calpain cleavage site in GluRIIA. (D) Different calpains act together, probably as a protein complex, to control GluR levels during development. In the absence of one calpain, the activity of other calpains is compromised, suggesting that the full activity of calpains requires the integrity of the calpain complex.

Publications

Jia, M., Meng, D., Chen, M., Li, T., Zhang, Y. Q. and Yao, A. (2019). *Drosophila* homolog of the intellectual disability-related long-chain acyl-CoA synthetase 4 is required for neuroblast proliferation. Journal of Genetics and Genomics 46(1): 5-17.

Metwally, E., Zhao, G., Li, W., Wang, Q. and Zhang, Y. Q. (2019). Calcium-activated calpain specifically cleaves glutamate receptor IIA but not IIB at the *Drosophila* neuromuscular junction. Journal of Neuroscience 39(15): 2776-2791.

Zhao, H., Wang, Q., Yan, T., Zhang, Y., Xu, H. J., Yu, H. P., Tu, Z., Guo, X., Jiang, Y. H., Li, X. J., Zhou, H. and Zhang, Y. Q (2019). Maternal valproic acid exposure leads to neurogenesis defects and autism-like behaviors in non-human primates. Translational Psychiatry 9(1): 267.

Center for Molecular Systems Biology

The center for molecular systems biology was established in 2006. The mission of the center is to pursue research related to human health and agricultural development using multidisciplinary approaches comprising computational biology, bioinformatics, systems biology, structural biology, evolutionary genomics. Research at the center focuses on the hidden regulatory mechanisms underlying gene expression, the assembly, modification and dynamics of macromolecules, the noise and robustness of biological systems. Currently, the center has six group leaders, including one recipient of the *National Science Fund for Distinguished Young Scholars,* three recipient of the *National Science Fund for Excellent Young Scholars* In 2019, the center has received many research funds from the Ministry of Science and Technology, National Natural Science Foundation of China, Chinese Academy of Sciences. The center has 3 patents approved, and has made substantive progresses in a variety of research directions with 18 SCI papers published.

Evolutionary Genomics: Dr. Wenfeng Qian's group constructed yeasts with complex aneuploid karyotypes and found that the overdosage of balanced protein complexes led to the reduced proliferation rate. The additional DNA copy of all subunits of protein complex helps the escape from the cellular surveillance systems, and the increase in the protein concentration of the whole complexes may lead to the imbalance among components of a cellular signaling pathway, which is deleterious and sometimes even lethal. They also showed that early- and late-replicating genes show dosage imbalance. Genes encoding the same protein complex tend to replicate at the same time during DNA synthesis, especially among fast proliferating cells such as stem cells and cancer cells, preventing the deleterious effects induced by dosage imbalance. These findings improve the understanding of the mechanisms to maintain dosage balance in a cell.

Non-coding RNAs: Dr. Xiu-Jie Wang's group studied the roles of long noncoding RNA *lnc-NAP* in embryonic stem cells (ESCs). The pluripotency of embryonic stem cells (ESCs) is controlled by a multilayer regulatory network, of which the key factors include core pluripotency genes OCT4, SOX2 and NANOG, and multiple microRNAs (miRNAs). Recently, long noncoding RNAs (lncRNAs) have been discovered as a class of new regulators for ESCs, and some lncRNAs could function as competing endogenous RNAs (ceRNAs) to regulate mRNAs by competitively binding to miRNAs. Here, we identify mmu-miR-139-5p as a new regulator for *Nanog* by targeting *Nanog* 3′ untranslated region (UTR) to repress *Nanog* expression in mouse ESCs and embryos. Such regulation could be released by an ESC-specifically expressed ceRNA named *lnc-NAP*. The expression of *lnc-NAP* is activated by OCT4, SOX2, as well as NANOG, through promoter binding. Downregulation of *lnc-NAP* reduces *Nanog* abundance, which leads to decreased pluripotency of mouse ESCs and embryonic lethality. These results reveal *lnc-NAP* as a new regulator for *Nanog* in mouse ESCs, and uncover a feed-forward regulatory loop of *Nanog* through the participation of *lnc-NAP*.

Functional Proteomics: Dr. Yingchun Wang's group applied label free quantitative proteomics to generate a proteome atlas of *Synechocystis* sp. PCC6803. Cyanobacteria are a group of oxygenic photosynthetic bacteria with great potentials in biotechnological applications and advantages as models for photosynthesis research. The subcellular locations of the majority of proteins in any cyanobacteria remain undetermined, representing a major challenge in using cyanobacteria for both basic and industrial researches. Here, using label free quantitative proteomics we mapped 2,027 proteins of *Synechocystis* sp. PCC6803, a model cyanobacterium, to different subcellular compartments, and generated a proteome atlas with such information. The atlas leads to numerous unexpected but important findings, including the predominant localization of the histidine kinases Hik33 and Hik27 on the thylakoid but not the plasma membrane. Such information completely changes the concept regarding how the two kinases are activated. Together, the atlas provides subcellular localization information for nearly 60% proteome of a model cyanobacterium, and will serve as an important resource for the cyanobacterial research community.

Structural Biology: The characterization of protein machinery involved in controlling different crop traits is a key step for molecular breeding. The deep understanding of the underlying mechanism will provide important information for genome editing to speed up crop seed design for better agricultural productivity. 4-Hydroxyphenylpyruvate dioxygenase (HPPD) is a key enzyme found in plants, which catalyzes metabolism of aromatic amino acid, such as phenylalanine and tyrosine. HPPD inhibitors are the newest class of herbicide for weed management in the field. Here, Dr. Yuhang Chen's team solved the crystal structure of rice HPPD in complex with an herbicide. The structure revealed that HPPD forms a dimer, where each monomer binds an herbicide molecule. Inspired by the HPPD-herbicide structure, Dr. Yuhang Chen's team further identified key residues involved in herbicide binding. This finding provides potential candidates for genome editing to generate herbicide-resistant crop.

Systems Developmental Biology: Chromatin state regulates diverse developmental processes by controlling gene expression. Mapping the chromatin activity landscape (CAL) in developing cells is crucial to understand the epigenetic basis of cell differentiation. Dr. Zhuo Du's group performed single-cell analysis of chromatin activity and revealed chromatin basis of cell lineage differentiation in a *C. elegans* embryo. Using transcriptional level of a reporter gene integrated at multiple genomic positions as a readout of chromatin activity, they constructed CAL in identity-resolved single cells at 0.88 Mb resolution during *C. elegans* embryogenesis. CAL varies considerably across the genome in a cell and across individual cells at a genomic position, and the distribution of the activity possesses a high information content. As the cell lineage unfolds, CAL diversifies gradually in general and dramatically in specific developmental contexts which predicts fate decision events. CAL is intrinsically coupled to lineage history and developmental fate of cells. Cells with an identical fate exhibit similar CAL but display lineage-origin-dependent differences, suggesting a memory of CAL following cell divisions. However, in a special type of the cells, the left-right symmetric cells, the nearly identical CAL does not exhibit lineage-dependent differences. It implies that chromatin state is predetermined in early progenitor cells from distinct cell lineages to direct the symmetry. Collectively, these findings reveal implications of chromatin regulation in lineage commitment, developmental fate decision and left-right symmetry establishment.

Medaka (*Oryzias latipes*) has become an important vertebrate model widely used in genetics, developmental biology, environmental sciences, and many other fields. A high-quality genome sequence and a variety of genetic tools are available for this model organism. However, existing genome annotation is still rudimentary, as it was mainly based on computational prediction and short-read RNA-seq data. Dr. Qiang Tu's team reported a dynamic transcriptome landscape of medaka embryogenesis profiled by long-read RNA-seq, short-read RNA-seq, and ATAC-seq. Integrating these datasets together, they constructed a much-improved gene model set including about 17,000 novel isoforms, identified 1600 transcription factors, 1100 long non-coding RNAs, and 50,000 potential *cis*-regulatory elements as well. Time-series datasets provided another dimension of information. With the expression dynamics of genes and accessibility dynamics of cis-regulatory elements, they investigated isoform switching, regulatory logic between accessible elements and genes during embryogenesis. They built user-friend web tools to present these datasets. This resource provides the first comprehensive omics datasets of medaka embryogenesis. Ultimately, They term these three assays as the minimum ENCODE toolbox and propose the use of it as the initial and essential profiling genomic assays for model organisms that have limited data available.

Structural and Functional Analysis on Biological Macromolecules

Yuhang Chen, Principal Investigator, Ph.D. (2002, Tsinghua University, China), Postdoctoral fellow and associate research scientist (2002-2012, Columbia University, USA).

Research Interests: Structural and functional analysis on membrane transport proteins; Structural and functional analysis on epigenetic regulators involved in chromatin assembly; Structure-based seed design for herbicide-resistance crop.

Email: yuhang.chen@genetics.ac.cn

HPPD structure-based herbicide-resistance crop design

The characterization of protein machinery involved in controlling different crop traits is a key step for molecular breeding. The deep understanding of the underlying mechanism will provide important information for genome editing to speed up crop seed design for better agricultural productivity. 4-Hydroxyphenylpyruvate dioxygenase (HPPD) is a key enzyme found in plants, which catalyzes metabolism of aromatic amino acid, such as phenylalanine and tyrosine. HPPD inhibitors are the newest class of herbicide for weed management in the field. Here, we solved the crystal structure of rice HPPD in complex with an herbicide. The structure revealed that HPPD forms a dimer, where each monomer binds an herbicide molecule. Inspired by the HPPD-herbicide structure, we further identified key residues involved in herbicide binding. This finding provides potential candidates for genome editing to generate herbicide-resistant crop.

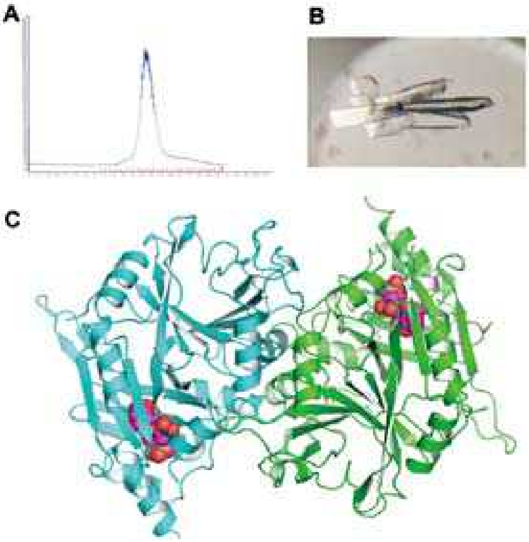

Figure: Crystal structure of HPPD-herbicide complex (A) Purification profile of HPPD; (B) Crystals of HPPD-herbicide complex; (C) Three-dimensional structure of HPPD-herbicide complex.

Publications

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Gao, D., Zhou, T., Da, L., Bruhn, T., Guo, L., Chen, Y., Xu, J. and Xu, M. (2019). Characterization and nonenzymatic transformation of three types of alkaloids from *Streptomyces albogriseolus* MGR072 and discovery of inhibitors of indoleamine 2,3-dioxygenase. Organic Letters 21(21): 8577-8581.

Dynamic Regulation of Embryogenesis

Zhuo Du, Principal Investigator. Ph.D. (2008, China Agricultural University, China). Postdoctoral researcher (2008-2009, Albert Einstein College of Medicine, USA; 2009-2014, Memorial Sloan Kettering Cancer Center, USA).

Research Interests: 1) Spatiotemporal regulation of gene expression during embryogenesis. 2) Mechanism of cell fate determination and differentiation. 3) Molecular and cellular basis of robustness and plasticity of embryogenesis.

Email: zdu@genetics.ac.cn

Publications

Li, X., Zhao, Z., Xu, W., Fan, R., Xiao, L., Ma, X. and Du, Z. (2019). Systems properties and spatiotemporal regulation of cell position variability during embryogenesis. Cell Reports 26(2): 313-321 e317.

Brandt, J. P., Rossillo, M., Du, Z., Ichikawa, D., Barnes, K., Chen, A., Noyes, M., Bao, Z. and Ringstad, N. (2019). Lineage context switches the function of a *C. elegans* Pax6 homolog in determining a neuronal fate. Development 146(8).

Xiao, L., Zhao, Z., He, F. and Du, Z. (2019). Multivariable regulation of gene expression plasticity in metazoans. Open Biology 9(12): 190150.

Single-cell analysis reveals chromatin basis of cell lineage differentiation in a *C. elegans* embryo

Chromatin state regulates diverse developmental processes by controlling gene expression. Mapping the chromatin activity landscape (CAL) in developing cells is crucial to understand the epigenetic basis of cell differentiation. Using transcriptional level of a reporter gene integrated at multiple genomic positions as a readout of chromatin activity, we constructed CAL in identity resolved single cells at 0.88 Mb resolution during *C. elegans* embryogenesis. CAL varies considerably across the genome in a cell and across individual cells at a genomic position, and the distribution of the activity possesses a high information content. As the cell lineage unfolds, CAL diversifies gradually in general and dramatically in specific developmental contexts which predicts fate decision events. CAL is intrinsically coupled to lineage history and developmental fate of cells. Cells with an identical fate exhibit similar CAL but display lineage-origin-dependent differences, suggesting a memory of CAL following cell divisions. However, in a special type of the cells, the left-right symmetric cells, the nearly identical CAL does not exhibit lineage-dependent differences. It implies that the chromatin state is predetermined in their early progenitor cells from distinct cell lineages to direct the symmetry. Collectively, our findings reveal implications of CAL in lineage commitment, developmental fate decision and left-right symmetry establishment.

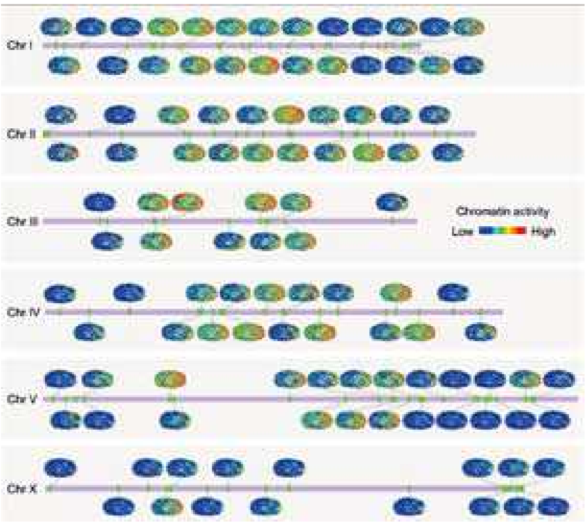

Figure: Mapping chromatin activity landscape at single-cell resolution by quantifying position effects on reporter expression. Figure shows cellular expression level of a reporter gene integrated into 113 specific genomic positions in 364 identity-resolved single cells as a readout of chromatin activity. Each ellipsoid represents an embryo with circles indicating single cells and color gradient showing chromatin activity level.

Quantitative Functional Genomics

Wenfeng Qian, Principal Investigator, Ph. D. (2012, University of Michigan, USA).

Research Interests: The long term goal of Qian lab is to understand basic rules in genome evolution with both high-throughput experimental and computational approaches. There are four major ongoing research topics in our lab: 1) translational regulation and protein homeostasis; 2) the construction of fitness landscape and adaptation mechanisms during the climbing of such landscape; 3) directed evolution and how epistasis affects evolutionary trajectories; 4) cell lineage tracing during the development of multicellular organisms.

Email: wfqian@genetics.ac.cn

Translational regulation by guanines in the poly(A) tail

Poly(A) tail plays a crucial role in the regulation of the eukaryotic mRNA, especially in determinating its stability. However, the bona fide sequences of the poly(A) tail has been mysterious, mainly due to the technical hurdles – DNA polymerase slips on A-runs which generates low-quality sequencing reads. We collaborated to directly sequence the full-length poly(A) tails in *Arabidopsis thaliana*. They showed that > 10% of poly(A) tails comprised at least one guanosine; among them, the G-content varies from 0.8–28%. They further constructed a series of mutants of the broadly expressed *Arabidopsis thaliana* PABs (AtPAB2, AtPAB4, and AtPAB8) that showed various phenotypic abnormalities. Further integration using CLIP-seq, ribo-seq, and mRNA stability assays revealed that the difference in G-content caused the variation in the AtPAB-binding efficiency among genes; G residues reduce the translational efficiency of mRNAs by inhibiting their binding to AtPABs. The study showcased the power of the next-generation genome-biology tools in understanding the basic principles underlying the central dogma, and shed light on the mechanisms of post-transcriptional controls in other species.

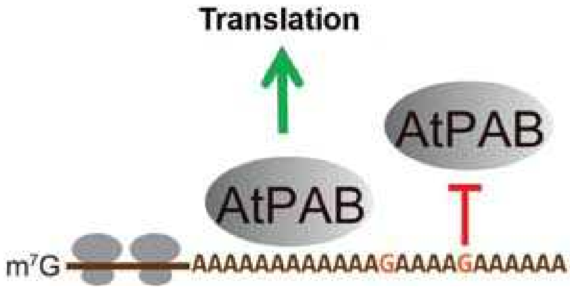

Figure: Guanosine (G) in poly(A) tail reduces the translational efficiency by inhibiting its binding to PABs.

Publications

Chen, Y., Chen, S., Li, K., Zhang, Y., Huang, X., Li, T., Wu, S., Wang, Y., Carey, L. B. and Qian, W. (2019). Overdosage of balanced protein complexes reduces proliferation rate in aneuploid cells. Cell Systems 9(2): 129-142 E125.

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Gene Regulatory Networks Controlling Development and Regeneration

Qiang Tu, Principal Investigator, Ph.D. (2003, Institute of Biochemistry and Cell Biology, SIBS, CAS, China); Postdoctoral scholar, Senior research fellow and Professional Staff (2004-2014, California Institute of Technology, USA).

Research Interests: Our lab is interested in developmental systems biology. We are striving to understand how thousands of genes logically interact with each other to drive various development and regeneration processes. Currently we focus on resolving gene regulatory networks that control sex determination using medaka fish as the model, and heart regeneration using zebrafish as the model.

Email: qtu@genetics.ac.cn

Dynamic transcriptional and chromatin accessibility landscape of medaka embryogenesis

Medaka (*Oryzias latipes*) has become an important vertebrate model widely used in genetics, developmental biology, environmental sciences, and many other fields. A high-quality genome sequence and a variety of genetic tools are available for this model organism. However, existing genome annotation is still rudimentary, as it was mainly based on computational prediction and short-read RNA-seq data. Here we report a dynamic transcriptome landscape of medaka embryogenesis profiled by long-read RNA-seq, short-read RNA-seq, and ATAC-seq (Figure 1). Integrating these datasets together, we constructed a much-improved gene model set including about 17,000 novel isoforms, identified 1600 transcription factors, 1100 long non-coding RNAs, and 50,000 potential cis-regulatory elements as well. Time-series datasets provided another dimension of information. With the expression dynamics of genes and accessibility dynamics of cis-regulatory elements, we investigated isoform switching, regulatory logic between accessible elements and genes during embryogenesis. We built user-friend web tools to present these datasets. This resource provides the first comprehensive omics datasets of medaka embryogenesis. Ultimately, we term these three assays as the minimum ENCODE toolbox and propose the use of it as the initial and essential profiling genomic assays for model organisms that have limited data available.

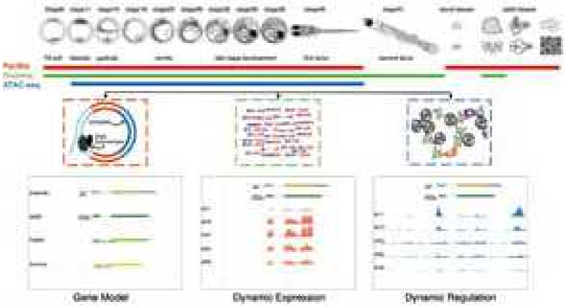

Figure: Overview of the study. Multiple samples including embryonic stages and adult organs were used for PacBio longread sequencing (red bar), Illumina short-read sequencing (green bar), and ATAC-seq (blue bar). The datasets generated were used for gene model construction, gene expression quantification, and genomic regulatory elements identification.

Functional Proteomics

Yingchun Wang, Principal Investigator, Ph.D. (2003, Genetics/Bioinformatics and Computational Biology, Iowa State University, USA).

Research Interests: The current focus of our research is to discover novel mechanisms that regulate cell polarization and pseudopodia dynamics of migrating cells using functional proteomics, and to identify new proteins and protein modifications that are critical for cell polarization and migration. The current focus is to quantitatively identify proteins on different membranes, including outer membrane, cytoplasmic membrane, and thylakoid membrane, of a model photosynthetic organism *Synechocystis* sp. PCC 6803. We will build a membrane proteome atlas for this organism. The same approach and workflow could also be applied for creating protein atlas for other organisms.

Email: ycwang@genetics.ac.cn

The quantitative proteome atlas of a model cyanobacterium

Cyanobacteria are a group of oxygenic photosynthetic bacteria with great potentials in biotechnological applications and advantages as models for photosynthesis research. The subcellular locations of the majority of proteins in any cyanobacteria remain undetermined, representing a major challenge in using cyanobacteria for both basic and industrial researches. Here, using label free quantitative proteomics we mapped 2,027 proteins of *Synechocystis* sp. PCC6803, a model cyanobacterium, to different subcellular compartments, and generated a proteome atlas with such information. The atlas leads to numerous unexpected but important findings, including the predominant localization of the histidine kinases Hik33 and Hik27 on the thylakoid but not the plasma membrane. Such information completely changes the concept regarding how the two kinases are activated. Together, the atlas provides subcellular localization information for nearly 60% proteome of a model cyanobacterium, and will serve as an important resource for the cyanobacterial research community.

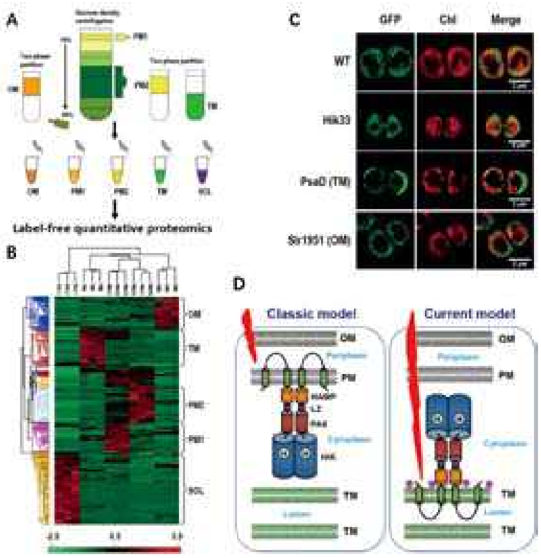

Figure: The quantitative proteome atlas of a model cyanobacterium. (A) The diagramed workflow for the large-scale label free quantitation of proteins from the different subcellular compartments of *Synechocystis*. (B) The heat map shows the hierarchy clustering analysis for the 2,027 quantified proteins. The clustering analysis was preformed using Z-scored LFQ values. (C) Fluorescence imaging of the indicated GFP-tagged proteins. PsaD is a known thylakoid protein, and Sll1951 is a known cell surface layer protein. The red channel is the autofluorescence from chlorophyll. (D) The models illustrating how Hik33 perceive environmental stimulus based on its subcellular localization.

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Zhang, Y., Huang, X., Wang, J., Wang, X., Liu, X., Chen, Y., Xu, W. and Wang, Y. (2019). Nitration-induced ubiquitination and degradation control quality of ERK1. Biochemical Journal 476(13): 1911-1926.

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Ding, S., Zhang, Y., Hu, Z., Huang, X., Zhang, B., Lu, Q., Wen, X., Wang, Y. and Lu, C. (2019). mTERF5 acts as a transcriptional pausing factor to positively regulate transcription of chloroplast *psbEFLJ*. Molecular Plant 12(9): 1259-1277.

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Bioinformatics and Systems Biology

Xiujie Wang, Principal Investigator, Ph.D. (2004, The Rockefeller University, USA).

Research Interests: The current focus the lab is to develop novel computational methods to analyze the fast increasing genomics, transcriptomics, proteomics and other large-scale biological data, to identify new non-coding regulatory RNA genes in eukaryotic genomes, to decipher their transcription regulatory mechanisms, and to study the functions of non-coding RNAs in regulating embryonic stem cell pluripotency and targeted differentiation of embryonic stem cells towards defined organs.

Email: xjwang@genetics.ac.cn

Long noncoding RNA *lnc-NAP* sponges mmu-miR-139-5p to modulate *Nanog* functions in mouse ESCs and embryos

The pluripotency of embryonic stem cells (ESCs) is controlled by a multilayer regulatory network, of which the key factors include core pluripotency genes OCT4, SOX2 and NANOG, and multiple microRNAs (miRNAs). Recently, long noncoding RNAs (lncRNAs) have been discovered as a class of new regulators for ESCs, and some lncRNAs could function as competing endogenous RNAs (ceRNAs) to regulate mRNAs by competitively binding to miRNAs. Here, we identify mmu-miR-139-5p as a new regulator for *Nanog* by targeting *Nanog* 3' untranslated region (UTR) to repress *Nanog* expression in mouse ESCs and embryos. Such regulation could be released by an ESC-specifically expressed ceRNA named *lnc-NAP*. The expression of *lnc-NAP* is activated by OCT4, SOX2, as well as *Nanog* through promoter binding. Downregulation of *lnc-NAP* reduces *Nanog* abundance, which leads to decreased pluripotency of mouse ESCs and embryonic lethality. These results reveal *lnc-NAP* as a new regulator for *Nanog* in mouse ESCs, and uncover a feed-forward regulatory loop of *Nanog* through the participation of *lnc-NAP*.

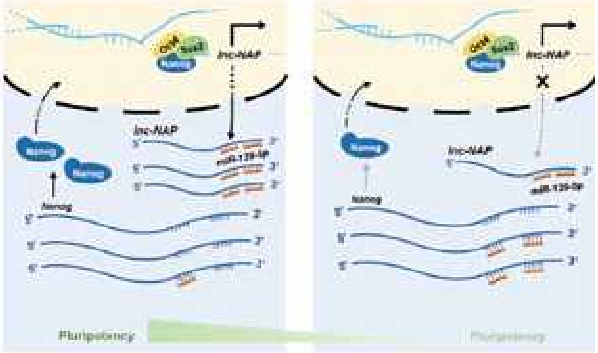

Figure: A schematic representation of the regulatory circuitry through which Oct4, Sox2, as well as Nanog fine-tune the expression of Nanog via ncRNAs *lnc-NAP* and mmu-miR-139-5p.

Publications

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Center for Agricultural Resources Research

The center's strategy is at ensuring the national demands on grain yield, water resources and ecological protection, focusing on the high efficient use of agricultural water resources; developing the innovative ecological resource theory and the modern agricultural technology systems for resource preservation; strengthening technological achievements transformation and service to society; gradually making the center to be an internationally well-known innovative institution.

The Center for Agricultural Resources Research has four key laboratories (i.e the Key Laboratory for Agricultural Water Resources of CAS, Hebei Key Laboratory of Water-saving Agriculture, Hebei Key Laboratory of Soil Ecology and Hebei Engineering Laboratory of Breeding and Germplasm Innovation for Plant Stress Tolerance). The center has four field stations (i.e Luancheng Agro-ecosystem Experimental Station, CAS, Nanpi Eco-agricultural Experimental Station, CAS, Taihang Mountain Mountain Ecosystem Experimental Station, CAS and NanDaGang Ecological Research Station of Coastal Wetland). There are three main research fields in the center (i.e water resource and water-saving agriculture, ecology and environment, and plant genetics and breeding). There are four research laboratories (i.e water resource and water-saving agriculture, ecology and environment, plant genetics and breeding, regional agriculture and agricultural policy). Now, the center has two professors from "National High-level Personnel of Special Support Program" In 2019, the center has achieved significant progresses in farmland hydrological process and high efficient use of agricultural water resources, crop germplasm selection and breeding, ecosystem process and management.

Water resources and water-saving agriculture: The major progresses achieved in 2019 can be summarized into 8 aspects: 1. Revealed the influence mechanism of agricultural land use types on groundwater quantity and quality from the perspective of groundwater recharge process. 2. Clarified the effects of planting structure adjustment on groundwater sustainability and grain production in piedmont plain. 3. Determined the nitrogen leaching rate of farmland under different precipitation years in North China Plain. 4. Analyzed the response law of vegetation change to meteorological drought in wind-sand source area of Beijing and Tianjin. 5. Revealed the photosynthetic basis of low light stress in early reproductive growth of wheat. 6. Got the effects of ridge mulching on the growth and water use of upland wheat and the dynamic changes of soil water, heat and salt. 7. Revealed the selection basis of summer maize varieties under the background of future climate change. 8. Found that crop breeding has increased the productivity and leaf wax n-alkane concentration in a series of five winter wheat cultivars developed over the last 60 years.

Plant genetics and breeding: The major progresses achieved in 2019 can be summarized into 5 aspects: 1. Transgenic experiments illustrated that overexpression of TaGS3.1/3.2/3.3/3.4/3.5 in wheat differentially affected thousand grain weight (TGW). The results imply that AS of TaGS3 may be an important regulation pattern involved in grain traits in wheat. 2. A set of new 4R translocations involving different arms was developed and characterized by GISH and marker analysis. The powdery mildew resistance was located on 4RL. A new powdery mildew resistance gene *pmDHT* were identified. These new translocation lines and *pmDHT* with diagnostic markers can efficiently used in wheat improvement for disease resistance. 3. Revealed the spatial-temporal distribution characteristic and interaction between agronomic traits of winter wheat and precipitation of growth period in Huang-Huai dryland. 4. Brassinosteroids (BRs) play vital roles in plant growth and development. We demonstrated that a DPY1-SiBAK1 complex mediates a negative feedback loop to prevent SiBRI1 from overactivation to modulate plant architecture in *Setaria*. 5. Two cytoplasmic receptor kinases known to be involved in plant innate immunity, PCRK1/2, were found to negatively regulate BR signal transduction by interacting with BRI1.

Ecology and environment: The major progresses achieved in 2019 can be summarized into 9 aspects: 1. Found that biochar could inhibit the production of N_2O in soil and promote the reduction of N_2O to N_2. 2. Found that in wheat-maize rotation system, nutrients should be supplied to wheat first under nutrient restriction conditions to increase soil carbon pool. 3. Found that halophytes can increase the carbon reserve, the utilization efficiency of salt water resources and the effect of lowering salt and cultivating fertilizer in the coastal heavy saline-alkali land. 4. Studied the spatial pattern characteristics of endangered and rare soils in Taihang Mountain area and discussed the main influencing factors. 5. Analyzed the comprehensive impact of the pig relocation policy and put forward the theoretical thinking and policy suggestions on the optimal spatial distribution of pigs and animal husbandry in the future. 6. Revealed that the wheat root microbiome changes with its developmental phase and is affected by nitrogen fertilizer, and wheat can recruit beneficial microorganisms to cope with high nitrogen input through root exudates. 7. Revealed that insect microbiomes depend on soil microbiomes, and that effects of plants on soil microbiomes can be transmitted to aboveground insects feeding later on other plants. 8. Quantified the adjustment effect of microtopography improvement measures on regional precipitation redistribution. 9. Revealed the nutrient utilization and balance mechanism of switchgrass under different nitrogen application rates and NPK nutrients.

In addition, the center has published 136 papers, among which 80 were included in SCI Journals; granted 23

Genetic Improvement & Germplasm Enhancement in Wheat

Diaoguo An, Principal Investigator, Ph.D. (2006, Research Center for Eco-environmental Sciences, CAS, China).

Research Interests: The laboratory is mainly interested in the development of new wheat germplasm resources by molecular chromosomesengineering; identifying, fine mapping and cloning of important genes/QTLs for disease resistance and important agronomic traits; molecular design breeding.

Email: dgan@sjziam.ac.cn

Development of novel wheat-rye chromosome 4R translocations and assignment of their powdery mildew resistance

Rye (*Secale ceraele* L.) is an important gene donor for wheat improvement because of its many valuable traits, especially disease resistance. Development of novel wheat-rye translocations with disease resistance can contribute to transferring the resistance into common wheat. Ina previousstudy, a wheat-rye T4BL·4RL and T7AS·4RS translocation line, WR41-1, was developed by distant hybridization, and it was speculated that its resistance to powdery mildew, caused by *Blumeria graminis* f. sp. *tritici* (*Bgt*), was derived from rye based on pedigree analysis. To make accurate use of chromosome 4R in wheat improvement, a set of new 4R translocations involving different arm translocations, such as 4RS monosomic,4RL monosomic, 4RL disomic, 4RS monosomic plus 4RL monosomic, 4RS monosomic plus 4RL disomic, and 4RS disomic plus 4RL disomic translocations, were developed from crosses with common wheat. Those translocations were characterized by genomic *in situ* hybridization (GISH) and EST-SSR (expressed sequence tag-simple sequence repeat) marker analysis. To confirm the source of powdery mildew resistance, the translocation plants were tested against *Bgt* isolate E09, the results indicated that all translocations with 4RL were resistant at all tested growth stages; while those with only 4RS translocation or no alien translocation were susceptible. This indicated that the powdery mildew resistance of WR41-1 was derived from the alien chromosome arm 4RL. To effectively use the 4RL resistance in wheat improvement, two kompetitive allele specific PCR (KASP) markers specific for chromosome arm 4RL were developed to detect the alien chromosome in the wheat genome. These new translocation lines with diagnostic markers can efficiently serve as important bridges for wheat improvement.

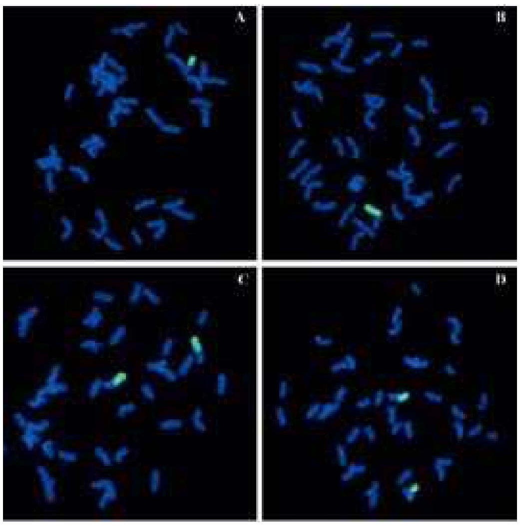

Figure: Genomic *in situ* hybridization identification of the WR41 derivatives. (A) 4RS monosomic translocation. (B) 4RL monosomic translocation. (C) 4RL disomic translocation. (D) 4RS monosomic plus 4RL monos omic translocation.

Publications

Ma, P., Han, G., Zheng, Q., Liu, S., Han, F., Wang, J., Luo, Q. and An, D. (2019). Development of novel wheat-rye chromosome 4R translocations and assignment of their powdery mildew resistance. Plant Disease: Doi:10.1094/PDIS-01-19-0160-RE

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Mountain Ecological Hydrological Process and Regulation Mechanism

Jiansheng Cao, Principal Investigator, Ph.D. (2012, University of Chinese Academy of Sciences, China), Deputy Head of Ecological Station in Taihang Mountain.

Research Interests: 1) Ecological hydrological process on slope for the rocky mountain area in North China; 2) Mechanism of flood and drought disasters for the rocky mountain area in North China; 3) Improvement of water conservation and regulation technology of rainfall; 4) Degraded mountain ecological restoration.

Email: caojs@sjziam.ac.cn

Advances in research on the effects of micro-topography changes on surface hydrological processes

The surface water cycle is a key link in the soil-plant-atmosphere continuum (SPAC) system, and micro-topography plays an important role in the process of rainfall redistribution. Here, we summarized the influence of micro-topography changes on surface hydrological processes and discuss the effects of micro-topography on overland flow, rainfall-infiltration, evapotranspiration, soil water transport, and feedback in SPAC systems. Previous studies regarding the effect of micro-topographic changes on surface hydrological processes were summarized and our understanding of the influential effect of micro-topography changes on runoff, infiltration, and evapotranspiration was advanced in this paper. We aimed at addressing the problems that the classification of micro-topography was unsystematic and that recent studies lacked thorough research into the coupling between micro-topography changes and surface hydrological processes. We proposed that micro-topography types should be divided according to different ecological types and micro-topography construction methods, and at the same time, combined with data from micro-topographic surveying tools and remote sensing technology, to define the micro-topographic scale more accurately. On this basis, long-term field observations should be combined with short-term lab simulations to reveal the coupling mechanism between microtopography changes and surface hydrological processes and to establish the quantitative relationship between them by creating model, and quantifying micro-topographic improvement measures to efficiently regulate the regional precipitation redistribution process. Ultimately, this paper may provide a theoretical basis for regional water resource regulation.

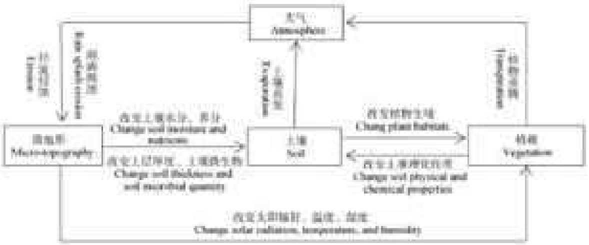

Figure: Feedback relationship between micro-topography and soil-plant-atmosphere continuum (SPAC) system.

Publications

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Xiao, D., Zhao, Y., Bai, H., Hu, Y. and Cao, J. (2019). Impacts of climate warming and crop management on maize phenology in northern China. Journal of Arid Land 11(6): 892-903.

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Regulation Mechanisms and Technologies for Highly Efficient and Eco-friendly Water Use of Crops

Baodi Dong, Young Investigator, Ph.D. (2008, University of Chinese Academy of Sciences)

Research Interests: Physio-ecological regulation mechanisms; Water saving technology; Rainfed agriculture; Improving crop water use efficiency.

Email: dongbaodi@sjziam.ac.cn

Publications

Dong, B., Yang, H., Liu, H., Qiao, Y., Zhang, M., Wang, Y., Xie, Z. and Liu, M. (2019). Effects of shading stress on grain number, yield, and photosynthesis during early reproductive growth in wheat. Crop Science 59: 363-378.

Photosynthetic base of reduced grain yield by shading stress during the early reproductive stage of two wheat cultivars

The young microspore (YM) stage, which is from the tetrad to the early phase of microspore development of wheat, is the stage most sensitive to abiotic stress affecting yield formation.In order to understand the effects of shading on the photosynthetic characteristics and grain yield in winter wheat during the YM stage, three levels of shading intensity: 100% (control), 40% (S1), and 10% (S2) of natural light were applied for 1, 3, 5, and 7 days during the YM stage of the shade-tolerant wheat cultivar (Henong825) and the shade-sensitive cultivar (Kenong9204) in the pot and two-year field experiments. Results showed that the grain yield extensively decreased as the shading intensity and duration increased.Moreover, the reduction in grain yield was more related to the decrease in grain number.With shading provision, the reduction of stomatal conductance (Gs), chlorophyll content, maximal photochemical efficiency of photosystem II (Fv/Fm), actual photochemical quantum efficiency (YII), saturation irradiance (PARsat), and maximum electron transport (Jmax) as well as the altered ultrastructure of chloroplast reduced the photosynthetic rate (Pn) and diminished the grain number of the cultivars. However, both cultivars showed different responses to shading. The Pn of Henong825 decreased with shading provision, but it rapidly increased to the control level after shading removal. This relieved damage to grain number formation and resulted in a smaller reduction in grain yield of Henong825 (-3.1% to 37.7%), which was less than that of Kenong9204 (14.0% to 79.4%). This study does not only supplement the research on the effects of shading intensity and duration on winter wheat during their YM stage, but it also provides technical support to the efficient utilization of select shade-tolerant cultivars.

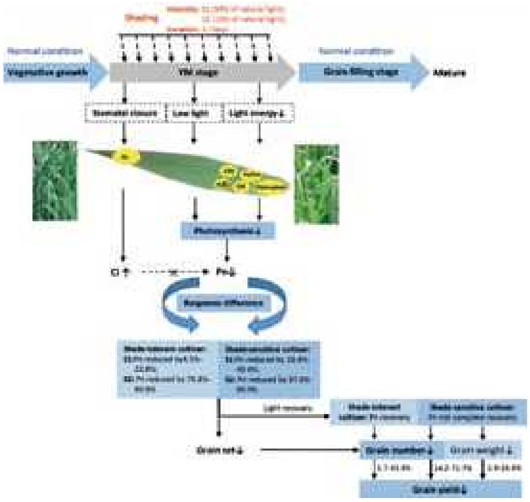
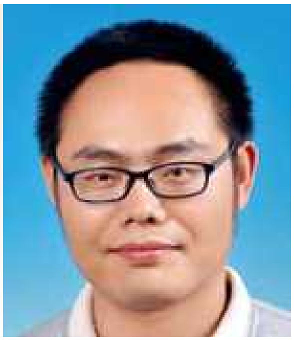


Figure: A model of wheat grown under low light stress. The downward black arrow indicates a descent; the upward black arrow indicates a rise.

Ecological Processes and Resource Utilization in Marginal Land



Lipu Han, Young Investigator, Ph.D. (2011, China Agricultural University).

Research Interests: we are focus on: (1) Ecological improvement mechanism of the interaction between saline-alkali lands and tolerant plants; (2) Research on key techniques of planting forage and energy plants; (3) Study for ecological response mechanism and sustainable development of forage and energy plants in sandy wasteland land; (4) Development and utilization for waste resource and plant residues in wetland-saline-alkaline land-farmland ecosystem.

Email: lphan@sjziam.ac.cn

Nutrient cycling of switchgrass planting for forage and bioenergy feedstock and soil nitrogen balance in a semiarid sandy wasteland

Understanding of switchgrass (*Panicum virgatum* L.) production response to nitrogen (N), phosphorus (P), and potassium (K) is essential for its management as a forage or bioethanol feedstock crop. To reveal the mechanism of nutrient utilization and balance on switchgrass, two experiments were carried out on sandy wasteland in Inner Mongolia. Different nitrogen application rate and NPK omission test were used to study the long-term sustainability of switchgrass as the forage and bioenergy feedstock quality. The optimum nitrogen fertilizer application significantly increased switchgrass crude protein content, protein yield, and theoretical ethanol yield. Harvest times affected crude protein content, theoretical ethanol yield, acid detergent fiber and neutral detergent fiber contents. Switchgrass biomass did not significantly increase at nitrogen application of 60 kg ha^{-1}. The lower rate of nitrogen application appears sufficient to produce good quality forage as well as biomass without negatively affecting feedstock quality, while avoiding the risk of NO_3^- loss via leaching on a sandy soil. The relevant research results have been published in the International Journal of Field Crops Research and Industrial Crops & Products.

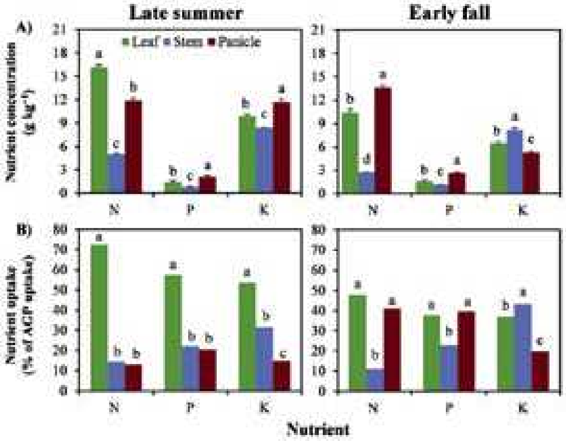


Figure: Switchgrass aboveground plant (AGP) nutrient concentration (A) and nutrient uptake (B) partitioning as determined by the fractions of leaf, stem, and panicle for late summer and early fall harvests (averaged across nitrogen rates and years). For each nutrient, different small letters indicate significant differences among plant organs at $p \leqslant 0.05$. The vertical bars denote standard errors.

Publications

Ameen, A., Liu, J., Han, L. and Xie, G. H. (2019). Effects of nitrogen rate and harvest time on biomass yield and nutrient cycling of switchgrass and soil nitrogen balance in a semiarid sandy wasteland. Industrial Crops and Products 136: 1-10.

Ameen, A., Tang, C., Liu, J., Han, L. and Xie, G. H. (2019). Switchgrass as forage and biofuel feedstock: Effect of nitrogen fertilization rate on the quality of biomass harvested in late summer and early fall. Field Crops Research 235: 154-162.

Ameen, A., Han, L. and Xie, G. H. (2019). Dynamics of soil moisture, pH, organic carbon, and nitrogen under switchgrass cropping in a semiarid sandy wasteland. Communications in Soil Science and Plant Analysis 50(7): 922-933.

Agrosystem Nutrient Cycling and Environmental Impacts

Chunsheng Hu, Principal Investigator Ph.D. (1996, Shenyang Institute of Applied Ecology, CAS, China), Vice Director of Center for Agricultural Resources Research of CAS.

Research Interests: The in situ processes and mechanisms of water and nitrogen leaching are studied using the isotope tracing technology and modeling. The study can provide scientific evidence for adopting reasonable water and fertilizer management strategies. Nitrogen nutrition diagnosis and transformation of middle-yielding and low-yielding lands are studied. The preferred fertilization plan is acquired based on the long-term fertilizer application experiments for the sustainable land use in northern China.

Email: cshu@sjziam.ac.cn

Biochar promotes the reduction of N_2O to N_2 and concurrently suppresses the production of N_2O in calcareous soil

Biochar additions may mitigate N_2O emissions from soil. The mechanisms underpinning the mitigation of emissions remain to be elucidated. A series of incubation experiments were performed to investigate the effects of biochar on N_2O production and reduction in columns with a low-fertility or high-fertility soil, with or without the injection of N_2O in the subsoil and with and without glucose (to stimulate denitrification).Biochar was added to the calcareous soils in 0 and 1% (w/w) amounts and moisture was maintained at 70%water-filled pore space (WFPS) over the incubation period. The results revealed that biochar reduced the emissions of soil-produced N_2O by 37%–47% and those of injected N_2O by 23%–44%. The addition of glucose solution strongly increased N_2O emissions, while biochar reduced total N_2O emissions by as much as 64%–81% and those of injected N_2O alone by 29%–51%. Differences between the low-fertility and high-fertility soils in the apparent N_2O emission mitigation by biochar were relatively small, but tended to be larger for the low-fertility soil. The results suggest that biochar addition can suppress the production of N_2O in soil and simultaneously stimulate the reduction of N_2O to N_2. Further studies are needed to elucidate the regulatory effects of biochar in soil.

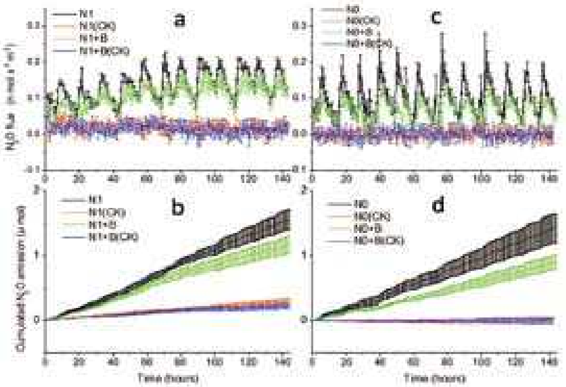


Figure: Fluxes of N_2O (a, c) and cumulative N_2O emissions (b, d) from unfertilized (N0) and fertilized soil (N1), with biochar (+B) or without biochar. During the incubation, N_2O was injected from the bottom of the soil through diffuse silicone tubing at a concentration of 998 ppmv every 12 h. Error bars denote the standard error of the mean (n = 3). The control treatments denoted as CK were not injected with N_2O but with N_2.

Publications

Bai, Z., Winiwarter, W., Klimont, Z., Velthof, G.,Misselbrook, T., Zhao, Z., Jin, X., Oenema, O., Hu,C. and Ma, L. (2019). Further improvement of air quality in China needs clear ammonia mitigation target. Environ Sci Technol 53(18): 10542-10544.

Chen, S., Waghmode, T. R., Sun, R., Kuramae, E. E., Hu, C. and Liu, B. (2019). Root-associated microbiomes of wheat under the combined effect of plant development and nitrogen fertilization. Microbiome 7(1): 136.

Chen, T., Oenema, O., Li, J., Misselbrook, T., Dong, W., Qin, S., Yuan, H., Li, X. and Hu, C. (2019). Seasonal variations in N2and N2O emissions from a wheat–maize cropping system. Biology and Fertility of Soils: 1-13.

He, C., Manevski, K., Andersen, M. N., Hu, C., Dong, W. and Li, J. (2019). Abiotic mechanisms for biochar effects on soil N2O emission. International Agrophysics 33(4): 537-546.

Li, J., Dong, W., Oenema, O., Chen, T., Hu, C., Yuan, H. and Zhao, L. (2019). Irrigation reduces the negative effect of global warming on winter wheat yield and greenhouse gas intensity. Science of the Total Environment 646: 290-299.

Wheat Genetics and Molecular Breeding

Junming Li, Principal Investigator.

Research Interests: Developing novel germplasms through exploitation of alien genes; Discovering related genes/QTLs of yield traits and analyzing their functional mechanisms; and breeding new varieties by molecular design.

Email: ljm@sjziam.ac.cn

Functional analysis of *TaGS3* in regulating grain traits of bread wheat

Heterotrimeric G-protein mediates growth and development by perceiving and transmitting signals in multiple organisms. G_γ subunit determines the specificity of the signal transduction pathways in plants. Alternative splicing (AS), a vital gene expression regulation process at the post-transcriptional level, plays a significant role in plant adaptation and evolution. Here we reported that there are five splicing isoforms of TaGS3 (G_γ), which translate five proteins with different domains. qRT-PCR result revealed that the five splicing isoforms of TaGS3 exhibited divergent tissue-specific expression patterns. *TaGS3.1*/3.2/3.3 were abundantly expressed in grains at different developmental stages, but *TaGS3.4* was abundantly expressed in leaves at booting stage, with *TaGS3.5* slightly expressed in both vegetative and reproductive organs. It was found that TaGS3.1/3.2/3.3/3.4/3.5 were located on the cell membrane and nuclear membranes. BiFC, Pull down and Yeast-two-hybrid assays revealed that TaGS3.1/3.2/3.3/3.4 interact with WGB1. Furthermore, Yeast-three-hybrid analyses demonstrated that TaGS3.1/3.2/3.3/3.4 coupled with WGB1 interact with WGA1. Transgenic experiments illustrated that overexpression of TaGS3.1/3.2/3.3/3.4/3.5 in wheat differentially affected thousand grain weight (TGW). Our results imply that AS of *TaGS3* may be an important regulation pattern involved in grain traits in wheat.

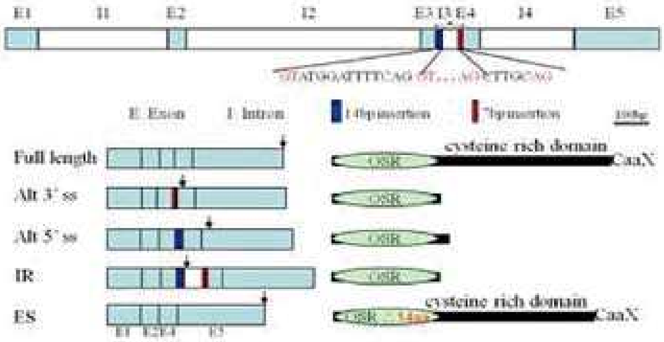


Figure: The five alternative splicing isoforms of TaGS3.

Publications

Fan, X., Cui, F., Ji, J., Zhang, W., Zhao, X., Liu, J., Meng, D., Tong, Y., Wang, T. and Li, J. (2019). Dissection of pleiotropic QTL regions controlling wheat spike characteristics under different nitrogen treatments using traditional and conditional QTL mapping. Frontiers in Plant Science 10:187.

Zhao, C., Zhang, N., Wu, Y., Sun, H., Liu, C., Fan, X., Yan, X., Xu, H., Ji, J. and Cui, F. (2019). QTL for spike-layer uniformity and their influence on yield-related traits in wheat. Bmc Genetics 20(1):23.

Microbial Ecology

Binbin Liu, Principal Investigator, Ph.D. (2006, Shanghai Jiao Tong University, China).

Research Interests: Dr. Liu's laboratory is mainly interested in using high throughput methods to investigate the microbial processes, focusing on soil microbial diversity, functional gene dynamics and expression related to nutrient turnover in agricultural ecosystems.

Email: binbinliu@sjziam.ac.cn

Publications

Chen, S., Waghmode, T. R., Sun, R., Kuramae, E. E., Hu, C. and Liu, B. (2019). Root-associated microbiomes of wheat under the combined effect of plant development and nitrogen fertilization. Microbiome 7(1): 136.

Liu, M., Chen, S., Wang, S., Hu, C. and Liu, B. (2019). High-quality draft genome sequence of pseudomonas songnenensis L103, a denitrifier isolated from a 100-Meter-deep aquifer in a heavily nitrogen-fertilized agricultural area. Microbiology Resource Announcements 8(36): e00373-00319.

Li, W., Xiao, Q., Hu, C., Liu, B. and Sun, R. (2019). A comparison of the efficiency of different urease inhibitors and their effects on soil prokaryotic community in a short-term incubation experiment. Geoderma 354: 113877.

Sun, R., D. D. Myrold, D. Wang, X. Guo and H. Chu (2019). AOA and AOB communities respond differently to changes of soil pH under long-term fertilization. Soil Ecology Letters 1(3-4): 126-135.

Sun, R., Li, W., Hu, C. and Liu, B. (2019). Long-term urea fertilization alters the composition and increases the abundance of soil ureolytic bacterial communities in an upland soil. FEMS Microbiol Ecol 95(5).

Response of root zone microbiomes of wheat to plant development and nitrogen fertilization

China is the largest chemical nitrogen (N) fertilizer producer and consumer in the world, the high rate N loss and low use efficiency are major problems in a large proportion of Chinese farmlands. In the China North Plain, one of the largest crop production areas in China, nitrogen fertilizer is deemed overused by more than 30%. The overuse of nitrogen fertilizer has resulted in a series of environmental issues. Since most N turnover processes are driven by microorganisms and are strongly affected by the nitrogen use efficiency of crops, understanding the mechanisms involved in these microbial-facilitated processes is of great importance.Through characterization of the bacterial and fungal microbiomes from the rhizosphere and roots of wheat (*Triticum aestivum* L.) at the three growth stages and under four levels of long-term N fertilization treatments, the researchers found that both plant growth status and N input drive the changes in the microbial community structure in the root zone of wheat. The plant growth stage showed a stronger effect on bacterial communities than that on fungal communities. The researchers also found a number of plant growth-promoting rhizobacteria positively responded to N fertilization, and their abundance was significantly correlated with the level of some organic acids, suggesting that the secretion of organic acids could be a strategy developed by plants to recruit beneficial microbes in the root zone to cope with high N input.

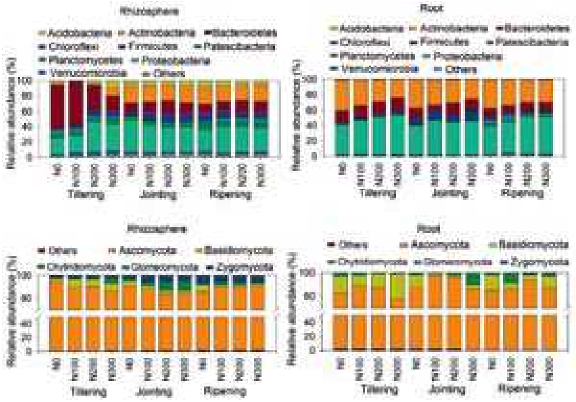


Figure: Bacterial and fungal community compositions of the rhizosphere (a) and root (b) samples at three growth stages and under four nitrogen fertilization levels.

Sustainable Management and Ecological Engineering for Ecosystem

Jintong Liu, Principal Investigator, Ph.D. (2000, Beijing Forestry University, China), Senior Visiting Scholar (1999-2000, Danish Royal University of Pharmaceutical Sciences, Denmark), Postdoctoral Fellow (2002-2004, Center for Central Agricultural Research, Japan).

Research Interests: Eco-engineering for drought prone mountain region, north China. Eco-engineering for coastal saline-alkali soil. Management for resources and ecosystem information.

Email: jtliu@sjziam.ac.cn

Rare and endangered soils in the Taihang Mountain region, North China

Loss of pedodiversity is a worsening land degradation issue worldwide. Knowledge of rare and endangered soils is critical for the protection of pedodiversity. However, such knowledge remains limited, especially for mountain regions with intensive human disturbance. In this paper, rare and endangered soils were identified using the Harmonized World Soil Database (HWSD), and their spatial distributions were determined for Taihang Mountain region, North China. The results showed that based on the second-level HWSD classification, a total of 94 soil types were identified in Taihang Mountain region, 36 of which were rare and 7 endangered soils. It implied that there was the need to protect soil resources in this region. Most of the rare and endangered soils were distributed in the northern of Taihang Mountain, indicating that the northern part needed more attention. Correlation analysis showed that the effect of human factors on rare and endangered soils was more important than that of natural factors, confirming that human activities were largely responsible for the occurrence of rare and endangered soils. Such results provided not only further understanding of pedodiversity but also useful information for protection of soil resources and control of land degradation.

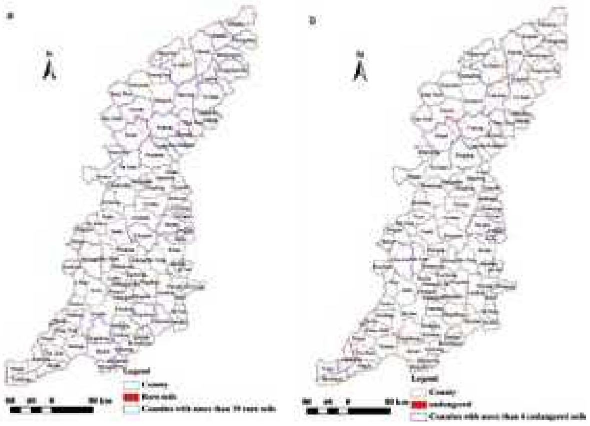


Figure: Spatial distribution of rare soils (a) and endangered soils (b) in the Taihang Mountain region.

Publications

Fu, T., Han, L., Gao, H., Liang, H. and Liu, J. (2019). Rare and endangered soils in the Taihang Mountain region, North China. Land Degradation & Development 30(14): 1739-1750.

Ameen, A., Tang, C., Liu, J., Han, L. and Xie, G. H. (2019). Switchgrass as forage and biofuel feedstock: Effect of nitrogen fertilization rate on the quality of biomass harvested in late summer and early fall. Field Crops Research 235: 154-162.

Ameen, A., Liu, J., Han, L. and Xie, G. H. (2019). Effects of nitrogen rate and harvest time on biomass yield and nutrient cycling of switchgrass and soil nitrogen balance in a semiarid sandy wasteland. Industrial Crops and Products 136: 1-10.

Efficient Water Use of Crops and Water-Saving Technology

Mengyu Liu, Principal Investigator, Ph.D. (2000, Hokkaido University, Japan).

Research Interests: Special efforts are devoted to eco-physiological mechanism of efficient water use, water saving and regulating technology, high efficient and safe production of vegetables, and relations between climate change and water use of agro-ecosystems.

Email: mengyuliu@sjziam.ac.cn

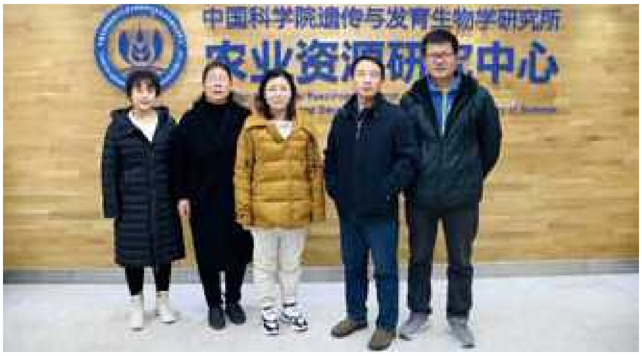
Publications

Dong, B., Yang, H., Liu, H., Qiao, Y., Zhang, M., Wang, Y., Xie, Z. and Liu, M. (2019). Effects of shading stress on grain number, yield, and photosynthesis during early reproductive growth in wheat. Crop Science 59(1): 363-378.

Effects of ridge and film mulching cultivation on dryland wheat growth and water use and dynamic changes of soil water, heat, and salt

Film mulching is an important way to protect and increase yield in many arid regions of the world. The subsurface film mulching technology we introduced from 2015 to 2018 has shown excellent performance in soil water conservation, salt suppression, yield increase effect, but the film may cause pollution to the soil ecological environment, so we introduced the ridge and mulch cultivation technology this year. The film used is a three-layer anti-aging black film, which can be used for 3-5 years and is easy to recycle. The groundwater level in the coastal area is low, and it is endangered by saline and alkali all year round, so the wheat yield is extremely low. In the one-year experimental study at Nanpi Experimental Station, ridge-cropped and mulched wheat increased yields by 12.44% (salinity 1.1‰-1.3‰) and 6.04% (salinity 1.7‰-1.9‰) compared with traditional flat-cropped wheat. From the analysis of the yield composition, the increase was due to an increase in the number of ears by 38.46% and 28.37%, respectively. Analysis from the perspective of dry matter distribution indicated increment in total biomass. Water use efficiency of ridge-cropped and mulched wheat was improved by 3%-9%. Ridge and film mulching technology in coastal dryland can effectively increase yield and water use efficiency of winter wheat.

Figure: Field test chart of ridge-covering and mulching.



Molecular Mechanisms of Plant Meristem Maintenance and Crop High-Yield

Xigang Liu, Principal Investigator, Ph.D. (2004, Hebei Normal University, China).

Research Interests: Our research is focused on: 1) the molecular mechanism of plant meristem maintenance and determinacy in monocot and dicot; 2) the molecular mechanisms of plant root development and the response to abiotic stress.

Email: xgliu@sjziam.ac.cn

DROOPY LEAF1 controls leaf architecture by orchestrating early brassinosteroid signaling

Brassinosteroids (BRs) play vital roles in plant growth and development. The tissue- and stage-specifically negative regulatiorsin early BR signaling are largely unknown. Here, using foxtail millet, a model plant of C4 grass, we demonstrate that DROOPY LEAF1 (DPY1) negatively regulates early brassinosteroid (BR) signaling to control leaf droop. *DPY1* expression is maximal at seedling stage and restricted to the vascular bundle, where DPY1 physically interacts with BRI1-ASSOCIATED KINASE1 (SiBAK1) to fine-tune the formation of the SiBAK1-BRASSINOSTEROID-INSENSITIVE1 (SiBRI1) complex, which affects the phosphorylation status of SiBRI1. Moreover, BR promotes DPY1 accumulation and the DPY1-SiBAK1 interaction to attenuate SiBRI1 phosphorylation. We uncover a brake mechanism in early BR signaling ensuring the properly spatiotemporal BR activity in stage-specific leaf architecture.

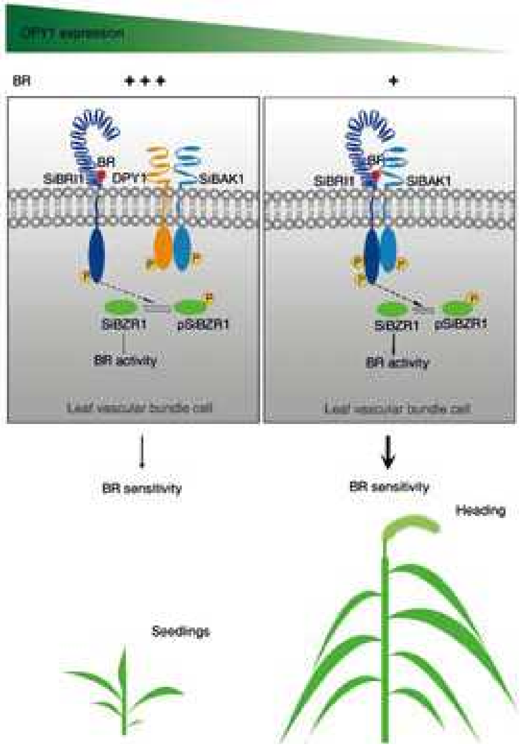
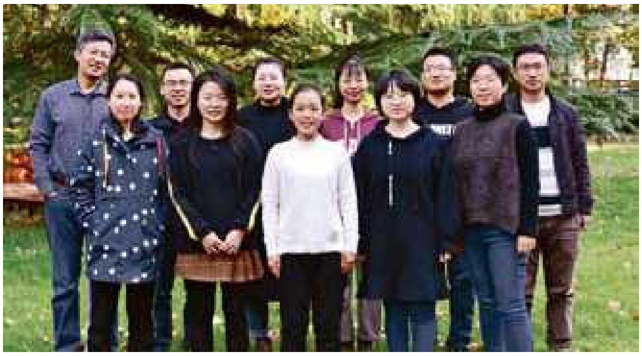


Figure: At the vegetative stage, high BR levels are required for fast development and growth of the C4 plant. While high BR levels enhance DPY1 accumulation and its phosphorylation, such an enhancement compromises early BR signaling as a feedback regulatory mechanism, particularly in leaf vascular tissues. As a result, the high BR-associated droopy leaf morphology is minimized. At the adult stage, the plant size reaches the maximum; DPY1 level and its phosphorylation decline as BR level drops, which in turn releases DPY1-mediated repression of BR signaling. Such a release may ensure transportation of assimilates from leaves to seeds as defects in either BR synthesis or signaling lead to smaller seed size.

Publications

Chen, L. G., Gao, Z., Zhao, Z., Liu, X., Li, Y., Zhang, Y., Liu, X., Sun, Y. and Tang, W (2019). BZR1 family transcription factors function redundantly and indispensably in BR signaling but exhibit BRI1-independent function in regulating anther development in *Arabidopsis*. Mol Plant 12(10): 1408-1415.

Zheng, Y. and Liu, X. (2019). Review: Chromatin organization in plant and animal stem cell maintenance. Plant Sci 281: 173-179.



Efficient Utilization of Saline Resources

Xiaojing Liu, Principal Investigator and Head of Nanpi Eco-agricultural Experimental Station, Ph.D. (2006, Tokyo University of Agriculture, Japan).

Research Interests: Reclamation and utilization of saline soils, saline water irrigation, and ecophysiology of plant salt tolerance.

Email: xjliu@sjziam.ac.cn

Publications

Chen, H., Yang, C., Ren, A., Guo, K., Feng, X., Li, J., Liu, X., Sun, H. and Wang, J. (2019). The Evapotranspiration of tamarix and its response to environmental factors in coastal saline land of China. Water 11(11):2273.

Feng, X., Guo, K., Yang, C., Li, J., Chen, H. and Liu, X. (2019). Growth and fruit production of tomato grafted onto wolfberry (Lycium chinense) rootstock in saline soil. Scientia Horticulturae 255: 298-305.

Guo, K. and Liu, X. (2019). Effect of initial soil water content and bulk density on the infiltration and desalination of melting saline ice water in coastal saline soil. European Journal of Soil Science 70(6):1249-1266.

Li, J., Hussain, T., Feng, X., Guo, K., Chen, H., Yang, C. and Liu, X. (2019). Comparative study on the resistance of Suaeda glauca and Suaeda salsa to drought, salt, and alkali stresses. Ecological Engineering 140:105593.

Ecological effect of Halophytes vegetation in coastal heavy saline land

Vegetation construction with halophytes in the coastal saline land not only significantly changes the landscape but also has a strong ecological effect. The studies on the vegetation of Haixing experimental base shows that the carbon storage of 10 a *Tamarix chinensis* plantation and 8 a *Lycium chinense* plantation respectively were 118.24 t · hm^{-2} and 96.27 t · hm^{-2}, which were 83.39 t · hm^{-2} and 61.42 t · hm^{-2} higher than that of bare land. From 2016 to 2018, the evapotranspiration of Tamarix plantation was 514.2-573.8 mm, Transpiration was accounting for 60.2% of the evapotranspiration. Water consumption had increased 377.6 mm compared with the bare land. In 2017, the water deficit of Tamarix plantation was 107.2 mm, while the remaining precipitation in the normal year (2016) and wet year (2018) was 77.8 mm and 187.5 mm respectively, indicating that the rainfall in coastal saline land could meet the consumption of Tamarix plantation. Although the salt tolerance of *Suaeda salsa* is higher than *S. glauca*, but its alkali tolerance is lower. Planting *S. salsa* in the saline soil had increased the soil porosity, and the water infiltration rate, which had promoted the salt leaching, and the plants also absorbed and brought away some salt; the salt brought away by leaching and plant absorption accounted for 94.40% and 5.60% of the total desalination, respectively.

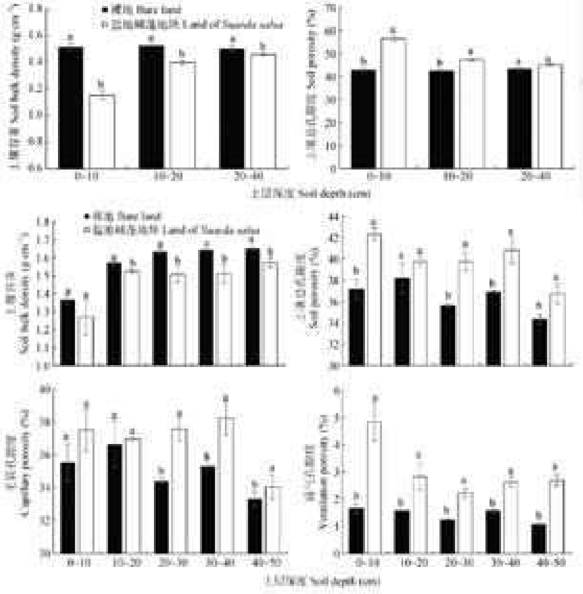


Figure: Soil bulk densities and porosities of native *Suaeda salsa* and bare land patches of the field investigation(top).Effects of *Suaeda salsa* growth on soil bulk density and porosity in the soil column experiment(lower).

Root Phenomics

Dr. Xiuwei Liu, scientist, graduated from the Center for Agricultural Resourses Research, Institute of Genetics and Developmental Biology, CAS in 2015. He was a post-doc at Texas A&M University and Noble Research Institute from 2015 to 2019.

Research Interests: Evaluating the leaf n-alkane carbon isotope as a surrogate for crop yield and water use efficiency, Investigating the effects of root phenes on root distribution, Using electrical capacitance to detect cotton roots.

Email: xgliu@sjziam.ac.cn

Crop breeding has increased the productivity and leaf wax n-alkane concentration in a series of five winter wheat cultivars developed over the last 60 years

Plant wax n-alkanes are a major constituent of the leaf and grain surface. In this study, we explored what can be learned from the abundance and carbon isotopic composition (δ^{13} C) of n-alkanes in historical winter wheat cultivars. We investigated leaf and grain wax n-alkane concentration (Σ_{alkL} and Σ_{alkG}) and carbon isotopes (δ^{13} C_{alkL} and δ^{13} C_{alkG}) on C_{29} as well as bulk leaf and grain carbon isotopes (δ^{13} C_{bulkL} and δ^{13} C_{bulkG}) to assess if these wax components changed across five wheat cultivars released from the 1950s to the early 2010s. Results showed that Σ_{alkL} and grain yield increased, while δ^{13} C_{alkL} and δ^{13} C_{bulkL} decreased across the historical wheat cultivars. We found a significant correlation between Σ_{alkL} and shoot biomass at the early growth stage, and a strong correlation between Σ_{alkL} at the grain-filling stage and grain yield. Grain measures, including Σ_{alkG}, δ^{13} C_{alkG}, and δ^{13} C_{bulkG} did not correlate with crop production. Although δ^{13} C_{alkL} and grain yield were not correlated at the flowering stage, they were correlated at the grain-filling stage under dry conditions. Our results indicate that increased Σ_{alkL} has been indirectly selected in breeding efforts to improve crop production in winter wheat, suggesting that greater leaf waxiness confers advantages for crop growth.

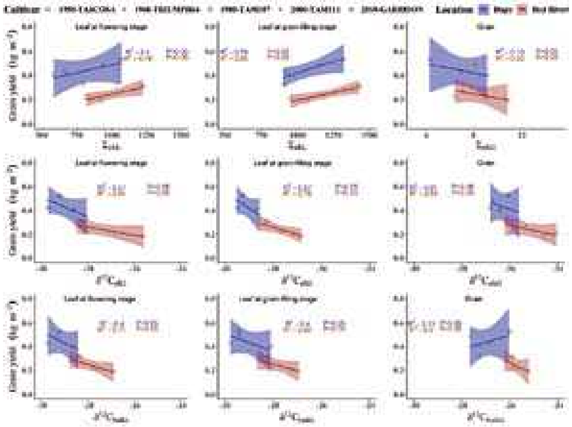


Figure: Relationships of S_{alkL}, d13CalkL, $d^{13}C_{bulkL}$, S_{alkG}, $d^{13}C_{alkG}$ and $d^{13}C_{bulkG}$ with grain yield in the field

Publications

Peng, B., Liu, X., Dong, X., Xue, Q., Neely, C. B., Marek, T., Ibrahim, A. M. H., Zhang, G., Leskovar, D. I. and Rudd, J. C (2019). Root morphological traits of winter wheat under contrasting environments. Journal of Agronomy and Crop Science 2019,00,1-15.

Liu, X., Feakins, S. J., Dong, X., Xue, Q., Han, J., Marek, T., Leskovar, D. I., Neely, C. B. and Ibrahim, A. M. H. (2019). Evaluating leaf wax and bulk leaf carbon isotope surrogates for water use efficiency and grain yield in winter wheat. Crop Science 59(2): 718-732.

Liu, X., Feakins, S. J., Ma, X.-F., Anderson, J. D., Vidal, E. and Blancaflor, E. B. (2019). Crop breeding has increased the productivity and leaf wax n-alkane concentration in a series of five winter wheat cultivars developed over the last 60 years. Journal of Plant Physiology 243: 153056.

Sun, H., Zhang, X., Liu, X., Liu, X., Shao, L., Chen, S., Wang, J. and Dong, X. (2019). Impact of different cropping systems and irrigation schedules on evapotranspiration, grain yield and groundwater level in the North China Plain. Agricultural Water Management 211: 202-209.

The Molecular Genetics of Plant Defense

Dongping Lu, Principal Investigator. Ph.D. (2007, University of Hawaii, USA).

Research Interests: Study on the plant pathogen resistance mechanism.

Email: dplu@sjziam.ac.cn

Publication

Huang, G., Sun, J., Bai, J., Han, Y., Fan, F., Wang, S., Zhang, Y., Zou, Y., Han, Z. and Lu, D. (2019). Identification of critical cysteine sites in brassinosteroid-insensitive 1 and novel signaling regulators using a transient expression system. New Phytologist 222(3): 1405-1419.

Fan, F., Zhang, Y., Huang, G., Zhang, Q., Wang, C. C., Wang, L. and Lu, D. (2019). AtERO1 and AtERO2 exhibit differences in catalyzing oxidative protein folding in the endoplasmic reticulum. Plant Physiology 180(4): 2022-2033.

Mao, D., Xin, Y., Tan, Y., Hu, X., Bai, J., Liu, Z. Y., Yu, Y., Li, L., Peng, C., Fan, T., Zhu, Y., Guo, Y. L., Wang, S., Lu, D., Xing, Y., Yuan, L. and Chen, C. (2019). Natural variation in the *HAN1* gene confers chilling tolerance in rice and allowed adaptation to a temperate climate. Proceedings of the National Academy of Sciences of the United States of America 116(9): 3494-3501.

PCRK1/2 can inversely modulate brassinosteroid and plant immune signaling pathways

The plant hormones brassinosteroids (BRs) modulate plant growth and development. There is a tradeoff between plant development and immunity. We used brassinolide-induced exogenous bri1-EMS-Suppressor 1 (BES1) dephosphorylation in *Arabidopsis thaliana* protoplasts as a readout, took advantage of the dramatic decrease of BR-insensitive 1 (BRI1, the receptor of BR) protein levels during protoplast isolation, and developed a protoplast transient system to reconstitute the BR signaling pathway. Using this transient system, we identified two negative regulators of BR signaling, pattern-triggered immunity compromised RLCK1 (PCRK1) and PCRK2 that were previously known to positively regulate innate immunity signaling (Figure). Furthermore, PCRK1/2 interact with BRI1 at the plasma membrane. This work reveals that PCRK1/2 can inversely modulate BR and plant immune signaling pathways.

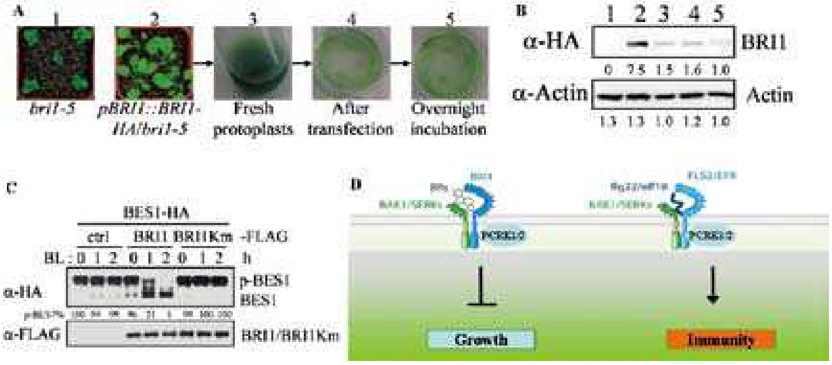
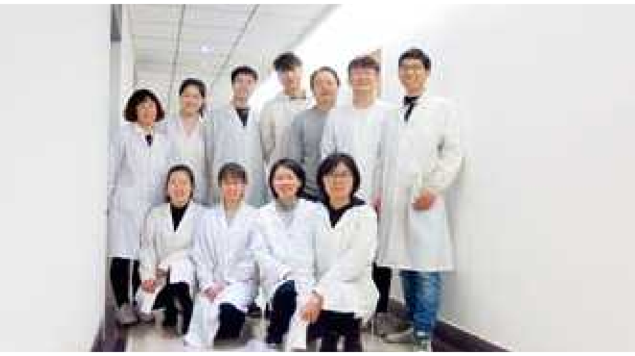


Figure: (A&B) Measurement of BRI1 protein levels during protoplast isolation and incubation using *pBRI1::BRI1-HA/bri1-5* plants. (C) The addition of exogenous BRI1 inprotoplasts could enable the exogenous BES1 to undergo dephosphorylation upon BL treatment. (D) Two receptor-like cytoplasmic kinases PCRK1/2 inversely regulate plant immune and brassinosteroid signaling pathways.



Agro-Ecology and Nutrient Management

Lin Ma, Principal Investigator, Ph.D. (2010, Agricultural University of Hebei, China). Postdoctoral fellow (2010-2014, Wageningen University, the Netherlands).

Research Interests: Sustainable development of agriculture and food systems by analyzing complex “soil-crop production-animal production-food processing-household consumption” chains, Mitigation options of non-point sources pollution from crop and animal production system, Techniques of manure management from “housing-storage-processing-application” chain.

Email: malin1979@sjziam.ac.cn

China’s pig relocation in balance

China’s pig relocation will protect water quality in the south, where people suffered from severe water pollution. However, such relocation may transfer the pollution to regions with large areas of forests and fragile natural grasslands.In 2015, the Chinese government banned livestock production in some regions (called non-livestock production regions, NLPRs) to control surface water pollution near vulnerable water bodies. In total, 90,000 NLPRs had been established by 2017, covering a land area of 0.82 million km^2 and shutting down 0.26 million pig farms. As a consequence, the number of slaughtered pigs decreased by 46 million head yr^{-1} between 2014 and 2017. The NLPRs policy is globally unprecedented in terms of the geographical area and number of farms affected, as well as its implementation speed. The NLPRs policy has reduced pork self-sufficiency in some provinces by up to 40%. However, it is unclear which farms and regions may take over the market share. This question is crucial because the consumption of pork in China is forecasted to increase from 690 to 1,000 million head yr^{-1} between 2018 and 2050. Pig production is expected to be transferred from watercourse-intense southern regions to southwest and northeast provinces — areas that the Chinese government designated as potential development regions. The main reasons to select these provinces are the current low pig population density and the large land area available for the application of pig manure, relative to other areas. This policy seems attractive at first: total nutrient losses to watercourses may decrease by up to 27% for nitrogen and up to 48% for phosphorus in southeast China, and more businesses and subsidies will arrive to economically less-developed regions, promoting local economies. However, the pollution burden associated with pig production may also be transferred. This is concerning because the potential development regions in the southwest and fragile natural grasslands, respectively. Besides, technology to manage manure and minimize ammonia emission does not appear to follow new production technology, due to a lack of appropriate investments and incentives6. Some recently established industrial-scale livestock farms in the northeast have simple manure or slurry lagoons that emit gaseous pollutants directly into the air. Estimated health costs of air pollution to citizens are comparable to the profits of pig production (€1.3 to 11 head^{-1} and approximately €4.2 head^{-1}, respectively). This suggests that the development regions may not benefit, on balance, when all of the costs are considered. Overall, the NLPRs and pig-relocation policies risk decreasing surface water pollution in the southeast at the expense of increasing air emission and groundwater pollution in the southwest and northeast, regions that already have high nitrogen losses. However, these trade-offs could be minimized through: (1) holistic spatial planning of livestock production that considers all economic, environmental and social constraints in an integrated manner; (2) adopting strategies to properly allocate manure to local cropping systems at sustainable nutrient loading rates; and (3) promoting the use of pollution mitigation technologies. In identifying nonlivestock production regions and potential development regions, we must consider the multiple risks to the environment, including surface water pollution, air pollution, soil degradation and threats to human health, but crucially, also the risks associated with long-distance transport of livestock, including the spreading of animal diseases.

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Cao, Y., Wang, X., Bai, Z., Chadwick, D., Misselbrook, T., G. Sommer, S., Qin, W. and Ma, L. (2019). Mitigation of ammonia, nitrous oxide and methane emissions during solid waste composting with different additives: A meta-analysis. Journal of Cleaner Production 235: 626-635.

Eco-Hydrological Modelling and Water Environmental Management

Yanjun Shen, Principal Investigator, Ph.D. (2018 Friedrich Schiller Universität Jena, Germany)

Research Interests: Eco-hydrological modelling based on hydro; logical models; Coupled modelling water quantity and quality at the basin scale surface water-groundwater interaction and solute transport; spatial data analysis and water resources management.

Email: shenyanjun@sjziam.ac.cn

Publications

Li, C., Li, H., Li, J., Lei, Y., Li, C., Manevski, K. and Shen, Y.-j. (2019). Using NDVI percentiles to monitor real-time crop growth. Computers Electronics in Agriculture 162: 357-363.

Shen, Y.-j., Shen, Y., Guo, Y., Zhang, Y., Pei, H. and Brenning, A. (2020). Review of historical and projected future climatic and hydrological changes in mountainous semiarid Xinjiang (northwestern China), central Asia CATENA. https://doi.org/10.1016/j.catena.2019.104343.

Response of vegetation coverage change to meteorological drought at different time scales in Beijing-Tianjin Sandstorm Source Region

Beijing-Tianjin Sandstorm Source Region is located in the arid and semi-arid region of China, which is a typically ecological fragile area with frequent drought disasters. Vegetation plays an important role in this region, but the response of vegetation to meteorological drought in this region is still unclear. Based on NDVI and SPEI, results showed that from 2000 to 2017, the vegetation coverage in most areas of the region has increased. The NDVI increased significantly ($P < 0.05$) in 47.66% of vegetation region, which was mainly located in the southern part. In growing season, 97.84% of the vegetation region was significantly negatively affected by drought. Under the negative influence of drought, the vulnerability of vegetation increased from April to July, reached the highest in July, and then decreased from July to October. Therefore, attention should be paid to avoid summer drought, especially to the negative impact of drought on vegetation in July. Compared with two subregions in south (I and V), the vegetation of three subregions in north (II, III and VI) was more vulnerable under the negative influence of drought. The negative influence of drought in grassland was most serious, followed by shrub, farmland and forest.

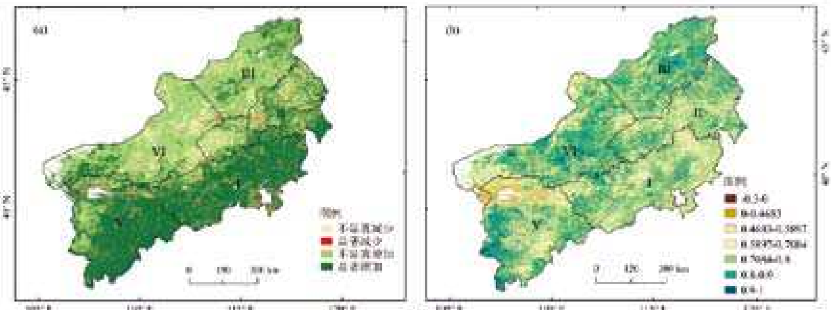

Figure: Trend of growing season NDVI change (a) and its max correlation with SPEI (b) in Beijing-Tianjin Sandstorm Source Region from 2000 to 2017.

Agricultural Hydrology and Water Resources

Yanjun Shen, Principal Investigator, Ph.D. (2004, Chiba University, Japan).

Research Interests: Our group is mainly interested in eco-hydrological processes, especially the processes related to agricultural water use and ecological conservation. By field observation, route survey, environmental tracing, remote sensing, and numerical modeling, we focus on the water cycles at plot, watershed, and regional scales. We are also involved in the research on hydrology and water resources change and adaptation to climate warming.

Email: yjshen@sjziam.ac.cn

Water-saving potential of subsurface drip irrigation for winter wheat

Using drip irrigation systems may significantly reduce the consumption of water. Lysimeter experiments were conducted under different irrigation treatments (flood, surface drip, and subsurface drip) to account for ET in the selection of a suitable irrigation method. Subsurface drip irrigation reduced ET by 26% compared to flood irrigation, and 15% compared to surface drip irrigation, with significant grain yield and biomass formation due to decreased evaporation losses. Grain yield, yield components, and above ground biomass were similar in subsurface drip and flood irrigation. However, these biomass parameters were lower with surface drip irrigation. Furthermore, subsurface drip irrigation increased the crop water productivity (24.95%) and irrigation water productivity (19.59%) compared to flood irrigation. The subsurface irrigated plants showed an increase in net photosynthesis (~10%), higher intrinsic water use efficiency (~36%), lower transpiration rate (~22%), and saved 80 mm of water compared to flood irrigation. Our findings indicate that subsurface drip irrigation can be adopted in the North China Plain to increase water use efficiency, optimize grain yield, and minimize water loss in order to address scarcity.

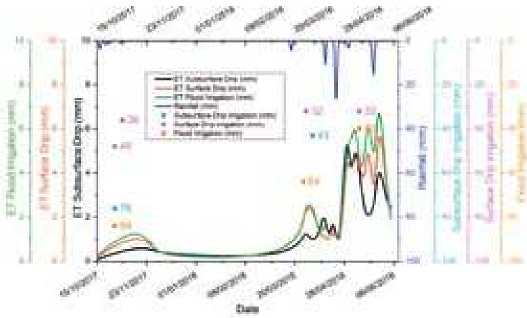

Figure: Relationship between solute front and wetting front under the impact of the ratio of initial soil water content to final water content.

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Zhang, J. and Shen, Y. (2019). Spatio-temporal variations in extreme drought in China during 1961-2015. Journal of Geographical Sciences 29(1): 67-83.

Min, L., Qi, Y., Shen, Y., Wang, P., Wang, S. and Liu, M. (2019). Groundwater recharge under irrigated agro-ecosystems in the North China Plain: From a critical zone perspective. Journal of Geographical Sciences 29(6): 877-890.

Zhang, Y., Qi, Y., Shen, Y., Wang, H. and Pan, X. (2019). Mapping the agricultural land use of the North China Plain in 2002 and 2012. Journal of Geographical Sciences 29(6): 909-921.

Water and Salt Movement Process and Regulation in Agro-Ecosystems

Hongyong Sun, Junior Investigator, Ph.D. (2007, Institute of Geographic Sciences and Natural Resources Research, CAS), Research Fellow (2009-2010, Commonwealth Scientific and Industrial Research Organisation, Australia), Deputy Director of the Nanpi Eco-agricultural Station.

Research Interests: 1) Water and salt movement process in GSPAC. 2) Mechanism of crop adaption to water and salt. 3) Water and salt regulation of field in water shortage saline area.

Email: hysun@sjziam.ac.cn

Wheat-derived SOC accumulates more than its maize counterpart in nutrients supplied wheat-maize cropping system

Fertilization is the most common way to supply nutrients to the soil and to maintain crop productivity in agricultural ecosystems, which may also influence soil organic carbon (SOC) accumulation rates. After 21 years of fertilization, N application did not increase soil total N content, but P application significantly increased soil total P contents by 33.9%. The single application of N or P did not significantly affect SOC content, while the NP combination significantly increased SOC contents by 22.1% and 29.6% compared to Ct in the no K and K treatments, respectively. The natural ^{13}C abundance approach and the SOC contents suggested that the NP combination increased wheat-derived SOC by 37.5% and 49.8% in the no K and K treatments; however, fertilization had no impact on maize-derived SOC content. Wheat-derived SOC was positively correlated to the wheat yield, while maizederived SOC was not correlated to the maize yield, which indicated that wheat-derived SOC accumulated more than maize-derived SOC in the wheat-maize cropping system. Our results indicate that N combined with P application is more beneficial than N or P alone to enlarge SOC sequestration, especially for wheat-derived SOC.

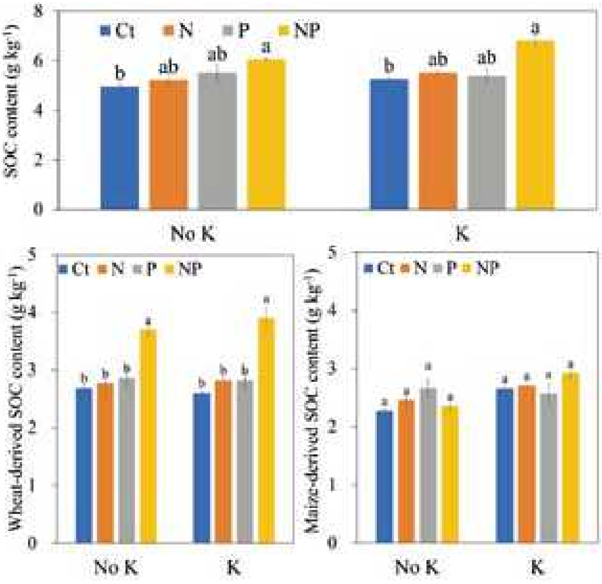

Figure: Fertilization effects on total soil organic carbon and different crop-derived soil organic carbon contents.

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Dong, X., Li, M., Lin, Q., Li, G. and Zhao, X. (2019). Soil Na+ concentration controls salt-affected soil organic matter components in Hetao region China. Journal of Soils and Sediments 19(3): 1120-1129.

Dong, X., Singh, B. P., Li, G., Lin, Q. and Zhao, X. (2019). Biochar has little effect on soil dissolved organic carbon pool 5 years after biochar application under field condition. Soil Use and Management 35(3): 466-477.

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Wang, J., Kang, S., Du, T., Tong, L., Ding, R. and Li, S. (2019). Estimating the upper and lower limits of kernel weight under different water regimes in hybrid maize seed production. Agricultural Water Management 213: 128-134.

Water Cycle and Groundwater Environment

Shiqin Wang, Principal Investigator, Ph.D. (Institute of Geographical Sciences and Natural Resources Research, CAS).

Research Interests: Hydro-geochemical processes of earth critical zone; Mechanism of water cycle, and nitrate transport within unsaturated zone and saturated zone; Interaction of surface water and groundwater; Sustainable development of groundwater resources based on the water quantity and water quality simulation.

Email: sqwang@sjziam.ac.cn

Nitrogen stock and leaching rates in a thick vadoses zone below areas of long-term nitrogen fertilizer application in the North China Plain: A future groundwater quality threat

Over-application of N-fertilizer may lead to nitrate leaching and pollution of groundwater, nitrate in groundwater displays an increasing trend in many aquifers of the world due to the excessive use of fertilize. In this study, deep soil cores down to 11 m were taken at three long-term N-fertilizer application treatments under a wheat-maize cropping system in the Piedmont Plain area and two land-uses in the headwater regions of the North China Plain. Groundwater recharge, leachate and the transport path of nitrate was identified. Results showed that leaching rates were lower than the declining rate of groundwater level (100 cm yr^{-1}) during normal precipitation year, it is unlikely for chemical N-fertilizer (abundantly applied in 1970's in the wheat-maize cropland) to enter groundwater based on the matrix flow hypothesis. Accumulation and denitrification of nitrate (particularly in upper 4 m depth of soil) limited the leaching flux of nitrate to deeper layers. However, groundwater recharge changed from matrix flow to bypass flow after extreme precipitation in wet year, which increased the risk of nitrate leaching and groundwater contamination. The results provided critical information for water and N fertilizer management practices in the agricultural fields in the future.

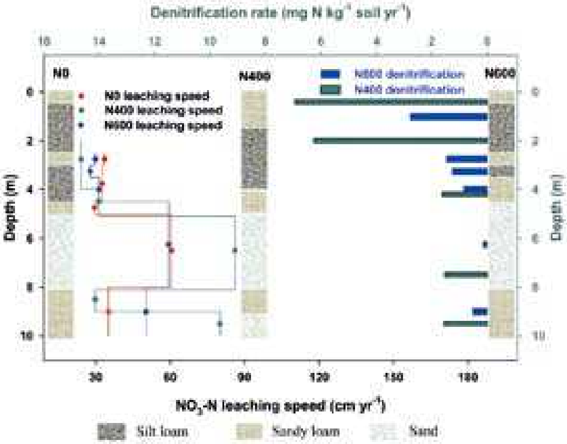

Figure: Leaching speed and denitrification rate in various texture soils in the N0, N400 and N600 treatments.

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Liu, B., Wang, S., Kong, X. and Liu, X. (2019). Soil matric potential and salt transport in response to different irrigated lands and soil heterogeneity in the North China Plain. Journal of Soils and Sediments: 1-12.

Liu, B., Wang, S., Kong, X., Liu, X. and Sun, H. (2019). Modeling and assessing feasibility of long-term brackish water irrigation in vertically homogeneous and heterogeneous cultivated lowland in the North China Plain. Agricultural water management 211: 98-110.

Water Resources and Food Security

Yonghui Yang, Principal Investigator, Ph.D. (2002, Chiba University, Japan), Vice Director of Center for Agricultural Resources Research of IGDB.

Research Interests: Accurate evaluation of key elements of hydrological cycle; Effect of human and climate change on hydrological cycle; Development of methods for agricultural water assessment; Land - Food - Water Nexus.

Email: yonghui.yang@sjziam.ac.cn

Publications

Zhou, X., Yang, Y., Sheng, Z. and Zhang, Y. (2019). Reconstructednatural runoff helps to quantify therelationship between upstream wateruse and downstream water scarcity in China's river basins. Hydrology and Earth System Sciences 23: 1-15.

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Hu, Q., Yang, Y., Han, S. and Wang, J. (2019). Degradation of agricultural drainage water quantity and quality due to farmland expansion and water-saving operations in arid basins. Agricultural Water Management 213: 8.

Han, S., Yang, Y., Li, H., Yang, Y., Wang, J. and Cao, J. (2019). Determination of crop water use and coefficient in drip-irrigated cotton fields in arid regions. Field Crops Research 236: 85-95.

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Evaluating the potentials of cropping adjustment for groundwater conservation and food production in the piedmont region of the North China Plain

As water saving by using technologies to alleviate groundwater depletion has its limitations, adjusting the cultivation patterns of water-intensive crops becomes an unavoidable measure to ensure water sustainability. Different cropping patterns (including fallowing) and water supply scenarios were set up, using the DSSAT crop model and a regression model, in order to predict the effects of cropping adjustments on groundwater sustainability and food production in the piedmont region of the plain. The results indicate that: (1) irrigation water requirement needs to be limited to a maximum level of 187 mm/a to sustain groundwater at the present level. Above this level, every 100 mm of irrigation pumping leads to a decline of 0.49 m in the groundwater level; (2) under the current water supply conditions, and taking groundwater sustainability, food supply, water use efficiency and soil fertility recovery into consideration, leaving 34% of the cropland fallow or leaving it fallow every 3 years seems to be the best option; (3) If an extra amount of water of 0.2 or 0.5 billion m^3 is supplied as a result of the SNWT Project, the percentage of cropland which should be left fallow can decrease to 25% or 11% respectively.

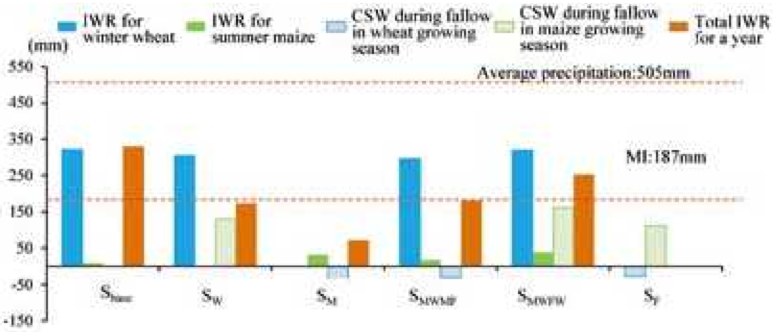

Figure:Comparison of water use for different cropping systems. 'MI' stands for the maximum irrigation within the range which will not cause a decline in groundwater levels. CSW refers to changes in soil water storage, where a negative value refers to a decrease in soil water and a positive value indicates an increase in soil water. The other notes: IWR-Irrigation water requirement; Sbase- two crops one year (winter wheat –summer maize); SW-one crop(winter wheat) one year; SM-one crop (summer maize) one year; SMWMF-three crops-in 2 years for maize–wheat–maize–fallow; SMWFW-three crops-in 2 years for maize-wheat-fallow-wheat; SF-fallow cropland throughout the year.

Improving Farmland Water Use Efficiency

Xiying Zhang, Principal Investigator. Ph.D. (2006, Graduate School of Agricultural and Life Sciences, University of Tokyo, Japan).

Research Interests: Focusing on crop-water relationship, root growth and soil water utilization, deficit irrigation scheduling, cultivars characters related to drought resistance and managing practices to improve crop water use efficiency.

Email: xyzhang@sjziam.ac.cn

Selecting traits to reduce seasonal yield variation of summer maize in the North China Plain

Due to the short growth duration of summer maize, which is planted after winter wheat harvest to form the annual double cropping system in the North China Plain (NCP), maize yield is significantly affected by weather conditions. Field results showed that seasonal yield variation was up to 47% of the average yield of the nine seasons. Grain kernel weight was the main yield component affecting annual yield variation under full irrigation. Further analysis showed that daily maximum temperature (Tmax), diurnal temperature range (DTR), and daily reference evapotranspiration (ET0) were each positively related to grain kernel weight from blister stage to maturity. Results from the cultivar tests showed that the yield difference among the cultivars was up to 35% of the average grain yield. Selecting cultivars with higher yield potential in each season could decrease the seasonal yield variation up to 32%. Cultivars with smaller leaf angle of upper leaves, higher final aboveground biomass, higher harvest index, and an earlier tasseling date would likely lead to more stable, higher yields for short season maize in the NCP.

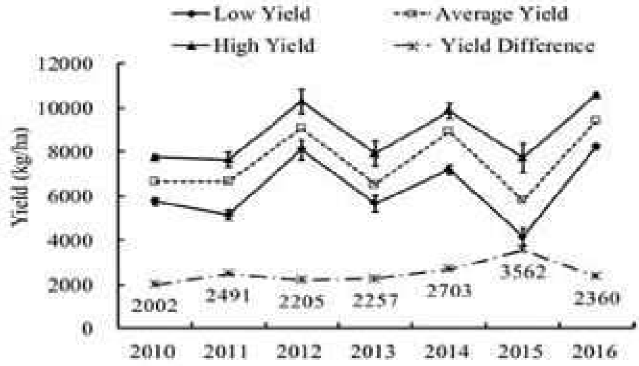

Figure: Changes in the average yield, high and low yield and yield difference among different cultivars for the 2010 to 2016 seasons.

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Rashid, M. A., Jabloun, M., Andersen, M. N., Zhang, X. and Olesen, J. E. (2019). Climate change is expected to increase yield and water use efficiency of wheat in the North China Plain. Agricultural Water Management 222: 193-203.

Rashid, M. A., Zhang, X., Andersen, M. N. and Olesen, J. E. (2019). Can mulching of maize straw complement deficit irrigation to improve water use efficiency and productivity of winter wheat in North China Plain? Agricultural Water Management 213: 1-11.

Fang, Q., Zhang, X. Y., Chen, S. Y., Shao, L. W., Sun, H. Y. and Yan, Z. Z. (2019). selecting traits to reduce seasonal yield variation of summer maize in the North China Plain. Agronomy Journal 111: 343-353.

Sun, H., Zhang, X., Liu, X., Liu, X., Shao, L., Chen, S., Wang, J. and Dong, X. (2019). Impact of different cropping systems and irrigation schedules on evapotranspiration, grain yield and groundwater level in the North China Plain. Agricultural Water Management 211: 202-209.

Ledgard, S. F., Wei, S., Wang, X., Falconer, S., Zhang, N., Zhang, X. and Ma, L. (2019). Nitrogen and carbon footprints of dairy farm systems in China and New Zealand, as influenced by productivity, feed sources and mitigations. Agricultural Water Management 213: 155-163.

Genetics and Breeding of Wheat Drought Resistance and Water Saving

Zhengbin Zhang, Principal Investigator, Ph.D. (1998, Northwest A&F University, China).

Research Interests: The cloning and function analysis of drought resistance and water ues efficiency related genes in wheat. The breeding of wheat drought resistance and water saving

Email: zzb@sjziam.ac.cn

Publications

- Elamin Hafiz Baillo, Roy Njoroge Kimotho, Zhengbin Zhang and Ping Xu (2019). Transcription Factors Associated with Abiotic and Biotic Stress Tolerance and Their Potential for Crops Improvement. Genes 10.771
- Roy Njoroge Kimotho, Elamin Hafiz Baillo and Zhengbin Zhang(2019). Transcription factors involved in abiotic stress responses in Maize (*Zea mays* L.) and their roles in enhanced productivity in the post genomics era. Peer J 9.8
- Lichao Zhai, Ping Xu, Zhengbin Zhang, Xiuling Jia, Lihua, Zhang, Ruizhi Xie, Shaokun, Li, Benhui Wei(2019). Improvements in grain yield and nitrogen use efficiency of summer maize by optimizing tillage practice and nitrogen application rate. Agronomy Journal 111(2).

Spatial-temporal distribution characteristic and interaction between agronomic traits of winter wheat and precipitation of growth period in Huang-Huai dryland

This article was to study the spatial-temporal distribution and interaction between agronomic traits of winter wheat and precipitation of growth period, and to provide a theoretical basis for variety improvement of winter wheat in Huang-Huai dryland under climate change.The data of agronomic traits and precipitation of the national regional trials of Huang-Huai dryland from 2010 to 2017 were used to analyze the spatial-temporal distribution and interaction by geographic methods and statistical methods. In terms of spatial distribution, the actual yield per unit area and 1000-kernel weight of winter wheat showed an increasing trend from west barren dryland to east fertile dryland. The plant height showed higher in the west barren dryland and lower in the middle and east fertile dryland. The total precipitation of different growth stages in the north of central and eastern Huang-Huai dryland was generally low, the south of central and eastern Huang-Huai dryland relatively high. In terms of time change, the total precipitation of germination to maturity period in the central and western dryland of Henan, Shanxi and Shaanxi showed a significant increasing trend. The total precipitation of germination to heading period was significantly positively correlated with actual yield, plant height, and number of effective ears. The results of path analysis showed that the plant height and the number of effective ears determined 53.2% of the actual yield variation in Huang-Huai fertile dryland, and the plant height and 1000-kernel weight determined 67% of the actual yield variation in Huang-Huai barren dryland. It was suggested that winter wheat breeding in Huang-Huai fertile dryland should increase plant height appropriately, improve the ability of efficient use of limited precipitation before flowering and increase ear development. Huang-Huai barren dryland breeding should stabilize plant height and improve the efficiency of transporting dry matter after flowering and harvest index.

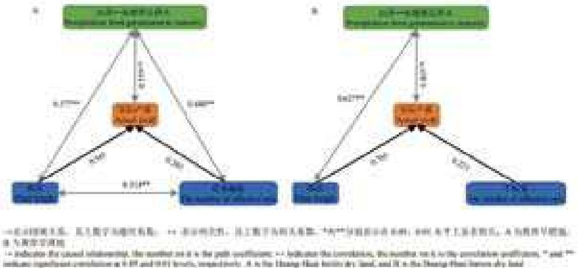

Figure: Relationship between agronomic traits of winter wheat and precipitation from germination to heading in Huang-Huai dry land.

Terrestrial Ecology and Plant Sciences

Feng Zhu, Principal Investigator, Ph.D. (2016, Wageningen University,the Netherlands). Postdoctoral fellow (2016-2018, Netherlands Institute of Ecology, the Netherlands).

Research Interests: Plant-mediated above- and below-ground species interactions: plant-soil feedback effects on aboveground plant-insect interactions; plant volatile-mediated species interactions up to the fourth trophic level; mechanisms of plant responses to biotic and abiotic stresses.

Email: zhufeng@sjziam.ac.cn

Foliar-feeding insects acquire microbiomes from the soil rather than the host plant

Microbiomes of soils and plants are linked, but how this affects microbiomes of aboveground herbivorous insects is unknown. We first generated plant- conditioned soils in field plots, then reared leaf-feeding caterpillars on dandelion grown in these soils, and then assessed whether the microbiomes of the caterpillars were attributed to the conditioned soil microbiomes or the dandelion microbiome. Microbiomes of caterpillars kept on intact plants differed from those of caterpillars fed detached leaves collected from plants growing in the same soil. Microbiomes of caterpillars reared on detached leaves were relatively simple and resembled leaf microbiomes, while those of caterpillars from intact plants were more diverse and resembled soil microbiomes. Plant-mediated changes in soil microbiomes were not reflected in the phytobiome but were detected in caterpillar microbiomes, however, only when kept on intact plants. Our results imply that insect microbiomes depend on soil microbiomes, and that effects of plants on soil microbiomes can be transmitted to aboveground insects feeding later on other plants.

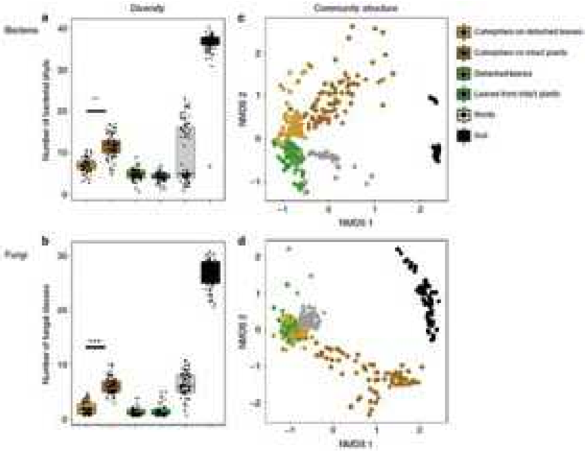

Figure: Diversity and community structure of bacteria and fungi in caterpillars, leaves, roots and soil. a,b) number of bacterial phyla and number of fungal classes of caterpillar, leaf, root and soil samples. c, d Non-metric multidimensional scaling (NMDS) of bacterial (c) and fungal (d) communities.

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Hannula, S. E., Zhu, F., Heinen, R. and Bezemer, T. M. (2019). Foliar-feeding insects acquire microbiomes from the soil rather than the host plant. Nature Communications 10: 1254.

Long, J. R. D., Heinen, R., Steinauer, K., Hannula, S. E., Huberty, M., Jongen, R., Vandenbrande, S., Wang, M., Zhu, F. and Bezemer, T. M. (2019). Taking plant–soil feedbacks to the field in a temperate grassland. Basic and Applied Ecology 40: 30-42.

Center for Core Facility & Advanced Technologies

Center for Core Facility & Advanced Technologies (CCFAT) were organized follow the principle that the center should prove technical service for the major project and tasks of the Country and the National Academy of Sciences, for the development of subjects and new layout ,for the development of the basic research capacity of the institute. CCFAT is currently composed of six specialized technical platforms (biological imaging analysis, lipidomic analysis, proteomics analysis, biological big data analysis, metabolomics analysis, plant hormone analysis), animal experiment center and isotope laboratory, which own the facilities and technologies that can strongly support genomics, proteomics, metabonomics, cell biology and mostly the whole life sciences research. There are 6 principle investigators, 4 senior engineers and 25 technicians work for CCAFT. In 2019, CCAFT has made further progress in technological innovation and development, technical services and support and technical training and communication.

The bio-imaging platform has plant CT imaging system, Structured Illumination Microscope, Two Photon Laser Scanning Fluorescence Microscope, Spinning Disk Confocal Microscope and Total Internal Reflection Microscope, Light Sheet, Laser Optical Tweezers, etc., with a total value of more than 25 million yuan. In 2019, the total service time of the biological image platform is 3769.5 hours, with a sharing rate of 66%. The bio-imaging platform has held 6 large-scale technical trainings, with a total number of 120 trainees, and received unanimous praise.

Table 1 Service Data of Bio-Imaging Platform in 2019

Name	Total Service Time (h)	Total Utilization Rate %	Sharing Rate %
SIM	394	22.1	67.0
LSM780	1378	77.7	86.9
SD-confocal	1997.5	112.0	44.1

In addition, the platform has developed a series of new imaging equipment and methods according to the needs of the Institute and customized instruments and use plans. 1) plant CT imaging system. Supported by the pre-research project of the national major research facility of crop phenotypic genomics (Shennong device), the plant CT imaging system (CropCT 1.0) independently developed by the platform has completed the installation and commissioning of the whole machine, entered the trial operation stage, and started to carry out relevant research on plant phenotypic genomics. 2) time delay imaging system. Due to the strong spontaneous fluorescence of plant samples, the acquisition of high-quality micro images of plant samples is seriously limited. In response to the practical needs of many research groups inside and outside the Institute, the bio-imaging platform has developed a delay imaging technology based on a new long-life nano fluorescence probe. After the laser excites the sample, it is delayed for a certain time, and after the short-lived spontaneous fluorescence signal is attenuated, the imaging of the target fluorescence can be performed by the gated ICCD, which can completely eliminate the interference of the spontaneous fluorescence. This technology will bring great help to plant sample imaging.

In 2019, the lipidomics platform has provided service for more than 20 research groups. The subjects of lipidomics tests include human, mouse, monkey, fruit fly, nematode, cave fish, rice, Arabidopsis, green pepper and many other species. In 2019, the service hours of the LC quadrupole linear ion trap tandem mass spectrometer was 5188.56 hours, the use efficiency was 249.45%, the total shared machine time was 3702.28 hours, and the sharing efficiency was 177.90%. The annual total time of the ion chromatography system is 1178.49 hours, the use efficiency is 56.66%, the annual shared time is 501.96 hours, and the sharing efficiency is 24.13%. The mass spectrometry pre-treatment system (bead mill / vacuum centrifuge / lyophilizer / ultracentrifuge) has a total time of 1441.73 hours, a use efficiency of 69.31%, a total shared machine time of 287.5 hours, and a sharing efficiency of 13.82%. The total time of the macro zoom microscope is 333.14 hours, the use efficiency is 16.02%, the total shared time is 76.04 hours, and the sharing efficiency is 3.66%. The total time of the seahorse is 331.4 hours, and the use efficiency is 15.93%. The TripleTOF 5600+ has an operating time of 681.33 hours and an operating efficiency of 32.76%. A total of 15 articles have been published in 2019.

The mission of biological big data analysis platform is to provide training and technical support to satisfy the needs of IGDB on bioinformatic data analysis. It aims to improve bioinformatic skills of all researchers and support the key researches of the institution through training services and project collaboration. To keep track of the new technology, a

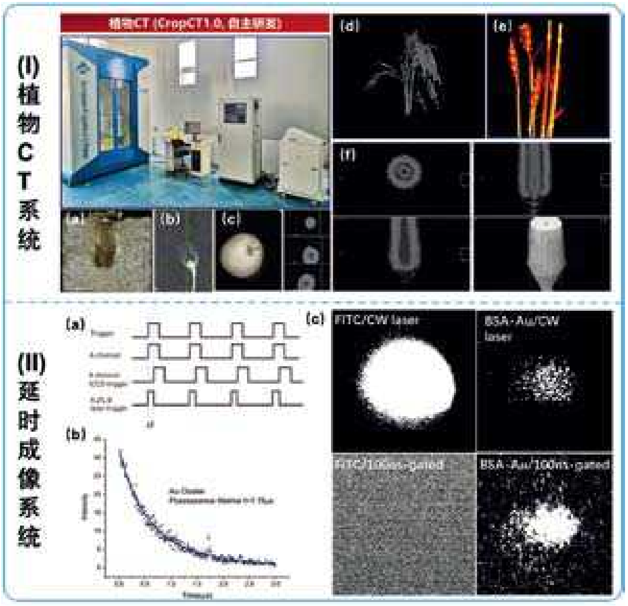

Figure 1. (I) Plant CT Imaging System and Its Typical Application. a) Root of rice in soil; b) Rose; c) Pear; d) Rice; e) Wheat; f) Corn. (II) Time-Delay Imaging System Based on Long-Lived Nanoprobes. a) time-delay imaging trigger signal setting; b) the lifetime of gold nanocluster measured by delay imaging system is about 1.15 µs; c) the spontaneous fluorescence can be removed by using delay imaging system and long-life gold nanocluster. The trigger signal triggers the laser to excite the sample, and then triggers ICCD to collect the signal after 100 ns. The FITC signal with short fluorescence life has been attenuated, leaving only the probe signal with long lifetime.

series of technical lectures and meetings were held by the platform, including the 2nd academic conference on advanced biotechnology, GWAS principle and application. In addition, the platform collaborated with many groups and completed the assembly of several rice, wheat, sorghum, tomato soybean and lettuce genomes. In 2019, the platform constructed a rice sub-database of an integrated omics knowledgebase (MBKbase-rice, www.mbkbase.org/rice), which integrates rice germplasm information, >7000 population sequencing data, phenotypic data, known alleles and gene expression data. The database provides online tools for finding target germplasms by genotype or phenotype information, as well as for analyzing the user submitted SNP or sequence data to find important alleles in the germplasm. The data and tools integrated in MBKbase will promote research in crop functional genomics and molecular breeding. The author of MBKbase gave a lecture to help users of IGDB. In 2019, High performance computer cluster run 3,921,868 hours and accomplished 2,301,996 tasks. It is a component of Beijing regional center of life science instrument and provided service for 32 groups of IGDB and many other institutes of scientific research.

The metabolomics facility was established and developed in recent years with the continuous support of the State Key Laboratory of Plant Genomics, and formally joined the Core Facilities of IGDB in 2014. From its inception, the facility has been envisioned as a field-leading research platform for China, and the long term aim is to develop a global reputation for quality and innovation in metabolomics research. The metabolomics facility focuses on profiling large numbers of metabolites to gain a high resolution view of the biochemical phenotypes of living organisms. These quantitative and qualitative chemical data are highly valuable in research focused on gene validation, biomarker discovery, and the elucidation of uncharacterized metabolic pathways, as well as in studies searching for mechanistic insights about the regulation of metabolism. The staff of the facility currently includes 4 technical personne. The facility has provided analytical services for more than one hundred customers, from both inside and outside IGDB, and published more than 30 papers with co-authorship in high-level journals including Nature Plants, Genome Biology, and PNAS. In addition to providing analytical chemistry services, the facility is actively involved in many national-level research projects including the NSFC programs, the Strategic Priority Research Program A of CAS, and the 973 Program of the Ministry of Science and Technology.

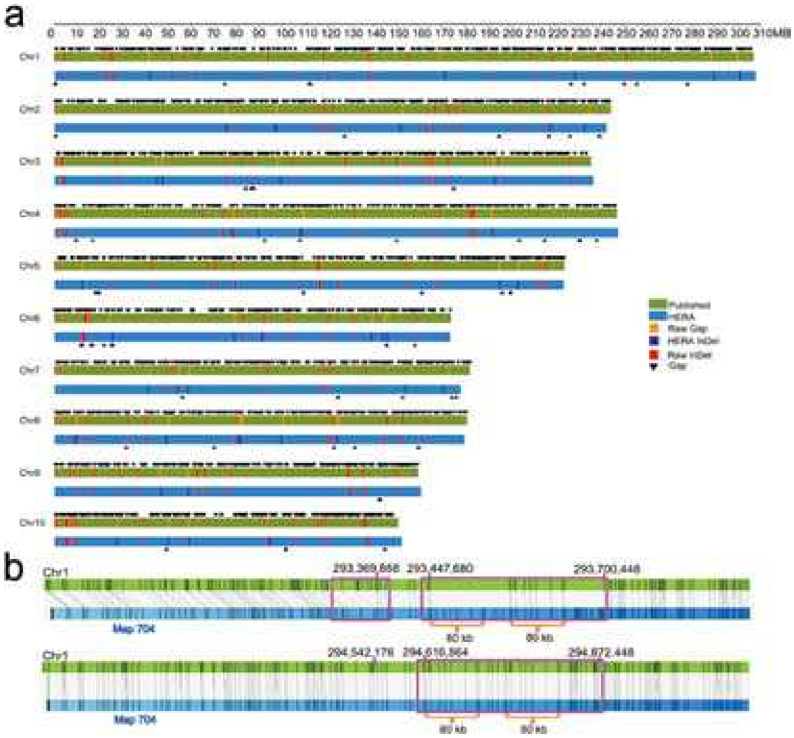

Figure.2 (a) comparison between Hera assembly genome and maize reference genome B73 refgen_v4. The number of sequence gaps in the whole genome has been reduced from 2523 to 76. (b) the missing or redundant sequences in the maize reference genome (above) were correctly filled or removed after Hera improvement (below).

Currently, the metabolomics facility has state-of-the-art mass spectrometry instruments and provides two kinds of metabolomics analytical services: untargeted analysis and targeted analysis. In 2019, total 8191analytical samples were tested, and 4 research articles and 4 collaborative papers were published from Core Facility for Metabolomics at IGDB.

The proteomics analysis platform has been equipped with the necessary hardware facilities for proteomic experiments, including the Thermofisher Orbitrap Fusion Lumos, the Thermofisher LTQ Orbitrap Elite and the AB Sciex TripleTOF 5600. Meanwhile, we also have supporting equipment for sample preparing and data analysis, including Waters e2695 HPLC, SpeedVac vacuum concentrators, and graphic workstation for mass spectrometry results search and analysis.

In 2019, we continuously improved the proteome analysis technology. By heating the temperature of the column, and increasing the inner diameter of the analytical column and the trap column, we prolong the service life of the analytical column without reducing the number of protein identification and the resolution of liquid chromatography, so as to reduce the operation cost of the platform. We also analyzed the proteome of dog's different brain regions at different development stages by TMT labeled quantitative proteome technology, and gets more than 7000 quantitative protein information, which provides an important resource for the research of brain development and mental disease mechanism of dogs.

During this year, we have provided proteomic analysis services for many research groups in our institute, as well as for many other institutions and universities, such as China Agricultural University, Zhejiang University, Academy of Agricultural Sciences, etc. Since 2019, the total operation time of the Orbitrap Fusion Lumos is 3191 hours, the service efficiency is 217%, the total sharing time is 2259 hours, and the sharing efficiency is up to 154%. The total operation time of the LTQ Orbitrap Elite is 4846 hours, the service efficiency is 330%, the total sharing time is 4092 hours, and the sharing efficiency is up to 279%. The total operation time of the combined high-resolution mass spectrometer is 3428 hours, the utilization efficiency is 233%, the annual sharing time is 2845 hours, and the sharing efficiency is 194%. The platform severed more than 1000 samples, and got about 1 million Yuan income in this year. In 2019, we and our collaborators published 8 articles in Nature Plant, Molecular Plant *etc*.

The Plant Hormone Platform is the first professional plant hormone analysis research platform established by the National Plant Genetic Research Center (Beijing). It is committed to developing high-efficient and comprehensive phytohormone analysis technology, providing reliable technical support for related research fields such as the mechanisms of hormone action and breeding by use of chemical means. The technical level of platform has been highly recognized by domestic and foreign botanists.

To meet various kinds of research needs, the platform has gradually established accurate quantitative analysis methods for various plant hormones based on their chemical property. Furthermore, a novel analysis technique was developed for simultaneously and accurately quantifying all kinds of plant hormones and their important metabolite, which includes indole acetic acid (IAA), cytokinins (CKs), ethylene, abscisic acid (ABA), jasmonic acid (JA), salicylic acid (SA), gibberellins (GAs), brassinosteroids (BRs), strigolactone (SL) and some plant peptide hormones. So far, the Plant Hormone Platform has several sets of mass spectrometer to provide shared services on the Chinese Academy of Sciences instrument and equipment sharing platform. Up to now, the instruments has been used for a total of 9470 hours in 2019, providing technical services to 35 research institutes. This year, platform received more than 2000 samples for phytohormon analysis, providing high-level technical services for domestic and foreign botanists. 13 co-author articles have been published at PNAS, Nature Plants, New Phytologist and other high-level magazines in 2019. Based on the development tenet of advancing with the times, the platform actively seek exchanges and cooperation with biologists to develop new analytical and screening technology systems for trace endogenous compounds with high physiological activity or aim to specific samples. During this year, plant hormone platform initially constructed a screening and identification system for plant endogenous small peptide, which provided convenience and technical support for researchers to explore new plant peptide hormones and stress resistance biomarkers. Above all, we anticipate to provide more comprehensive technical support for botanists.

Animal Facility can provide high-quality, multi-mode number of animals and standardized model rearing environment for the CAS system and other research institutions. Animal Facility have mice, rats, rabbits, guinea pigs reared foster care standard laboratory facilities, but also have zebrafish, Xenopus laevis standardized rearing experiment facilities. Animal Facility have a highly efficient operating mechanism and management system, with a number of experimental and technical personnel. Animal Facility provide animal experiments, embryo cryopreservation, embryo transfer technology, transgenic technology, antibody technology and other technical services. In the future, according to CAS and IGDB for the development of science and technology development needs, to build non-profit service system, improve infrastructure, support laboratory equipment, improve the experimental technique, offer a variety of advanced, shared experimental operation. Form a unique and operate efficiently, resource sharing research support system, provide basic conditions for research.

There are 810 m^2 of barrier environment facilities and 1676 m^2 of conventional environment facilities. Provide qualified animal breeding facilities, standardization of laboratory facilities, and standard laboratory animal. 859 m^2 of barrier environment facilities and 3006 m^2 of conventional environment facilities will be used after the renovation is completed in 2020. We have provided animals and animal foster care services for IGDB, Institute of Biophysics, Institute of Zoology, China Agriculture University, and so on. Provide antibody technology, embryo cryopreservation, embryo transfer technology for CAS, The Chinese Academy of Agricultural Sciences, Peking University, Tsinghua University and so on. We have a good breeding infrastructure and establish an effective mechanism for sharing service. This not only solves the scientific research of the demand for animal experiments, but also helps for close cooperation and mutual support and complements each other of the Institute of CAS. It became public resources and technical support system of Olympic Village Science Park Chinese Academy of Science, to achieve sharing of resources.

In 2019, Center for Core Facility & Advanced Technologies (CCFAT) provided more than 98,000 hours of machine service time, which has an increase of 51.0% over last year. CCFAT provided technical support and services for the publication of 53 papers of the Institute. A total of 15 technical lectures and training sessions were organized by the center, with nearly 1100 trainees. In Aug 2019, the Second IGDB frontier Biotechnology Academic Conference was successfully held by CCFAT. Holding the large-scale academic conferences not only improved the theoretical communication of the technical support staff of the institute, but also increased the influence of CCFAT. Moreover, CCFAT was rated as good in the Evaluation and assessment of open sharing of major scientific research infrastructure and large scientific research instruments in Central Universities and scientific research institutes, ranking has been greatly improved compared with the previous year.

State Key Laboratory of Plant Genomics

The State Key Laboratory of Plant Genomics was approved in 2003 by the Ministry of Science and Technology of China, and roots back to the Key Laboratory of Plant Biotechnology of the Chinese Academy of Sciences (CAS), founded in 1990. The Laboratory has passed the Nationwide Evaluation of State Key Laboratories (5-year-peroid), and ranked outstanding (Rank A) in 2006 and 2011, and excellent (Rank B) in 2016.

The Laboratory combines multidisciplinary approaches to address fundamental questions in plant growth and development, with an emphasis on dissecting the molecular mechanisms of complex agronomic traits of crops. A mission of the Laboratory is to extend knowledge from basic research to crop improvement. Using rice and *Arabidopsis* as model systems, main research fields of the Laboratory include, but not limited to, the structure and function of plant genomes, functional genomics of important agronomic traits, molecular mechanisms of plant signal transduction, plant-environment and plant-pathogen interactions, and molecular breeding.

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VICE DIRECTORS: Chengcai Chu, Wei Qian, Yonghong Wang

PRINCIPAL INVESTIGATORS: Yang Bai, Xiaofeng Cao, Mingsheng Chen, Shouyi Chen, Zhukuan Cheng, Chengcai Chu, Rongxiang Fang, Huishan Guo, Yantao Jia, Danhua Jiang, Yuling Jiao, Zhaosheng Kong, Chuanyou Li, Jiayang Li, Chengzhi Liang, Shaoyang Lin, Jun Liu, Dongping Lv, Wei Qian, Wenfeng Qian, Jinlong Qiu, Guodong Wang, Yonghong Wang, Guixian Xia, Qi Xie, Cao Xu, Yongsheng Yan, Shanguo Yao, Jian Ye, Jie Zhang, Jinsong Zhang, Lili Zhang, Jian-min Zhou, Yihua Zhou, Lihuang Zhu, Zhen Zhu, Jianru Zuo

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SCIENTIFIC ADVISORY BOARD: Shouyi Chen, Rongxiang Fang, Yaoguang Liu, Zhihong Xu, Yongbiao Xue, Qifa Zhang, Lihuang Zhu, Zhen Zhu

WEBSITE: http://http://plantgenomics.genetics.cas.cn/

MAJOR RESEARCH PROGRESSES

In 2019, scientists in the State Key Laboratory of Plant Genomics published 125 papers in *Science, Nat Biotechnol, Annu Rev Plant Biol, Trends Plant Sci, Genome Biol, Nat Commun, Nat Plants, Sci Adv, Genome Res, Mol Plant, Proc Natl Acad Sci USA, Plant Cell* and etc. 7 varieties of rice and sorghum have obtained national or provincial approvals, and 21 patents have been granted. In the past year, scientists in the Laboratory have made important advances in several research fields. In the area of plant genomics, Wenfeng Qian's group revealed a synchronized replication of genes encoding the same protein complex in fast-proliferating cells (Chen et al., *Genome Res*, 2019). The Qian group and collaborators founded that unbalanced protein complexes could reduce the proliferation rate of aneuploidy cells (Chen et al., *Cell Syst*, 2019). Xiaofeng Cao's group and Wenfeng Qian's group reported a new mechanism, in which translational efficiency of a gene can be regulated through the G-content-dependent PAB binding (Zhao et al., *Genome Biol*, 2019). Xiaofeng Cao's group and collaborators illustrated that DNA methylation is important in regulating histone demethylase REF6 targeting (Qiu et al., *Nat Commun*, 2019). The Cao group and collaborators also revealed a fine regulation mechanism of miR528 accumulation in rice (Yang et al., *Mol Plant*, 2019). The Cao group and collaborators reported a regulatory mechanism in transgenerational thermomemory in *Arabidopsis* (Liu et al., *Cell Res*, 2019). The Cao group and collaborators founded that H3K27me3 demethylase JMJ13 served as a temperature- and photoperiod-dependent flowering inhibitor (Zheng et al., *Nat Commun*, 2019). The Cao group and collaborators found that the JMJ16 protein of *Arabidopsis* was a H3K4-specific demethylase, and could negatively regulate leaf senescence (Liu et al., *Plant Cell*, 2019). Chengzhi Liang's group developed an innovative genome assembly method HERA which resolved repeats efficiently by constructing a connection graph from an overlap graph (Du and Liang, *Nat Commun*, 2019). The Liang group constructed the MBKbase, an integrated omics knowledge base for molecular breeding in rice (Peng et al., *Nucleic Acids Res*, 2019).

In the area of functional genomics, Jiayang Li's group reported a molecular explanation for the coordination between of plant height and tiller number in rice by GAs, SLR1 and MOC1 (Liao et al., *Nat Commun*, 2019), and established a new framework for the control of tiller bud formation and outgrowth (Shao et al., *Mol Plant*, 2019). Yonghong Wang's group and Jiayang Li's group jointly revealed a new mechanism of LA1 and OsBRXL4 regulation of rice tiller angle (Li et al., *Mol Plant*, 2019). Chengcai Chu's group and collaborators revealed a mechanism underlying nitrate activation of both phosphate and nitrate utilization in rice (Hu et al., *Nat Plants*, 2019). Zhukuan Cheng's group confirmed that the ultimate bipolar spindle in meiosis was transformed from the multipolar spindle (Xue et al., *Proc Natl Acad Sci USA*, 2019). Yihua Zhou's group identified a novel polysaccharide acetylase, DARX1, which helps us to understand cell wall structure (Zhang et al., *Plant Cell*, 2019). Zhaosheng Kong's group and collaborators found that cotton fibers elongate via a unique tip-biased diffuse growth mode by live-cell imaging (Yu et al., *Nat Plants*, 2019). Qi Xie's group and collaborators showed that sorghum gene *Tannin1* controled bird feeding behavior by modulating the biosynthesis of polyphenols and fatty acid-derived volatiles (Xie et al., *Mol Plant*, 2019).

In the area of plant signal transduction, Guodong Wang's group identified a P450 enzyme responsible for gibberellin 13-hydroxylation (He et al., *Nat Plants*, 2019). Jiayang Li's group elucidated the direct regulatory relationship between strigolactone and cytokinin in rice (Duan et al., *Proc Natl Acad Sci USA*, 2019). Chuanyou Li's group elucidated a transcriptional regulatory role of MYC2 in the jasmonic acid signaling pathway (You et al., *Plant Cell*, 2019). The same group and collaborators showed that the MYC2-MED25 functional complex could terminate the jasmonic acid signaling (Liu et al., *Plant Cell*, 2019). They and collaborators identified enhancers of jasmonic acid signaling pathway (Wang et al., *Nat Plants*, 2019). The Li group and collaborators revealed a molecular mechanism of anthocyanin accumulation in tomato flesh in response to light (Sun et al., *Mol Plant*, 2019). Yuling Jiao's group reported a domain-specific gene expression map of *Arabidopsis* shoot domains (Tian et al., *Nat Commun*, 2019).

In the area of plant-environment and plant-pathogen interactions, Yang Bai's group and Chengcai Chu's group revealed a role of the microbiome in the utilization efficiency of nitrogen in rice (Zhang et al., *Nat Biotechnol*, 2019). Yang Bai's group and collaborators analyzed the function and mechanism of triterpenoids in regulating root microbiome of *Arabidopsis* (Huang et al., *Science*, 2019). Jian-min Zhou's group and collaborators reconstituted the resistosome ZAR1 complex and clarified its biochemical functions, providing a structural template for understanding plant NLRs, which was a major milestone in plant immunity research (Wang et al., *Science*, 2019a; 2019b). Huishan Guo's group revealed a molecular mechanism of chitin oligomer deacetylation, which increases virulence in soil-borne fungal pathogens (Gao et al., *Nat Plants*, 2019). Jian Ye's group revealed that virus *Begomovirus* could affect the interaction between plants and vector insects and non-vector insects by infecting plants (Zhao et al, *Sci Adv*, 2019). Jun Liu's group demonstrated the mechanism that a chitinase MoChia1 secreted by *Magnaporthe oryzae* activated the immune response of rice (Yang et al., *Plant Cell*, 2019). Guixian Xia's group found that the cotton apoplastic protein CRR1 stabilized chitinase 28 to facilitate defense against the fungal pathogen *Verticillium dahlia* (Han et al., *Plant Cell*, 2019).

In the area of plant biotechnology and molecular breeding, Jinlong Qiu's groups showed that Cas9-mediated editing was more efficient in open chromatin regions than in closed chromatin regions in rice (Liu et al., *Genome Biol*, 2019). Chengcai Chu's group and collaborators identified a dominant precocious promoting gene *EF-cd* and revealed its mechanism in rice precocious and high yield (Fang et al., *Proc Natl Acad Sci USA*, 2019). Jiayang Li's team has released a rice elite variety Zhongkefa 928. The Li team and collaborators have also released rice varieties Zhonglonggeng 100, Qianxiangyou 220, Quanyou 220, and Jiaheyou 5. Qi Xie's team has bred sweet sorghum varieties Zhongketian 048, and Zhongketian 060. All these varieties have obtained national or provincial approvals in 2019.

To recognize the contributions in their research fields, Profs. Xiaofeng Cao, Jiayang Li, Yang Bai, Huishan Guo, Yuling Jiao, Qi Xie, Chuanyou Li, Zhaosheng Kong, Jian-min Zhou Jianru Zuo have been invited to write review papers, spotlight papers or commentaries for *Annul Rev Plant Biol, Plant Cell, Curr Opin Microbiol, Curr Opin Genet Dev, Mol Plant, Trends Plant Sci, J Exp Bot, Philos T R Soc B*, and *J Integr Plant Biol.*

AWARDS AND RECOGNITIONS

In the past year, Zhaosheng Kong was awarded the National Science Fund for Distinguished Young Scholars. Bin Hu, Wenfeng Qian, Baocai Zhang and Jie Zhang were selected by the Outstanding Youth Science Foundation. Bing Wang was elected to the CAS Youth Innovation Promotion Association. Jiayang Li was elected a vice president of the China Science Center of International Eurasian Academy of Sciences (IEAS), and awarded the Lifetime Contribution Award by the Chinese Society for Cell Biology. Xiaofeng Cao was elected an IEAS Academician, and awarded the 2019 Outstanding Achievement Award by the Chinese Society for Plant Biology (CSPB). Yuling Jiao received a 2019 Outstanding Young Scientist Award by CSPB. Jiayang Li, Jian-min Zhou and Chengcai Chu were recognized as Highly-Cited Researchers in 2019 by Clarivate Analytics. Naiqin Zhong's team was awarded the CAS Science and Technology Promotion and Development Prize.

State Key Laboratory of Plant Cell and Chromosome Engineering

The State Key Laboratory of Plant Cell and Chromosome Engineering (PCCE) was founded in 1989. The mission of PCCE is to conduct plant genetic and breeding research in the major crops, with emphases on studying the molecular mechanisms underlying important agronomic traits and the development of new crop varieties. PCCE aims to systematically dissect genetic basis of important agronomic traits of major crops and identify gene function underlying the control of plant growth and development, and adaption to environmental changes. It also aims to develop efficient key gene pyramiding technologies, such as genome editing and molecular design breeding, to facilitate elite genes or alleles assembling for crop breeding of elite varieties. In order to broaden the genetic basis of wheat germplasm, PCCE also create novel germplasms that with excellent agronomic traits including high yield, superior quality, high nutrient efficiency or improved tolerance to biotic and abiotic stresses through chromosome engineering.

DIRECTOR: Xiangdong Fu
VICE DIRECTORS: Fangpu Han, Caixia Gao, Zhixi Tian
PRINCIPAL INVESTIGATORS: Huabang Chen, Xiangdong Fu, Caixia Gao, Fangpu Han, Zanmin Hu, Junming Li, Yunhai Li, Zhensheng Li, Hongqing Ling, Cuimin Liu, Xigang Liu, Zhiyong Liu, Fei Lu, Qianhua Shen, Zhixi Tian, Yiping Tong, Daowen Wang, Jun Xiao, Yongbiao Xue, Aimin Zhang, Xiangqi Zhang, Baoge Zhu
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ADVISORY COMMITTEE: Rongxiang Fang, Tingyun Kuang, Zhensheng Li

WEBSITE: http://pcce.genetics.cas.cn

MAJOR RESEARCH PROGRESSES

In 2019, PCCE scientists have published 39 scientific papers in peer-reviewed academic journals, including *Science, Nature Protocols, Nature Plants, Plant Cell* etc. PCCE scientists got 18 authorized patterns, and 4 protection of new varieties of plants. PCCE got 3 new crop variety approvals, including corn cultivar “Keyu 153” and “Keyu 175”(approval of national variety committee), wheat cultivar “Keyi 6259” (approval of local variety committee). PCCE scientists have made several important progresses in the research on genetic basis of complex agronomic traits, new genome-editing techniques and improvements of nitrogen use efficiency, etc. The representative achievements are as follows:

Analysis of Genetic Control Network of Important Agronomic Traits: Xiangdong Fu’s lab obtained the *NAL1* gene by QTL analysis and map-based cloning. Pyramiding of the *dep1-1* and *NAL1*^{NJ6} alleles achieves sustainable improvements in nitrogen-use efficiency and grain yield in japonica rice breeding (Xu et al. *J Genet Genomics*, 2019). NGR5 was cloned and characterized and the expression level and protein level of NGR5 were induced by nitrogen. NGR5 can interact with the subunit LC2 of PRC2 complex to regulate the growth and the nitrogen utilization efficiency. Yiping Tong’s Lab constructed the gene regulatory network of TaNAC2, and identified that the TaNAC2-NRT2.5 module has a key role in regulating grain nitrate accumulation and seed vigour (Li et al., *New Phytol*, 2019); Another project uncovered that TabZIP60 and TaNADH-GOGAT interaction plays important roles in mediating N use and wheat growth, and these data provided valuable information for engineering N use efficiency and yield in wheat (Yang et al., *Plant Biotechnol J*, 2019). HongQing Ling’s lab summarized the regulation mechanisms of FIT and its binding proteins in the plant iron absorption (Wu et al, *Front Plant Sci*, 2019). Aimin Zhang’s Lab completed the fine mapping and genetic effect analysis of Rht12, an important dwarf gene in wheat (Sun et al., *Plant J*, 2019); Another project unraveled the genetic architecture of grain size in einkorn wheat through linkage and homology mapping and transcriptomic profiling (Yu et al., *J Exp Bot*, 2019). Yunhai Li’s lab was invited to make a systematic review on the mechanisms controlling plant seed size. This review summarizes several signaling pathways that control seed size through maternal tissues, including or involving the ubiquitin-proteasome pathway, G-protein signaling (Xu et al., *J Integr Plant Biol*, 2019), mitogen-activated protein kinase (MAPK) signaling, phytohormone perception and homeostasis, and some ranscriptional regulators. Meanwhile, growth of the zygotic tissues is regulated in part by the HAIKU (IKU) pathway and phytohormones (Li et al., *Annu Rev Plant Biol*, 2019); Meanwhile, they showed that the Mediator complex subunit MED16 acts as a negative regulator of endoreduplication to influence cell growth, and MED16 was partially dependent on *CCS52A1/A2* to control endoreduplication and cell growth in Arabidopsis (Liu et al., *Plant Cell*, 2019). Qian-Hua Shen's lab investigated the functions of multiple CSEPs of *Blumeria graminis f. sp. hordei* and analyzed the variation of the *Pm60* locus in *Triticum urartu* accesstions. Two molecular markers were developed for screening functional Pm60 alleles that can confer disease resistance to *Blumeria graminis f.sp. tritici* E09 (Zhao et al., *Crop J*, 2019). Zhiyong Liu's lab cloned a powdery mildew resistance gene *Pm24* which encoded a tandem kinase protein WTK3 with putative kinase-pseudokinase domains. Haplotype analysis and transgenic assay revealed that a rare 6-bp natural deletion of lysine-glycine codons is critical for the gain of powdery mildew resistance function. Zhensheng Li's lab carried out an RNA-Seq analysis of different varieties subjected to salt and control treatments and suggested that PUFAs could contribute to salt tolerance in common wheat by enhancing the photosynthetic system and JA-related pathways (Luo et al., *Crop J*, 2019). Zhixi Tian's Lab updated soybean Zhonghuang 13 genome to a golden reference (Shen et al., *Sci China Life Sci*, 2019). The decrease of gene expression diversity during domestication of animals and plants was revealed at the genome-wide level (Liu et al., *BMC Evol Biol*, 2019); Participated in writing the review of the genomics of *Oryza* species provides insights into rice domestication and heterosis.

Genome Editing and Precision Plant Breeding : Caixia Gao's Lab used whole-genome sequencing to analyze specificity for base editors, including BE3, high-fidelity BE3 (HF1-BE3) and ABE, and found that BE3 and HF1-BE3, but not ABE, induced substantial unpredictable genome-wide off-target mutations in rice plant (Jin et al., *Science*, 2019). In addition, they used the base editing technology to modify the wheat acetolactate synthase gene ALS and acetyl-coenzyme A carboxylase genes ACC, and generated transgene-free wheat germplasms bearing herbicide tolerance mutations, which would facilitate better weed control (Zhang et al., *Nat Plants*, 2019). Furthermore, they developed a protocol for manipulating gene translation efficiency in plants by editing uORF, and this method can achieve fine-tuning of gene translation in transgene-free derivatives, which accelerates the analysis of gene function and the improvement of crops (Si et al., *Nat Protoc*, 2019).

Plant Chromosome Engineering and Breeding: Fangpu Han's Lab identified two functional centromeric satellites that are abundant in the wheat subgenomes,and highlighted role of rearrangement of centromere organization in asymmetry found in polyploid wheat, which may function in homologous chromosome pairing during meiosis, ultimately leading to speciation (Su et al., *Plant Cell*, 2019). Another project characterized the deposition of CENH3 in maize by over-expression and mutational analysis (Feng et al., *Plant J*, 2019). Daowen Wang's lab carried out a RNAi cassette for suppressing lipoxygenase (LOX) gene expression in wheat grains using a double right border T-DNA vector via Agrobacterium-mediated transformation, and developed marker-free and transgene insertion site-defined transgenic wheat with improved grain storability and fatty acid content (Cao et al., *Plant Biotechnol J*, 2019). Huabang Chen's Lab bred maize varieties 'Keyu 153' (National Reg. 20190298) and 'Keyu 175' (National Reg. 20190097). 'Keyu 153' is authorized Plant Variety Protection right (CNA20181994.2). Aimin Zhang's Lab bred wheat varieties 'Keyi 6259' which approval of Hebei province. Baoge Zhu's Lab selected soybean variety Kedou 13 with wide adaptability and high yield and soybean variety Kedou 10 with high quality and high yield, and is participating in the national regional test.

State Key Laboratory of Molecular Developmental Biology

The State Key Laboratory of Molecular Developmental Biology is hosted in the Institute of Genetics and Developmental Biology. Our mission is: 1) to address fundamental questions in development of both plants and animals using model organisms such as *C. elegans*, *Drosophila*, *Xenopus*, zebrafish, mouse, monkey, *Arabidopsis* and rice; and 2) to develop innovative technology to meet national needs in agriculture and human health.

DIRECTOR: Weicai Yang
VICE DIRECTORS: Xun Huang, Fan Chen, Zhiheng Xu
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MEMBERS: Shumin Duan, Xiang Gao, Jiayang Li, Peng Li, Wei Li, Lingfei Luo, Weihua Wu, Weicai Yang, Xu Zhang, Zuoyan Zhu

SCIENTIFIC ADVISORY COMMITTEE: Aike Guo, Naihe Jing, Yixun Liu, Zhihong Xu

WEBSITE: http://mdb.genetics.ac.cn

In 2019, the laboratory published 89 papers. Eleven eminent scientists spoke at the FORUM on DEVELOPMENT, GENETICS, and DISEASE. During 2019, the laboratory achieved significant advances in the following fields:

Cell Differentiation and Organ Formation: RNA poly (a) tail is an essential component of mature mRNA and lncRNA, important for RNA stability and translation regulation. Dr. Falong Lu's lab established a new accurate and sensitive method to analyze RNA poly (A) tails. This method is able to read the full-length RNA isoforms with the entire poly (A) tail sequences using the PacBio sequencing platform. They found more than 17% of the mRNAs harbor non-A (U, G and C) residues within the body of poly (A) tails in mouse GV oocytes, besides those known non-A residues at the 3' ends. These findings along with the PAIso-seq method may open the door to a new layer of RNA post-transcriptional regulations (Liu et al., *Nat Commun*, 2019). Little is known about the function of histone arginine methylation in acute lymphoblastic leukemia (ALL). Dr. Shilai Bao's group and Dr. Huyong Zheng's lab of Beijing Children's Hospital found that enhanced protein arginine methyltransferase 5 (PRMT5) promotes pediatric B-cell precursor acute lymphoblastic leukemia (BCP-ALL) leukemogenesis partially by the dysregulation of B-cell lineage differentiation. The symmetric dimethylation of H4R3 (H4R3sme2) and PRMT5 may serve as potential sensitive biomarkers of pediatric BCP-ALL. Suppression of the activation of PRMT5 may offer a promising therapeutic strategy against pediatric BCP-ALL (Mei et al., *Clin Cancer Res*, 2019). Dr. Yuqiang Jiang's group developed an efficient *in vivo* photodynamic therapy system based on a nanomaterial, dihydrolipoic acid-coated gold nanocluster (AuNC@DHLA), that combined the advantages of large penetration depth in tissue, extremely high twophoton (TP) absorption cross-section (σ2~106 GM), efficient ROS generation, a Type I photochemical mechanism, and negligible *in vivo* toxicity. This system has very important clinical application value (Han et al., *ACS Nano*, 2019). Dr. Weicai Yang's group discovered that that BICE1 interacts with MCM4 and MCM7 of the pre-replication complex and suggested that BICE1 plays a role in modulating DNA replication via interaction with MCM4 and MCM7 (Long et al., *New Phytol*, 2019). Trimeric intracellular cation (TRIC) channels are thought to provide counter-ion currents that facilitate the active release of Ca^{2+} from intracellular stores. Dr. Yuhang Chen's lab described high-resolution crystal structures of vertebrate TRIC-A and TRIC-B channels, both in Ca^{2+}-bound and Ca^{2+}-free states, and found the TRIC channels are symmetric trimers with diacylglycerol as a regulatory factor at interprotomer interfaces (Wang et al., *PNAS*, 2019).

Neurodevelopment and Regeneration: Adult neurogenesis exhibits distinct characteristics from the embryonic counterpart. However, the intrinsic mechanism underlying the differential regulation of neurogenesis between these two stages remains unclear. Dr. Weixiang Guo's lab found that RNA-binding protein HuR is predominantly expressed in the cytoplasm of embryonic neural stem cells (NSCs) but translocates into the nucleus of adult NSCs. Transcriptomic analysis of HuR-deficient adult NSCs revealed that HuR primarily regulates alternative splicing of numerous premRNA transcripts, including focal adhesion kinase (FAK). These findings provide mechanistic insights into the differential regulation of embryonic and adult neurogenesis through developmental cytoplasmicto-nuclear translocation of HuR (Wang et al., *Cell Rep*, 2019). Dr. Zhuo Du's group discovered that the variability of cell position during *C. elegans* embryogenesis is highly deterministic and temporally dynamic, regulated by intrinsic and extrinsic mechanisms. Fate specification and cell-cell junctions contribute to the reduction of variability. These results provide insight into systems properties and spatiotemporal control of cellular variability during development (Li et al., *Cell Rep*, 2019). Coronary arteries occlusion results in ischemic myocardial tissue and progressively negative ventricular remodeling. At or after the initial period of myocardial infarction (MI), matrix metalloproteinases (MMPs) are upregulated and cause degradation of the extracellular matrix (ECM) and further decrease of tissue mechanical properties, which contributes to progressive thinning and global dilatation of the ventricular wall in the infarcted area, leading to a deterioration in cardiac function. Dr. Jianwu Dai's group developed a dual-function MI-responsive on-demand growth factor delivery system to promote angiogenesis and inhibit cardiac remodeling by targeting the upregulated MMP-2/9 after MI. The new system increases the local protein concentration and reduces unnecessary diffusion, which resultes in significantly improved cardiac function, increased vascularization, and ameliorates adverse myocardial remodeling (Fan et al., *Adv Mater*, 2019).

Tissue Metabolism and Aging: Comprehensive assessment of serum lipidomic aberrations before type 2 diabetes (T2DM) onset has remained lacking in Han Chinese. Dr. Guanghou Shui's lab evaluated changes in lipid coregulation antecedent to T2DM and identified novel lipid predictors for T2DM in individuals with normal glucose regulation (NGR). Through the analysis large amounts of data, they further improved prediction of incident diabetes over conventional clinical indices (Lu et al., *Diabetes Care*, 2019). The gut microbiome has been shown to have diverse impacts on human and animal physiology and health. During cold exposure it is well established that animals maintain their body temperature by activating heat production from a specialized tissue known as Brown Adipose Tissue (BAT) and promoting "browning" of white adipose tissue. Dr. John Speakman's lab used different antibiotic recipes to eradicate gut microbiota. They subsequently found that animals lacking gut microbiota had impaired thermoregulation. Therefore, the results reveal that the function of gut microbiota plays an important role in the activation of BAT (Li et al., *Cell Rep*, 2019)

Luancheng National Station of Agricultural Ecosystem, China National Ecosystem Observation and Research Network

Luancheng station, established in 1981, is one of the field stations of the Chinese Ecosystem Research Network (CERN) and a member of Global Terrestrial Observation System (GTOS). The station is also a demonstration base for modern agricultural technologies in Hebei province. In 2005, the station became one of the stations of the Chinese National Ecosystem Observation and Research Network (CNERN). In 2016, the station joined the International Long TERM Ecological Research Network (ILTER).

The primary goals of the station are to implement long-term comprehensive observations on the structure, function, and evolvement of the agro-ecosystem; to clarify the mechanisms of the energy, water, and nutrient transfer processes of the farmland ecosystem and the theoretical basis for interface regulation; and to study the structural functions of the integrated system of agro-ecology and economy.

DIRECTOR: Yanjun Shen
VICE DIRECTOR: Yisong Cheng
PRINCIPAL INVESTIGATOR: Chunsheng Hu, Xiying Zhang, Yanjun Shen, Mengyu Liu, Junming Li, Diaoguo An, Zhenngbin Zhang, Lin Ma, Shiqin Wang, Xigang Liu, Binbin Liu, Xiaofang Li, Feng Zhu, Xiuwei Liu, Hongyong Sun, Baodi Dong
SECRETARY: Yisong Cheng

COMMITTEE OF SCIENCE
DIRECTOR: Mingan Shao
COMMISSARY: Fusuo Zhang, Keling Wang, Ganlin Zhang, Chunming Liu, Chunsheng Hu, Xiying Zhang, Yi Luo, Yanjun Shen

Main outputs in 2019

1) Totally, up to 88 papers were published in 2019, of which 70 were on the SCI indexed journals.

2) Ten patents were granted in 2019, of which two were invention patents. And thirteen patents, including four inventive, have been applied for certification.

Main progresses in 2019

1) The results suggest that biochar addition can suppress the production of N_2O in soil and simultaneously stimulate the reduction of N_2O to N_2. Further studies are needed to elucidate the regulatory effects of biochar in soil.

2) It studies and analyzes the possibility that China's animal husbandry policy may increase the risk of animal husbandry pollution in the northern region, and puts forward the theoretical thinking and policy suggestions for the future pig and the spatial optimization layout of animal husbandry in China.

3) Taking the different types of farmland thick aeration zone in the deep buried area of groundwater in North China Plain as the research object, the water movement rate, salt accumulation and leaching characteristics of the deep aeration zone are estimated, the potential impact of different agricultural land use types on the shallow groundwater quality is analyzed, and the lag time of groundwater vertical supply (water quantity and water quality) under the condition of groundwater level decline is evaluated From the process point of view, the mechanism of agricultural land use type on groundwater quantity and quality was revealed.

4) The research results of Luancheng station from 2008 to 2016 show that the annual variation of summer maize yield is as high as 47%, and the grain weight under full irrigation is the most important factor affecting the annual variation of summer maize yield.

5) Through characterization of the bacterial and fungal microbiomes from the rhizosphere and roots of wheat (*Triticum aestivum* L.) at the three growth stages and under four levels of long-term N fertilization treatments, the researchers found that both plant growth status and N input drive the changes in the microbial community structure in the root zone of wheat. The plant growth stage showed a stronger effect on bacterial communities than that on fungal communities.

6) Based on the data of the agronomic characters and precipitation of the national Huang Huai Winter Wheat Regional test control varieties in different regional test sites from 2010 to 2017, the relationship between the agronomic characters and the total precipitation from seedling to maturity of the dry land winter wheat in Huang Huai was analyzed.

Key Laboratory of Agricultural Water Resources, Chinese Academy of Sciences
Hebei Key Laboratiory for Water-Saving Agriculture

Heibei Key Laboratory for Water-saving Agriculture was founded in 2005 by the Science and Technology Department of Hebei Province. Based on this laboratory, Key Laboratory of Agricultural Water Resources of Chinese Academy of Science was established in 2008.

The laboratory focus on improving agricultural water use efficiency in individual, field and regional levels, guarantying food security in North China, achieving sustainable development of agriculture, carrying on theoretical and technological innovation of high efficient use on agricultural water resources, providing theoretical and technical support for regional shortage of agricultural water resources.

DIRECTOR: Yanjun Shen
VICE DIRECTOR: Xiying Zhang, Shiqin Wang
PRINCIPAL INVESTigators: Diaoguo An, Jiansheng Cao, Chunsheng Hu, Xiaofang Li, Binbin Liu, Jintong Liu, Mengyu Liu, Xiaojing Liu, Lin Ma, Shenyan Jun, Shenyan Jun, Shiqin Wang, Yonghui Yang, Wanjun Zhang, Xiying Zhang, Zhengbin Zhang, Zhu Feng, Xiuwei Liu
SECRETARY: Yukun Hu

SCIENTIFIC ADVISORY COMMITTEE:
STRATEGIC COMMITTEE: Changming Liu, Guihai Wang, Zhensheng Li, Lun Shan, Junliang Tian
DIRECTOR: Dahe Qin
VICE DIRECTOR: Bojie Fu, Chunsheng Hu
MEMBERS: Shaozhong Kang, Jun Xia, Fengchang Wu, Wenjun Ding, Xiaoyan Li, Xurong Mei, Jianhua Wang, Yanfen Wang, Yonghui Yang, Huijun Wang, Zhaoji Zhang, Zhenghui Xie

WEBSITE: http://lawr.sjziam.ac.CN:8085/

MAIN RESEARCH PROGRESSES:

Substantial progresses in several aspects have been achieved by the key laboratory in 2019: The Academic Committee conference and annual conference were held in 2019 by the key laboratory. Hydro geochemistry test platform for vadose zone work smoothly and a subsurface drip system was finished in Luancheng Station. One "outstanding science and technology achievement prize of CAS "and one "agricultural water saving technology award" were won by the key Lab., and 50 SCI papers were published in this year.

Crop physiological and genetic basis for high efficient water use: Professor Dong Baodi's group studied photosynthetic base of reduced grain yield by shading stress during the early reproductive stage of two wheat cultivars, the results showed that the grain yield extensively decreased as the shading intensity and duration increased. This study supplements the research on the effects of shading intensity and duration on winter wheat during their young microspore stage, but it also provides technical support to the efficient utilization of resources. Liu Xiuwei's group analysis he productivity and leaf wax n-alkane concentration in a series of five winter wheat cultivars over the last 60 years, Plant wax n-alkanes are a major constituent of the leaf and grain surface. In this study indicate that increased ΣalkL has been indirectly selected in breeding efforts to improve crop production in winter wheat, suggesting that greater leaf waxiness confers advantages for crop growth. Zhang Xiying's group selected traits to reduce seasonal yield variation of summer maize, the results showed than cultivars with smaller leaf angle of upper leaves, higher final aboveground biomass, higher harvest index, and an earlier tasseling date would likely lead to more stable, higher yields for short season maize in the NCP. Professor Zhang studied the spatial-temporal distribution and interaction between agronomic traits of winter wheat and precipitation of growth period, and to provide a theoretical basis for variety improvement of winter wheat in Huang-Huai dryland under climate change.

Hydrological Process in farmland: Professor Liu Mengyu and his collaborators analyzed the effects of ridge and film mulching cultivation models on dry land wheat growth, water use and dynamic changes of soil water, heat, and salt. This study find that ridge-cropped and mulched wheat increased average yields by 12.44% and 6.04% compared with traditional flat-cropped wheat and this technology can effectively increase winter wheat yield and increase water use efficiency of winter wheat. Shen Yanjun's group using Lysimeter experiments under different irrigation treatments (flood, surface drip, and subsurface drip) to account for ET in the selection of a suitable irrigation method. Results showed that subsurface drip irrigation reduced ET by 26% compared to flood irrigation, and 15% compared to surface drip irrigation, with significant grain yield and biomass formation due to decreased evaporation losses. Grain yield, yield components, and above ground biomass were similar in subsurface drip and flood irrigation. Wang Shiqin's group studied deep soil cores down to 11 m at three long-term N-fertilizer application treatments under a wheat-maize cropping system in the Piedmont Plain area and two land-uses in the headwater regions of the North China Plain. The results provided critical information for water and N fertilizer management practices in the agricultural fields in the future.

Optimal allocation of regional agricultural water resources: Professor Yonghui Yang' s group evaluated the potentials of cropping adjustment for groundwater conservation and food production in the piedmont region of the North China Plain using the DSSAT crop model and a regression model. The results indicate that irrigation water requirement needs to be limited to a maximum level of 187 mm/a or leaving 34% of the cropland fallow to sustain groundwater at the present level, and if an extra amount of water of 0.2 or 0.5 billion m3 is supplied as a result of the SNWT Project, the percentage of cropland which should be left fallow can decrease to 25% or 11% respectively. Shen Yanjun's group studied the response of vegetation coverage change to meteorological drought at different time scales in Beijing-Tianjin Sandstorm Source Region based on NDVI and SPEI from 2000 to 2017. This research showed the negative influence of drought in grassland was most serious, followed by shrub, farmland and forest. Cao Jiansheng's group advanced in research on the effects of micro-topography changes on surface hydrological processes and discuss the effects of micro-topography on overland flow, rainfall-infiltration, evapotranspiration, soil water transport, and feedback in SPAC systems. This studied provided a theoretical basis for regional water resource regulation.

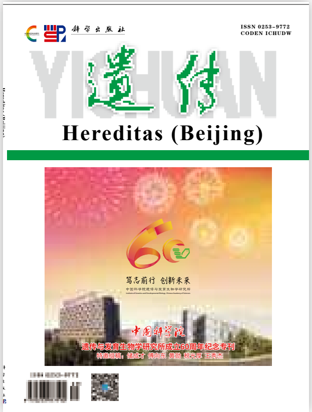
Journal of Genetics and Genomics

Journal of Genetics and Genomics (JGG, formerly known as *Acta Genetica Sinica*, founded in 1974) is sponsored by both Institute of Genetics and Developmental Biology of Chinese Academy of Sciences and Genetics Society of China, and jointly published by Elsevier Ltd. and Science Press. Its current Editor-in-Chief is Prof. Yongbiao Xue. JGG is currently indexed by Science Citation Index Expanded (SCI-E), PubMed, Scopus, etc. The JCR impact factor of JGG in 2018 is 4.650 and ranked 31 among all 174 journals indexed by SCI in the field of genetics.

JGG publishes peer-reviewed articles of novel and significant discoveries in molecular genetics, developmental genetics, cytogenetics, epigenetics, medical genetics, population and evolutionary genetics, genomics and functional genomics as well as bioinformatics and computational biology. Focusing on international cutting-edge research, JGG attracts high-quality papers, organizes special issues on topical research areas, and timely reports important discoveries. In 2019, one special issue on *Drosophila* and Human Diseases and one special section on On-Target vs Off-Target have been published, attracting a close attention from experts in the related fields.

JGG aims to publish high quality genetics and genomics research and important discoveries. To better serve the scientific community, JGG will further enhance its academic quality and global impact, strengthen its editorial team and provide professional services. Both editorial board and office will strive to promote JGG to be a leading international journal in the fields of genetics and genomics.

Hereditas (Beijing)



Founded in 1979, *Hereditas* (*Beijing*) is sponsored by Institute of Genetics and Developmental Biology of Chinese Academy of Sciences and Genetics Society of China, and published monthly by Science Press in China. *Hereditas* (*Beijing*) is a national academic journal, Chinese core journal, and top-notch Chinese science and technology journal. Its current Editor-in-Chief is Prof. Yongqing Zhang.

Hereditas (*Beijing*) has been indexed by more than 20 retrieval systems and databases, such as PubMed/MEDLINE, Biological databases, Index Medicus (IM), Russian Abstract Journal (AJ), Chemical Abstract (CA). *Hereditas* (*Beijing*) is also released on many databases and websites, such as CNKI, Wanfang Database, Chongqing VIP Database, and the website www.chinagene.cn. Its contents comprise innovative research articles in the fields of genetics, genomics, developmental biology, evolution, biotechnology, etc.

In 2019, to further improve the academic quality of *Hereditas* (*Beijing*), high-quality papers were invited national wide and two special issues were published, one of which was to show the Genetic Studies in Guangdong Province and another was to celebrate the 60th Anniversary of Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, respectively. According to the latest Chinese S&T Journal Citation Reports (CJCR) (Core Edition) in 2019, *Hereditas* (*Beijing*) obtained a core impact factor of 1.043 and a total citation of 1780. Out of the total of 28 basic biology journals, it was ranked the 3rd by the core impact factor, the 6th by the total citations, and the 3rd by the core comprehensive value.

Chinese Journal of Eco-Agriculture

Chinese Journal of Eco-Agriculture (CJEA, formerly known as Eco-Agriculture Research) was founded in 1993, and is sponsored by Institute of Genetics and Developmental Biology of Chinese Academy of Sciences (IGDB, Beijing), undertaken by Center for Agricultural Resources Research of IGDB (Shijiazhuang), published monthly by Sciences Press in Chinese or English. The Editor-in-Chief of CJEA is Academician LIU Changming, and Executive Editor-in-Chief is Prof. HU Chunsheng.

CJEA is a per-reviewed academic journal. The goal of the journal is to provide a platform for scientists, academicians, and engineers to promote, share, and discuss various new issues and developments in different areas of eco-agriculture, such as agroecosystem and its regulation, crop cultivation and physiological ecology, agricultural resources and environment, agricultural ecologic economics and ecoagriculture.

CJEA has been included in various databases, such as CNKI, Wanfang Date, CSCD, VIP, Chaoxing, SCOPUS, CABI, CA, JST. The impact factor and total citation of CJEA are 1.800 and 4359, ranking the second and fourth in the total 37 agriculture academic journals according to the Chinese S&T Journal Citation Report (Core Edition) in 2019.

In 2019, the special column for “Rural Revitalization and Ecoagriculture” was published in February.

Major Events

2 January

New progress in Rice Molecular Design and Breeding in China" was selected into the top ten science and technology progress news of China in 2018.

2 January

The "Research on the Water Cycle Evolution Process and Dynamic Response Mechanism of Vegetation in Arid Areas under Changing Environments" project hosted by the Center for Agricultural Resources Research won the first prize of Hebei Province Natural Science in 2018.

河北省科学技术奖

证　书

为表彰河北省科学技术奖获得者，特颁发此证书。

项目名称：

奖种类别：

奖励等级：一等

获 奖 者：

3 January

Center for Agricultural Resources Research held 2018 Annual Academic Conference.

6 January

The State Key Laboratory of Molecular Developmental Biology held the annual meeting of Academic Committee in 2018.

9 January

The State Key Laboratory of Plant Cell and Chromosome Engineering held 2018 Academic Committee Meeting.

15 January

2019 Annual Meeting of IGDB was held.

15-18 January

2019 Scientific Annual Meeting of IGDB was held successfully.

25 January

President Bai Chunli attends the democratic life meeting of Party members and leading cadres of IGDB.

25 January

The State Key Laboratory of Plant Genomics held the annual meeting of Academic Committee in 2018.

4 March

Yu Yingjie, Director of Bureau of Major R&D Programs, CAS, visited the Innovative Academy for Seed Design.

5 March

Prof. Patrick Hussey, PVC Science and Head of Faculty of Science and Engineering of Durham University, UK ,visited IGDB.

8 March

The Forum on Women's Day was held.

14 March

The first meeting of the first Council of CAS Innovative Academy for Seed Design was held.

22 March

Forum on Life Science Rrontier and Seed Innovation was held in Lingshui, Hainan Province.

22 March

The First Chinese and Latin American Young Scientists Forum was held at IGDB.

24 March

The IGDB, the Department of Agriculture and Rural Areas of Hainan Province and Sanya Municipal People's government signed an agreement to jointly establish Innovative Academy for Seed Design.

29 March

2017 special repair and purchase project of IGDB passed the acceptance check.

8 April

The CAS Strategic Priority Research Program (Class A) on the molecular module design and breeding innovation system has passed the acceptance of the archives.

11 April

Discipline Inspection Commission of IGDB deployed the related activities in 2019.

11 April

Wu Jianguo, Executive Vice President of Beijing Branch, visited Center for Agricultural Resources Research.

15 April

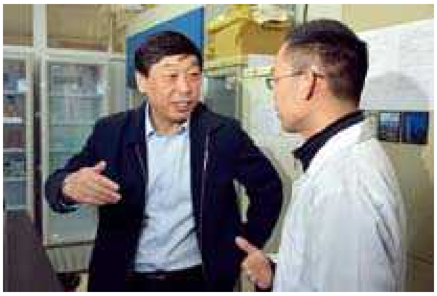
The Party Committee of IGDB held the first central group learning meeting in 2019.

17 April

A Delegation from the National Institute of Agricultural Research of Uruguay visited the Institute.

6 May

Shi Qingshuang, Deputy Governor of Hebei Province, visited Center for Agricultural Resource Research.



18 May

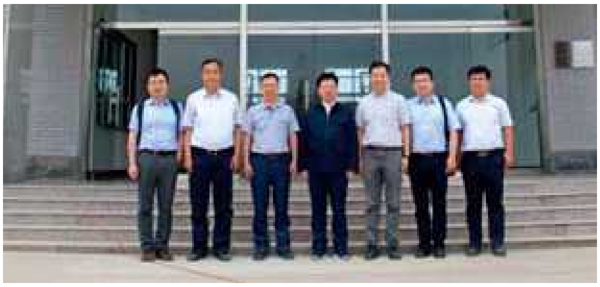
The 15th Public Science Day of IGDB was held.

18-19 May

The 7th Young Scholars Forum on Interdisciplinary Research of Mathematics, Computer and Life Sciences was held successfully.

24 May

Li Shushen, Deputy President of the Chinese Academy of Sciences, visited the Nanpi Eco-agricultural Experimental Station, CAS.



24-27 May

4th International Symposium on Animal Models of Diseases was held.

31 May

The 5th IGDB Parent-Children Activities on Children's Day was held.

3-5 June

2nd International Conference of Plant Chromosomes Engineering and Functional Genomics for Breeding was held.

10 June

Students from the 23rd class of backbone of science and technology management in the Party School of Chinese Academy of Sciences visited the Institute.

10 June

The 2019 ceremony for graduation and degree awarding of IGDB was successfully held.

14 June

The 2019 Youth Innovation Academic Forum of IGDB was successfully held.

15 June

IGDB successfully held the special science popularization activity of "Science Communication Month" of Beijing Branch of CAS.

4 July

Bai Chunli, CAS President, visited IGDB for the campaign on the theme of "staying true to our founding mission".

12 July

The opening ceremony of the research and practice Summer Camp for college students in 2019 was held.

19 July

The Party Committee of IGDB held a series of symposiums on education and learning with the theme of "staying true to our founding mission ".

27 July

Joint research center of crop phenotypic genomics opened in Wuhan, Hubei Province.

15 August

Chinese Academy of Agricultural Sciences paid a visit to the Institute for for the campaign on the theme of "staying true to our founding mission"

15-18 August

Epigenetics and Chromatin Conference was held.

25 August

Center for Agricultural Resources Research held training course on Efficient Cultivation and Management Technologies for modern agriculture.

2 September

IGDB signed strategic cooperation agreement with Yunnan University.

4 September

Dongying Molecular Design and Breeding Research Center was established in Shandong Province.

6 September

The opening ceremony and entrance education of 2019 new students of IGDB were held.

11 September

The demonstration site meeting of Zhongkefa No.5, a new rice variety with high yield, high quality and stress resistance, was successfully held in Jilin City.

19 September

The annual walking activity was held by the Institute.

25 September

Joint Academic Forum of 60th Anniversary of IGDB was successfully held.

25 September

Special Academic Forum on the 60th Anniversary of IGDB was successfully held.

26 September

The fifth session of the fourth Labor Union Congress of IGDB was held.

11-14 October

5th Lipidall International Conference on Lipid Metabolism was held.

15 October

CAS Center for Excellence in Molecular Plant Sciences visited the Institute.

24 October -11 November

General skills training forum was organized by the Institute.

28-29 October

IGDB held training for the new employees in 2019.

29 October

On October 29, 2019, An Memorandum of Understanding between the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, and the Center for Plant Biotechnology and Genomics (CBPG) of Spain was signed.

2 November

IGDB organized the second Science Festival of Chinese Academy of Sciences

5 November

IGDB launched the special Party class of "staying true to our founding mission ".

5-7 November

2019 training course for the potential member of the Party of Beijing Branch of CAS was successfully held in the Institute.

6-7 November

2019 Annual Forum of Young Scholars of the State Key Laboratory of Molecular Developmental Biology was held.

10-17 November

International Students Conference among NAIST, UC Davis and IGDB was held in Japan.

16 November

Dr. Li Jiayang was elected as Vice-president of International Eurasian Academy of Sciences (China), while Dr. Cao Xiaofeng was elected as Academician of International Eurasian Academy of Sciences.

18 November

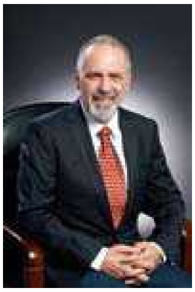
A meeting to announce the new executive leadership of IGDB was held.

19 November

Four researchers from IGDB were selected as "highly cited scientists" in 2019.

22 November

Dr. John Speakman was elected as a Foreign Member of CAS.



3 December

Center for Agricultural Resources Research signed strategic cooperation agreement with Gansu Agricultural University.

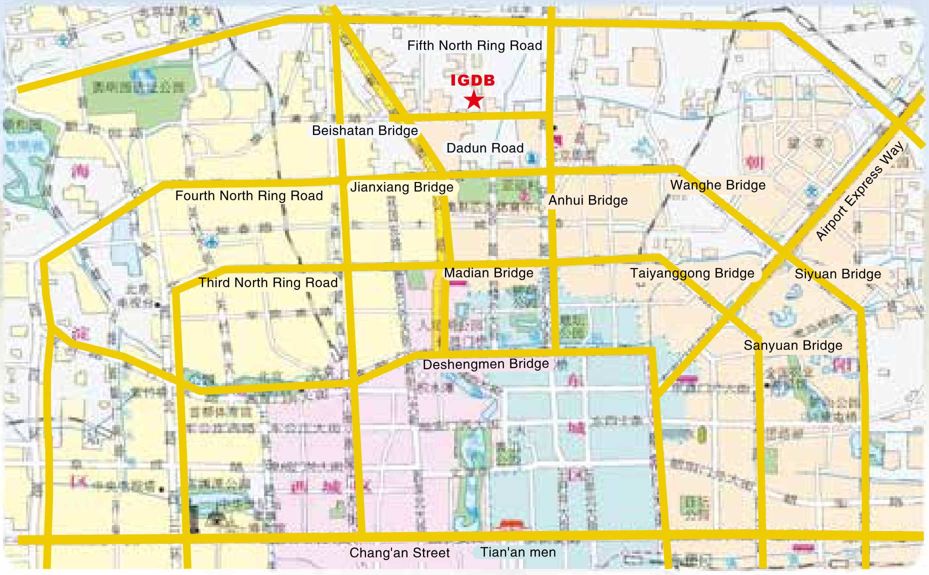
11 December

Joint theme Party day activity of "Party building promotes scientific and technological innovation" between Bureau of Frontier Science and Education of CAS and IGDB was held.

Institute of Genetics and Developmental Biology
Chinese Academy of Sciences
Address: No.1 West Beichen Road, Chaoyang District, Beijing
100101, China

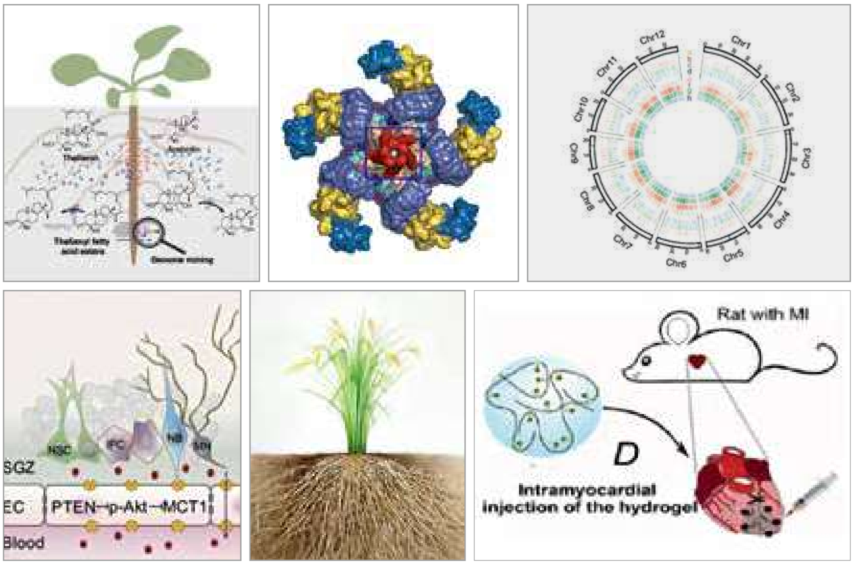
Institute of Genetics and Developmental Biology is located five kilometers north of the city center, between the Fourth and Fifth North Ring Road, near the Olympic Park.

Center for Agro–Resources Research
Address: No.286, Huaizhong Road,
Shijiazhuang, Hebei 050021, China



Editorial Committee of Annual Report

Cover image: Bird Feeding Behavior Control by *Tannin1* (Provided by Dr. Qi Xie)



Figures are taken from published papers by Yang Bai's group (Huang et al., *Science*, 2019), Jianmin Zhou's group (Wang et al., *Science*, 2019a, 2019b), Caixia Gao's group (Jin et al., *Science*, 2019), Weixiang Guo's group (Wang et al., *Cell Stem Cell*, 2019), Yang Bai's group and Chengcai Chu's group (Zhang et al., *Nat Biotechnol*, 2019), Jianwu Dai's group (Fan et al., *Advanced Materials*, 2019)

2019 Annual Report

Institute of Genetics and Developmental Biology
Chinese Academy of Sciences

Address: No.1 West Beichen Road, Chaoyang District, Beijing 100101, China
Tel: +86-10-64803652
E-mail: igdb.news@genetics.ac.cn
Website: http://www.genetics.ac.cn