Zika Virus Disrupts Neural Progenitor Development and Leads to Microcephaly in Mice
Li et al., 2016, Cell Stem Cell

MDIS1–MIK mediates the male perception of female attractants in plants
Wang et al., 2016, Nature
The past year has seen many progresses at the Institute of Genetics and Developmental Biology (IGDB) of Chinese Academy of Sciences (CAS). Most importantly, the “1-3-5” mission proposal and the 13th FIVE YEAR PLAN of the IGDB were approved by CAS.

Scientists in IGDB have made impressive advances in sciences, research funding, and public recognitions in 2016. In total, 342 SCI-indexed papers were published, 46 patents and 17 crop variety rights were granted. IGDB scientists secured 53 research proposals including 7 projects from the MOST Key Research Plan initiated in 2016, and earned 20.8 million RMB from technology transfer. Six young PIs were recruited and three of them were funded by the National Youth Thousand Talents Program. IGDB, for the first time, initiated Young Investigator Program for eminent young staff. Dr. Xiaofeng Cao was elected as a member to the Third World Academy of Sciences; Dr. John R. Speakman was elected as fellow of the American Association for the Advancement of Science (AAAS); Dr. Caixia Gao was awarded China Science Stars of the year by Nature magazine; Dr. Qi Xie was one of the highest cited scientists worldwide by Thomson Reuters.

In 2016, IGDB signed a strategic collaboration agreement with Zhongnongfa Seed Industry Group Limited, a member of the China National Agricultural Development Group Corporate Limited (CNDAC), and Tarim University, and formed partnership with Shijiazhuang Modern Agricultural Innovation Center. The Centre of Excellence for Plant and Microbial Science (CEPAMS), jointly established by CAS and John Innes Centre (JIC, UK), was officially launched in Beijing and Shanghai. I strongly believe that these partnerships will further strengthen IGDB’s competitiveness and international visibility.

Finally, I would like to take this opportunity to thank our sponsors and funding agencies for their enormous support as well as our staff and students for making this year very exciting and successful. I am pleased to present this annual report and wish you a prosperous year of the rooster.
<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Center for Genome Biology</td>
<td>1</td>
</tr>
<tr>
<td>Plant and Microbiota Interactions</td>
<td>2</td>
</tr>
<tr>
<td>Epigenetic Regulation in Higher Plants</td>
<td>3</td>
</tr>
<tr>
<td>Plant Comparative Genomics</td>
<td>4</td>
</tr>
<tr>
<td>Molecular Mechanisms of Abiotic Stress Response in Higher Plants</td>
<td>5</td>
</tr>
<tr>
<td>Plant Molecular Cytogenetics</td>
<td>6</td>
</tr>
<tr>
<td>Rice Functional Genomics and Agrobiotechnology</td>
<td>7</td>
</tr>
<tr>
<td>Molecular Systems Biology of Plant Pattern Formation</td>
<td>8</td>
</tr>
<tr>
<td>Molecular Mechanisms of Jasmonate Actions</td>
<td>9</td>
</tr>
<tr>
<td>Molecular Mechanism Underlying Plant Architecture and Grain Quality</td>
<td>10</td>
</tr>
<tr>
<td>Genomics and Bioinformatics Facility</td>
<td>11</td>
</tr>
<tr>
<td>Crop Molecular Breeding</td>
<td>12</td>
</tr>
<tr>
<td>Plant Functional Metabolomics</td>
<td>13</td>
</tr>
<tr>
<td>Genetic Control of Plant Morphogenesis</td>
<td>14</td>
</tr>
<tr>
<td>Molecular Mechanisms of Ubiquitination and Plant Abiotic Stress Signaling</td>
<td>15</td>
</tr>
<tr>
<td>Plant Genetics and Breeding</td>
<td>16</td>
</tr>
<tr>
<td>Rice Ethylene Signaling and Soybean Functional Genomics</td>
<td>17</td>
</tr>
<tr>
<td>Molecular Basis of Plant-Microbe Interactions</td>
<td>18</td>
</tr>
<tr>
<td>Molecular Genetics and Cell Wall Biology</td>
<td>19</td>
</tr>
<tr>
<td>Plant Functional Genomics and Genetic Engineering Technology</td>
<td>20</td>
</tr>
<tr>
<td>Molecular Genetics on Plant Development and Disease Resistance</td>
<td>21</td>
</tr>
<tr>
<td>Nitric Oxide-Mediated Signal Transduction and Nitrogen Nutrition in Plants</td>
<td>22</td>
</tr>
</tbody>
</table>
### Center for Molecular Agrobiology

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maize Genetics and Breeding</td>
<td>24</td>
</tr>
<tr>
<td>Plant Genetics and Molecular Biology</td>
<td>25</td>
</tr>
<tr>
<td>Plant Genetic Transformation and Genome Editing</td>
<td>26</td>
</tr>
<tr>
<td>Plant Chromosome Biology</td>
<td>27</td>
</tr>
<tr>
<td>Plant Biotechnology</td>
<td>28</td>
</tr>
<tr>
<td>Plant Molecular and Developmental Biology</td>
<td>29</td>
</tr>
<tr>
<td>Distant Hybridization between Wheat and <em>Thinopyrum ponticum</em></td>
<td>30</td>
</tr>
<tr>
<td>Molecular Biology of Plant Nutrition and Wheat Genomics</td>
<td>31</td>
</tr>
<tr>
<td>Biochemistry of Photosynthetic Proteins</td>
<td>32</td>
</tr>
<tr>
<td>Wheat Genomics, Genetics &amp; Breeding</td>
<td>33</td>
</tr>
<tr>
<td>Molecular Mechanism of Plant Disease Resistance</td>
<td>34</td>
</tr>
<tr>
<td>Molecular Plant-Microbe Interactions</td>
<td>35</td>
</tr>
<tr>
<td>Functional Genomics and Genetics of Soybean</td>
<td>36</td>
</tr>
<tr>
<td>Genetic Control of N and P Use in Wheat</td>
<td>37</td>
</tr>
<tr>
<td>Molecular Studies of Important Agronomic Traits and Genetic Improvement of Wheat</td>
<td>38</td>
</tr>
<tr>
<td>Plant Molecular Genetics and Molecular Breeding</td>
<td>39</td>
</tr>
<tr>
<td>Wheat Molecular Breeding</td>
<td>40</td>
</tr>
<tr>
<td>Molecular Biology and Chromosome Engineering of Wheat</td>
<td>41</td>
</tr>
<tr>
<td>Soybean Genetics and Breeding</td>
<td>42</td>
</tr>
</tbody>
</table>

### Center for Developmental Biology

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Epigenetics and Cell Differentiation</td>
<td>44</td>
</tr>
<tr>
<td>Plant Molecular Control and Response</td>
<td>45</td>
</tr>
<tr>
<td>Regenerative Medicine and Tissue/Organ Construction</td>
<td>46</td>
</tr>
<tr>
<td>Neural Development</td>
<td>47</td>
</tr>
<tr>
<td>Neural Stem Cells and Neurogenesis</td>
<td>48</td>
</tr>
<tr>
<td>Lipid Metabolism and Development</td>
<td>49</td>
</tr>
</tbody>
</table>
Bio-Imaging and Micro/Nano Optics 50
Neurodegenerative Diseases and Developmental Biology 51
Molecular Mechanisms and Functions of Retrograde Vesicular Transport 52
Functional Genomics of Human and Animals 53
Cytoskeletal Dynamics and Function 54
Lipidomics and Lipid Metabolism 55
Molecular Energetics 56
Molecular Genetics of Mitochondrial Stress Signaling 57
The Genetic Program of Gonad Development 58
Signal Transduction, Diseases & Development 59
Plant Molecular and Reproductive Biology 60
Mechanisms of Lysosome-Mediated Cellular Clearance 61
Molecular Genetics of Sexual Plant Reproduction 62
Vertebrate Early Development 63
Developmental Neurobiology and Genetic Modeling of Neurological Diseases 64

**Center for Molecular Systems Biology** 65
Structural Biology of Macromolecules 66
Systems Biology of Animal Embryogenesis 67
Quantitative Functional Genomics and Single Cell Genetics 68
Systems Developmental Biology 69
Functional Proteomics 70
Bioinformatics and Systems Biology 71

**Center for Agricultural Resources Research** 72
Wheat Genetic Improvement & Germplasm Enhancement 73
Mountain Eco-Engineering and Eco-Hydrology 74
Nutrient Cycling and Environmental Impacts in Agricultural Ecosystem 75
Wheat Molecular Breeding 76
<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Remediation of Heavy Metal Polluted Farmland</td>
<td>77</td>
</tr>
<tr>
<td>Microbial Ecology</td>
<td>78</td>
</tr>
<tr>
<td>Sustainable Management and Ecological Engineering for Ecosystem</td>
<td>79</td>
</tr>
<tr>
<td>Physiological and Ecological Mechanismin of Efficient Water Use of Crops</td>
<td>80</td>
</tr>
<tr>
<td>Plant Molecular and Developmental Biology</td>
<td>81</td>
</tr>
<tr>
<td>High Efficient Utilization of Water and Soil Resources</td>
<td>82</td>
</tr>
<tr>
<td>Molecular Genetics of Plant Defense</td>
<td>83</td>
</tr>
<tr>
<td>Agro-Ecology and Nutrient Management</td>
<td>84</td>
</tr>
<tr>
<td>Agricultural Hydrology and Water Resources</td>
<td>85</td>
</tr>
<tr>
<td>Experimental Mechanism &amp; Modeling of Hydrologic Cycle and Solute Transport</td>
<td>86</td>
</tr>
<tr>
<td>Sustainable Agricultural Water Management</td>
<td>87</td>
</tr>
<tr>
<td>Mechanisms and Techniques to Improve Farmland Water Use Efficiency</td>
<td>88</td>
</tr>
<tr>
<td>Genetics and Breeding of Wheat Drought Resistance and Water Saving</td>
<td>89</td>
</tr>
<tr>
<td>Center for Core Facility &amp; Advanced Technologies</td>
<td>90</td>
</tr>
<tr>
<td>Key Laboratories</td>
<td>92</td>
</tr>
</tbody>
</table>
The mission of the Center for Genome Biology (the Center, thereafter) is to develop and apply genomics tools to understand how plants regulate growth and development.

In 2016, scientists in the Center have made important advances in multiple fronts, including the plant genome structure and regulation, molecular dissection of complex agricultural traits, and plant interactions with environment and pathogenic organisms. In plant genomics studies, Xiaofeng Cao’s group reported that REF6 uses four zinc fingers to directly recognize a CTCTGYTY motif, allowing genome-wide, site-specific demethylation of H3K27me3. These results identify a new targeting mechanism of an H3K27 demethylase to counteract Polycomb-mediated gene silencing (Cui et al., Nat Genet, 2016). Her team also applied genetics, transcriptomics, proteomics and biochemistry to show that AtPRMT5 modulates constitutive and alternative pre-mRNA splicing, uncovering a key process through which arginine methylation impacts diverse developmental processes (Deng et al., PNAS, 2016). Jiayang Li and colleagues proposed a regulatory framework for precision breeding with "genome-edited crops" (GECs) so that society can fully benefit from the latest advances in plant genetics and genomics, which showed pioneering influence in the application of genome-edited technology (Huang et al., Nat Genet, 2016). Jiayang Li’s group and collaborators successfully carried out efficient intron-mediated site-specific gene replacement through the non-homologous end joining (NHEJ) pathway assisted by the CRISPR/Cas9 system, and these newly developed technology can be generally applied to molecular breeding and analysis of plant genes (Li et al., Nat Plants, 2016).

In functional genomics studies, Jiayang Li’s group identified a defective soluble starch synthase gene (SSIIIa) responsible for resistant starch (RS) production. This discovery holds great promise in improving cooking quality of rice especially in the indica varieties which are dominating in southern Asia (Zhou et al., PNAS, 2016). Yonghong Wang and Jiayang Li’s groups discovered a new molecular mechanism controlling shoot branching. They showed that the MKK7-MPK6 cascade phosphorylates Ser337 on PIN1, establishing a molecular link between the MAPK cascade and auxin-regulated plant development (Jia et al., PLoS Biol, 2016). Lihuang Zhu’s group and collaborators conducted integrated genetics and omics analyses in a model two-line rice hybrid system, Liang-youpei 9 (LYP9) and its parents to identify multiple quantitative trait loci (QTLs) involved in yield heterosis, and proposed a common mechanism for yield heterosis in the present commercial hybrid rice (Li et al., PNAS, 2016). Chengcai Chu’s group analyzed a newly identified a dominant panicle enclosure mutant regulator of eui1 (ree1-D) to show that HOX12 acts directly through EU1 to regulate panicle exertion in rice (Gao et al., Plant Cell, 2016). Zhukuan Cheng’s group showed that P31comet is a functional synaptonemal complex (SC) protein and is essential for double-strand break (DSB) formation and SC installation in rice (Ji et al., PNAS, 2016). The same group and collaborators demonstrate that MS5 participates in progression of meiosis during early prophase I and that its allelic variants alter fertility in oilseed rape (Brassica napus L.), which may provide a promising strategy for pollination control for heterosis breeding (Xin et al., Plant Cell, 2016). Chuanyou Li’s group and collaborators identified DA3 as a negative regulator of endoreduplication and showed that endoreduplication is linked to cell and organ growth via interaction of DA3 with key cell-cycle regulators (Xu et al., Plant Cell, 2016). Yuling Jiao’s group reported that the initiation of axillary meristems requires a meristematic cell population continuously expressing the meristem marker SHOOT MERISTEMLESS (STM), and proposed a threshold model for axillary meristem initiation (Shi et al., PLoS Genet, 2016).

In studying of plant-environment/pathogen interactions, Jian-Min Zhou’s group reported a novel serine protease from Pseudomonas syringae that specifically destroys a key immune co-receptor precisely following its activation, leading to enhanced virulence while avoiding detection by the plant surveillance system (Li et al., Cell Host Microbe, 2016). The same group demonstrated that heterotrimERIC G proteins are directly coupled to an immune receptor kinase complex to regulate immune signaling through both pre-activation and post-activation mechanisms (Liang et al., eLife, 2016). Qi Xie’s group reported that the two major complexes involved in the ER-associated protein degradation (ERAD) system closely interact with each other, which is conserved between plants and mammals (Chen et al., Nat Plants, 2016).

AWARDS AND RECOGNITIONS
Prof. Xiaofeng Cao was elected as a member to the Third World Academy of Sciences. Prof. Qi Xie was highlighted in Thomson Reuters China Citation Laureates. Prof. Chuanyou Li received a Leading Talent award from the Scientific and Technological Innovation Program.
Plant and Microbiota Interactions

Dr. Yang Bai, Principal Investigator, Ph.D. (2010, University of Cologne, Germany). Dr. Bai’s group are mainly interested in plant root microbiota’s functions in disease resistance and nutrient uptake by metagenomic approaches, such as 16S and metagenomic sequencing, high throughput microbial cultivation and reconstitution.

Email: ybai@genetics.ac.cn

Plant root-associated microbes and agricultural productivity

Baoyuan Qu, Yongxin Liu, Jingying Zhang, Xiaoxuan Guo, Ting Jiang, Zishan He, Na Zhang, Xiaoning Zhang, Yang Bai

In nature, healthy plants associate with abundant and diverse microbial communities, called microbiota. Classical studies on plant-microbe interaction mainly focus on just a few pathogenic and beneficial microbial strains. With the development of DNA sequencing and microbial cultivation technologies, we are able to understand the function of these plant-associated microbiota at the microbial community level. Current progress shows that these microbes contain a huge number of functional genes, and can play important roles in plant’s disease resistance, nutrient uptake and stress tolerance. Our group are exploring multiple functions of microbiota associated with both model plants and crops. We believe that a better understanding of plant microbiota will be essential to the development of global sustainable agriculture, especially for reducing the application of chemical fertilizer and improving global food security.

Publication


Figure: Root microbiota protects Arabidopsis plant growth in F. oxysporum infection.
Epigenetic Regulation in Higher Plants

Dr. Xiaofeng Cao, Principal Investigator, Member of Chinese Academy of Sciences, Academician of TWAS (Third World Academy of Sciences). The laboratory uses both Arabidopsis and rice as model systems to identify key components involved in dynamic histone methylation and small RNA biogenesis. The laboratory currently focuses on elucidating the RNA regulatory network and its role in ambient temperature response and plant development.

Email: xfcao@genetics.ac.cn

REF6 recognizes a specific DNA sequence to demethylate H3K27me3 and regulate organ boundary formation in Arabidopsis

Xia Cui, Falong Lu, Qi Qiu, Bing Zhou, Lianfeng Gu, Shuaibin Zhang, Yanyuan Kang, Xiekui Cui, Xuan Ma, Qingqing Yao, Jinbiao Ma, Xiaoyu Zhang, Xiaofeng Cao

In metazoans and plants, trimethylation of histone H3 lysine27 (H3K27me3) facilitates the maintenance of developmentally regulated genes in a transcriptionally repressed state. The establishment and the removal of H3K27me3 at specific genes are therefore critically important for normal development. The RELATIVE OF EARLY FLOWERING 6 protein (REF6, also known as JM1J2) specifically demethylates H3K27me3 at its target loci for transcriptional activation. Loss of REF6 leads to the ectopic accumulation of H3K27me3 at hundreds of genes in seedlings, as well as a number of developmental phenotypes. However, how REF6 is targeted to specific genes remains unknown.

Our work demonstrates that function and genome-wide targeting of REF6 protein require its four Cys2-His2 zinc fingers, which directly recognize the CTCTGYTY motif (Fig. a, d, e). By analyzing the genome-wide distribution of the motif, we found REF6 preferred to bind motifs clustering together and located in loci with active chromatin states (Fig. b, c). In addition, we found REF6-targeted CUP-SHAPED COTYLEDON 1 (CUC1) and CUC3 genes, which are important for cotyledon separation. This study reveals a novel targeting mechanism of an H3K27me3 demethylase to counteract Polycomb-mediated gene silencing that regulates plant development, including organ boundary formation (Fig. f).

Figure: ZnF domain is essential for REF6 targeting by interacting with a specific DNA motif. (a) The truncated REF6 without the C2H2-ZnF domains (REF6ΔZnF-HA) transgene cannot bind its target genes. (b) CTCTGYTY-motif is enriched in REF6-binding regions. (c) Distribution of the CTCTGYTY motif in REF6 binding peaks. (d) GST-REF6C containing the C2H2-ZnF cluster but not GST binds the NAC004 probe in vitro. ZnF mutants (cysteine to alanine) abolished (ZnF2mu-ZnF4mu) or severely attenuated (ZnF1mu) the protein-DNA interaction. (e) Single-base mutations in the CTCTGTTT motif of the NAC004 probe either abolish or weaken the interaction between GST-REF6C and the DNA probe. (f) Single-base mutations in the CTCTGTTT motif of the NAC004 probe either abolish or weaken the interaction between GST-REF6C and the DNA probe.

Publications


Plant Comparative Genomics

Dr. Mingsheng Chen, Principal Investigator, Ph.D. (1998, Purdue University, USA).
The laboratory is mainly interested in plant comparative genomics, bioinformatics,
genome evolution and molecular cloning of important agronomic genes in rice.
Email: mschen@genetics.ac.cn

Revisiting the protein-coding gene of *Oryza sativa* using evolutionary signatures

Qun Yang, Mingsheng Chen

With the progress of the International *Oryza* Map Alignment Project (I-OMAP), nearly a dozen of completely sequenced genomes of *Oryza* have become available. Such genomic resources make it possible to systematically discover functional elements in rice using comparative genomic analysis. Here we use 9 *Oryza* genomes for *de novo* discovery of protein-coding genes in rice. After building a multiple alignment based on 2876 homologous regions, we chose 757 well-studied genes as training set to calculate evolutionary signatures, including reading frame conservation (RFC), codon substitution frequencies (CSF) and PhyloCSF. Tests showed that the sensitivity and specificity of each signature are more than 85%. We next used RFC and CSF as evolutionary constraint feature functions combining with maximal dependence decomposition and weight array model as splice site feature functions to build a robust Semi-Markov Conditional Random Field (SMCRF) model program, called Agares-lite. Agares-lite can identify conserved protein-coding sequences missing from the current annotation of rice. We ran Agares-lite on chromosome 1, 9, 10 data set and predicted 1605 new protein-coding exons not overlapping with any coding exons in MSU Rice Genome Annotation Project Release 7 annotation, of which 61% are located in intergenic regions. We also used PhyloCSF as a strict evolutionary signature test searching the whole rice genome to identify 754 potential stop-codon readthroughs. Validation of these potential novel protein-coding exons and stop-codon read-throughs is on-going.

**Publications**


---

Figure: Gene annotations predicted by Agares-lite. The top part shows the RNA-seq reads around a gene, the middle blue squares demonstrate annotations of Agares-lite, and the MSU release 7 structures are revealed on the bottom.
Soybean miR172a improves salt tolerance as a long distance signal

Wenjia Pan, Jianjun Tao, Tong Cheng, Xiaohua Bian, Wei Wei, Wanke Zhang, Biao Ma, Shouyi Chen, Jinsong Zhang

Our previous study has identified a series of miRNAs from soybean. In this research, we found that miR172a was induced by salt and drought treatments and this miRNA may play roles in stress responses of soybean. Soybean transgenic hairy roots overexpressing pre-miR172a were generated by Agrobacterium K599-mediated root transformation. Soybean with the miR172a-OE hairy roots exhibited tolerance to 80 mM NaCl treatment, and plant height and fresh weight were also increased compared to the control. Through degradome sequencing, target genes of the known miRNAs were analyzed, and 12 target genes for the miR172a were identified. The cleavage site of 6 target genes were further confirmed by using RLM-5' RACE method. Soybean with RNAi-transgenic hairy roots for four target genes were further generated and only plants with the GmSSAC1-RNAi hairy roots exhibited tolerance to 80 mM NaCl treatment. In contrast, soybean with GmSSAC1-OE hairy roots exhibited sensitivity to 80 mM NaCl treatment. GmSSAC1 encodes an AP2-type transcription factor. A further downstream gene GmTHI1, which encodes a key enzyme involved in the vitamin B1 formation, was identified by using RNA-seq and qRT-PCR. Soybean with GmTHI1-OE hairy roots exhibited tolerance to 80 mM NaCl treatment, while soybean with GmTHI1-RNAi hairy roots exhibited sensitivity to 80 mM NaCl treatment. The AP2-type transcription factor GmSSAC1 suppressed the expression of GmTHI1. Hence, miR172a may enhance salt stress tolerance of soybean by regulating AP2 transcription factor gene and release its suppression to GmTHI1. Moreover, soybean miR172a was found to improve salt tolerance as a long distance signal from transgenic hairy roots to untransgenic shoots by grafting experiment.
Plant Molecular Cytogenetics

Dr. Zhukuan Cheng, Principal Investigator, Ph.D. (1999, Institute of Genetics, CAS, China). Dr. Cheng’s laboratory mainly focuses on plant molecular cytogenetics, especially on the molecular mechanism of homologous chromosome pairing and recombination.

Email: zkcheng@genetics.ac.cn

OsMTOPVIB promotes meiotic DNA double-strand break formation in rice

Zhihui Xue, Yafei Li, Lei Zhang, Wenqing Shi, Chao Zhang, Fanfan Zhang, Ding Tang, Zhukuan Cheng

Meiotic recombination is initiated by DNA double-strand breaks (DSBs). In budding yeast, Spo11 and its accessory proteins are required for introducing DSBs. However, few of these proteins are conserved across species. Here, we identified a gene in rice, designated OsMTOPVIB for its homology with Arabidopsis MTOPVIB. In OsmtopVIB mutants, DSB markers (e.g., γH2AX and OsDMC1) are absent (Fig. A), while the DSB repair defects of the Osrad51c and Oshus1 mutants are abolished in the OsmtopVIB background (Fig. B). OsMTOPVIB physically interacts with OsSPO11-1 and OsSPO11-2, suggesting that OsMTOPVIB forms part of a multi-protein complex with OsSPO11 subunits and is involved in mediating DSB formation (Fig. C). Consistent with a direct role in meiotic DSB formation, OsMTOPVIB is localized to chromatin loops, to which recombining DNA sequences are mapped (Fig. D). OsMTOPVIB is a key component in rice meiotic DSB formation.

Publications

<table>
<thead>
<tr>
<th>Authors</th>
<th>Title</th>
<th>Journal</th>
<th>Year</th>
<th>Pages</th>
</tr>
</thead>
</table>

Figure: OsMTOPVIB is essential for meiotic DSB formation. (A) Immunolocalization of γH2AX and OsCOM1 in the wild type and OsmtopVIB. OsREC8 signals indicate meiotic chromosomes. (B) Fragmentations observed in Osrad51c and Oshus1 are abolished in the OsmtopVIB background. (C) The full-length (FL) and truncated proteins of OsMTOPVIB interact with OsSPO11-1 and OsSPO11-2 in Y2H assays. (D) The chromosome axis indicated by OsREC8 (red) is surrounded with OsMTOPVIB (green) foci. Bars, 5μm.
Rice Functional Genomics and Agrobiotechnology

Dr. Chengcai Chu, Principal Investigator, Ph.D. (1996, Martin-Luther University, Germany). The work of laboratory covers rice functional genomics and agrobiotechnology, mainly focusing on the leaf senescence, grain size, and nutrient use efficiency, the key agronomic traits in rice production.

Email: ccchu@genetics.ac.cn

Rice HOX12 regulates panicle exsertion by directly modulating the expression of ELONGATED UPPERMOST INTERNODE1

Shaopei Gao, Jun Fang, Fan Xu, Wei Wang, Chengcai Chu

Bioactive gibberellins (GAs) are key endogenous regulators of plant growth. Previous work identified ELONGATED UPPERMOST INTERNODE1 (EUI1) as a GA deactivating enzyme which plays an important role in panicle exsertion in rice (Oryza sativa). However, the mechanism that controls EU1 activity during development is still largely unexplored. In this study, we identified a dominant panicle enclosure mutant regulator of eui1 (ree1-D), which is caused by the activation of a homeodomain-leucine zipper transcription factor HOX12. Diminished HOX12 expression by RNA interference enhances the panicle exsertion, mimicking the eui1 phenotype. Quantification of GA levels in the uppermost internodes revealed that the HOX12 knockout plants contain higher levels of the major biologically active GAs (such as GA1 and GA4) than these in the wild type. The expression of EUI1 is elevated in the ree1-D mutant but lowered in HOX12 knockout plants. Interestingly, both HOX12 and EUI1 genes are predominantly expressed in panicles, where GA4 is highly accumulated. Yeast one-hybrid, electrophoretic mobility shift assay, and chromatin immunoprecipitation analyses showed that HOX12 physically interacts with EUI1 promoter both in vitro and in vivo. Furthermore, overexpression of HOX12 in eui1 mutant background remains the elongated uppermost internode phenotype. These results reveal a novel regulatory module that HOX12 acts directly through EUI1 to regulate panicle exsertion in rice.

Publications


Feedback from leaves controls shoot apical meristem growth by modulating auxin transport

Bihai Shi, Xiaolu Guo, Ying Wang, Ken-ichiro Hayashi, Jinzhi Lei, Lei Zhang, Yuling Jiao

Stem cells must balance self-renewal and differentiation; thus, stem cell activities are precisely controlled. In plants, the control circuits that underlie division and differentiation within meristems have been well studied but those that underlie feedback on meristems from lateral organs, such as leaves, remain largely unknown. Here we show that long-distance auxin transport mediates this feedback in a non-cell-autonomous manner. A low-auxin zone is associated with the shoot apical meristem (SAM) organization center, and is required for regulation of SAM size. Using computational model simulations, we show that auxin transport from leaves can inhibit auxin transport from the SAM through an auxin transport switch, and thus maintain SAM auxin homeostasis and SAM size. Genetic and microsurgical analyses confirmed the model’s predictions. In addition, the model explains the surprising observation that yabby mutants exhibit oscillations of SAM size. Our study shows that plants use a distinct feedback control mechanism for long-distance regulation of stem cell activities.

Figure: Auxin transportation in the shoot apex. Longitudinal sections of the inflorescence shoot apex with floral buds removed, and beads containing 20 μM NBD-3BA (A) or 20 μM NBD-NAA (B) applied to the incision sites. Arrowheads mark the inflorescence meristem and triangles indicate the incision sites where floral buds were removed. Bars, 50 μm.
Molecular Mechanisms of Jasmonate Actions

Dr. Chuanyou Li, Principal Investigator, Ph.D. (1999, Institute of Genetics, CAS, China). The laboratory is uncovering the molecular mechanisms of jasmonate-signaled plant immunity. We are also interested in the cross-talks of jasmonate with other phytohormones in coordinating plant immunity and development. A long-term goal of our research is to develop an environment-friendly strategy for crop protection.

Email: cyli@genetics.ac.cn

Mediator links the jasmonate receptor to the promoters of MYC2 direct targets

Lin Li, Chunpeng An, Qingzhe Zhai, Chuanyou Li

Jasmonates are important plant hormones that play well-established roles in regulating plant immunity and developmental processes. JA-Ile, the active form of the hormone, is perceived by the nuclear-localized F-box protein COI1 that forms a functional E3 ubiquitin ligase. Perception of JA-Ile leads to the degradation of JAZ repressor proteins and thereby triggers genome-wide transcriptional reprogramming that is regulated by the master transcription factor MYC2. These conceptual advances highlight that MYC2-orchestrated transcriptional reprogramming, which occurs on transcriptionally active chromatin, is a central theme of JA signaling. In this context, a challenge to further understand the JA signaling lies in unraveling the determinants that enable the JA-Ile co-receptor complex transmits hormone-unique regulatory signals to the Pol II general transcription machinery to guide the specific transcription of JA-responsive genes.

Recent research in our lab has established a direct linkage between the JA-Ile receptor COI1 and the general transcription machinery. We showed that, in addition to interacting with the master transcription factor MYC2, MED25 also physically and functionally interacts with the receptor COI1 (Fig. a-c). Using chromatin ChiP-PCR assays, we found that COI1 occupies on the core promoter of MYC2 target genes and this occupancy is regulated by JA-Ile (Fig. d). More importantly, in the med25 mutant, the enrichment levels of COI1 on the core promoter of MYC2 target genes is dramatically reduced, suggesting that the promoter occupancy of COI1 on MYC2 targets depends on MED25 (Fig. d). This study elucidates a detailed mechanism by which MED25 directly bridges the communication of COI1 with the Pol II general transcription machinery.

Our work shed new light to further understand the molecular details of JA-Ile perception and the subsequent activation of MYC2-directed transcriptional reprogramming.

Figure: MED25 links COI1 to the promoter of MYC2 targets. (a) Y2H assays show that MED25 interacts with COI1. (b) In vitro pull-down assays between MED25-MBP and COI1-His. (c) MED25 associates with COI1 in LCI assays. (d) The occupancy of COI1 on the core promoter of MYC2 targets is regulated by JA-Ile in a MED25 dependent manner.

Publications


Molecular Mechanism Underlying Plant Architecture and Grain Quality

Dr. 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. The laboratory is mainly interested in the development and metabolism of higher plants, focusing on the molecular basis of plant architecture, phytohormones and the regulation of starch biosynthesis. The laboratory is also working on molecular design of new elite rice varieties with higher yield, better grain quality, and resistance to pests and stresses.

Email: jyli@genetics.ac.cn

Critical roles of soluble starch synthase SSIIIa and granule-bound starch synthase Waxy in synthesizing resistant starch in rice

Hongju Zhou, Lijun Wang, Guifu Liu, Xiangbing Meng, Yanhui Jing, Xiaoli Shu, Xiangli Kong, Jian Sun, Hong Yu, Steven M. Smith, Dianxing Wu, Jiayang Li

Changes in human lifestyle and food consumption have resulted in a large increase in the incidence of type-2 diabetes, obesity, and colon disease, especially in Asia. These conditions are a growing threat to human health, but consumption of foods high in resistant starch (RS) can potentially reduce their incidence. Strategies to increase RS in rice are limited by a lack of knowledge of its molecular basis. Through map-based cloning of a RS locus in indica rice, we have identified a defective soluble starch synthase gene (SSIIIa) responsible for RS production and further showed that RS production is dependent on the high expression of the Waxy (Wxa) allele, which is prevalent in indica varieties. The resulting RS has modified granule structure; high amylose, lipid, and amylose-lipid complex; and altered physicochemical properties. This discovery provides an opportunity to increase RS content of cooked rice, especially in the indica varieties, which predominates in southern Asia.

Email: jyli@genetics.ac.cn

Publications


Genomics and Bioinformatics Facility

Dr. Chengzhi Liang, Principal Investigator, Ph.D. (1995, Institute of Genetics, CAS, China), Master degree of Mathematics in Computer Science (2001, University of Waterloo, Canada). The major research areas of this core facility include: 1) genome sequencing and analysis, including genome de novo sequencing or resequencing, RNA-seq, population sequencing, genome assembly, population genetic analysis, gene or QTL mapping; 2) bioinformatics development, including developing algorithm and software for genome annotations, construction of gene regulatory networks, and databases for integrating genotypic and phenotypic data.

Email: cliang@genetics.ac.cn

De novo assembly of plant genomes using an integrative strategy

Chengzhi Liang, Huilong Du, Bin Ma, Hui Liu, Ying Yu, Yanfei Ma, Qiang Gao, Yinghao Cao, Ming Qi, Kunfan Liu, Xin Yang

A high-quality reference genome is critical for understanding genome content, structure, genetic variation, and evolution of an organism. Genomes assembled for the next-generation short read sequencing technologies are usually highly fragmented with thousands to tens of thousands of sequence contigs. The long reads generated from single molecule, real-time (SMRT) sequencing technology have been used to assemble complete microbial genomes and high-quality animal or plant draft genomes. However, for large eukaryotic genomes, especially plants, additional work is still required to obtain chromosome-scale contiguity and to fix errors introduced by the assembly programs. Here we report the de novo genome assembly of an indica rice (Oryza sativa ssp. indica cultivar Shuhui498, or R498) by integrating whole-genome shotgun SMRT sequences, fosmid clone sequence tags, genetic maps, and BioNano single-molecule mapping data. The near complete R498 assembly consists of seven single-contig and five double-contig pseudomolecules, with a total size of 390.3 megabases, which were estimated to account for more than 99% of the R498 genomic sequences. It is more continuous than the current reference genomes of rice (MSU7) (O. sativa ssp. japonica cultivar Nipponbare) and Arabidopsis thaliana (TAIR10) that have been obtained by clone-based Sanger sequencing. We identified genome-specific genes and structural variations between R498 and Nipponbare and presence/absence variations by comparing them to 17 draft genomes in cultivated rice and its closest wild relatives. Our results demonstrate how to de novo assemble a highly contiguous and near complete plant genome through the integration of easy-reaching technologies. The R498 genome serves as a new reference for the discovery of genes and structural variations in rice.

Table: Comparison of R498 and Nipponbare genomes. *Only gaps ≥100 bp were counted in Nipponbare. A presence variation (PV) in R498 is equivalent to an absence variation (AV) in Nipponbare, and vice versa. (Unpublished data)

<table>
<thead>
<tr>
<th></th>
<th>R498</th>
<th>Nipponbare</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genome length (bp)</td>
<td>390,322,188</td>
<td>373,245,519</td>
</tr>
<tr>
<td>Gap number</td>
<td>5</td>
<td>239*</td>
</tr>
<tr>
<td>Telomere number</td>
<td>24</td>
<td>13</td>
</tr>
<tr>
<td>mtDNA length (bp)</td>
<td>527,116</td>
<td>490,520</td>
</tr>
<tr>
<td>cpDNA length (bp)</td>
<td>134,546</td>
<td>134,525</td>
</tr>
<tr>
<td>Gene number</td>
<td>38,714</td>
<td>36,775</td>
</tr>
<tr>
<td>Repeat content (%)</td>
<td>42.05</td>
<td>40.43</td>
</tr>
<tr>
<td>SNP number</td>
<td>2,548,071</td>
<td>2,548,071</td>
</tr>
<tr>
<td>PV (10-50 kb) number</td>
<td>1,524</td>
<td>726</td>
</tr>
<tr>
<td>PV (&gt;50 kb) number</td>
<td>170</td>
<td>92</td>
</tr>
</tbody>
</table>

Publications


Crop Molecular Breeding

Dr. Shaoyang Lin, Principal Investigator, Ph.D. (1993, Chiba University, Japan). Dr. Lin’s laboratory is mainly interested in crop molecular breeding, including improvement of the rice blast resistance, lodging resistance, yields and quality in an elite variety KY131 in Heilongjiang Province.

Email: sylin@genetics.ac.cn

Seed number design of an elite rice variety KY131 in Heilongjiang Province

Xiaomin Feng, Guoqiang Jiang, Qingbo Yuan, Shaoyang Lin

Seed number is one of important component factors of rice yield. Through QTL analysis, we found a seed number related QTL, named MLq1, from an indica variety GKBR. The QTL was then backcrossed into KY131 in order to increase its seed number. So far, the F1 plants from the cross between GKBR and KY131 were backcrossed thrice with KY131 to generate a BC1F1 population. One individual was selected from the BC1F1 segregation population, and the genome recovery rate was 99.42%. Through introduction of the MLq1 from GKBR, the panicle became larger and more compact (Fig. A), and the primary branch number and the seed number were significantly increased in lines with MLq1 (Fig. B, C). However, the plant height and morphology of selected BC1F1 individuals with MLq1 grown in Nanjing were not changed (Fig. D). And the yield of a selected line with MLq1 grown in Jiamusi increased to 1254 Jin per Mu, 13.9% higher than that of KY131, which was 1101 Jin per Mu (Fig. E).

Figure: The seed number and yield of KY131 was significantly increased by the QTL MLq1 introduction. (A) Picture of the main panicles of KY131 and plants with different types of MLq1 from a BC1F1 segregation population. (B) Primary branch number of KY131 and plants with different types of MLq1 from a BC1F1 segregation population. (C) Seed number of KY131 and plants with different types of MLq1 from a BC1F1 segregation population. (D) The plant height and morphology of selected BC1F1 individuals containing MLq1 grown in Nanjing. (E) The yield of a selected line with MLq1 grown in Jiamusi increased to 1254 Jin per Mu, 13.9% higher than that of KY131.
Plant Functional Metabolomics

Dr. Guodong Wang, Principal Investigator, Ph.D. (2003, Shanghai Institute of Plant Physiology and Ecology, CAS, China). The overall interest in our laboratory is to study how plant synthesizes so many small-molecule natural products \textit{in planta}, the key enzymes potentially involved in these biosynthesis pathways and the mechanism of the unexplored enzymatic reactions. Currently, we are exploring the flavor/nutrition quality for hops and soybean by using integrated omics techniques, including comparative metabolomics, genomics and transcriptomics, as well as the traditional molecular and biochemical approaches.

Email: gdwang@genetics.ac.cn

Molecular mechanism of volatile production in cucumber plants

Guo Wei, Fengxia Zhang, Hao Qin, Qingwen Chen, Zhongyi Hu, Guodong Wang

Plant volatile organic compounds (VOCs), which are generated in a tissue-specific manner, play important ecological roles in the interactions between plants and their environments, including the well-known functions of attracting pollinators and protecting plants from herbivores/fungi attacks. However, to date, there have not been reports of holistic volatile profiling of the various tissues of a single plant species, even for the model plant species. In this study, we qualitatively and quantitatively analyzed 85 volatile chemicals, including 36 volatile terpenes, in 23 different tissues of cucumber plants (Cucumis sativus L.) using solid phase micro-extraction combined with gas chromatography-mass spectrometry (SPME-GC-MS). Most volatile chemicals were found to occur in a highly tissue-specific manner. The consensus transcriptomes for each of the 23 cucumber tissues were generated with RNAseq data and used in VOC-Gene correlation analysis to screen for candidate genes likely to be involved in cucumber volatile biosynthetic pathways. \textit{In vitro} biochemical characterization of the candidate enzymes demonstrated that TPS11/TPS14, TPS01, and TPS15 were responsible for volatile terpenoid production in the roots, flowers, and fruit tissues of cucumber plants, respectively. A functional heteromeric geranyl(geranyl) pyrophosphate synthase, composed of an inactive small subunit (type I) and an active large subunit, was demonstrated to play a key role in monoterpene production in cucumber. In addition to establishing a standard workflow for the elucidation of plant volatile biosynthetic pathways, the knowledge generated from this study lays a solid foundation for future investigations of both the physiological functions of cucumber volatiles and aspects of cucumber flavor improvement.

Figure: \textit{In vitro} enzymatic assays of the CsaTPSs.

Publications


Genetic Control of Plant Morphogenesis

Dr. Yonghong Wang, Principal Investigator, Ph.D. (2004, Institute of Genetics and Developmental Biology, CAS, China). The laboratory is mainly interested in elucidating the molecular basis of plant morphogenesis. Using Arabidopsis and rice as model systems, we focus on dissecting the molecular networks involved in formation and development of the shoot auxillary 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

Mitogen-activated protein kinase cascade MKK7-MPK6 plays an important role in plant development and regulates shoot branching by phosphorylating PIN1 in Arabidopsis

Weiyan Jia, Baohua Li, Shujia Li, Yan Liang, Xiaowei Wu, Mei Ma, Jiayao Wang, Jin Gao, Yueyue Cai, Yuanya Zhang, Yingchun Wang, Jiayang Li, Yonghong Wang

MAPK cascades play important roles in transducing environmental and developmental signals into adaptive and programmed responses. Because of the complexity of MAPK cascades, revealing the specificity of the MAPK modules is key to forming a functional and fully connected signal transduction system in higher plants. In the MAPK signaling module, MAPK kinases (MKKs) are of particular importance because they serve as the convergence and divergence points in the MAPK signal transduction. Our previous study has characterized an Arabidopsis bushy and dwarf1 (bud1) mutant, in which the MAP Kinase Kinase 7 (MKK7) was constitutively activated, leading to multiple auxin-related developmental defects. Here, we used the bud1 mutant to discover the signaling events of MKK7 downstream modules. Our results demonstrated that MPK6 and MPK3 are two major downstream targets of MKK7. Genetic analysis showed that the MKK7-MPK6 cascade is specifically responsible for the regulation of shoot branching, hypocotyl gravitropism, filament elongation, and lateral root formation, while MKK7-MPK3 cascade is mainly involved in leaf morphology (Fig.). Furthermore, we found that MKK7-MPK6 cascade phosphorylates the Ser 337 (S337) site of PIN1, affecting PIN1 polar localization and thus modifying shoot branching (Fig.). Our findings specify the functions of the MKK7-MPK6 cascade and explain how the MKK7-MPK6 signaling pathway regulates polar auxin transport to determine shoot branching in Arabidopsis.

Publications


Molecular Mechanisms of Ubiquitination and Plant Abiotic Stress Signaling

Dr. Qi Xie, Principal Investigator, Ph.D. (1994, Universidad de Madrid, Spain). Dr. Xie’s laboratory is mainly interested in molecular mechanisms of ubiquitination and signal transduction of plants under abiotic stress.

Email: qxie@genetics.ac.cn

Endomembrane pathways in ABA and abiotic stress signaling

Feifei Yu, Lijuan Lou, Miaomiao Tian, Qingliang Li, Xiaqiang Cao, Yaorong Wu, Qi Xie

Protein post-translational modification by ubiquitination participates in many aspects of plant growth, development and stress responses. Covalent attachment of ubiquitin to targets is sequentially catalyzed by three enzymes (E1, E2 and E3). Abscisic acid (ABA) is a major phytohormone that affects plant growth and development as well as various biotic and abiotic stress responses. Recently, the regulatory role of ubiquitination in ABA signaling has been extensively studied, especially the subtle modulation of PYR/PYL/RCAR-type ABA receptors by two multi-units E3 ubiquitin ligase complexes and one single-unit E3 ubiquitin ligase through 26S proteasome system. Most studies focused on identification and function analysis of E3 ubiquitin ligase, but the function of E2 or E2-like in ABA signaling is poorly understood. We found that E2-like VPS23A is a key component of ESCRT-I, and negatively regulates ABA signaling. Deletion of VPS23A enhances the activity of key kinase OST1 in ABA signaling under ABA treatment. VPS23A has epistatic relation with PYR/PYL/RCAR type ABA receptors. VPS23A may recognize both the unmodified PYR/PYLs and the K63-linked diubiquitin chains of PYR/PYLs. VPS23A affects the subcellular localization of PYR1 and stability of the PYL4 by the analysis of vps23a mutant. These findings support that VPS23A affects PYR1/PYL4 via vacuole-mediated degradation besides 26S proteasome system, further strengthen our understanding of both the turnover of ABA receptors and ESCRTs in plant hormone signaling.

Publications


Plant Genetics and Breeding

Dr. Shanguo Yao, Principal Investigator, Ph.D. (2004, Ehime University, Japan). The lab is mainly interested in molecular design for new rice variety in north China. In addition to utilize known functional genes, the lab is also engaged in identifying molecules of potential value in rice breeding. By pyramiding these genes, the lab is trying to find an ideal combination by which the variety could be developed with coordinately improved productivity, quality and stress tolerance.

Email: sgyao@genetics.ac.cn

Molecular design for new rice variety in north China

Ruci Wang, Li Zhang, Yueming Wang, Shanguo Yao

The rapid economic development in China greatly increases the demand for rice of good eating quality, and rice grown in Heilongjiang is extremely popular for the superior grain quality. The rice planting area in Heilongjiang could be divided into three major accumulative temperature zones, and varieties planted in these regions are differed in several traits including cold tolerance, heading date, plant height, and seed shape. Based on the evaluation of comprehensive traits of the major varieties cultivated so far in Heilongjiang, we focused on the improvement of three receptors of Kongyu131 (strong cold tolerance and better eating quality but poor blast resistance), Jite639 (good grain quality, stronger cold tolerance and higher yield but poor blast resistance and longer growth period), and Daohuaxiang2 (good grain quality but poor lodging resistance), and try to apply the improved lines in practical production in the first, second, and third accumulative temperature zone, respectively. To achieve this aim, we first investigated thoroughly the genotypes of agronomically important genes compromised in the cultivated varieties in Heilongjiang, and screened for novel alleles and created thereafter various NILs under the background of the three receptors by whole-genome background selection. Pyramiding of the alleles for blast resistance, heading date and grain quality under the background of Jite639 identified one combination that showed overall traits obviously better than that of the control variety Longjing21. The pyramided line was named Zhongke621, and will join the Regional Try for New Rice Varieties of Good Grain Quality in Heilongjiang province in 2017.

Publications


Figure: Breeding for new rice variety Zhongke621. (A) The receptor variety Jite639. (B) The control variety Longjing21 for the second accumulative temperature zone. (C) Field performance of Zhongke621. (D) Alleles introduced into Zhongke621. Indicating that the heading date of Zhongke621 was improved similar to that of the control variety Longjing21.
**Rice Ethylene Signaling and Soybean Functional Genomics**

Dr. JinSong Zhang, Principal Investigator, Ph.D. (1991, Peking University, China). Dr. Zhang’s laboratory is mainly interested in roles of ethylene signaling in plant growth, development and stress responses of rice. The laboratory focuses on new components and new mechanisms of ethylene signaling in rice. Regulatory genes for oil accumulation and stress tolerance were also investigated in soybean.

Email: jszhang@genetics.ac.cn

**Transcriptomic signature of developing soybean seeds reveals genetic basis of seed trait formation during domestication**

Xiang Lu, Qingtian Li, Qing Xiong, Wei Li, Yingdong Bi, Yongcai Liu, Weiqun Man, Wanke Zhang, Biao Ma, Shouyi Chen, JinSong Zhang

Soybean is an important crop providing oil and proteins for human. The soybean seed traits are controlled by multiple factors and may have been selected during domestication. In this study, a comprehensive assessment of the evolution of gene co-expression networks based on the analysis of 40 transcriptomes from developing soybean seeds in cultivated and wild soybean accessions was performed. Totally 2,680 differentially expressed genes during seed maturation were identified and two cultivar-specific gene co-expression networks were established. Through analysis of the two networks and integration with quantitative trait locus data, two potential key drivers GA20OX and NFYA for seed trait formation were identified. GA20OX encodes an enzyme in a rate-limiting step of GA biosynthesis, and NFYA encodes a transcription factor. Overexpression of the GA20OX and NFYA enhanced seed size/weight and oil contents respectively in seeds of transgenic plants. The two genes showed significantly higher expressions in cultivated soybeans than those in wild soybeans, and the increases in expression were associated with the genetic variations in the promoter region of the two genes (Fig.). Moreover, the expressions of the GA20OX and NFYA in seeds of soybean accessions correlated with seed weight and oil contents respectively. These studies reveal transcriptional adaption during soybean domestication and may identify a mechanism of selection by expression for seed trait formation, providing strategies for future breeding practice.

**Publications**


Molecular Basis of Plant-Microbe Interactions

Dr. Jianmin 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). Dr. Zhou’s team aims to understand how plants recognize pathogens to confer disease resistance and how pathogens cause disease on plants.

Email: jmzhou@genetics.ac.cn

Heterotrimeric G proteins regulate plant immunity

Xiangxiu Liang, Jinlong Wang, Miaomiao Ma, Xiaojuan Zhang, Jian-Min Zhou

The Arabidopsis immune receptors such as FLS2 perceive a variety of microbial molecules to activate a variety of immune responses through the central kinase BIK1. Recent reports showed that the heterotrimeric G proteins composed of the non-canonical Gα protein XLG2/3, the Gβ protein AGB1, and the Gγ proteins AGG1/2 are required for FLS2-mediated immune responses, but underlying mechanism remains unknown. We reported that the heterotrimeric G proteins positively regulate plant immunity by directly interacting with the FLS2 receptor. eLife 2016, 5: e13568.


Publications


Figure: Model for G protein-coupled FLS2 signaling. In the pre-activation state, the heterotrimeric G proteins composed of XLG2/3, AGB1, and AGG1/2 interact with the FLS2-BIK1 complex. Stimulation by flg22 induces BAK1-FLS2 interaction and activation of the receptor complex. This leads to the activation of the G proteins and phosphorylation of XLG2 in the N terminus. The activated XLG2 further regulates immunity likely through interacting with RbohD and other downstream effectors. This study demonstrates that the G proteins are directly coupled to the FLS2 receptor complex and regulate immune signaling through both pre-activation and post-activation mechanisms, highlighting remarkable similarities and striking differences in heterotrimeric G protein-coupled receptor signaling in animals and plants.
Molecular Genetics and Cell Wall Biology

Dr. Yihua Zhou, Principal Investigator, Ph.D. (1998, Institute of Genetics and Developmental Biology, CAS, China). Dr. Zhou’s laboratory is mainly interested in molecular mechanism of cell wall formation and its biological roles in plant development and growth, focusing on characterizing key components for the control of secondary wall biosynthesis and regulation, and on improving the lodge resistance of rice plants.

Email: yhzhou@genetics.ac.cn

Understanding the mechanism of xylan O-acetylation in rice

Yaping Gao, Congwu He, Dongmei Zhang, Xiangling Liu, Zuopeng Xu, Baocai Zhang, Yihua Zhou

Acetylation is a ubiquitous modification on cell wall polymers, which play a structural role in plant growth and stress defenses. However, the mechanisms for how crop plants accomplish cell-wall polymer O-acetylation are largely unknown. Here, we report on the isolation and characterization of two trichome birefringence-like (tbl) mutants in rice, which are affected in xylan O-acetylation. ostbl1 and ostbl2 single mutant and the tbl1 tbl2 double mutant displayed a stunted growth phenotype with varied degree of dwarfism. As shown by chemical assays, the wall acetylation level is affected in the mutants and the knock-down and overexpression transgenic plants. Furthermore, nuclear magnetic resonance (NMR) spectroscopy analyses showed that all those mutants have varied decreases in xylan monoacetylation. The divergent expression level of OsTBL1 and OsTBL2 explained the chemotype difference and indicated that OsTBL1 is a functionally dominant gene. OsTBL1 was found to be Golgi-localized. The recombinant OsTBL1 protein expressed in Pichia incorporates acetyl groups onto xylan. By using xylopentaose (X5), a preferring acceptor substrate, OsTBL1 can transfer up to four acetyl residues onto X5 and this activity showed saturable kinetics. 2D-NMR spectroscopy specified that OsTBL1 transfers acetate to 2-O or 3-O site of xylosyl residues. In addition, ostbl1 and tbl1 tbl2 displayed susceptibility to rice blight disease, indicating that this xylan modification is required for pathogen resistance. This study offers us the insights into the mechanisms and functions of xylan acetylation in crop plants.

Publications


Figure: OsTBL1 is involved in xylan acetylation in rice. (A) Phenotype analysis of ostbl1. (B) HSQC spectra, showing the reduced xylan acetylation in ostbl1. (C) MALDI-TOF spectra, showing that xylopentaose is acetylated by purified OsTBL1 expressed in Pichia. (D) Diagram of the products shown in panel C.
Plant Functional Genomics and Genetic Engineering Technology

Dr. Zhen Zhu, Principal Investigator, Ph.D. (1988, Institute of genetics, CAS, China). Dr. Zhu’s laboratory is mainly interested in plant functional genomics, molecular biology and agricultural biotechnology, focusing on rice biotechnology, to address the rice pest control, better use of rice heterosis, and high efficient and stable expression of foreign genes in rice.

Email: zzhu@genetics.ac.cn

Dissection of photosynthesis related molecular modules in rice

Yonggang Peng, Lei Zhang, Xiaoli Wei, Yan Dai, Yangyang Pan, Lijiao Zhang, Mi Ni, Yufei Lu, Zhen Zhu

Rice is a main food crop in China and its production is directly related to food security. The photosynthetic efficiency and the crop yield are influenced by illumination time, light intensity, temperature, moisture, fertilizing conditions and CO$_2$ deficiency during the growth stage. It is significant for improvement of photosynthetic efficiency, further increasing the grain yield in crops to illuminate the photosynthesis related molecular modules. Based on the commercial japonica rice varieties in northeast China, we investigated the main photosynthetic traits including net photosynthetic rate (Pn) and maximum quantum yield of PS II (Fv/Fm) in 240 rice varieties (Fig.), and screened high photosynthetic efficiency materials and varieties which need to be improved. We hybridized varieties between high photosynthetic efficiency materials and popularized varieties, and produced several reciprocal hybrid crosses. The F$_1$ hybrids in two hybrid crosses which showed higher photosynthetic efficiency than parental varieties were identified. We selected high photosynthetic efficiency materials of hybrid rice with the breeding potential from different ecological zones in paddy fields of northeast China. Genome-wide association study (GWAS) of Pn and Fv/Fm in 240 rice varieties was carried out using the mixed linear model (MLM). Two significant SNP loci were obtained for Pn on rice chromosome 10 in a region of 94.7 kb. Four significant SNP loci were obtained for Fv/Fm, on rice chromosome 8, in a region of 35 bp. The above research laid a foundation for further exploration of rice photosynthetic modules and cultivation of new high photosynthetic efficiency varieties.

Figure: Maximum quantum yield of PS II (Fv/Fm) in 240 rice varieties. HL0, high light 0 hour (before high light treatment). HL4, high light treatment for 4 hours. LL2, low light recovery for 2 hours. LL4, low light recovery for 4 hours.
Molecular Genetics on Plant Development and Disease Resistance

Prof. Lihuang Zhu, Principal Investigator Emeritus. The focus of Zhu’s research team is to understand how plant implements its resistance to fungal or bacterial disease, and how it regulates organ differentiation by using rice as a model. The current studies focus on the analyses of heterosis-related loci in hybrid rice and the molecular mechanisms of rice defense against blast disease.

Email: lhzhu@genetics.ac.cn

Integrated analysis of phenome, genome, and transcriptome of hybrid rice uncovered multiple heterosis-related loci for yield increase

Dayong Li, Zhiyuan Huang, Shuhui Song, Yeyun Xin, Donghai Mao, Qinming Lu, Ming Zhou, Dongmei Tian, Mingfeng Tang, Qi Wu, Xue Liu, Tingting Chen, Xianwei Song, Xiqin Fu, Bingran Zhao, Chengzhi Liang, Aihong Li, Guozhen Liu, Shigui Li, Songnian Hu, Xiaofeng Cao, Jun Yu, Longping Yuan, Caiyan Chen, Lihuang Zhu

Hybrid rice is the dominant form of rice planted in China, and its use has extended worldwide since the 1970s. It offers great yield advantages and has contributed greatly to the world’s food security. However, the molecular mechanisms underlying heterosis have remained a mystery. In this study we integrated genetics and omics analyses to determine the candidate genes for yield heterosis in a model two-line rice hybrid system, Liang-you-pei 9 (LYP9) and its parents (Fig. A). Phenomics study revealed that the better parent heterosis (BPH) of yield in hybrid is not ascribed to BPH of all the yield components but is specific to the BPH of spikelet number per panicle (SPP) and paternal parent heterosis (PPH) of effective panicle number (EPN) (Fig. B). Genetic analyses then identified multiple quantitative trait loci (QTLs) for these two components. Moreover, a number of differentially expressed genes and alleles in the hybrid were mapped by transcriptome profiling to the QTL regions as possible candidate genes (Fig. C). In parallel, a major QTL for yield heterosis, rice heterosis 8 (RH8), was found to be the DTH8/Ghd8/LHD1 gene. Based on the shared allelic heterozygosity of RH8 in many hybrid rice cultivars, a common mechanism for yield heterosis in the present commercial hybrid rice is proposed.

Publications


Regulation of carbon-nitrogen balance by rice Fd-GOGAT

Xiaolu Yang, Jinqiang Nian, Qingjun Xie, Jian Feng, Fengxia Zhang, Hongwei Jing, Jian Zhang, Guojun Dong, Yan Liang, Juli Peng, Guodong Wang, Qian Qian, Jianru Zuo

Plants assimilate inorganic nitrogen absorbed from soil into organic forms as Gln and Glu through the glutamine synthetase/glutamine:2-oxoglutarate amidotransferase (GS/GOGAT) cycle. Whereas GS catalyzes the formation of Gln from Glu and ammonia, GOGAT catalyzes the transfer of an amide group from Gln to 2-oxoglutarate to produce two molecules of Glu. We identified and characterized a rice mutant abnormal cytokinin response 1 (abc1). The weak mutant allele abc1-1 mutant shows a typical nitrogen-deficient syndrome, including the reduction in plant height, tiller number and chlorophyll content, accompanying with the loss of grain yield (Fig. A, B, C). Molecular genetics and biochemical analyses revealed that ABC1 encodes a ferredoxin-dependent (Fd)-GOGAT, a key enzyme of the GS/GOGAT cycle (Fig. D, E). In abc1-1, the Fd-GOGAT activity was significantly reduced (Fig. D), resulting in dramatic alterations in levels of the substrates and products of the GS/GOGAT cycle (Fig. F). We have identified five non-synonymous single-nucleotide polymorphisms in the ABC1 coding region, belonging to three distinct haplotypes, which have been highly and specifically differentiated between japonica and indica subspecies. These results suggest that ABC1/OsFd-GOGAT is essential for plant growth and development by modulating nitrogen assimilation and the carbon–nitrogen balance.

Publications
Center for Molecular Agrobiology

The main mission of the Center for Molecular Agrobiology (CMA) is to conduct genetic and breeding research in the major crops, with emphases on studying the molecular mechanisms underlying agronomic traits and the development of new crop varieties. In 2016, CMA scientists have made a series of important progresses in the research on genetic control of complex agronomic traits, genome editing techniques, the improvement of nutrient use efficiency and molecular mechanisms of pathogen resistance, etc.

Genetic Architecture of Complex Agronomic Traits: Yunhai Li’s Group revealed that the F-box protein SAP controls meristemoid cell proliferation and organ size by targeting PPD proteins for degradation (Wang et al., Nat Commun, 2016). They showed that DA3 controls seed and organ size by regulating the stability of cyclin (CYCA2;3) and cyclin-dependent kinase (CDKB1;1) (Xu et al., Plant Cell, 2016). In addition, they defined a regulatory mechanism of the miR396-652/OSGRF4-OsGIFs module in grain size control (Duan et al., Nat Plants, 2016). Using 809 diverse soybean accessions worldwide and genome-wide association studies, Zhixi Tian’s group identified 245 significant genetic loci and network analyses demonstrated that some associated loci exhibited pleiotropy, whereas others were linked on short fragments. This study provides insights into the genetic correlation among complex traits and will facilitate future soybean functional studies and breeding by molecular design. Cuimin Liu’s Group successfully resolved the structure of GPI, a key enzyme in starch metabolic pathways in wheat. They found two amino acid residues can significantly improve the activity of GPI, while one residue can severely reduce its activity. It will insight into the studies of biochemical properties, protein structures and regulation networks of GPI, and also provides new strategies of breeding wheat for grain quality.

Molecular Mechanisms of Pathogen Resistance: Qianhua Shen’s group identified an E3 ubiquitin ligase which was interact with several barley MLA immune receptors against powdery mildew fungus, and revealed a mechanism for stability control of immune receptors and for the attenuation of defense signaling via the ubiquitin proteasome system (Wang et al., Plant Physiol, 2016). Zhiyong Liu’s group identified and constructed fine genetic linkage map and physical map of wheat spot blotch resistance gene Sb3, providing a framework for map-based cloning of Sb3 and marker-assisted selection (MAS) of spot blotch resistance in wheat breeding programs (Lu et al., Theor Appl Genet, 2016). Daowen Wang’s group found the gene co-expression networks (GCN) and regulation mechanism, the major modules and the hub genes of the powdery mildew resistance regulated genes in immune (IM) and hypersensitive reaction (HR) resistance responses. These findings provide a new insight into the molecular mechanism in wheat resistance to *Blumeria graminis f.sp. tritici* (*Bgt*) (Zhang et al., Sci Rep, 2016). Dingzhong Tang’s group showed that an *Arabidopsis* mutant cyb3a1-3 exhibited enhanced defense responses to the powdery mildew fungus *Golovinomyces cichoracearum*. The CYP83A1A gene encodes cytochrome P450 83A1 monoxygenase, which functions in glucosinolate biosynthesis. Decreasing camalexin levels by mutation of the camalexin synthetase gene PAD3 or the camalexin synthesis regulator AtWRKY33 compromised the powdery mildew resistance. These results indicated that CYP83A1A may regulate the accumulation of camalexin through WARK33 to modulate powdery mildew resistance (Liu et al., Front Plant Sci, 2016).

The Improvement of Nutrient Use Efficiency: Yiping Tong’s group generated a wheat plant of knocking out *TaPHO2-A1* significantly increased phosphorus uptake and grain yield under low phosphorus conditions. It provides useful cue to improve wheat yield with less phosphorus fertilizer input through engineering *PHO2* expression level by genome editing approach (Ouyang et al., Sci Rep. 2016). Hongjing Ling’s group analyzed the molecular characterization of the *AtSPX3* promoter, and demonstrated that both P1BS (AtPHR1 binding site) and AtMyb4 (MYB4 putative binding site) elements were two main cis-elements in the *AtSPX3* promoter. They found that AtPHR1, a key transcription factor in Pi homeostasis of plant, was required for the negative regulation function of AtMyb4 element in shoots (Li et al., Plant Cell Physiol, 2016). Xiangdong Fu’s group found that *Arabidopsis* ENLARGED HYPOCOTYL5 (HY5), a bZIP transcription factor that regulates plant growth in response to light, is a shoot-to-root mobile signal that coordinates light-responsive carbon and nitrogen metabolism, and hence shoot and root growth, in a whole-organismal response to ambient light fluctuations. The finding enhances understanding of how plant C and N nutrient balance is maintained in fluctuating environments and suggests novel strategies for the improvement of nutrient-use efficiency in crops (Chen et al., Curr Biol, 2016).

Genome Editing Techniques: Caixia Gao’s group developed the efficient intron-mediated site-specific gene replacement and insertion approaches using the CRISPR-Cas9 system, which generate mutations using the nonhomologous end joining (NHEJ) pathway (Li et al., Nat Plants, 2016). They also developed an efficient and transgene-free genome editing in wheat through transient expression of CRISPR/Cas9 DNA or RNA (Zhang et al., Nat Commun, 2016).

Plant Chromosome Engineering: Zhensheng Li’s group developed a translocation line Xiaoyan 447 and an addition line Xiaoyan85 derived from the crosses between *Th. ponticum*, wheat-Th. ponticum partial amphidiploids and wheat, respectively. Both Xiaoyan 447 and Xiaoyan 85 display acceptable resistance to Ug99 races at seedling and adult stages (Li et al., J Genet Genomics, 2016). Fangpu Han’s group investigated two maize *de novo* centromeres atypically located in euchromatin, and found that seeding of CENH3, the centromere-specific histone, was affected by intrinsic DNA methylation patterns before neocentromere formation and that CENH3 loading can also shape the DNA methylation patterns after *de novo* centromere formation (Su et al., Plant J, 2016).

In addition, Huabang Chen’s group performed map-based cloning and abortion mechanism analysis of maize *ABNORMAL POLLEN ACULATION GENE 1* (*APV1*). Aimin Zhang’s group carried on genome-wide QTL mapping and gain further knowledge on genetic architecture of grain size in einkorn wheat. Xiangqi Zhang’s group identified several new high-molecular-weight glutenin subunit genes from *Roegneria nakaii* and *R. alashonica*, and investigated their structural characteristics and phylogenetic relationships. These studies provide new clues and resources for dissection of complex agronomic traits.

Breeding of New Varieties: Zhiyong Liu’s group developed new wheat lines for National Yellow & Huai Rivers Regional Test and Henan Provincial Regional Test in 2016. Baoge Zhu’s group created several the special nutrient soybean germplasms and bred excellent lines by molecular breeding system, and twelve breeding lines were participated the National Regional Test or Provincial Regional Test in 2016.
Maize Genetics and Breeding

Dr. Huabang Chen, Principal Investigator, Ph.D. (1999, Purdue University, USA). The Laboratory is mainly interested in corn genetics and breeding, including: 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. We are currently working on Ga1-S, and Ga2-S, the strong alleles of the gametophytic factors that control maize cross-incompatibility; Rf3, the restorer gene of CMS-S; and genes that show highly resistance to salt stresses.

Email: hbchen@genetics.ac.cn

Publication


ABNORMAL POLLEN VACUOLATION1 (APV1) is required for male fertility by contributing to anther cuticle and pollen exine formation in maize

Yamuna Somaratne, Youhui Tian, Hua Zhang, Mingming Wang, Yanqing Huo, Fengge Cao, Li Zhao, Huabang Chen

Anther cuticle and pollen exine are the major protective barriers against various stresses. The proper functioning of genes expressed in the tapetum is vital for the development of pollen exine and anther cuticle. Here, we report a tapetum-specific gene, Abnormal Pollen Vacuolation1 (APV1), in maize that affects anther cuticle and pollen exine formation. The apv1 mutant was completely male sterile. Its anther epidermal surface was smooth, shiny, and plate-shaped. Its microspores were swollen, less vacuolated, with a flat and empty anther locule. Only a few unevenly distributed Ubisch bodies were formed on the apv1 mutant, leading to a more apparent inner surface. A significant reduction in the cutin monomers was observed in the mutant. APV1 encodes a member of the P450 subfamily. APV1 appeared to be widely expressed in the tapetum at the vacuolation stage, and its protein signal colocalized with the endoplasmic reticulum (ER) signal. We suggest that APV1 functions in the fatty acid hydroxylation pathway which is involved in forming sporopollenin precursors and cutin monomers that are essential for the development of pollen exine and anther cuticle in maize.

Figure: Role of APV1 in anther cuticle and pollen exine development in maize. APV1 is expressed in the endoplasmic reticulum of the tapetum and acts on the C12 fatty acid to form the hydroxylated C12 fatty acid. Hydroxylated C12 fatty acid is then converted to hydroxylated C16/C18 fatty acids. Tapetum expressed MS26 acts on the hydroxylated C16/C18 fatty acids and converts them to ω-hydroxy C16/C18 fatty acid, which is a constituent of sporopollenin precursors and wax and cutin monomers.
Mobile transcription factor HY5 coordinates plant carbon and nitrogen acquisition

Xiangbin Chen, Qinfang Yao, Xihua Gao, Caifu Jiang, Nicholas P. Harberd, Xiangdong Fu

It has been known that coordination of shoot photosynthetic carbon fixation with root inorganic nitrogen uptake optimizes plant performance in a fluctuating environment. However, the molecular basis of this long-distance shoot-root coordination is little understood. Here we show that Arabidopsis elongated hypocotyl 5 (HY5), a bZIP transcription factor that regulates growth in response to light, is a shoot-to-root mobile signal that mediates light promotion of root growth and nitrate uptake. Shoot-derived HY5 auto-activates expression of root HY5 and also promotes root nitrate uptake by activating NRT2.1, a gene encoding a high-affinity nitrate transporter. In the shoot, HY5 promotes carbon assimilation and translocation, whereas in the root, HY5 activation of NRT2.1 expression and nitrate uptake is potentiated by increased carbon photoassimilate (sucrose) levels. We further show that HY5 function is fluence-rate modulated and enables homeostatic maintenance of carbon-nitrogen balance in different light environments. Thus, mobile HY5 coordinates light-responsive carbon and nitrogen metabolism, and hence shoot and root growth, in a whole-organismal response to ambient light fluctuations.

Figure: Shoot-to-root translocation of HY5 coordinates plant growth and nutrition in responses to fluctuating light environments. (A) and (B) HY5 is a shoot-to-root translocated protein. (C) EMSA demonstrated binding of HY5 to the NRT2.1 promoter. (D) Sucrose-promoted root NO3- uptake is dependent upon HY5. (E) HY5 maintains homeostatic balance between C and N metabolism at varying light fluence.
Efficient and transgene-free genome editing in wheat through transient expression of CRISPR/Cas9 DNA or RNA

Yi Zhang, Zhen Liang, Yuan Zong, Yanpeng Wang, Jinxiang Liu, Kunling Chen, Jin-Long Qiu, Caixia Gao

The CRISPR/Cas9 mediated genome editing system has been widely used to introduce targeted mutations in various organisms including plants. However, the commonly used genetic segregation based genome editing method has several disadvantages: the CRISPR/Cas9 DNA transgenic intermediates increases the chance of off-target changes and causes legislation concerns about genetically modified organisms (GMOs); it is still challenging to create mutations in some transformation-recalcitrant species, such as wheat, soybean, sorghum, cotton and woody plants; and it is impossible for vegetatively propagated crops such as potato, banana, and cassava to be modified by this method.

Our research team developed two simple and efficient genome editing methods, that is the transient expression of CRISPR/Cas9 DNA (abbreviated as TECCDNA) or RNA (abbreviated as TECCRNA) methods. These methods were used for the first time to edit both hexaploid bread wheat (Triticum aestivum L., AABBDD, 2n=6x=42) and tetraploid durum wheat (T. turgidum L. var. durum, AABB, 2n=4x=28). The mutagenesis frequencies of different seven genes in hexaploid bread wheat and tetraploid durum wheat ranged from 1.0% - 9.5%. Furthermore, the tissue culture procedures are free of lengthy, costly and labor intensive herbicide selection, and homozygous mutant plants with no detectable transgenes were identified in T0 populations.

Side-by-side experiment showed that the mutagenesis frequency of TECCDNA based genome editing (3.3%) was comparable to that of conventional DNA integration based genome editing (3.0%), and much higher than that of TECCRNA based genome editing (1.1%). All the mutations obtained by these two genome editing methods transmitted to the next generation faithfully, and the homozygous mutants showed the expected phenotype. We believe the two methods, especially the TECCRNA based genome editing, will accelerate molecular breeding studies in wheat, and help to stimulate basic and applied plant genome-engineering research.

Figure: Overview of the genome-editing methods based on transient expression of CRISPR/Cas9 DNA or RNA.
Non-homologous chromosomal recombination and gene exchange via the Cre/lox system in wheat engineered chromosomes

Jing Yuan, Qinghua Shi, Xiang Guo, Yalin Liu, Handong Su, Fangpu Han

Engineered minichromosomes have been produced using a telomere-mediated truncation technique in many plants, such as maize, barley, Arabidopsis and rice. However, the transfer of genes to minichromosomes has rarely been reported. Common wheat was used to perform chromosomal truncation and recombination. Telomere truncation was successfully performed in common wheat by telomere seeding with a 2.6-kb-long Arabidopsis-type telomere array to generate stable truncated chromosomes, which accompanied by a relatively high frequency of chromosomal rearrangement, especially the A-D translocation group. Using the Cre/lox system, a promoterless DsRed gene inserted in one chromosome was transferred to another chromosome behind a maize ubiquitin promoter. DsRed transcripts and red fluorescent proteins were detected in the recombinant plants. In one recombinant seedling, transgenic signals were detected by FISH analysis at the centric terminus of chromosome 4D and the distal terminus of chromosome 3A. Intriguingly, clear translocations could be detected at the transgenic loci of these two chromosomes. Furthermore, signals of centric-specific sequences were co-localized with the translocated D-group chromosomal segment in the terminal region of chromosome 3A (Fig.). Taken together, the results indicate that, besides the gene exchange into the target chromosome, non-homologous chromosomal recombination was also induced via the Cre/lox system. These approaches could offer a platform to transfer large DNA fragments or even terminal chromosomal segments to other non-homologous chromosomes of the natural genome.

Figure: Cytological detection of the cross combination of Cre1301-30 × pWY86-2011-3-20. Root metaphase chromosomes were detected using probes for 6C6, a cereal-specific centromere repeat sequence, (green) and Cre1301 (red) probes. Chromosome 3A was confirmed using the pAs1 and pSc119.2 probes.
Effects of drought and salt-stresses on gene expression in *Caragana korshinskii* seedlings revealed by RNA-seq

Shaofeng Li, Chengming Fan, Yan Li, Jianhui Zhang, Jingshuang Sun, Yuhong Chen, Changyan Tian, Xiaohua Su, Mengzhu Lu, Chengzhi Liang, Zanmin Hu

Drought and soil salinity are major abiotic stresses. The mechanisms of stress tolerance have been studied extensively in model plants. *Caragana korshinskii* is characterized by high drought and salt tolerance in northwestern China; unique patterns of gene expression allow it to tolerate the stress imposed by dehydration and semi-desert saline soil. There have, however, been no reports on the differences between *C. korshinskii* and model plants in the mechanisms underlying their drought and salt tolerance and regulation of gene expression. In this research, we investigated transcriptome changes of *C. korshinskii* whole-seedling plants in response to drought and salt stresses. On comparison of the transcriptomes of the control, drought- and salt-treated plants, 1,630 and 1,521 contigs showed significant differences in transcript abundance under drought and salt stresses. Compared to the differentially expressed genes (DEGs) in drought- or salt-treated *Arabidopsis* in the database, 542 DEGs in drought-treated *C. korshinskii* and 529 DEGs in salt-treated samples were presumably unique to *C. korshinskii*. The transcription profiles revealed that genes related to transcription factors, protein kinases, and antioxidant enzymes are relevant to the tolerance of drought and salt stress in this species. The present study identified potential genes involved in drought and salt tolerance in *C. korshinskii*, as well as many DEGs uniquely expressed in drought- or salt-treated *C. korshinskii* samples compared to *Arabidopsis*. These results will facilitate the discovery of specific stress-resistance-related genes in *C. korshinskii*, possibly leading to the development of novel plant cultivars through genetic engineering.

Figure: Venn diagrams illustrate the DEGs under drought and salt treatment in *C. korshinskii*. The red and blue colors represent the upregulated and downregulated transcripts under drought treatment, respectively. The yellow and green colors represent the upregulated and downregulated transcripts under salt treatment, respectively.
SCF\textsuperscript{SAP} controls organ size by targeting PPD proteins for degradation in \textit{Arabidopsis thaliana}

Zhibiao Wang, Na Li, Shan Jiang, Nathalie Gonzalez, Xiahe Huang, Yingchun Wang, Dirk Inzé, Yunhai Li

Control of organ size by cell proliferation and growth is a fundamental process, but the mechanisms that determine the final size of organs are largely elusive in plants. We have previously revealed that the ubiquitin receptor DA1 regulates organ size by repressing cell proliferation in \textit{Arabidopsis}. Here we report that a mutant allele of STERILE APETALA (SAP) suppresses the \textit{da1-1} mutant phenotype. We show that SAP is an F-box protein that forms part of a SKP1/Cullin/F-box E3 ubiquitin ligase complex and controls organ size by promoting the proliferation of meristemoid cells. Genetic analyses suggest that SAP may act in the same pathway with PEAPOD1 and PEAPOD2, which are negative regulators of meristemoid proliferation, to control organ size, but does so independently of DA1. Further results reveal that SAP physically associates with PEAPOD1 and PEAPOD2, and targets them for degradation. These findings define a molecular mechanism by which SAP and PEAPOD control organ size.

Figure: SAP regulates the proliferation of meristemoid cells. A model of SAP controlling organ size. The SCF\textsuperscript{SAP} complex-mediated degradation of PPD proteins causes an increased period of meristemoid cell proliferation, resulting in large organs.
Establishment and characterization of new wheat-\textit{Thinopyrum ponticum} addition and translocation lines with resistance to Ug99 races

Hongwei Li, Qi Zheng, Zacharias A. Pretorius, Bin Li, Dingzhong Tang, Zhensheng Li

Ug99 (TTKSK) is a race of \textit{Puccinia graminis} Pers.:Pers f. sp. \textit{tritici} Eriks. and E. Henn, (Pgt) with broad virulence to wheat. It was the first known Pgt race possessing virulence to Sr31, a widely used stem rust resistance gene. Ug99 spreads and evolves very fast. Up to now, a total of 13 Ug99 variants have been detected in 13 countries in Africa. Although the proportion of cultivars and lines resistant to Ug99 races has been increasing in recent years, a need still exists to discover and utilize additional sources of resistance. \textit{Thinopyrum ponticum} is the donor of stem rust resistance genes Sr24, Sr25, Sr26, and Sr43. Recent evidence demonstrated that \textit{Thinopyrum} species are rich sources of resistance to Ug99 races. With the help of Prof. Zacharias A. Pretorius, we developed a translocation line Xiaoyan 447 and an addition line Xiaoyan85 from the crosses between Th. ponticum, wheat-\textit{Th.ponticum} partial amphiploids and wheat, respectively. Both Xiaoyan 447 and Xiaoyan 85 show acceptable resistance to Ug99 both at seedling and adult stages. By using the diagnostic molecular markers for Sr24, Sr25, Sr26, and Sr43, we found that the resistance in both Xiaoyan 85 and Xiaoyan 447 is not regulated by any of these known Sr genes from \textit{Th. ponticum}. Therefore, the resistance to Ug99 races in Xiaoyan 85 and Xiaoyan 447 may be controlled by novel gene(s). We now are developing new translocation lines and new wheat varieties with high resistance to Ug99 by using Xiaoyan 85 and Xiaoyan447.

Figure: Infection responses to Ug99 race PTKST the wheat-\textit{Th.ponticum} addition line Xiaoayn 85 and translocation line Xiaoayn 447. A: Infection responses of wheat-Th.ponticum partial amphiploids to PTKST. Xiaoayn 81, Jing 411, and Federation4*/Kavkaz were used as susceptible controls. B: Infection responses of Xiaoayn 85 and Xiaoayn 447 to PTKST of \textit{P. graminis} f. sp. \textit{tritici}. 

Molecular Biology of Plant Nutrition and Wheat Genomics

Dr. 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). The laboratory is mainly interested in the molecular biology of plant nutrition and wheat genomics, focusing on studying the molecular mechanisms of iron and phosphate uptake, and on sequencing of wheat genomes and comparative analysis.

Email: hqling@genetics.ac.cn

Characterization of the AtSPX3 promoter elucidates its complex regulation in response to phosphorus deficiency

Ye Li, Huilian Wu, Huajie Fan, Ting Zhao, Hong-Qing Ling

AtSPX3, responding to phosphate (Pi) deficiency at its expression, is an important gene involved in Pi homeostasis in Arabidopsis. For understanding its transcriptional regulation, we characterized AtSPX3 promoter by distal truncation, internal deletion, and mutation of the predicted cis-elements, and identified multiple cis-elements responsive to Pi status. We found that the AtSPX3 promoter had a length limitation for activating the gene expression. The P1BS (AtPHR1 binding site) and AtMyb4 (MYB4 putative binding site) elements were two main cis-elements in the AtSPX3 promoter (Fig.). P1BS is essential and has dosage effect for activating the gene expression under Pi deficiency (Fig. B), while the element AtMyb4 possesses a dual function: one was to enhance the AtSPX3 expression in roots under Pi deficiency, and the other one was to repress AtSPX3 expression in shoots under both Pi deficiency and sufficiency (Fig. D). Moreover, we confirmed that AtPHR1, a key transcription factor in Pi homeostasis of plant, was required for the negative regulation function of AtMyb4 element in shoots (Fig. B). Generally, our findings in this work are useful for understanding the molecular regulation mechanism of genes involved in Pi uptake and homeostasis.

Figure: Functional analysis of the P1BS and AtMyb4 elements of AtSPX3 promoter. (A) Schematic outlines showing the expression cassettes of GUS driven by the full-length (FUL), P1BS-1-mutated (mP1BS-1), P1BS-2-mutated (mP1BS-2), P1BS-1 and P1BS-2 mutated (mP1BS-1–2) and containing four P1BS cis-elements (4xP1BS) promoter of AtSPX3. (B) Quantitative GUS activity analysis in roots of the plant lines transformed with the indicated vectors under Pi-deficiency (-P) and Pi-sufficiency (+P) by fluorimetric assay. (C) Schematic maps showing the expression cassettes of GUS controlled by the full length (FUL), AtMyb4-1-mutated (mMYB-1) and AtMyb4-2-mutated (mMYB-2) AtSPX3 promoter. (D) Quantitative GUS activity analysis of the transgenic plant lines with indicated vector by fluorimetric assay.

Publications


Diverse combinations of co-chaperonin subunits expanding chloroplast chaperonin system

Qian Zhao, Lixia Hu, Cuimin Liu

Many proteins can only attain their biological active conformation in the assistance of double ring cylindrical-shaped chaperonin system. In chloroplast, form I Rubisco (ribulose 1,5-bisphosphate carboxylase/oxygenase), key enzyme in Calvin cycle and also the most abundant protein on earth, depends on chloroplast chaperonin system to fold and assemble. Chloroplast chaperonin system is far more complicated than its prokaryotic ancestry due to gene duplication and specialization. In this study, we use *Chlamydomonas reinhardtii* as a model system to investigate the complexity of chloroplast co-chaperonins and how diverse co-chaperonin complexes can contribute to adaptability and flexibility of the intact chaperonin system.

Three co-chaperonin subunits exist in *Chlamydomonas* chloroplast, CrCPN10, whose size is similar to GroES. While CrCPN20 and CrCPN23, both consisting of two tandem GroES-like domain, may provide novel functional module. A complementation assay conducted in GroE-deficient *E. coli* showed a single CrCPN20 and all the possible combinations of co-chaperonin subunits could replace GroES, whereas neither a single CrCPN11 nor CrCPN23 could. But only complex consists of all three co-chaperonin subunits co-operates with its native partner CrCPN60 can fully complement GroES-GroEL system in high temperature stress. CrCPN20 and all co-chaperonin combinations could be purified in a stable complex when they are co-expressed in *E. coli*. They can all functionally interact with both GroEL and CrCPN60 according to co-migration assay and ATPase activity assay. An *in vitro* refolding assay using several model substrates with different sizes indicated different combinations of co-chaperonin may offer different chamber volumes for the intact chaperonin complex and accommodate different protein clients.

Figure: Diverse combinations of chloroplast co-chaperonin subunits endows chaperonin system extra ability. (a) Simulation model of chloroplast co-chaperonin. (b) Negative-stain Electron micrograph of CrCPN60-CrCPN112023 complex. (c) All co-chaperonin combinations can replace GroES in physiological 37°C condition. (d) ATPase activity of GroEL, CrCPN60 in the absence or presence of different co-chaperonin combinations.
Wheat Genomics, Genetics & Breeding

Dr. Zhiyong Liu, Principal Investigator, Ph.D. (1999, China Agricultural University, China). Postdoctoral researcher, (1999-2001, ETH Zurich, Swiss; 2001-2004, Hawaii Agriculture Research Center, USA). He worked as full professor at China Agricultural University from 2004-2015 and joined the Institute in 2016. Dr. Liu’s laboratory is mainly interested in wheat genetics and breeding, focusing on wheat disease resistance genes mapping and cloning.

Email: zyliu@genetics.ac.cn

Fine genetic mapping of spot blotch resistance gene Sb3 in wheat (Triticum aestivum)

Ping Lu, Yong Liang, Delin Li, Zhengzhong Wang, Wenbin Li, Guoxin Wang, Yong Wang, Shenghui Zhou, Qiuong Wu, Jingzhong Xie, Deyun Zhang, Yongxing Chen, Miaomiao Li, Yan Zhang, Qian Sun, Chenggui Han, Zhiyong Liu

Wheat spot blotch disease, caused by Bipolaris sorokiniana, is a devastating disease that can cause severe yield losses. Although inoculum levels can be reduced by planting disease-free seed, treatment of plants with fungicides and crop rotation, genetic resistance is likely to be a robust, economical and environmentally friendly tool in the control of spot blotch. We found that winter wheat line 621-7-1 conferred immune resistance against B. sorokiniana. Genetic analysis indicates that the spot blotch resistance of 621-7-1 is controlled by a single dominant gene, provisionally designated Sb3. Bulked segregant analysis (BSA) and simple sequence repeat (SSR) mapping showed that Sb3 is located on chromosome arm 3BS linked with markers Xbarc133 and Xbarc147. Nineteen polymorphic markers were developed from the Chinese Spring 3BS shotgun survey sequence contigs and 3BS reference sequences for the Sb3 gene. Finally, Sb3 was mapped in a 0.094 cM genetic interval spanning a 380 kb physical genomic region of Chinese Spring chromosome 3BS. The genetic and physical maps of Sb3 provide a framework for map-based cloning and marker-assisted selection (MAS) of the spot blotch resistance.

Publications


Molecular Mechanism of Plant Disease Resistance

Dr. Qianhua Shen, Principal Investigator, Ph.D. (2004, Max Planck Institute for Plant Breeding Research, Germany). Dr. Shen’s laboratory is interested in the molecular mechanisms of plant-microbe interactions, focusing on plant NLR receptor-mediated immunity and transcription regulation in disease resistance, non-coding sRNAs in plant-fungus interactions, and mechanism of fungal pathogen virulence.

Email: qhshen@genetics.ac.cn

SnRK1 enhances barley disease resistance by phosphorylation and destabilization of a transcription repressor

Xinyun Han, Ling Zhang, Pengya Xue, Chunlei Zhang, Qianhua Shen

Following pathogen recognition, plant immune receptors trigger immune responses that usually involve massive defense transcription reprogramming. Although many transcription factors (TFs) have been identified to regulate plant defense, the activity and stability regulation of TFs remains largely unknown. Previously, we have identified two barley TFs, WRKY1 and WRKY2, downstream of barley NLR receptor MLA activation, and each acts as a repressor in barley basal and MLA-mediated resistance against powdery mildew fungus. Here, we show that a barley protein kinase SnRK1 specifically interacts with WRKY3 to regulate its stability and defense responses. In yeast two-hybrid, SnRK1 interacted with both MLA1 and WRKY3 through their N-terminus. The interaction of SnRK1 and WRKY3 was further confirmed by in vitro pull-down assay and by bimolecular fluorescence complementation analysis (BiFC). SnRK1, upon activation by the upstream kinase GRIK1, induced the phosphorylation of WRKY3 in vitro shown by phosphor-protein mobility shift assay. We further identified two Serine residues in WRKY3, Serine83 and Serine112, as two major SnRK1 phosphorylation sites. In Nicotiana benthamiana, we showed that activation of SnRK1 induced WRKY3 phosphorylation and thus enhanced WRKY3 protein degradation dependent on 26S proteasome. WRKY3 mutants, WRKY3(S83A) or WRKY3(S112A) and WRKY3(S83A/S112A) mimicking phosphorylation-null status for the respective site(s), were more stable compared to WRKY3 wildtype. Overexpression of WRKY3 compromised basal and MLA1-mediated disease resistance to B. graminis fungus, while SnRK1 overexpression increased basal resistance to the fungus. Interestingly, coexpression of SnRK1 and WRKY3 resulted enhanced disease resistance similar to SnRK1 overexpression, suggesting that SnRK1 derepressed WRKY3 function as a defense negative regulator. Our results suggest that SnRK1 acts upstream of WRKY3 to positively regulate defense responses through phosphorylation and destabilization of WRKY3.
Molecular Plant-Microbe Interactions

Dr. Dingzhong Tang, Principal Investigator, Ph.D. (1998, Fujian Agricultural University, China). Dr. Tang’s laboratory is mainly interested in how plants transduce signals to control defense responses and how plants regulate pathogen-induced cell death. As a long-term goal, Dr. Tang’s laboratory would like to identify the major signaling pathways that regulate plant defense responses and elucidate how these pathways control plant disease resistance.

Email: dztang@genetics.ac.cn

Mutation of the glucosinolate biosynthesis enzyme cytochrome P450 83A1 monooxygenase increases camalexin accumulation and powdery mildew resistance

Simu Liu, Lisa M. Bartnikas, Sigrid M. Volko, Frederick M. Ausubel, Dingzhong Tang

Small secondary metabolites, including glucosinolates and the major phytoalexin camalexin, play important roles in plant defence responses. We isolated an Arabidopsis mutant cyp83a1-3 that exhibited enhanced defense responses to the powdery mildew fungus Golovinomyces cichoracearum, and identified a mutation in the gene encoding cytochrome P450 83A1 monooxygenase (CYP83A1), which functions in glucosinolate biosynthesis. Double mutant analysis showed that this enhanced resistance against G. cichoracearum requires NPR1, EDS1, and PAD4, but not SID2 or EDS5. In cyp83a1-3 mutants, the upregulated expression of genes related to camalexin synthesis induced by G. cichoracearum infection. Significantly, the cyp83a1-3 mutant also accumulated higher levels of camalexin. Decreasing camalexin levels by mutation of the camalexin synthetase gene PAD3 or the camalexin synthesis regulator AtWRKY33 compromised the powdery mildew resistance in these mutants. Consistent with these observations, overexpression of PAD3 increased camalexin levels and enhanced resistance to G. cichoracearum. Taken together, our data indicate that accumulation of higher levels of camalexin contributes to increased resistance to powdery mildew.

Publications

Dissection of the genetic networks underlying 84 agronomical traits in soybean

Chao Fang, Yanming Ma, Shiwen Wu, Yanting Shen, Yi Pan, Zhiwu Zhang, Guodong Wang, Baoge Zhu, Zhixi Tian

Soybean (Glycine max [L.] Merr.) is one of the most important oil and protein crops. The ever increasing soybean consumption demands challenge soybean breeding. Both the correlations among different traits and the genetic interactions among genes within a trait add the complexity of breeding process. To understand the genetic networks underlying phenotypic correlations, we collected 809 diverse soybean accessions worldwide, and phenotyped them for two years in three locations for 84 agronomic traits. Genome-wide association studies identified 245 significant genetic loci, among which 95 genetically interacted with other loci. Network analyses demonstrated that some associated loci exhibited pleiotropy, whereas others were linked on short fragments, indicating their coordinate or specific effects across different traits (Fig.). The linkage disequilibrium among the associated loci reflected the phenotypic correlations. This study provides insights into the genetic correlation among complex traits and will facilitate future soybean functional studies and breeding by molecular design.
Genetic Control of N and P Use in Wheat

Dr. Yiping Tong, Principal Investigator, Ph.D. (1999, Institute of Genetics, CAS, China). The laboratory is mainly interested in mapping QTLs for N and P use efficiency in wheat, isolating genes regulating root morphology in relation with N and P use in wheat, and molecular breeding for N and P efficient wheat varieties.

Email: yptong@genetics.ac.cn

Knock out of the TaPHO2-A1 gene improves phosphorus uptake and grain yield under low phosphorus conditions in common wheat

Xiang Ouyang, Xia Hong, Xueqiang Zhao, Wei Zhang, Xue He, Wenyong Ma, Wan Teng, Yiping Tong

MiR399 and its target PHOSPHATE2 (PHO2) play pivotal roles in phosphate (Pi) signaling in plants. Loss of function mutation in PHO2 leads to excessive Pi accumulation in shoots and growth retardation in diploid plants like Arabidopsis thaliana and rice (Oryza sativa). We isolated three PHO2 homologous genes, TaPHO2-A1, -B1 and -D1, from hexaploid wheat (Triticum aestivum). These TaPHO2 genes all contained miR399-binding sites and were able to be degraded by tae-miR399. TaPHO2-D1 was expressed much more abundantly than TaPHO2-A1 and -B1. In consist with these results, the overall expression of TaPHO2 in the roots of the tapho2-a1, -b1 and -d1 mutants was reduced to 55.8%, 70.1% and 21.1% of the wild type level (Fig. A). Among the mutants, tapho2-d1 had the strongest, tapho2-a1 the moderate, and tapho2-b1 the weakest phenotype in term of leaf Pi concentration under both low and high phosphorus conditions when the wheat seedlings were grown hydroponically. Two consecutive field experiments showed that knocking out TaPHO2-D1 reduced plant height and grain yield under both low and high phosphorus conditions. However, knocking out TaPHO2-A1 significantly increased phosphorus uptake and grain yield under low phosphorus conditions (Fig.), with no adverse effect on grain yield under high phosphorus conditions. Our results indicated that TaPHO2s involved in phosphorus uptake and translocation, and molecular engineering TaPHO2 shows potential in improving wheat yield with less phosphorus fertilizer.

Figure: Knock out of TaPHO2-A1 improves wheat growth under low P conditions. (A) Relative expression level of TaPHO2 in roots. (B) Growth performance of tapho2 mutants and wild type Xiaoyan 81 (XY81) under low P conditions.

Publications


Molecular Studies of Important Agronomic Traits and Genetic Improvement of Wheat

Dr. Daowen Wang, Principal Investigator, Ph.D. (1993, University of East Anglia and John Innes Center, UK). Research direction is to understand and improve the genetic basis of important agronomic traits in common wheat. Research projects include 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.

Publications


Coexpression network analysis of the genes regulated by two types of resistance responses to powdery mildew in wheat

Juncheng Zhang, Hongyuan Zheng, Yiwen Li, Hongjie Li, Xin Liu, Huanju Qin, Lingli Dong, Daowen Wang

Powdery mildew disease caused by Blumeria graminis f. sp. tritici (Bgt) inflicts severe economic losses in wheat crops. A systematic understanding of the molecular mechanisms involved in wheat resistance to Bgt is essential for effectively controlling the disease. Here, using the diploid wheat Triticum urartu as a host, the genes regulated by immune (IM) and hypersensitive reaction (HR) resistance responses to Bgt were investigated through transcriptome sequencing. Four gene coexpression networks (GCNs) were developed using transcriptomic data generated for 20 T. urartu accessions showing IM, HR or susceptible responses. The powdery mildew resistance regulated (PMRR) genes whose expression was significantly correlated with Bgt resistance were identified, and they tended to be hubs and enriched in six major modules. A wide occurrence of negative regulation of PMRR genes was observed. Three new candidate immune receptor genes (TRIUR3_13045, TRIUR3_01037 and TRIUR3_06195) positively associated with Bgt resistance were discovered. Finally, the involvement of TRIUR3_01037 in Bgt resistance was tentatively verified through cosegregation analysis in a F2 population and functional expression assay in Bgt susceptible leaf cells (Fig.). This research provides insights into the global network properties of PMRR genes, and suggests that Triticum urartu is a valuable model for elucidating the molecular mechanism underlying wheat resistance to Bgt infection.

Figure: Comparative analysis of resistance associated allele (RAA) and susceptibility associated allele (SAA) of the NLR gene TRIUR3_01037. (A) A diagram illustrating the two SNP sites (sites 1 and 2) in the coding region of RAA and SAA. The first SNP caused a serine to phenoalanine substitution whereas the second one rendered an alanine to threonine replacement. (B) The effects of ectopically expressing RAA or SAA on Bgt haustorium index in single-cell functional expression assay. The cells were transiently transformed by pUbi-GUS alone (as control), pUbi-RAA + pUbi-GUS (for expressing RAA) or pUbi-SAA + pUbi-GUS (for expressing SAA), followed by Bgt inoculation. About 200 infected cells were examined for haustorium growth in each treatment. Haustorium index (mean ± SD) was calculated as the percentage of examined cells with haustorium presence. The means marked by different letters are statistically different (ANOVA, P < 0.05).
Plant Molecular Genetics and Molecular Breeding

Dr. Wenxue Zhai, Principal Investigator, Ph.D. (1999, Institute of Genetics, CAS, China). 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 Xa21 gene, rice and maize molecular breeding.

Email: wxzhai@genetics.ac.cn

The Fd-GOGAT1 mutant lc7 confers resistance to Xanthomonas oryzae pv. oryzae in rice

Honglin Chen, Chunrong Li, Liping Liu, Jiying Zhao, Guanghuai Jiang, Wenxue Zhai

Bacterial blight (BB) is a serious disease in rice that is caused by the Gram-negative bacterium Xanthomonas oryzae pv. oryzae (Xoo) and can cause yield losses of up to 50%. Xoo is a serious threat to agriculture and global food security. The use of resistance genes in breeding programs has been regarded as the most effective and economical strategy for controlling bacterial blight. To date, a total of 38 BB resistance genes (R genes) have been identified. Of these genes, eight BB resistance genes, namely Xa21, Xa1, Xa26, Xa5, Xa13, Xa27, Xa10 and Xa23, have been cloned, and the protein structures that they encode are diverse. This diversity indicates that the molecular mechanism of BB resistance is very complicated in rice. We identified and characterized a rice leaf color mutant, lc7, which is defective in chlorophyll synthesis and photosynthesis but confers resistance to Xoo. Map-based cloning revealed that lc7 encodes a mutant ferredoxin-dependent glutamate synthase1 (Fd-GOGAT1). Fd-GOGAT1 has been proposed to have great potential for improving nitrogen-use efficiency, but its function in bacterial resistance has not been reported. The lc7 mutant accumulates excessive levels of ROS in the leaves, causing the leaf color to become yellow after the four-leaf stage. Compared to the wild-type, lc7 mutants have a broad-spectrum high resistance to seven Xoo races (PXO86, PXO79, PXO71, PXO99, PXO145, PXO280 and PXO339). Differentially expressed genes (DEGs) and qRT-PCR analysis indicate that many defense pathways that are involved in this broad-spectrum resistance are activated in the lc7 mutant. These results suggest that Fd-GOGAT1 plays an important role in broad-spectrum bacterial blight resistance, in addition to modulating nitrogen assimilation and chloroplast development.

Figure: Map-based cloning of the lc7 gene. (A) The lc7 gene was mapped to a 78-kb region between the markers S16 and S22 on chromosome 7 with nine candidate genes. The LOC_Os07g46460 gene encoding Fd-GOGAT1 with a single-base substitution at the 983rd position is the best candidate gene of lc7. (B, C) PCR amplification of Hyg and lc7 from the control and transgenic plants. M = Trans2k plus DNA Marker. (D, E) The relative expression level of Fd-GOGAT1 in transgenic plants. (F) The expression patterns of Fd-GOGAT1 in different tissues. (G) The Fd-GOGAT activity in wild-type, lc7 and complemented lc7 plants. (H) The phenotypes of T1 transgenic plants and their parents at the booting stage. (I) The lesion length of lc7 mutant and complemented lc7 plants 14 days after inoculation with Xoo strain PXO99. Nip-V and lc7-V are transgenic plants from the Nipponbare and lc7 mutant transformed with the pCAMBIA1301 vector, respectively; lc7-C is the function-complemented lc7 plant; and NRI is the OsFd-GOGAT1 RNAi plant.

Publications


Genome-wide QTL mapping reveals genetic architecture of grain size in einkorn wheat

Kang Yu, Wenlong Yang, Jiazhu Sun, Xin Li, Kehui Zhan, Dangqun Cui, Chunming Liu, Dongcheng Liu, Aimin Zhang

High-density genetic map is an important tool to locate agronomic traits along the chromosomes. Genetic architecture of grain size is still less understood in wheat. In this study, a high-density genetic map was developed using restriction-associated DNA sequencing (RAD-seq) on 109 recombinant inbred lines (RILs) derived from a cross of KT1-1 (Triticum monococcum ssp. boeoticum) × KT3-5 (T. monococcum ssp. monococcum). The map contained ~10K SNP markers and 936 other types of molecular markers assigned to 1,551 bins, and covered the 1,873-cM with an average marker interval of 0.2 cM. We examined seven agronomic traits in five location-year environments, including thousand grain weight (TGW), grain length (GL), grain width (GW), grain length/width ratio (GLW), grain circumference (GC), grain area (GA), and grain roundness (GR). All these traits possess high broad-sense heredity (> 80%). The total explained phenotypic variations of 46 consistent QTLs for each trait ranged from 45.7% to 66.7% (Fig. a). QTL regions, 200.8-224.3 cM on chromosome 1A and 162.2-190.1 cM on chromosome 2A contained the QTLs for GL, GLW, GA, GC, GR and TGW. By aligning with barley and Chinese Spring A genome physical map (Fig. b, c) and mapping in this RIL population, AGPL and NAL1 were located on these respective regions. Therefore, the genes or gene pathways underlying QTL, AGPL-starch syntheses and NAL1-hormone transport pathways, might be the genetic factors contributing the formation of grain. However, RT-PCR and RNA-sequencing experiments were needed to validate the mechanisms. Furthermore, the genetic map revealed that 4AL/5AL translocation and pericentric inversion 4A on hexaploid wheat (Fig. b, c). Thus, this high-density genetic map and QTL data not only provide valuable genetic information to dissect genetic architecture of grain shape associated traits in einkorn wheat, but also contribute to the genome research.
Molecular Biology and Chromosome Engineering of Wheat

Dr. Xiangqi Zhang, Principal Investigator, Ph.D. (1990, Northeast Normal University, China). Dr. Zhang’s laboratory is mainly interested in Triticeae molecular biology and chromosome engineering, focusing on resistance to disease, improvement of processing quality and development of novel germplasm.

Email: xqzhang@genetics.ac.cn

Structural characterization and evolutionary relationship of high-molecular-weight glutenin subunit genes in *Roegneria nakaii* and *Roegneria alashanica*

Lujun Zhang, Zhixin Li, Renchun Fan, Bo Wei, Xiangqi Zhang

High-molecular-weight glutenin subunits (HMW-GSs) are the major seed storage proteins in the endosperm of Triticeae species and are the critical determinants of flour processing quality of bread wheat (*Triticum aestivum* L., AABBDD). The *Roegneria* is a large genus of Triticeae, including about 130 allopolyploid species. Little is known about its high-molecular-weight glutenin subunits (HMW-GSs). In this study, we isolated six novel HMW-GS genes from two tetraploid *Roegneria* species (StStYY) native to China, *R. nakaii* Kitag and *R. alashanica* Keng, the four of them derived from *R. nakaii* and the other two from *R. alashanica*. Sequencing indicated that Rny1, Rny3, and Ray1 possessed intact open reading frames (ORFs), whereas Rny2, Rny4, and Ray2 harbored in-frame stop codons. All of the six genes possessed a similar primary structure to known HMW-GS, while showing some unique characteristics. Their coding regions were significantly shorter than Glu-1 genes in wheat (Table). The amino acid sequences revealed that all of the six HMW-GSs were intermediate towards the y-type. The phylogenetic analysis showed that the HMW-GSs from species with St, StY, or StH genome(s) clustered in an independent clade, varying from the typical x- and y-type clusters. Thus, the Glu-1 locus in *R. nakaii* and *R. alashanica* is a very primitive glutenin locus across evolution. The six genes were phylogenetically split into two groups clustered to different clades, respectively, each of the two clades included the HMW-GSs from species with St (diploid and tetraploid species), StY, and StH genomes. Hence, it is concluded that the six *Roegneria* HMW-GS genes are from two St genomes undergoing slight differentiation. The evolutionary significance and perspective on wheat improvement of these novel HMW-GSs merit further studies.

<table>
<thead>
<tr>
<th>Genes</th>
<th>GenBank Accession Number</th>
<th>ORF Size</th>
<th>Signal Peptide</th>
<th>N-terminal</th>
<th>Repetitive Domain</th>
<th>C-terminal</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rny1</td>
<td>KP121402</td>
<td>1371 bp</td>
<td>18</td>
<td>102</td>
<td>5</td>
<td>293</td>
<td>0</td>
</tr>
<tr>
<td>Rny2</td>
<td>KP121403</td>
<td>1253 bp</td>
<td>21</td>
<td>105</td>
<td>5</td>
<td>250</td>
<td>0</td>
</tr>
<tr>
<td>Rny3</td>
<td>KP121404</td>
<td>1452 bp</td>
<td>18</td>
<td>102</td>
<td>5</td>
<td>320</td>
<td>0</td>
</tr>
<tr>
<td>Rny4</td>
<td>KP121405</td>
<td>1280 bp</td>
<td>21</td>
<td>105</td>
<td>5</td>
<td>259</td>
<td>0</td>
</tr>
<tr>
<td>Ray1</td>
<td>KP121399</td>
<td>1389 bp</td>
<td>18</td>
<td>102</td>
<td>5</td>
<td>299</td>
<td>0</td>
</tr>
<tr>
<td>Ray2</td>
<td>KP121399</td>
<td>1271 bp</td>
<td>21</td>
<td>105</td>
<td>5</td>
<td>238</td>
<td>0</td>
</tr>
</tbody>
</table>

Table: A summary of some information of the six new HMW-GS genes from *R. nakaii* and *R. alashanica*
Soybean Genetics and Breeding

Dr. Baoge Zhu, Principal Investigator, Ph.D. (2005, Institute of Genetics and Developmental Biology, CAS, China). Baoge Zhu’s lab has been engaged in soybean genetics and breeding research. An efficient soybean breeding system was built and 19 excellent soybean varieties were bred. Three excellent varieties, i.e. Kefeng No.14, Kexin No.3 and Kedou No.1, have been widely released in China.

Email: bgzhu@genetics.ac.cn

Development of special nutrient soybean germplasms and breeding of excellent varieties

Baoge Zhu, Guoan Zhou, Yi Pan, Xiwen Chen

Several elite soybean lines with more seeds per pod were developed using a new molecular module by sexual hybridization and backcrosses, such as KH5-2, K25-1, K25-5, LZ904-1 and LZ904-7. The best two of these lines, LZ904-7 and KH5-2, were evaluated for field trial in Suzhou of Anhui Province and Zhoukou of Henan Province, respectively. The results showed that: 1) In Suzhou field trial, the seed yield of LZ904-7 is 3114.0 kg/ha, which is 11.79% higher than the control, while the seed yield of KH5-2 is 2977.5 kg/ha, which is 5.47% higher than the control; 2) In Zhoukou field trial, the seed yields of LZ904-7 is 3093.0 kg/ha, which is 8.24% higher than the control, while the seed yield of KH5-2 is 3225.0 kg/ha, which is 10.43% higher than the control; 3) the ratios of multiple seeds per pod of LZ904-7 and KH5-2 are increased 21.47% and 18.55% respectively compared to the controls.

Moreover, several special nutrient soybean germplasms were created using an efficient soybean molecular breeding system. The characteristics of Zhongke8 seed include large grain (35g/100 seeds), cyan coat and high oligosaccharide content, and soymilk sweet flavor. Zhongke8 is suitable for producing soy milk. The characteristics of Zhongke103 seed include high isoflavone content (0.385 mg, 92.5% higher than control), high yield (over 3000 kg/ha, 15% higher than control), and high yield of bean sprout (7.5 kg seeds, 15.4% higher than control). Zhongke103 is suitable for producing “health-nutrient” bean sprouts. A few of excellent soybean lines were also developed, twelve of which were taken for a National Regional Test or Provincial Regional Test in 2016.

Figure: Special nutrient soybean germplasms.
The missions of the Center for Developmental Biology (CDB) are focusing on fundamental questions of development of both plants and animals using model organisms such as *C. elegans*, *Drosophila*, *Xenopus*, zebrafish, mouse, monkey, *Arabidopsis* and rice, and to develop innovative technology to meet our national needs in agriculture and human health. Currently CDB has 24 research groups. There are 12 principal investigators (PI) who were awarded the *National Science Fund for Distinguished Young Scholars*, and 17 PIs who were funded by the *CAS Hundred Talents Program*. Xiaojiang Li and John Speakman were funded by the *National Thousand Talents Program*. During 2016, the Center for Developmental Biology has made substantial progress in the following fields.

**Early Development:** Weicai Yang’s group reported the identification of a cell-surface receptor heteromer, MDIS1-MIK, on the pollen tube that perceives the female attractant LURE1 in *Arabidopsis thaliana*. This finding identified the long-puzzled receptor heteromer of the LURE1 attractant and revealed the activation mechanism and will contribute to the full understanding of male-female recognition during plant reproduction. Meanwhile, this study establishes the theory of through inter-species expressing of receptor to break down the reproductive isolation and will shed light on the crop breeding (Wang et al., *Nature*, 2016). In the Solanaceae, Rosaceae and Plantaginaceae, the S-locus encodes a single S-RNase and a cluster of S-locus F-box (SLF) proteins to control the pistil and pollen expression of *SI*, respectively. Yongbiao Xue’s group revealed that the electrostatic potentials act as a major physical force between cytosolic SLFs and S-RNases, providing a mechanistic insight into the self/non-self-discrimination between cytosolic proteins in angiosperms (Li et al., *Plant J.*, 2016). Large numbers of maternal RNAs are deposited in oocytes and are reserved for later development. Jian Zhang’s group reported loss of Zar1 causes markedly upregulation of zona pellucida (ZP) family proteins, while overexpression of ZP proteins in oocytes causes upregulation of stress related activating transcription factor 3 (atf3), arguing that tightly controlled translation of ZP proteins is essential for ER homeostasis during early oogenesis. Furthermore, Zar1 binds to zona pellucida (zp) mRNAs and represses their translation (Miao et al., *Development*, 2016).

**Neurodevelopment and Disease:** Zhiheng Xu’s group and Guoli Ming’s group at Johns Hopkins University revealed that Crmp2 (collapsing response mediator protein 2), a schizophrenia risk gene, plays a critical role in neural development, circuit integrity and brain function. They provided a valuable mouse model for better understanding the aetiology of schizophrenia and targeted strategies for drug development (Zhang et al., *Nat Commun*, 2016). Xu’s group also demonstrated MEA6 plays a critical role in lipid transportation through the coordinated regulation of the COPII machinery, which provided insights into mechanisms underlying VLDL transportation. More importantly, this mouse model provides a useful tool for potential biomarkers or drug screening related to fatty liver disease (Wang et al., *Cell Res.*, 2016). Mei Ding’s group found that the single calponin homology (CH) domain-containing protein CHDP-1 induces the formation of cell protrusions by coupling membrane expansion to Rac1-mediated actin dynamics in *Caenorhabditis elegans* (Guan et al., *PLoS Genet*, 2016). Xiaojiang Li’s group revealed age- and cell type-dependent vital functions of Htt (huntingtin, Huntington’s disease protein) and the safety of knocking down neuronal Htt expression in adult brains as a treatment (Wang et al., *PNAS*, 2016; Liu et al., *PLoS Genet*, 2016). The study of Yongqing Zhang’s group study sheds new light onto the neuronal functions of UBE3A (E3 ubiquitin ligase) and provides novel perspectives for understanding the pathogenesis of UBE3A-associated Angelman syndrome and autism (Li et al., *PLoS Genet*, 2016).

**Stem Cell and Tissue Engineering:** Zhiheng Xu’s group gave direct evidence that Zika infection causes microcephaly in a mammalian animal model. They found the virus infected the neural progenitor cells, and infected brains reveal expression of genes related to viral entry, altered immune response, and cell death. Further study showed passive transfer of convalescent serum containing high-titer neutralizing antibodies to pregnant mice can not only suppress ZIKV replication but also inhibit cell death and reduction of neural progenitor cells in infected fetal brains, thus preventing microcephaly (Wang et al., *Cell Res.*, 2016). Jianwu Dai’s group screened a functional scaffold, on which the cultured neural stem cells (NSCs) show high neuronal differentiation rate and generate both sensory and motor mature neurons. They transplanted the functional scaffold into a rat severe spinal cord injury model, which showed that higher endogenous neurogenesis efficiency as well as in vivo survival and neuronal differentiation rate of the grafted NSCs are observed (Li et al., *Adv Funct Mater*, 2016).

**Lipid Metabolism and Development:** John Speakman’s group used public domain data to locate signatures of positive selection based on derived allele frequency, genetic diversity, long haplotypes, and differences between populations at SNPs identified in genome-wide association studies (GWASs) for BMI. The widespread absence of signatures of positive selection, combined with selection favoring leanness at some alleles, does not support the suggestion that obesity provided a selective advantage to survive famines, or any other selective advantage (Wang et al., *Cell Metab.*, 2016). Using state-of-the-art lipidomic approach, Guanghou Shui’s group found a breakdown in DHA esterification into neural membranes may prove more detrimental than a diminished dietary supply of DHA per se (Lam et al., *Oncotarget*, 2016).

**Vesicle Trafficking and Development:** Together with Xiaojiaing Hao’s group at Kunming Institute of Botany, CAS, Chonglin Yang’s group showed that protein kinase C couples activation of the TFEB transcription factor with inactivation of the ZKSCAN3 transcriptional repressor through two parallel signaling cascades. It revealed that PKC activators are viable treatment options for lysosome-related disorders (Li et al., *Nature Cell Biol.*, 2016). Phosphatidylinositol 3-phosphate (PtdIns3P) plays a central role in endosome fusion, recycling, sorting, and early-to-late endosome conversion. Yang’s group identified two new factors, SORF-1 and SORF-2, as essential PtdIns3P regulators in *C. elegans*. These findings revealed a conserved mechanism that controls appropriate PtdIns3P levels in early-to-late endosome conversion (Liu et al., *J Cell Biol.*, 2016).
Loss of the golgin GM130 causes golgi disruption, purkinje neuron loss, and ataxia
Chunyi Liu, Mei Mei, Qiuling Li, Peristera Roboti, Qianqian Pang, Zhengzhou Ying, Fei Gao, Martin Lowe, Shilai Bao

The golgi apparatus lies at the heart of the secretory pathway where it is required for secretory trafficking and cargo modification. Disruption of golgi architecture and function has been widely observed in neurodegenerative disease, but whether golgi dysfunction is causal with regard to the neurodegenerative process, or is simply a manifestation of neuronal death, remains unclear. Here we report that targeted loss of the golgin GM130 leads to a profound neurological phenotype in mice. Global knockout of mouse GM130 results in developmental delay, severe ataxia, and post-natal death. We further show that selective deletion of GM130 in neurons causes fragmentation and defective positioning of the golgi apparatus, impaired secretory trafficking, and dendritic atrophy in Purkinje cells. These cellular defects manifest as reduced cerebellar size and Purkinje cell number, leading to ataxia. Purkinje cell loss and ataxia first appear during post-natal development but progressively worsen with age. Our data therefore indicate that targeted disruption of the mammalian golgi apparatus and secretory traffic results in neuronal degeneration in vivo, supporting the view that Golgi dysfunction can play a causative role in neurodegeneration.

Figure: Loss of GM130 resulted in dentritic atrophy. (A) Golgi staining shows that dendritic atrophy in Purkinje cells appeared during post-natal development (P30). (B) Defective positioning of the Golgi apparatus in Purkinje cells in GM130 loss mice. (C) Model for GM130 function in dendrite maintenance in Purkinje cells.
Plant Molecular Control and Response

Dr. Fan Chen, Principal Investigator, Ph.D. (1997, Ehime University, Japan). The laboratory mainly focuses on plant molecular response and control mechanism. The signal transduction during plant development 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

The mechanism of abscisic acid signaling and stress response in rice

Lei Wang, Jianying Liu, Meijuan Zou, Fang Zhang, Guanlin Zhu, Jun’e Jiang, Haibo Ren, Xiaohua Fang, Fan Chen

Abscisic acid (ABA) is an essential phytohormone that not only regulates seeds dormancy, germination and seedling growth, but also is involved in responding to environmental stresses such as drought, high salinity and chilling. The identified ABA receptors, PYR/PYL/RCAR was found to directly bind and regulate the activity of the protein phosphatase 2C (PP2C). The Sucrose Non-fermentation Kinase Subfamily 2 (SnRK2s) protein kinases, a central signaling complex (ABA-PYR-PP2Cs-SnRK2s) that is responsible for ABA signal perception and transduction is supported by abundant genetic, physiological, biochemical and structural evidence. Ten PYLs orthologs with the special structure of ABA receptor were identified in rice. Though the common signal transduction pathway was characterized among the members of PP2C family, the function and stress response of the OsPYLs were based on their ABA binding activity in rice. The basic leucine zipper (bZIP) factors are involved in ABA signaling pathway and play an important regulator during environmental stress response. There are 10 clades of bZIPs in rice, from clade A to clade J. The function of several rice bZIP-type transcription factors was analyzed and they are involved in the regulation of the adaptive stress response and plant fertility of rice. The result of phosphorylation by OsSnRK2s show that members from both clade A and clade G are involved in ABA signal pathway, but the signal transduction pathway of members from clade G may be different from those from clade A.

Figure: Different pathway of ABA signal transduction with the phosphorylation of bZIP proteins in rice.

Publications


Regenerative Medicine and Tissue/Organ Construction

Dr. Jianwu Dai, Principal Investigator, Ph.D. (1998, Duke University, USA). The main focus of his laboratory is to develop the intelligent biomaterials for tissue regeneration and to construct of artificial tissue or organ in vitro.

Email: jwdai@genetics.ac.cn

Publications


The clinical study of spinal cord injury by treatment of NeuroRegen scaffold

Zhihong Xiao, Yannan Zhao, Bing Chen, Sufang Han, Xing Li, Jin Han, Jianwu Dai

The objective of the clinical study was to assess the safety and feasibility of the collagen scaffold transplantation, named NeuroRegen scaffold, in complete chronic spinal cord injury (SCI) patients. Different lengths of scars ranging from 0.5–4.5 cm were surgically resected in five complete chronic SCI patients under nerve electrophysiology instructions. The NeuroRegen scaffold along with autologous bone marrow mononuclear cells (BMMCs), which have been proven to promote neural regeneration and SCI recovery in animal models, were transplanted into the gap in the spinal cord following scar tissue resection (Fig. A-C). No obvious adverse effects related to scar resection or NeuroRegen scaffold transplantation were observed immediately after surgery or at the 12-month follow-up. The significant progresses of this study are as below: firstly, we use the nerve electrophysiology method to distinguish scar tissue from normal neural tissue, and resected the scar from patients’ spinal cords; secondly, the safety and feasibility of NeuroRegen scaffold transplantation was proven. The results indicate that NeuroRegen scaffold transplantation could be a promising clinical approach to treating SCI (Xiao et al., 2016).

Soon after, eight patients with chronic complete SCI were enrolled to examine the safety and efficacy of implanting NeuroRegen scaffold with human umbilical cord mesenchymal stem cells (MSCs). No adverse events were observed during 1 year of follow up. During one year of observation of neurological function after scaffold implantation, we found that 62.5% of subjects demonstrated expansion of sensation level (Fig. D), and three patients with cervical lesions showed increased finger flexibility (Fig. F). We also analyzed MEPs in patients and found marked expansion of the MEP-responsive area in 87.5% of patients (Fig. E), which suggests partial recovery of neurological function. Increased stability and trunk equilibrium in the sitting position were reported in four patients. Autonomic dysfunction is a common clinical consequence of SCI; we detected autonomic neural function recovery, such as enhanced skin sweating below the injury level, in some patients after the treatment (Fig. F) (Accepted).

Our study suggests that construction of a regenerative microenvironment using a scaffold-based strategy may be a possible future approach to SCI repair.
Neural Development

Dr. Mei Ding, Principal Investigator, Ph.D. (2004, University of California, Santa Cruz, USA). Dr. Ding’s laboratory is interested in discovering the molecular mechanisms underlying neural development using *Caenorhabditis elegans* as a model system.

Email: mding@genetics.ac.cn

The calponin family member CHDP-1 interacts with Rac1/CED-10 to promote cell protrusions

Liying Guan, Xuehua Ma, Jingyan Zhang, Mei Ding

In response to intra- and extracellular cues, remodeling of the sub-membranous cortical actin cytoskeleton constantly reorganizes the plasma membrane. Thus, distinct types of actin-rich invaginations or protrusions, such as filopodia and lamellipodia, enable cells to explore territory and pull themselves around. Extensive research has shown that the plasma membrane is tightly coupled to the motility machinery. However, how the continuous reorganization of the actin cytoskeleton is coupled with appropriate restructuring of the plasma membrane at the molecular level in vivo is unclear. We discovered that the protein CHDP-1, which contains a single type III CH domain and shares homology to calponin in mammals, plays a crucial role in protrusion formation in *C. elegans*. With its additional amphipathic helix motif in its C-terminal, CHDP-1 localizes to the cell cortex and induces the formation of membrane protrusions. The CH domain of CHDP-1 does not bind to either G- or F-actin, but instead binds to the Rac1 homolog CED-10. This suggests that CHDP-1 may influence actin cytoskeleton dynamics by directly regulating Rac1/CED-10. Intriguingly, CHDP-1 preferentially binds to the GTP-bound active form of the CED-10 protein and preserves the membrane localization of GTP-CED-10. Hence, by coupling membrane expansion to Rac1-mediated actin dynamics, CHDP-1 promotes the formation of cellular protrusions in *C. elegans*.

Figure: CHDP-1 associates with CED-10. (A) Protein-protein interactions between CHDP-1 and CED-10 in immunoprecipitation assays. (B-C) GFP::CED-10 colocalizes with RFP::CHDP-1 at the periphery (B) and in protrusions (C) of the PLM cell. Asterisks label the nucleus within the cell body. (D) CHDP-1 co-precipitates the GTP-bound active form of the CED-10 protein. (E) The membrane localization of CED-10 is defective in chdp-1(xd27) mutant animals. (F) The membrane localization of GFP::CHDP-1 is not altered in ced-10(n1993) mutants.

Publication

Neural Stem Cells and Neurogenesis

Dr. Weixiang Guo, Principal Investigator, Ph.D. (2008, Institute of Zoology, CAS, China). Dr. Guo’s laboratory is mainly interested in 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

Positive feedback between RNA-binding protein HuD and transcription factor SATB1 promotes neurogenesis

Feifei Wang, Joseph J. Tidei, Eric D. Polich, Yu Gao, Huashan Zhao, Nora I. Perrone-Bizzero, Weixiang Guo, Xinyu Zhao

The mammalian embryonic lethal abnormal vision (ELAV)-like protein HuD is a neuronal RNA-binding protein implicated in neuronal development, plasticity, and diseases. Although HuD has long been associated with neuronal development, the functions of HuD in neural stem cell differentiation and the underlying mechanisms have gone largely unexplored. Here we show that HuD promotes neuronal differentiation of neural stem/progenitor cells (NSCs) in the adult subventricular zone by stabilizing the mRNA of special adenine–thymine (AT)-rich DNA-binding protein 1 (SATB1), a critical transcriptional regulator in neurodevelopment. We find that SATB1 deficiency impairs the neuronal differentiation of NSCs, whereas SATB1 overexpression rescues the neuronal differentiation phenotypes resulting from HuD deficiency. Interestingly, we also discover that SATB1 is a transcriptional activator of HuD during NSC neuronal differentiation. In addition, we demonstrate that NeuroD1, a neuronal master regulator, is a direct downstream target of SATB1. Therefore, HuD and SATB1 form a positive regulatory loop that enhances NeuroD1 transcription and subsequent neuronal differentiation. Our results here reveal a novel positive feedback network between an RNA-binding protein and a transcription factor that plays critical regulatory roles in neurogenesis.

Figure: Model for the HuD and SATB1 regulatory network for the regulation of adult NSC neuronal differentiation through NeuroD1.
Lipid Metabolism and Development

Dr. Xun Huang, Principal Investigator, Ph.D. (2003, University of California, Santa Cruz, USA). The laboratory is mainly interested in discovering the regulation of lipid metabolism and the role of lipid metabolism during animal development.

Email: xhuang@genetics.ac.cn

Publications


Qi Y., Kapterian T., Du X., Ma Q., Fei W., Zhang Y., Huang X., Dawes I., Yang H. CDP-diacylglycerol synthases regulate the growth of lipid droplets and adipocyte development. J. Lipid Res. 57: 767-780.


Drosophila TRF2 and TAF9 regulate lipid droplet size and phospholipid fatty acid composition

Wei Fan, Sin Man Lam, Xiao Yang, Zhonghua Liu, Yuan Liu, Guanghou Shui, Xun Huang

Lipid droplets (LD) are main lipid storage structures in most cells. The size of LDs varies greatly in different cell types to accommodate distinct cellular functions. It is well known that the content of the lipid core, the composition of monolayer phospholipids and the protein machinery for LD fusion affect the size of LDs. In addition, taking advantage of genetic and cell based-RNAi screens, systematic studies have identified numerous genes and cellular pathways involved in the regulation of lipid storage and LD dynamics. However, our understanding of the lipid storage network and regulation of LD dynamics is far from clear. In this study, we identified that several components of the general transcription factor TFIIID complex, including a specific TBP (TATA-box binding protein) family protein TRF2 (TBP-related factor 2) and several TAFs (TBP-associated factors), regulate LD size in the Drosophila larval fat body (Fig.). Lipidomic analysis reveals that TRF2 and TAF9 also affect the fatty acid composition of several classes of phospholipids. When we compared the relative amounts of major phospholipids based on the total fatty acid chain length, there are more phospholipid species with longer fatty acid chains in trf2 and taf9 RNAi fat bodies compared with controls. These results suggest that several classes of phospholipids in trf2 and taf9 RNAi tend to be composed of fatty acids with long chain lengths. These data reveal specific roles of general transcription factors in lipid metabolism and lipid storage.

Figure: TRF2 and TAFs affect LD size in Drosophila larval fat body and phospholipid fatty acid composition.
Bio-Imaging and Micro/Nano Optics

Dr. Yuqiang Jiang, Principal Investigator, Ph.D. (2004, Shanxi University, China). The laboratory is mainly interested in the development of optical micromanipulation (laser tweezers) and bio-imaging techniques, and their applications in biology. We have found some novel phenomena based on none linear polarization, such as “trap split”, in optical trapping nanoparticles with ultrafast pulsed laser; and realized live cells imaging with two-photon induced luminescence from gold nanoparticles.

Email: yqjiang@genetics.ac.cn

PINK1 and Parkin cooperatively protect neurons against constitutively active TRP channel-induced retinal degeneration in *Drosophila*

Zengyi Huang, Yuqiang Jiang, Tao Wang

Calcium has an important role in regulating numerous cellular activities. However, extremely high levels of intracellular calcium can lead to neurotoxicity, a process commonly associated with degenerative diseases. Despite the clear role of calcium cytotoxicity in mediating neuronal cell death in this context, the pathological mechanisms remain controversial. We used a well-established *Drosophila* model of retinal degeneration, which involves the constitutively active TRPP365 channels, to study calcium-induced neurotoxicity. We found that the disruption of mitochondrial function was associated with the degenerative process. Further, increasing autophagy flux prevented cell death in TRPP365 mutant flies, and this depended on the PINK1/Parkin pathway. In addition, the retinal degeneration process was also suppressed by the coexpression of PINK1 and Parkin. Our results provide genetic evidence that mitochondrial dysfunction has a key role in the pathology of cellular calcium neurotoxicity. In addition, the results demonstrated that maintaining mitochondrial homeostasis via PINK1/Parkin-dependent mitochondrial quality control can potentially alleviate cell death in a wide range of neurodegenerative diseases.

Publications


Figure: Modifying mitochondrial quality control pathways modulates the severity of photoreceptor cell death in TRPP365 flies. (a–h) TEM images of cross-sections from 8-day-old flies. (a) Wild-type. (b) TRPP365+/+. (c) ninaE>opa1 (ninaE-gal4/UAU-opa1). (d) ninaE>opa1;TRPP365+/+. (e) ninaE>drp1 (ninaE-gal4/UAU-drp1). (f) ninaE>drp1;TRPP365+/+. (g) ninaE>vcp (ninaE-gal4/UAU-vcp). (h) ninaE>vcp;TRPP365+/+. Scale bar, 2 μm. (i) Histogram of the mean number of rhabdomeres per ommatidium from 8-day-old flies. The quantification is based on the examination of TEM images of ≥150 ommatidia from three flies. Error bars indicate S.E.M.s (***P< 0.001).
Neurodegenerative Diseases and Developmental Biology

Dr. Xiaojiang Li, Principal Investigator, Ph.D. (1991, Oregon Health Science University, USA). Since 1996, Dr. Li has been a faculty member and was promoted to Professor in 2005. Dr. Li was appointed as Distinguished Professor of Emory University in USA in 2007. Dr. Li’s laboratory is mainly interested in transgenic animal models and pathogenesis of neurodegenerative diseases.

Email: xjli@genetics.ac.cn

Ablation of huntingtin in adult neurons is nondeleterious but its depletion in young mice causes acute pancreatitis

Guohao Wang, Xudong Liu, Marta A. Gaertig, Shihua Li, Xiaojiang Li

The Huntington’s disease (HD) protein, huntingtin (HTT), is essential for early development. Because suppressing the expression of mutant HTT is an important approach to treat the disease, we must first understand the normal function of Htt in adults versus younger animals. Using inducible Htt knockout mice, we found that Htt depletion does not lead to adult neurodegeneration or animal death at > 4 months of age, which was also verified by selectively depleting Htt in neurons. On the other hand, young Htt KO mice die at 2 months of age of acute pancreatitis due to the degeneration of pancreatic acinar cells. Importantly, Htt interacts with the trypsin inhibitor, serine protease inhibitor Kazal-type 3 (Spink3), to inhibit activation of digestive enzymes in acinar cells in young mice, and transgenic HTT can rescue the early death of Htt KO mice. These findings point out age- and cell type-dependent vital functions of Htt and the safety of knocking down neuronal Htt expression in adult brains as a treatment.

Figure: Inactivation of Htt does not cause neurodegeneration but lead to pancreatitis. (A) Morphology of control and wHtt-KO mice brain was photographed at 2-month-old. (B) Brain volume were measured after tamoxifen injection 5 days (n=7, n.s. represents no significant differences). (C) Immunostaining of GFAP, LC3I/II, and beta-tubulin III in the cortex of different aged wHtt-KO and control mice.

Publications

Hong Y., Zhao T., Li X., Li S., Mutant huntingtin Impairs BDNF release from astrocytes by disrupting Rab3a GTP/GDP exchange. J. Neurosci. 2016, 36: 8790-8801.
Molecular Mechanisms and Functions of Retrograde Vesicular Transport

Dr. Jia-Jia Liu, Principal Investigator, Ph.D. (2000, University of Chicago, USA). The laboratory is mainly interested in membrane trafficking, focusing on molecular mechanisms of retrograde vesicular transport in mammalian cells and role(s) of vesicular transport in neurodevelopment.

Email: jjliu@genetics.ac.cn

Retrolinkin recruits the WAVE1 protein complex to facilitate BDNF-induced TrkB endocytosis and dendrite outgrowth

Chenchang Xu, Xiuping Fu, Shaoxia Zhu, Jia-Jia Liu

Retrolinkin, a neuronal membrane protein, coordinates with endophilin A1 and mediates early endocytic trafficking and signal transduction of the ligand-receptor complex formed between brain-derived neurotrophic factor (BDNF) and its receptor, tropomyosin related Kinase B (TrkB), in dendrites of CNS (CNS) neurons. Here we report that retrolinkin interacts with the CYFIP1/2 subunit of the WAVE1 complex, a member of the WASP/WAVE family of nucleation promoting factors (NPF) that binds and activates the Arp2/3 complex to promote branched actin polymerization. WAVE1, not N-WASP, is required for BDNF-induced TrkB endocytosis and dendrite outgrowth. Disruption of the interaction between retrolinkin and CYFIP1/2 impairs recruitment of WAVE1 to neuronal plasma membrane upon BDNF addition and blocks internalization of activated TrkB. We also show that WAVE1-mediated endocytosis of BDNF-activated TrkB is actin-dependent and clathrin-independent.

These results not only reveal the mechanistic role of retrolinkin in BDNF-TrkB endocytosis, but also indicate that WASP/WAVE-dependent actin polymerization during endocytosis is regulated by cell type-specific and cargo-specific modulators.

Publications


Mps1 kinase regulates tumor cell viability via its novel role in mitochondria

Xiaojuan Zhang, Yu Guo, Fuxing Gong, Pingping Tan, Runlin Z. Ma

Targeting mitotic kinase monopolar spindle 1 (Mps1) for tumor therapy has been investigated for many years. Although it was suggested that Mps1 regulates cell viability through its role in spindle assembly checkpoint (SAC), the underlying mechanism remains less defined. In an endeavor to reveal the role of high levels of mitotic kinase Mps1 in the development of colon cancer, we unexpectedly found the amount of Mps1 required for cell survival far exceeds that of maintaining SAC in aneuploid cell lines. This suggests that other functions of Mps1 besides SAC are also employed to maintain cell viability. Mps1 regulates cell viability independent of its role in cytokinesis as the genetic depletion of Mps1 spanning from metaphase to cytokinesis affects neither cytokinesis nor cell viability. Furthermore, we developed a single-cycle inhibition strategy that allows disruption of Mps1 function only in mitosis. Using this strategy, we found the functions of Mps1 in mitosis are vital for cell viability as short-term treatment of mitotic colon cancer cell lines with Mps1 inhibitors is sufficient to cause cell death. Interestingly, Mps1 inhibitors synergize with microtubule depolymerizing drug in promoting polyploidization but not in tumor cell growth inhibition. Finally, we found that Mps1 can be recruited to mitochondria by binding to voltage-dependent anion channel 1 (VDAC1) via its C-terminal fragment. This interaction is essential for cell viability as Mps1 mutant defective for interaction fails to main cell viability, causing the release of cytochrome c. Meanwhile, deprivation of VDAC1 can make tumor cells refractory to loss of Mps1-induced cell death. Collectively, we conclude that inhibition of the novel mitochondrial function Mps1 is sufficient to kill tumor cells.
Cytoskeletal Dynamics and Function


Email: wxmeng@genetics.ac.cn

Functional analysis of CAMSAP3 in the formation of noncentrosomal microtubules

Congcong Dong, Honglin Xu, Wenxiang Meng

The epithelium has apico-basal axis polarity that plays an important role in absorption, excretion and other physiological functions. In epithelial cells, a substantial number of noncentrosomal microtubules (MTs) are scattered in the cytoplasm with an apico-basal polarity to adapt to these complex functions. Several previous studies have found that noncentrosomal MTs are nucleated at the centrosome, and then released and translocated elsewhere. However, the detailed process and molecular mechanism remains largely unknown. In this study, we found that Nezha, also called CAMSAP3 (calmodulin-regulated spectrin-associated protein 3), a noncentrosomal MT minus-end protein, accumulated in the pericentrosomal area and accompanied the release of MTs from the centrosome; whereas depletion of CAMSAP3 prevented MT release and instead caused focusing of MTs at centrosomes. Further studies demonstrated CAMSAP3 precisely coordinated with dynein and katanin to regulate the MT detachment process. In conclusion, our results indicate CAMSAP3 is a key molecule for generation of noncentrosomal MT.

Publications


Figure: CAMSAP3 promotes release of centrosomal MTs from the centrosome. (A) Time-lapse recording of CAMSAP3-GFP and α-tubulin-RFP expressed in a DLD1 cell during regrowth. (B) DLD1 cells transfected with the indicated siRNAs were immunostained for CAMSAP3, α-tubulin, and γ-tubulin when regrowth for 10 min. (Right) Quantity of microtubule intensities at pericentrosomal area. (C) Stable cell lines for GFP and CAMSAP3-GFP were immunostained for α-tubulin and γ-tubulin when regrowth for 30 min. (Right) Quantity of microtubule intensities at pericentrosomal area. Scale bars, 6 μm. ***P < 0.001, n≥30.
Lipidomics and Lipid Metabolism

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

Biological relevance of fatty acyl heterogeneity to the neural membrane dynamics of Rhesus macaques during normative aging.

Sin Man Lam, Gek Huey Chua, Xiao-Jiang Li, Bing Su, Guanghou Shui

Using state-of-the-art lipidomic approaches, we report herein an extensive lipidomic atlas of the changing membrane lipid landscape in the frontal cortex of Rhesus macaques across three selected age groups (i.e., young, sexually-mature and old) to the details of individual fatty acyls. Remarkably, our lipidomic analysis revealed an intriguing pattern of PUFA-esterification across phospholipids on a temporal scale, with docosahexaenoic acids (DHAs) displaying notable accretions in sexually-mature macaques for all phospholipid classes examined, which is not observable in all remaining polyunsaturated fatty acids (PUFAs). On the other hand, arachidonic acid (ARA) exhibited sharp attritions in the membrane lipidesomes of sexually-mature macaques, a decline which was attenuated only for cardiolipins (CLs). Interestingly, DHA enrichment in phospholipids was lost in old macaques, with accompanying augmentations in very-long-chain sphingomyelins (VLC-SMs). Correlation matrix analysis demonstrated an escalating degree of membrane lipid co-regulation with aging, and point to an attractive possibility that a complex temporal interplay between DHA-enriched membrane microdomains and SM-/cholesterol-rich rafts may exist in neural membranes. Lipid co-regulation data also suggest that these membrane microdomains may foster global changes in membrane dynamics principally via altering CL level, which subsequently prompts alternative membrane lipid synthetic pathways driven by a compromised energy availability in the aging brain.

Figure: Schematic diagram illustrating the proposed role of changing membrane lipid dynamics that governs normative brain aging in Rhesus macaques. The temporal switching of between DHA-enriched membrane microdomains and raft membrane microdomains may serve as competing platforms to modulate distinct pathways that constitute the molecular basis of aging, principally resulting in a gradual reduction in total CLs and a decline in energy availability from mitochondrial oxidative phosphorylation. The brain turns to alternative, energy-saving phospholipid synthetic pathways in place of de novo biosynthesis to maintain membrane dynamics under a compromised energy supply, leading to increasingly intense degree of membrane lipid co-regulation with aging.

Publications


Molecular Energetics

Dr. John R. Speakman, Principal Investigator, Ph.D. (1984, University of Stirling, UK), FRSE (2004), FMedSci (2008), Fellow of the Academy of Europe (2012). The focus of our group is to understand 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

Analysis of positive selection at single nucleotide polymorphisms associated with body mass index does not support the “Thrifty Gene” hypothesis

Guanlin Wang, John Speakman

Proposed in 1962 one of the most popular ideas for the genetic basis of human obesity is the Thrifty gene hypothesis. This suggests that ancestraly genes promoting obesity were positively selected for because they enhanced the ability to survive periods of famine. I have argued against this idea and proposed in 2007 the ‘drifty gene’ hypothesis which suggests that obesity susceptibility is a product of genetic drift. This is proposed to occur because in our past we probably controlled our body weight very well as a mechanism to avoid predation. Around 2 million years ago however Homo erectus developed weapons and fire and also social behaviour. These were sufficient to remove the selective pressure against body weight gain. The machinery underlying the upper regulation point for body weight was therefore able to mutate and drift. We tested between these ideas by searching for signatures of positive selection in the human genome at SNPs linked to BMI. The thrifty gene idea suggests that such signatures would be evident at loci related to obesity, while the drifty gene idea suggests such signatures will be absent. We found using multiple metrics in multiple populations that the occurrence of positive selection in BMI related SNPs was no higher than for randomly selected SNPs, and lower than in positive control SNPs already known to be under positive selection (eg in the lactase gene and two genes linked to lighter skin colour in Europeans). The figures show the comparison of tests in the BMI associated randomly selected and positive control SNPs.

Publications


Mitochondrial stress induces chromatin reorganization to promote longevity and UPR\textsuperscript{mt}

Ye Tian, Gilberto Garcia, Qian Bian, Kristan K. Steffen, Larry Joe, Suzanne Wolff, Barbara J. Meyer, Andrew Dillin

Organisms respond to mitochondrial stress through the upregulation of an array of protective genes, often perpetuating an early response to metabolic dysfunction across a lifetime. We find that mitochondrial stress causes widespread changes in chromatin structure through histone H3K9 di-methylation marks traditionally associated with gene silencing. Mitochondrial stress response activation requires the di-methylation of histone H3K9 through the activity of the histone methyltransferase met-2 and the nuclear co-factor lin-65. While globally the chromatin becomes silenced by these marks, remaining portions of the chromatin open up, at which point the binding of canonical stress responsive factors such as DVE-1 occurs. Thus, a metabolic stress response is established and propagated into adulthood of animals through specific epigenetic modifications that allow for selective gene expression and lifespan extension.

Figure: Model for Mitochondrial Stress Signaling Pathway. (A) Under non-stressed conditions, MET-2 produces H3K9me1/2 histone subunits in the cytoplasm. ATFS-1 translocates to the mitochondria and is degraded. DVE-1 and LIN-65 do not accumulate in the nucleus and the UPR\textsuperscript{mt} is not induced, animals are normal lived and the nucleus is not compacted. (B) During mitochondrial stress, MET-2 continues to produce H3K9me2 histone subunits, ATFS-1 now translocates to the nucleus to induce UPR\textsuperscript{mt}. DVE-1 and LIN-65 accumulate in the nucleus. Animals are long-lived, the UPR\textsuperscript{mt} is induced, nuclei become compacted, and H3K9me2 levels remain unchanged. (C) Loss of met-2 during mitochondrial stress results in reduced nuclear H3K9me2 levels, nuclei that are less compacted, reduced DVE-1 and LIN-65 nuclear accumulation, reduced UPR\textsuperscript{mt} induction, and partial suppression of increased lifespan. (D) Loss of lin-65 during mitochondrial stress results in reduced nuclear H3K9me2 levels, nuclei that are less compacted, reduced DVE-1 nuclear accumulation, reduced UPR\textsuperscript{mt} induction, and partial suppression of increased lifespan. (E) Loss of both met-2 and atfs-1 during mitochondrial stress results in nuclei that are less compacted, reduced nuclear accumulation of DVE-1 and LIN-65, no UPR\textsuperscript{mt} induction, and complete suppression of lifespan extension.
The Genetic Program of Gonad Development

Dr. Zhaohui Wang, Principal Investigator, Ph.D. (1998, University of Chicago, USA). Using Drosophila as the model system, we have been studying how the somatic and the germline components of the gonad communicate with each other to establish the correct cell fate and to reach the proper cell number.

Email: zhwang@genetics.ac.cn

Rab5 in somatic cells regulates germline proliferation via JNK and BMP signaling in drosophila testis

Yaning Tang, Qing Geng, Di Chen, Shaowei Zhao, Zhaohui Wang

Signals derived from the microenvironment contribute greatly to tumorigenesis. The underlying mechanism requires thorough investigation. Here, we use Drosophila testis as a model system to address this question, taking the advantage of the ease to distinguish germline and somatic cells and to track the cell numbers. In an EMS mutagenesis screen, we identified Rab5, a key factor in endocytosis, for its non-autonomous role in germline proliferation. The disruption of Rab5 in somatic cyst cells, which escort the development of germline lineage, induced the over-proliferation of under-differentiated but genetically wild-type germ cells. We demonstrated that this non-autonomous effect was mediated by the transcriptional activation of Dpp (the fly homolog of BMP) by examining the Dpp-reporter expression and RNAi knocking down Dpp to block germline overgrowth. Consistently, the protein levels of Bam, the germline pro-differentiation factor normally accumulated in the absence of BMP/Dpp signaling, decreased in the over-proliferating germ cells. Further, we discovered that JNK signaling pathway operated between Rab5 and Dpp, because simultaneously inhibiting JNK pathway and Rab5 in cyst cells prevented both dpp transcription and germline tumor growth. Additionally, we found that multiple endocytic genes, such as avl, TSG101, Vps25, or Cdc42, were required in the somatic cyst cells to restrict germline amplification. These findings indicate that when the endocytic state of the surrounding cells are impaired, genetically wild-type germ cells overgrow. This non-autonomous model of tumorigenesis provides a simple system to dissect the relation between tumor and its niche.

Figure: JNK pathway mediated Rab5's negative regulation on dpp. (A) puc is expressed in cyst cells. Only the apical tip of a testis is shown. (B) Removal of one copy of puc enhanced the tumorigenic phenotype of Rab5 RNAi (genotype: tj-GAL4/UAS-Rab5-RNAi; tubGAL80/W). The 5G-tumor containing testes are divided into weak, moderate and severe categories, according to the amount of the over-proliferating cells. Examples are given in BI-BIII. The scoring of each category in different genotypes is presented in BIV. The white lines indicate the segments occupied by tumor cells. The numbers of testes scored in BIV are: for tj>Rab5 RNAi, n=35; for tj>Rab5 RNAi; puc+/+, n=48. (C-E) Expression of bsk in somatic cells suppressed the dpp expression and germline over-proliferation phenotype of somatic Rab5 RNAi. (C) Genotype: tj-GAL4 dpp-lacZ/UAS-Rab5-RNAi; tubGAL80. (D) Genotype: UAS-ask/Y; tj-GAL4 dpp-lacZ/+; tubGAL80. (E) Genotype: UAS-bsk/Y; tj-GAL4 dpp-lacZ/UAS-Rab5-RNAi; tubGAL80. (F) Somatic expression of hepCA induced ectopic dpp expression in cyst cells and led to SG accumulation (genotype: tj-GAL4 dpp-lacZ/+; tubGAL80/UAS-hep). Scale bars: 25 μm (A); 100 μm (B-F).
Transfer of convalescent serum to pregnant mice prevents Zika virus infection and microcephaly in offspring

Shuo Wang, Shuai Hong, Yong-Qiang Deng, Qing Ye, Ling-Zhai Zhao, Fu-Chun Zhang, Cheng-Feng Qin, Zhi-Heng Xu

Due to the ongoing fetal risk from endemic ZIKV infection, an effective vaccine is imperative and, more urgently, is utilizing existing counter measurements to treat the infected pregnant woman. Recent studies have shown that several antibodies are able to neutralize ZIKV and inhibit viremia in mouse model of ZIKV infection. However, how to protect pregnant woman, especially those with potential fetus brain ZIKV infection is a much more grave challenge. We showed that passive transfer of convalescent serum with high-titer neutralizing antibodies to pregnant mice not only suppressed the replication of ZIKV but also inhibited the cell death and the reduction of NPCs in infected embryonic brains, thus preventing the development of microcephaly. This indicates that antibodies in the serum can pass through both placenta barrier of pregnant mice and the blood-brain barrier of fetuses. Our study indicates that convalescent serum has the potential to be used for the prevention and treatment of ZIKV infection in pregnant women.

Figure: Transfer of convalescent serum to pregnant mice prevents Zika virus infection and microcephaly in offspring. (A) In vitro neutralizing activity of human convalescent serum. (B-I) Fetal brains were injected with ZIKV or medium at E13.5 and inspected at E18.5 with or without treatment with human convalescent serum. (B, C) Human convalescent serum protects embryos from ZIKV infection and cell death. (D, E) Human convalescent serum prevents the development of microcephaly. (F) The thinning of the cortical plate was also effectively rescued by the serum treatment. (G-I) Convalescent serum rescues the reduction of NPCs and the thinning of VZ/SVZ caused by ZIKV infection.
Dr. Yongbiao Xue, Principal Investigator, Ph.D. (1989, University of East Anglia and John Innes Centre, UK). 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 mechanisms controlling adaptive growth and development in plants.

Email: ybxue@genetics.ac.cn

**Publications**


**Electrostatic potentials of the S-locus F-box proteins contribute to the pollen S specificity in self-incompatibility in *Petunia hybrida***

Junhui Li, Yue Zhang, Yanzhai Song, Hui Zhang, Jiangbo Fan, Qun Li, Dongfen Zhang, Yongbiao Xue

Self-incompatibility (SI) is a self/non-self discrimination system widely found in angiosperms and, in many species, is controlled by a single polymorphic S-locus. In the Solanaceae, Rosaceae and Plantaginaceae, the S-locus encodes a single S-RNase and a cluster of S-locus F-box (SLF) proteins to control the pistil and pollen expression of SI, respectively. Previous studies have shown that their cytosolic interactions determine their recognition specificity, but the physical force between their interactions remains unclear. In this study, we show that the electrostatic potentials of SLF contribute to the pollen S specificity through a physical mechanism of “like charges repel and unlike charges attract” between SLFs and S-RNases in Petunia hybrid (Fig.). Strikingly, alteration of a single C-terminal amino acid of SLF reversed its surface electrostatic potentials and subsequently the pollen S specificity. Collectively, our results reveal that the electrostatic potentials act as a major physical force between cytosolic SLFs and S-RNases, providing a mechanistic insight into the self/non-self discrimination between cytosolic proteins in angiosperms.

![Image](image-url)
Protein kinase C controls lysosome biogenesis independently of mTORC1

Yang Li, Meng Xu, Xiao Ding, Chen Yan, Zhiqin Song, Lianwan Chen, Xiahe Huang, XinWang, Youli Jian, Guihua Tang, Changyong Tang, Yingtong Di, Shuzhen Mu, Xueziao Liu, Kai Liu, Ting Li, Yingchun Wang, Long Miao, Weixiang Guo, Xiaojiang Hao, Chonglin Yang

Lysosomes respond to environmental cues by controlling their own biogenesis, but the underlying mechanisms are poorly understood. Here we describe a protein kinase C (PKC)-dependent and mTORC1-independent mechanism for regulating lysosome biogenesis, which provides insights into previously reported effects of PKC on lysosomes. By identifying lysosome-inducing compounds we show that PKC couples activation of the TFEB transcription factor with inactivation of the ZKSCAN3 transcriptional repressor through two parallel signaling cascades. Activated PKC inactivates GSK3β, leading to reduced phosphorylation, nuclear translocation and activation of TFEB, while PKC activates JNK and p38 MAPK, which phosphorylate ZKSCAN3, leading to its inactivation by translocation out of the nucleus. PKC activation may therefore mediate lysosomal adaptation to many extracellular cues. PKC activators facilitate clearance of aggregated proteins and lipid droplets in cell models and ameliorate amyloid plaque formation in APP/PS1 mouse brains. Thus, PKC activators are viable treatment options for lysosome-related disorders.

Publications


Molecular Genetics of Sexual Plant Reproduction

Dr. Weicai Yang, Principal Investigator, Director of the Institute, Ph.D. (1994, Wageningen University, The Netherlands). Dr. Yang’s laboratory is mainly interested in molecular genetics of plant reproduction, focusing on female gametogenesis, male-female gametophytic interaction and early embryo development.

Email: wcyang@genetics.ac.cn

Publications


A receptor heteromer mediates the male perception of female attractants in plants

Tong Wang, Liang Liang, Yong Xue, Peng-Fei Jia, Wei Chen, Meng-Xia Zhang, Ying-Chun Wang, Hong-Ju Li, Wei-Cai Yang

Sexual reproduction requires recognition between the male and female gametes. In flowering plants, the immobile sperms are delivered to the ovule-enclosed female gametophyte by guided pollen tube growth. Although the female gametophyte-secreted peptides have been identified to be the chemotactic attractant to the pollen tube, the male receptor(s) is still unknown. Here we identify a cell-surface receptor heteromer, MDIS1–MIK, on the pollen tube that perceives female attractant LURE1 in Arabidopsis thaliana. MDIS1, MIK1 and MIK2 are plasma-membrane-localized receptor-like kinases with extracellular leucine-rich repeats and an intracellular kinase domain. LURE1 specifically binds the extracellular domains of MDIS1, MIK1 and MIK2, whereas mdis1 and mik1 mik2 mutant pollen tubes respond less sensitively to LURE1. Furthermore, LURE1 triggers dimerization of the receptors and activates the kinase activity of MIK1. Importantly, transformation of AtMDIS1 to the sister species Capsella rubella can partially break down the reproductive isolation barrier. Our findings reveal a new mechanism of the male perception of the female attracting signals.

Figure: AtMDIS1 as a female signal receptor can break down the reproduction isolation at micropylar guidance stage between A. thaliana and C. rubella. (A) The phylogenetic tree of crucifer species. (B) The untransformed C. rubella pollen tubes do not enter the ovule of A. thaliana. (C) The C. rubella expressing AtMDIS1 enter the ovule of A. thaliana.
Vertebrate Early Development

Dr. Jian Zhang, Principal Investigator, Ph.D. (1996, University of Miami, USA). The laboratory is mainly interested in vertebrate embryogenesis. Current projects include genetic regulation of cellular differentiation in early embryos. We use zebrafish and mouse as model systems.

Email: jianzhang84@genetics.ac.cn

Study of Zar1 in zebrafish oogenesis and sex differentiation

Liyun Miao, Yue Yuan, Feng Cheng, Junshun Fang, Fang Zhou, Weirui Ma, Yan Jiang, Xiahe Huang, Yingchun Wang, Lingjuan Shan, Dahua Chen, Jian Zhang

Large numbers of maternal RNAs are deposited in oocytes and are reserved for later development. Control of maternal RNA translation during oocyte maturation has been extensively investigated and its regulatory mechanisms are well documented. However, translational regulation of maternal RNAs in early oogenesis is largely unexplored. In this study, we generated zebrafish zar1 mutants which result in early oocyte apoptosis and fully penetrant male development. Loss of p53 suppresses the apoptosis in zar1 mutants and restores oocyte development. zar1 immature ovaries show upregulation of proteins implicated in endoplasmic reticulum (ER) stress and the unfolded protein response (UPR). More importantly, loss of Zar1 causes markedly upregulation of zona pellucida (ZP) family proteins, while overexpression of ZP proteins in oocytes causes upregulation of stress related activating transcription factor 3 (atf3), arguing that tightly controlled translation of ZP proteins is essential for ER homeostasis during early oogenesis. Furthermore, Zar1 binds to zona pellucida (zp) mRNAs and represses their translation. Together our results indicate that regulation of translational repression and derepression are essential for precisely controlling protein expression during early oogenesis.

Figure: Zar1 represses translation of ZP proteins in zebrafish oocytes. (A-D) Zar1 binds to zp mRNAs. (A) Zar1 protein was precipitated in heterozygous ovaries. (B) qPCR analysis of zp mRNAs immunoprecipitated from heterozygotes. Relative level of immunoprecipitated ef1a mRNA compared to the input ef1a mRNA was assigned as 1. (C) Analyzing interaction of zebrafish Zar1 and zp mRNAs with a yeast three-hybrid system. (D) Western blot analysis indicates expression of Zar1 and Zar1-mu in yeast. (E-G) Zar1 represses translation of Zp proteins in oocytes. (E) Statistics of relative luciferase activity. Zar1 repressed Zp3b translation. Mutation of Zar1 Znf domain abolished its translational repression activity. (F) RT-PCR of injected RNA reporters. (G) Western blot analysis shows expression of RFP-Flag, Zar1, and Zar1-mu.

Publications


Dr. Yongqing Zhang, Principal Investigator, Ph.D. (1991, China Agricultural University, China). His main interest is to understand how the normal and diseased brain function using Drosophila melanogaster as a model organism. As the molecular and cellular features of vertebrate nervous system are conserved in Drosophila, the studies on Drosophila will help reveal the mechanisms of human brain development and function.

Email: yqzhang@genetics.ac.cn

Publications


Ube3a regulates synaptic growth and endocytosis by inhibiting BMP signaling

Wenhua Li, Aiyu Yao, Hui Zhi, Yong Q. Zhang

Altered expressions of the E3 ubiquitin ligase UBE3A which is involved in protein degradation through the proteasome pathway are associated with neurodevelopmental and behavioral defects observed in Angelman syndrome (AS) and autism. However, little is known about the neuronal function of UBE3A and the pathogenesis of UBE3A-associated disorders. To understand the in vivo function of UBEA in the nervous system, we generated multiple mutations of ube3a, the Drosophila ortholog of UBE3A. We found a significantly increased number of total boutons and satellite boutons in conjunction with compromised endocytosis in the neuromuscular junctions (NMJs) of ube3a mutants compared to wild type. Genetic and biochemical analysis showed an upregulation of bone morphogenetic protein (BMP) signaling in the nervous system of ube3a mutants. Consistently, immunohistochemical study revealed a specific increase in the protein level of Thickveins (Tkv), a type I BMP receptor, but not Wishful thinking (Wit), a type II BMP receptor, in ube3a mutants. Biochemically, Ube3a associated with and specifically ubiquitinated lysine 227 within the cytoplasmic tail of Tkv, and promoted its proteasomal degradation in Schneider 2 cells. Furthermore, the negative regulation of Tkv by Ube3a was conserved in mammalian cells. These results together uncover a critical role for Ube3a in regulating NMJ synapse development by repressing BMP signaling. This study sheds new light onto the neuronal functions of UBE3A and provides novel perspectives for understanding the pathogenesis of UBE3A-associated brain disorders.
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 genetics and omics. 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, one recipient of the National Science Fund for Excellent Young Scholars, three fellows of the National One Thousand Talents Program for Young Scientists, one fellow of the National Ten Thousand Talents Program for Scientific and Technological Innovation Leading Talents, and three fellows of the CAS Hundred Talents Program. In 2016, the center has received research funds from the 973 program, the 863 program, the key research projects of NSFC and the strategic projects of CAS. The center has two patents approved, and has made substantive progresses in a variety of research directions with 19 SCI papers published. The center, as participants, received the second prize of National Natural Science Awards and the first prize of S&T Excellent Achievement Awards for Universities. Two graduate students of the center won the National Scholarship.

Transcriptomics: Xiujie Wang’s group reports that ubiquitously expressed genes participate in cell-specific functions via alternative promoter usage. They identified 110 mouse embryonic stem cell (mESC) specifically expressed transcripts with cell-stage-specific alternative transcription start sites (SATS isoforms) from 104 ubiquitously expressed genes, majority of which have active epigenetic modification-or stem cell-related functions. These SATS isoforms are specifically expressed in mESCs, and tend to be transcriptionally regulated by key pluripotency factors through direct promoter binding. Knocking down the SATS isoforms of Nmnat2 or Usp7 leads to differentiation-related phenotype in mESCs. These results demonstrate that cell-type-specific transcription factors are capable to produce cell-type-specific transcripts with alternative transcription start sites from ubiquitously expressed genes, which confer ubiquitously expressed genes novel functions to involve in the establishment or maintenance of cell-type-specific features.

Functional Proteomics: Yingchun Wang’s group focuses on the study of growth factor-induced nucleocytoplasmic shuttling proteins. They identified 203 nucleocytoplasmic shuttling proteins containing 46 imported proteins and 157 exported proteins in response to epidermal growth factor (EGF) stimulation using quantitative proteomics techniques. More than a half of the exported proteins contain predicted nuclear export sequence (NES). Furthermore, they found that phosphorylation of Serine 1055 of XPO1, a potential substrate of RSK2, plays an important role in nucleocytoplasmic shuttling.

Structural Biology: Yuhang Chen’s group focuses on the structural and functional studies of CENP-A anti-loading factor Ccp1 in centromeres. CENP-A is a centromere-specific histone H3 variant and also localized in centromere. Ccp1 could prevent CENP-A from improperly loading into chromosome in centromere and non-centromeric regions. According to molecular replacement and single wave length anomalous diffraction, they solved the structure of Ccp1. Ccp1 is belonged to NAP family and forms a homodimer in solution. Ccp1 is composed of three domains and has a ‘headphone’ topology. Long α1 helix in N terminal is dimerization domain, responsible for binding two Ccp1 monomers. Five α helixes and four β sheets form a hydrophobic core. The C terminal of Ccp1 is highly flexible for its abundance in acidic amino acids. By introducing mutation into Ccp1, they disrupted the dimer structure, resulting in loss of function in vivo. In order to explore the interaction between Ccp1 and histones, we respectively reconstituted the CENP-A/H4 dimer and H3/H4 dimer in vitro. The evidence from pull-down experiment demonstrated that Ccp1 prioritized to bind CENP-A rather than H3. This finding may explain how the Ccp1 regulate the CENP-A assembly in centromeric regions.

Evolutionary Genomics: Wenfeng Qian’s group revealed the impact of individual synonymous codons on mRNA levels by a codon-resolution analysis. They attempted to quantify this impact using 3,556 synonymous variants of the heterologous gene encoding green fluorescent protein (GFP) and 523 synonymous variants of the endogenous gene (TDH3) in yeast. They found the mRNA level to be strongly correlated with codon usage bias (CUB) for both genes, demonstrating a direct role of CUB in regulating the transcript concentration, likely via regulating mRNA degradation. They further estimated that the impact of CUB on mRNA level explains ~36% of the correlation between CUB and mRNA level among yeast genes. Their study revealed pleiotropic effects of synonymous codon usage, provided an alternative explanation for the well-known correlation between CUB and gene expression level, and called for re-evaluation of the theories on the evolution of CUB.

Systems Developmental Biology: Zhuo Du’s group analyzed the developmental properties and dynamics of cell position noise during embryogenesis. Using live imaging, automated lineage tracing and quantitative single-cell analyses they have systematically measured and analyzed the noise of cell positions during every minute of the first half of embryogenesis in C. elegans. Results show that each cell's position exhibits characteristic and dynamic noise profile during the course of embryogenesis. Noise of cell positions is largely independent of cell division pattern, localization, migration distance, movement velocity and cell fate, but is strongly coupled to the lineage identity, lineage distance, and morphological organization. These findings establish that instead of being stochastic, noise of cell position is subjected to tight developmental constraints. On the basis of these results they are performing mechanistic analyses to explore the regulation and implications of cellular noise during embryogenesis.

QiangTu’s group performs a systematic functional analysis of long non-coding RNAs in medaka embryonic development and sex determination. They identified 890 IncRNA genes with dynamic expression profiles during embryogenesis, 104 IncRNA genes with sexually dimorphic expression patterns during sex determination stages. They also characterized many spatial expression patterns of these IncRNA genes. They are employing a functional analysis strategy combining both multiplex knockdown screening and individual knockout in vivo, together with bioinformatics and developmental biology techniques, to perform a large-scale analysis of IncRNAs in embryonic development and sex determination in medaka. Their study could gain a better understanding of the biological function of IncRNAs in vertebrate development.
It’s known to us all that chromosome structure is conserved in eukaryotes. Chromosome is highly conserved and can be organized into different regions, for example centromeres. Centromeres are defined as genetic loci and they are the places that kinetochore assemble. Therefore, centromeres are very important for proper segregation of chromosomes in mitosis. CENP-A is a centromere-specific histone H3 variant and also localized in centromere. It is considered as an important epigenetic mark. How the proper ratio of CENP-A to H3 is maintained in centromere region is unknown for now. Li Fei group in NYU identified a new protein, called Ccp1, in fission yeast. Ccp1 could prevent CENP-A from improperly loading into chromosome in centromere and non-centromeric regions. According to molecular replacement and single wave length anomalous diffraction, we solved the structure of Ccp1. Ccp1 belongs to NAP family and forms a homodimer in solution. Similar to other NAP family protein, Ccp1 is composed of three domains and has a ‘headphone’ topology. Long α1 helix in N terminal is dimerization domain, responsible for binding two Ccp1 monomers. Five α helixes and four β sheets form a hydrophobic core. The C terminal of Ccp1 is highly flexible for its abundance in acidic amino acids. By introducing mutation into Ccp1, we disrupted the dimer structure, resulting in loss of function in vivo. In order to explore the interaction between Ccp1 and histones, we respectively reconstituted the CENP-A/H4 dimer and H3/H4 dimer in vitro. The evidence from pull-down experiment demonstrated that Ccp1 prioritized to bind CENP-A rather than H3. This finding may explain how the Ccp1 regulate the CENP-A assembly in centromeric regions.

**Figure:** Ccp1 prioritizes to bind (CENP-A/H4) complex rather than (H3/H4) complex. (A) Characterization of CENP-A/H4 dimer and H3/H4 dimer. (B) In vitro binding assay of Ccp1 against CENP-A/H4 dimer and H3/H4 dimer.
Developmental properties and dynamics of cell position noise during embryogenesis

Xiaoyu Li, Zhuo Du

Biological processes are intrinsically noisy which could be both detrimental and beneficial to organismal fitness. While biological noises at the molecular level such as gene transcription and protein synthesis have been subjected to extensive investigations, the properties, mechanisms and implications of cellular noise during in vivo development are poorly understood. The clarity and invariance of *C. elegans* cell lineage make it a unique model system to study developmental noises at cellular resolution. Using live imaging, automated lineage tracing and quantitative single-cell analyses we have systematically measured and analyzed the noise of cell positions during every minute of the first half of embryogenesis. Comparison of relative cell positions in over 30 wild-type embryos under identical conditions revealed a highly reproducible 3D cell positions over space and time. Focusing on the noise of cell positions (defined as the variability of cell position among wild-type embryos) we found each cell’s position exhibits characteristic and dynamic noise profile during the course of embryogenesis. We analyzed the relationship between noise of cell positions and many other key developmental properties. We found noise of cell positions is largely independent of cell division pattern, localization, migration distance, movement velocity and cell fate, but is strongly coupled to the lineage identity, lineage distance, and morphological organization. These findings establish that instead of being stochastic, noise of cell position is subjected to tight developmental constraints. On the basis of these results we are performing mechanistic analyses to explore the regulation and implications of cellular noise during embryogenesis.

**Figure:** Properties of cell position noise. (A) Cell position noise is coupled to founder cell lineage identity. (B) Cell position noise is coupled to lineage history. (C) Cell position noise is coupled to embryonic morphological organization. (D) Dynamics of position noise is highly concordant during embryogenesis. (E) Cell position noise is controlled during cell cycle.
Codon-resolution analysis reveals the impact of individual synonymous codons on mRNA levels
Siyu Chen, Ke Li, Wenqing Cao, Jia Wang, Tong Zhao, Qing Huan, Shaohuan Wu, Yu-Fei Yang, Wenfeng Qian

Codon usage bias (CUB) refers to the observation that synonymous codons are not used equally frequently in a genome. CUB is stronger in more highly expressed genes, a phenomenon commonly explained as a result from natural selection on translational accuracy and efficiency. Nevertheless, this phenomenon could also occur if CUB regulates gene expression at the mRNA level, a simple hypothesis that has been neglected for decades. Here, we attempt to quantify the impact of synonymous mutations on mRNA levels in yeast using 3,556 synonymous variants of the heterologous gene encoding green fluorescent protein (GFP) and 523 synonymous variants of the endogenous gene TDH3. We found the mRNA level to be strongly correlated with CUB for both genes, demonstrating a direct role of CUB in regulating the transcript concentration, likely via regulating mRNA degradation, as our additional experiments suggest. We further estimated that the impact of CUB on mRNA level explains about 36% of the correlation between CUB and mRNA level among yeast genes. Our study reveals pleiotropic effects of synonymous codon usage, provides an alternative explanation for the well-known correlation between CUB and gene expression level, and calls for re-evaluation of the theories on the evolution of CUB.

Figure: Synonymous codon usage regulates mRNA level among GFP synonymous variants. (A) The flowchart of the experimental design. DNA oligos were synthesized with doped nucleotides and yeast transformation was performed to generate the variants. (B) The yeast variants were pooled and the expression of GFP was induced in 2% galactose. DNA and RNA were extracted from the pooled cells and frequencies of variants were estimated with Illumina sequencing read counts. The ratio between the frequency of mRNA in the pooled library and that of DNA reflects the mRNA levels per cell. (C) mRNA level increases with the number of preferred codons in a GFP variant.

Publications
Large-scale functional analysis of long non-coding RNAs in medaka embryonic development and sex determination

Yongjie Liu, Hanqiao Shang, Ting Zhang, Qiang Tu

Non-coding RNAs (ncRNAs) are pervasively expressed in organisms. In recent years, while small ncRNAs have been well studied, the biological function of major long non-coding RNAs (lncRNAs) remains enigmatic. With the advent and popularization of next-generation sequencing of transcriptome, a tremendous amount of lncRNAs are now being identified in various genomes. However, in vivo functions of most lncRNAs are still unclear. Some pioneering functional studies suggested that these molecules regulate diverse biological processes. However, these studies were mainly based on single gene studies, or knockdown experiments using cell lines, instead of systematic characterization of in vivo functions of lncRNAs based on genetic approaches. To reveal in vivo functions of lncRNAs, we are performing a systematic functional analysis of lncRNAs in embryonic development and sex determination, using medaka fish as the model animal. Firstly, we identified 890 lncRNA genes with dynamic expression profiles during embryogenesis (Fig. 1A, B), 104 lncRNA genes with sexually dimorphic expression patterns during sex determination stages (Fig. C, D). We also characterized many spatial expression patterns of these lncRNA genes (Fig. D). Secondly, we are employing a functional analysis strategy combining both multiplex knockdown screening and individual knockout in vivo, together with bioinformatics and developmental biology techniques, to perform a large-scale analysis of lncRNAs in embryonic development and sex determination in medaka. Thus, our study could gain a better understanding of the biological function of lncRNAs in vertebrate development.

Figure: lncRNAs expressed during embryogenesis and sex determination stages. (A) lncRNAs dynamically expressed during embryogenesis. (B) One example of such lncRNAs. (C) lncRNAs with sexually dimorphic expression pattern. Circles indicate known protein-coding genes which functioning in sex determination. Red dots indicate lncRNAs enriched in female embryos. Blue dots indicate lncRNAs enriched in male embryos. (D) WMISH of one example of such lncRNAs. Arrow indicates the gonad. This lncRNA is expressed exclusively in female gonads.
Center for Molecular Systems Biology

Functional Proteomics

Dr. Yingchun Wang, Principal Investigator, Ph.D. (2003, Genetics/Bioinformatics and Computational Biology, Iowa State University, USA). Our research focuses on large scale quantitative analysis of the cross talk between phosphorylation and ubiquitination. Our research interest is to use state-of-the-art proteomics technology to study the signaling mechanism that control cell migration and cancer metastasis.

Email: ycwang@genetics.ac.cn

Functional proteomics study of growth factor-induced nucleocytoplasmic shuttling proteins

Jinglong Wang, Yuanya Zhang, Xiahe Huang, Xiaorong Wang, Yingchun Wang

Nucleocytoplasmic shuttling of proteins is an important process for signal transduction of cells. Numerous signal proteins are transported into nucleus, whereas the other set of proteins are exported from nucleus in response to the growth factor stimulation. This process involves a complicated mechanism of transporter/cargo complex across the NPC (nuclear pore complex). However, at a global level, scarce information has been available regarding the identities and amount of shuttling proteins in response to a certain growth factor stimulation. Here, we identified 203 nucleocytoplasmic shuttling proteins containing 46 imported proteins and 157 exported proteins in response to epidermal growth factor (EGF) stimulation using quantitative proteomics techniques (Fig. A). More than a half of the exported proteins contain predicted nuclear export sequence (NES) (Fig. B). Furthermore, we found that phosphorylation of Serine 1055 of XPO1, a potential substrate of RSK2, plays an important role in nucleocytoplasmic shuttling (Fig. C, D).

Publications


Figure: Functional proteomics study of EGF-induced nucleocytoplasmic shuttling proteins. (A) Workflow for the identification of nucleocytoplasmic shuttling proteome. (B) Enrichment analysis of predicted nuclear localization sequence (NLS) and NES motifs in shuttling proteins. (C) Western blot shows the levels of ectopically expressed GFP-XPO1 in the nuclear compartment of cells overexpressing GFP-RSK2 or GFP at the indicated times of EGF stimulation. (D) The model of XPO1 shuttling between cytoplasm and nucleus.
Ubiquitously expressed genes participate in cell-specific functions via alternative promoter usage

Guihai Feng, Man Tong, Baolong Xia, Guanzheng Luo, Meng Wang, Dongfang Xie, Haifeng Wan, Ying Zhang, Qi Zhou, Xiuijie Wang

How do different cell types acquire their specific identities and functions is a fundamental question of biology. Previously significant efforts have been devoted to search for cell-type-specifically expressed genes, especially transcription factors, yet how ubiquitously expressed genes participate in the formation or maintenance of cell-type-specific features remains largely unknown. Here, we have identified 110 mouse embryonic stem cell (mESC) specifically expressed transcripts with cell-stage-specific alternative transcription start sites (SATS isoforms) from 104 ubiquitously expressed genes, majority of which have active epigenetic modification-or stem cell-related functions. These SATS isoforms are specifically expressed in mESCs, and tend to be transcriptionally regulated by key pluripotency factors through direct promoter binding. Knocking down the SATS isoforms of Nmnat2 or Usp7 leads to differentiation-related phenotype in mESCs. These results demonstrate that cell-type-specific transcription factors are capable to produce cell-type-specific transcripts with alternative transcription start sites from ubiquitously expressed genes, which confer ubiquitously expressed genes novel functions to involve in the establishment or maintenance of cell-type-specific features.

Figure: Gene Ontology enrichment analysis of mESC-specific SATS genes. Circles are the enriched biological processes ($P$-value<0.01, two-sided hypergeometric test with Benjamini–Hochberg correction) among SATS genes identified by ClueGO. The names of processes and their related GO terms are shown in the same colors. Circles are connected according to the hierarchical relationships of GO terms. The sizes of circles are negatively correlated with the enrichment $P$-values of GO terms.

Publications


Center for Agricultural Resources Research

The center’s missions are: 1) to ensure the national demands on grain yield, water resources and ecological protection, by focusing on the high efficient use of agricultural water resources; 2) to develop the innovative ecological resource theory and the modern agricultural technology systems for resource preservation; and 3) to strengthen technological achievements transformation and service to society.

The Center for Agricultural Resources Research has three key laboratories (i.e., the Key Laboratory for Agricultural Water Resources of CAS, Hebei Province Key Laboratory for Water-Saving Agriculture, and Hebei Province Engineering Laboratory of Breeding and Germplasm Innovation for Plant Stress Tolerance). The center has three field stations (i.e., Luancheng Agro-ecosystem Experimental Station, CAS, Nanpi Eco-agricultural Experimental Station, CAS, and Taihang Mountain Mountain Ecosystem Experimental Station, CAS). The center has one fellow of the National One Thousand Talents Program for Young Scientists, two fellows of the National High-Level Personnel of Special Support Program, six fellows of the CAS Hundred Talents Program. In 2016, 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:** Mengyu Liu’s group proposed a series of technologies to save irrigation water through altering the sowing date and spaces according to effective rainfall. Xiying Zhang’s group determined the best timing for irrigation using brackish water and revealed that increase of soil organic matter could help to maintain soil fertility and root zone salt balance. Yonghui Yang’s group rectified ET algorithm using a P-T model under a film-mulched farmland and found that the annual water consumption from pear garden is about 70 mm larger than that from croplands (Ai et al., J Hydrometeorol, 2016). Yanjun Shen’s group quantified fied that water in deep vadose zone moves mainly as a type of matric flow by a rate of ~1.14 m/y with loading large amount of solutions. Denitrification acts as a major factor to reducing nitrate leaching to aquifiers in plain region, while denitrogen is little in mountain aquifiers (Min et al., Hydrof Process, 2017). Yanjun Shen’s group also clarified the nexus relations among regional cropping pattern, water resources, and grain yield in semiarid NCP, and pointed out that the upper limit of irrigation land should be restrained as much as 4 million ha in the NW arid region (Guo and Shen, J Hydrol, 2016). These findings posed great understanding to agricultural water saving practices at the dimension of crop drought resistance physiology, brackish water utilization, efficient water and nitrogen management at field scale, as well as understanding to the agriculture-water-ecology nexus relations or even the appropriate reclamation extent at region scale.

**Plant Genetics and Breeding:** Diaoguo An’s group characterized a new Pm2 allele, PmFG, which confers powdery mildew resistance in the wheat germplasm Line FG-1, and seven closely linked markers were developed for PmFG (Ma et al., Front Plant Sci, 2016). The new variety of wheat "Kenong 2011" developed by Junming Li’s group was certified. In addition, they characterized a number of quantitative trait loci for wheat kernel size, quality and tolerance to low-N stress using a recombinant inbred line population derived from Kenong 9204 × Jing 411 (Cui et al., Theor Appl Genet, 2016). Xigang Liu’s group uncovered the mechanisms by which the FHY3, a key factor in light signaling, is involved in plant meristem maintenance and determinacy, which shed new light on how plant development coordinated with environmental signals (Li et al., PNAS, 2016). Zhengbin Zhang’s group performed transcriptomic analysis of the responses of Triticum urartu to water deprivation and resupply, providing gene and molecular marker resources for the genetic improvement of drought resistance in wheat and related crops. Dongping Lu’s group found that a Xanthomonas oryzae pv. oryzae effector, XopR, associates with receptor-like cytoplasmic kinases and suppresses PAMP-triggered stomatal closure (Wang et al., Sci China Life Sci, 2016).

**Ecology and Environment:** Chunsheng Hu’s group determined the soil organic/inorganic carbon storage in the soil profile at 0–100 cm depths and the concentration of dissolved inorganic carbon in soil leachate in four kinds of N application treatments (0, 200, 400, and 600 kg N ha⁻¹ y⁻¹) for 15 years in the North China Plain (Dong et al., Sci Total Environ, 2016). Lin Ma’s group quantified nutrient flows and losses in the whole management chain (from animal feeding to manure application to land) in China and potential to reduce nutrient losses and increase the amount of manure applied to crop land and replace fertilizer NPK (Bai et al., Environ Sci Technol, 2016). Binbin Liu’s group established the nitrification-related pathways (including ammonia oxidation) and heterotrophic denitrification as the most predominant sources of N₂O emissions from soil ecosystems. Xiaojing Liu’s group developed the diversified crop-planting patterns to adapt to the characteristics of regional soil and water resources in coastal plain of Hebei province (Yang et al., Eur J Agron, 2016). Jintong Liu’s group developed an evaluation model for underground water used as irrigation to analysis benefit-cost of three underground water irrigation scenarios in North China Plain (Yu et al., Irrig Drain, 2016). Jiansheng Cao’s group developed the automatic control system of wide-and narrow-spacing partial root alternate irrigation and the modern sensor technology and intelligent control technology.

In addition, the center was awarded a second prize of Hebei Nature Science, a second prize of Hebei Progress in Scientific and Collective Technology, and a first prize of Xinjiang Progress in Scientific and Collective Technology; published 76 papers, of which 43 were included in SCI Journals; administered 8 consulting reports to the local and central government; granted 11 patents; draw a national standard; registered 2 softwares in 2016.
Wheat Genetic Improvement & Germplasm Enhancement

Dr. Diaoguo An, Principal Investigator, Ph.D. (2006, Research Center for Eco-environmental Sciences, CAS, China). The laboratory is mainly interested in: 1) the development of new wheat germplasm resources by molecular chromosomes engineering; 2) identifying, fine mapping and cloning of important genes/QTLs for disease resistance and important agronomic traits; 3) molecular design breeding.

Email: dgan@sjziam.ac.cn

Molecular cytogenetic identification of a new wheat-rye 6R chromosome disomic addition line with powdery mildew resistance

Diaoguo An, Qi Zheng, Qiaoling Luo, Pengtao Ma, Hongxing Xu, Yunfeng Xu

Rye (Secale cereale L.) possesses many valuable genes that can be used for improving disease resistance, yield and environment adaptation of wheat (Triticum aestivum L.). It is necessary to develop desirable germplasm and search for novel resistance gene sources against constantly accumulated variation of the virulent isolates. In the present study, a new wheat-rye line designated as WR49-1 was produced through distant hybridization and chromosome engineering protocols between common wheat cultivar Xiaoyan 6 and rye cultivar German White. Using sequential GISH (genomic in situ hybridization), mc-FISH (multicolor fluorescence in situ hybridization), mc-GISH (multicolor GISH) and EST (expressed sequence tag)-based marker analysis, WR49-1 was proved to be a new wheat-rye 6R disomic addition line. As expected, WR49-1 showed high levels of resistance to wheat powdery mildew (Blumeria graminis f. sp. tritici, Bgt) pathogens prevalent in China at the adult growth stage and 19 of 23 Bgt isolates tested at the seedling stage. According to its reaction pattern to different Bgt isolates, WR49-1 may possess new resistance gene(s) for powdery mildew, which differed from the documented powdery mildew gene, including Pm20 on chromosome arm 6RL of rye. Additionally, WR49-1 was cytologically stable and had improved agronomic characteristics; therefore, it could serve as an important bridge for wheat breeding and chromosome engineering.

Figure: PCR amplification of expressed sequence tag (EST)-based markers. CGG143 (a) specific for rye chromosome 6R, and SWES78 (b), SWES206 (c) and SWES231 (d) specific for 6RL, respectively, in wheat-rye lines and controls for detection of 6R in WR49-1. The 110, 260, 200 and 260 bp bands indicate the diagnostic DNA fragments specific for 6R or 6RL, respectively.

Publications


Center for Agricultural Resources Research

Mountain Eco-Engineering and Eco-Hydrology

Dr. Jiansheng Cao, Associate Professor, Principal Investigator, Ph.D., Vice-Station-Master of Hilly Ecosystem Experimental Station in Taihang Mountain, Chinese Academy of Sciences. Our group is mainly interested in ecohydrology processes and effective utilization of precipitation resources in mountain basins, restoration and reconstruction of degraded mountain ecosystem, automatic monitoring and control of hydrology factors.

Email: caojs@sjziam.ac.cn

Publications


Zhao X., Li F., Zhang W., Ai Z., Shen H., Liu X., Cao J., Manevski K. Soil respiration at different stand ages (5, 10, and 20/30 Years) in coniferous (Pinus tabulaeformis Carrière) and deciduous (Populus davidiana Dode) Plantations in a sandstorm source area. Forest 2016, 7: 153.


Study on automatic control system and method of partial root alternate irrigation

Jiansheng Cao, Xiaohua Hao, Xiuping Liu, Hehui Wang, Wanjun Zhang

With the growing shortage of freshwater resources and increasing demand for water, the development of water-saving agriculture has become an important countermeasure to achieve sustainable utilization of water resources. Controlled partial rootzone alternative irrigation is to keep the crop root system drying in a horizontal or vertical profile, and the drying area appears alternately through artificial control, which is to say that part of the crop root always growing in the dry or relative dry soil environment. As a new water-saving technology, the study of controlled partial rootzone alternate irrigation is still at an early stage, although the possibility in theory and implementation and the huge potential of water-saving have been proved, there are still some problems in the implementation process. To solve the problems of extensive agricultural water use and low water-saving irrigation automation, and to advance agricultural modernization and water resources security, the automatic control system of wide- and narrow-spacing partial rootzone alternate irrigation was developed, and the modern sensor technology and intelligent control technology were integrated to realize the automatic control: 1) Realization of automatic control and alternative irrigation for narrow row-spacing crop. There are horizontal interactions of water movement because of the close distance between two driplines. Based on two soil moistures auto monitored respectively below two driplines and the single irrigation threshold, irrigation begins from one dripline and automatically stops when soil moisture reaches field capacity. Then irrigation occurrence in the other dripline delays because of the horizontal interaction of water movement. 2) Realization of automatic control and alternative irrigation for wide row-spacing crop. In contrast to narrow row-spacing crop, there aren’t horizontal interactions of water movement because of the far distance between two driplines. Based on four soil moistures (two in each dripline) and two irrigation thresholds, irrigation begins from one dripline firstly and then changes to the other dripline.

Figure: The automatic control system of wide-spacing partial rootzone alternate irrigation.
Nutrient Cycling and Environmental Impacts in Agricultural Ecosystem

Dr. Chunsheng Hu, Principal Investigator, Ph.D. (1996, Shenyang Institute of Applied Ecology, CAS, China). Vice Director of Center for Agricultural Resources Research of CAS, Head of Luancheng Eco-agricultural Experimental station. The laboratory is mainly interested in nutrients cycling of farming ecosystems and farming precision technology, focusing on nutrient leaching, green-house gas emission, and precision farming technology development.

Email: cshu@ms.sjziam.ac.cn

Reassessing carbon sequestration in the North China Plain via addition of nitrogen

Wenxu Dong, Yuming Zhang, Yuying Wang, Xiaoxin Li, Chunsheng Hu

Soil inorganic carbon (SIC) exerts a strong influence on the carbon (C) sequestered in response to nitrogen (N) additions in arid and semi-arid ecosystems, but limited information is available on in situ SIC storage and dissolution at the field level. This study determined the soil organic/inorganic carbon storage in the soil profile at 0–100 cm depths and the concentration of dissolved inorganic carbon (DIC) in soil leachate in 4 N application treatments (0, 200, 400, and 600 kg N ha\(^{-1}\) y\(^{-1}\)) for 15 years in the North China Plain. The objectives were to evaluate the effect of nitrogen fertilizer on total amount of carbon sequestration and the uptake of atmospheric CO\(_2\) in an agricultural system. Results showed that after 15 years of N fertilizer application the SOC contents at depths of 0-100 cm significantly increased, whereas the SIC contents significantly decreased at depths of 0-60 cm. However, the actual measured loss of carbonate was far higher than the theoretical maximum values of dissolution via protons from nitrification. Furthermore, the amount of HCO\(_3^{-}\) and the HCO\(_3^{-}/(\text{Ca}^{2+} + \text{Mg}^{2+})\) ratio in soil leachate were higher in the N application treatments than no fertilizer input (CK) for the 0-80 cm depth. The result suggested that the dissolution of carbonate was mainly enhanced by soil carbonic acid, a process which can absorb soil or atmosphere CO\(_2\) and less influenced by protons through the nitrification which would release CO\(_2\). To accurately evaluate soil C sequestration under N input scenarios in semi-arid regions, future studies should include both changes in SIC storage as well as the fractions of dissolution with different sources of acids in soil profiles.

Table: A budget for CO\(_2\) sinks after applying nitrogen at different rates in calcareous soil.

<table>
<thead>
<tr>
<th></th>
<th>CK</th>
<th>N(_{200}) (Mg ha(^{-1}))</th>
<th>N(_{400}) (Mg ha(^{-1}))</th>
<th>N(_{600}) (Mg ha(^{-1}))</th>
</tr>
</thead>
<tbody>
<tr>
<td>ΔSOC in 0-100cm (1)</td>
<td>–</td>
<td>15.3</td>
<td>20.2</td>
<td>20.8</td>
</tr>
<tr>
<td>ΔSIC in 0-60cm (2)</td>
<td>–</td>
<td>–18.6</td>
<td>–13.6</td>
<td>–15.2</td>
</tr>
<tr>
<td>Theory dissolution by nitrification (3)</td>
<td>–</td>
<td>–2.6</td>
<td>–5.1</td>
<td>–7.7</td>
</tr>
<tr>
<td>Min CO(_2) sinks (1)+(3)</td>
<td>–</td>
<td>12.7</td>
<td>15.1</td>
<td>13.1</td>
</tr>
<tr>
<td>Max CO(_2) sinks (1)–(2)–(3)*2)</td>
<td>–</td>
<td>28.7</td>
<td>23.7</td>
<td>20.6</td>
</tr>
</tbody>
</table>

Publications


Registration of winter wheat cultivar Kenong 2011

Junming Li, Jun Ji, Wei Zhang, Zhiguo Wang, Fa Cui

Kenong 2011 was developed from cross of Kenong 9204/PZW-9. Kenong 9204 is a high-yield wheat cultivar with excellent nitrogen-using efficiency, and PZW-9, an alien translocation line between common wheat and *Agropyron cristatum*, was introduced from the Institute of Crop Science, CAAS. Kenong 2011 possesses a number of favorable alleles at key yield-related loci, such as *gpw2119-7A* (controlling valid tiller number), *gwm131-3B* and *cfe273-6A* (controlling kernel number per spike) and *cfd233-2D* (controlling kernel weight). Its tillering capacity is stronger and spike-forming capacity is higher, with 705 spikes/m² and 36 kernels per spike in average. It averagely yielded 7900.5, 7777.5, 9055.5 and 8430.0 kg/ha (accordingly 5.18%, 7.42%, 4.97% and 5.05% higher than control, *P*<0.05) respectively in 2012~2015 Hebei Provincial Wheat Performance Trial of Regional Nursery. Kenong 2011 harbors favorable alleles at two major stable QTLs for the maximum root length, i.e., *QMRL-2B* and *QMRL-7B*. The large root system is significantly positively correlated with nitrogen uptake and grain output. Under 20% reduction of N input, Kenong 2011 yielded 5.4%~9.0% more than the control cultivars in 2013~2015 (*P*<0.05).

For disease resistances, according to the official test, Kenong 2011 is intermediate resistant to stripe rust, leaf rust and powdery mildew. Kenong 2011 is 75 cm tall, with strong straw, and good resistance to lodging. Juvenile plant growth is semi-erect. Plant color at booting is green and anthers are yellow. The stem does not have anthocyanin. Stem internodes are hollow and the last internode is short. The flag leaf is erect, twisted, and has no waxy bloom. Spikes are spindle, awned, and yellow at maturity. Seeds are ovate, cheeks are rounded, kernel weight is 41-44 mg.

Figure: Kenong 2011 in Hebei Provincial wheat performance trial of regional nursery in 2014.
Remediation of Heavy Metal Polluted Farmland

Dr. Xiaofang Li, Principal Investigator, Ph.D. (2010, Research Centre for Eco-Environmental Sciences, China). Dr. Li’s laboratory is dedicated to the ecological remediation of heavy metal polluted farmland, with a special interest in novel biotechnologies.

Email: xfli@sjziam.ac.cn

Community genomics infers negative environment-biodiversity feedback in revegetated sulphidic tailings

Xiaofang Li, Philip L. Bond, Longbin Huang

Increased risks of salinity and metal release induced by revegetation in sulphidic metal tailings have been implied but still lack robust long-term field evidence. Further, as known critical factors in bioweathering in tailings, microbial mechanisms related to such risks have not been resolved at an individual genomic level. In this study, by taking advantage of a long-term field trial of tailings revegetation at northwest Queensland, we explored the two-year pore water chemistry, cell abundance using fluorescent in situ hybridization (FISH) and metagenome-based community genomics in the tailings. It is found that revegetation measures did not ameliorate the tailings’ hydrogeochemistry; rather, obviously higher median values of pore water salinity, Cd, Cu, Zn and other toxic metals were found. Meanwhile, around $10^7$ cells/g tailings were detected using FISH in the tailings. Assembly of 10 population genomes, with 5 nearly complete, allowed a fine decoding of the community metabolic potentials. Besides the powerful resistance genetic systems for osmotic, metal and oxidative stresses, dominant species possess genes to potentially impact sulphides oxidation directly or indirectly, replenishing saline and metal pool against leaching and possibly leading to N depletion.

Taken together, this study provides direct field evidence for increased risks of saline and metal toxicity induced by revegetation and the possible mechanisms for negative biodiversity-environment feedback in the tailings, which explains the difficulties in reinstating microbial diversity and functions for tailings revegetation.

Figure: A conceptual diagram depicting the microbial sulphides oxidation resulting salinity and N depletion in the tailings.
Effects of long-term nitrogen fertilization on soil nitrification/denitrification and microbial community structure

Fenghua Wang, Shuaimin Chen, Yuying Wang, Chunsheng Hu, Binbin Liu

The continuous increase of the greenhouse gas nitrous oxide (N₂O) in the atmosphere due to the increasing anthropogenic nitrogen input in agriculture has become a global concern. In spite of the complex and multiple routes of N₂O formation, the nitrification-related pathways (including ammonia oxidation) and heterotrophic denitrification have been established as the most predominant sources of N₂O emissions from soil ecosystems. The long-term N fertilization field experiment was conducted at Luancheng research station in the North China Plain since 1998 with a wheat-maize rotation system, which including four N fertilizer application rates: 0 (control, N0), 200 (N200), 400 (N400) and 600 (N600) kg N ha⁻¹ yr⁻¹. It was found that N fertilization rates significantly reduced soil pH and C/N ratio, while significantly increased the OM, TN, TC, NO₃⁻-N, PNA, and PDA after 17-year application of N fertilizer. qPCR results showed that nitrogen fertilizer increased the abundance of amoA, nirK, nirS, and nosZ genes. RDA analysis revealed that pH and C/N ratio had significantly negative correlation with the abundance of functional genes. Bacterial amoA, nirK, and nirS genes were more susceptible to environmental factors (Fig. a). Long-term application of N fertilizer changed bacteria diversity, and microbial community structure was different between summer and winter samples (Fig. b). According to MRT analysis, variation of pH and NH₄⁺-N were the main factors that caused this phenomenon in summer and winter soil samples, respectively (Fig. c, d). This study was important to better understand the underlying mechanisms leading to soil N₂O formation.

Figure: Long-term fertilization altered microbial community structure. (a) RDA analysis. (b) PCoA analysis. (c) MRT analysis of summer samples. (d) MRT analysis of winter samples.
Sustainable Management and Ecological Engineering for Ecosystem

Dr. Jintong Liu, Principal Investigator, Ph.D. (2000, Beijing Forestry University, China). Dr. Liu’s laboratory is mainly interested in sustainable management and ecological engineering for ecosystem, aiming to key scientific issues in different ecosystems, especially degraded ecosystems.

Email: jtliu@sjziam.ac.cn

An economic valuation of groundwater management for agriculture in Luancheng county of North China Plain

Fengjiao Ma, Hui Gao, A. Egrinya Eneji, Zhanzhong Jin, Lipu Han, Jintong Liu

The North China Plain (NCP) is one of the most productive and intensively cultivated agricultural regions in China but it experiences severe water shortage; thus field irrigation relies heavily on groundwater. The extraction of groundwater for irrigation has sustained increased grain yield, although the value of the irrigation water has not been estimated. Here, we propose an evaluation model for underground water used for irrigation, which took into account the infrastructure price, resource price and environment price based on monetary values. We classified underground water into total extracted, actual consumption and over-exploited water according to the hydrological cycle. We then performed a benefit-cost analysis of three underground water irrigation scenarios—actual irrigation, equilibrium irrigation and maximum water productivity (WP) irrigation—using the proposed model and Luancheng County of NCP as a case study. The results showed that (1) the volume of irrigation water varied in the order of actual irrigation scenario > equilibrium irrigation scenario > maximum WP irrigation scenario. The amount of different components of water—extracted groundwater, actually consumed groundwater and over-exploited groundwater—varied similarly, although the yearly variations in extracted groundwater were smaller (Fig.); (2) the total water price should include the infrastructure price, resource price and environment price, although farmers merely pay for the infrastructure price; the resource price constituted the largest proportion of the total water price, especially in the dry years; (3) equilibrium irrigation was the most suitable scenario based on net benefits by our valuation method of underground irrigation water.

Figure: The amount of different underground water irrigation in three scenarios during 1984–2008 in Luancheng County. Note that $A = $actual irrigation; $E = $equilibrium irrigation; $M = $maximum WP irrigation. $V_1$, $V_2$, $V_3$ = the amount of extracted groundwater, actual groundwater consumed and over-exploited groundwater, respectively.

Publications

Physiological and Ecological Mechanisms of Efficient Water Use of Crops

Dr. Mengyu Liu, Principal Investigator, Ph.D. (2000, Hokkaido University, Japan). 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: mengyuli@ms.sjziam.ac.cn

Publications

The wheat GT factor TaGT2L1D negatively regulates drought tolerance and plant development

Xin Zheng, Haipei Liu, Hongtao Ji, Youning Wang, Baodi Dong, Yunzhou Qiao, Mengyu Liu, Xia Li

GT factors are trihelix transcription factors that specifically regulate plant development and stress responses. Recently, several GT factors have been characterized in different plant species; however, little is known about the role of GT factors in wheat. Here, we show that TaGT2L1A, TaGT2L1B, and TaGT2L1D are highly homologous in hexaploid wheat, and are localized to wheat chromosomes 2A, 2B, and 2D, respectively. These TaGT2L1 genes encode proteins containing two SANT domains and one central helix. All three homologs were ubiquitously expressed during wheat development and were responsive to osmotic stress. Functional analyses demonstrated that TaGT2L1D acts as a transcriptional repressor; it was able to suppress the expression of AtSDD1 in Arabidopsis by binding directly to the GT3 box in its promoter that negatively regulates drought tolerance. TaGT2L1D overexpression markedly increased the number of stomata and reduced drought tolerance in gtl1-3 plants. Notably, ectopic expression of TaGT2L1D also affected floral organ development and overall plant growth. These results demonstrate that TaGT2L1 is an ortholog of AtGTL1, and that it plays an evolutionarily conserved role in drought resistance by fine-tuning stomatal density in wheat. Our data also highlight the role of TaGT2L1 in plant growth and development.

Figure: Schematic diagrams of AtGTL1, PtaGTL1 and TaGT2L1. (a) Biological function of TaGT2L1. (b) The plant water-deficit tolerance of two-week-old plants was evaluated. (c) The number of stomata per mm² in the abaxial epidermis of fully expanded rosette leaves. (d) How TaGT2L1D regulates plant drought resistance.
Plant Molecular and Developmental Biology

Dr. Xigang Liu, Principal Investigator, Ph.D. (2004, Hebei Normal University, China). The laboratory mainly focuses on the molecular mechanism of plant floral meristem maintenance and determinacy. Combing forward genetics with molecular and cellular biology, biochemistry and bioinformatics, we aim to dissect the multiple genes involved network controlling floral meristem determinacy by regulation WUS expression. Our laboratory is also interested in multiple molecular networks controlled spike development in wheat.

Email: xgliu@sjziam.ac.cn

A gene loop represses WUSCHEL expression in Arabidopsis

Lin Guo, Xiuwei Cao, Yuhao Liu, Jun Li, Yongpeng Li, Dongming Li, Caixia Gao, Aiwu Dong, Xigang Liu

Plant meristems are responsible for producing all parts of the plant body. While shoot apical meristem (SAM) keeps lifelong “stemness” activity, floral meristem (FM) reaches a programmed termination termed FM determinacy once a defined number of floral organs are developed. WUSCHEL (WUS) is critical for plant meristem maintenance and determinacy. Regulatory elements are essential for regulating spatial and temporal expression of WUS. Here, using chromosome conformation capture (3C) and chromatin immunoprecipitation-3C (ChIP-3C), we demonstrated that two particular regions flanking WUS gene body form a gene loop that is directly mediated by TERMINAL FLOWER2 (TFL2) and AGAMOUS (AG) during flower development in a physical distance and chromatin content independent manner. Transgenic plants and CRISPR/Cas9-edited lines showed that the gene loop represses host gene expression. Therefore, we shed new light on the mechanism of chromatin conformation change in gene expression.

Publications


Figure: Gene loop at the WUS locus. (A) Diagram of the WUS locus showing the DpnII sites (red triangles), primer locations, CArG-boxes (green ellipses) and WUS’ and WUS3’ CRE regions in this study. (B-E) 3C-PCR (B, D) and 3C-qPCR (C, E) examining the gene loop at the WUS locus. The specific 3C product is marked by the red arrow (B). Error bars represent SD from three biological repeats (C, E). **P<0.01. (F) 3C-PCR examining the gene loops at the GUS and WUS loci in the indicated plants. (G) 3C-qPCR examining the WUS gene loop in Ler and SALK_114398.
Integrate technologies and demonstration for adaptive cultivation of plants in coastal saline soils

Xiaojing Liu, Xiumei Zhang, Zhaoqiang Ju, Kai Guo, Zhenzhen Liu, Zhixia Xie, Lilin Yang

The coastal plain is the frontier area for implementing the developmental strategy in Hebei Province, which has plenty of arable land resources. However, the developmental obstacles exist in the coastal plain saline area, including high salt content in the soil, the lack of fresh water resources, the unreasonable farming structure, and the low comprehensive efficiency of the agriculture. This study focuses on the adaptability of the efficient cultivation technology, by applying the resources in saline water, heat, and cold weather in the region. The diversified crop-planting patterns were built to adapt to the characteristics of regional soil and water resources.

We invented the technology for reclamation of heavy coastal saline soil by freezing saline water irrigation in winter. The separation process of saline water and freshwater was clarified in the process of saline water freezing and thawing. The effects of freezing saline water irrigation on soil salt leaching were explicated. Moreover, the suitable planting patterns with freezing saline water irrigation were integrated in coastal region. In arid saline region, the summer maize deep tillage-winter wheat furrow sowing method was applied to increase crop yield. Meanwhile, the synergistic patterns for planting economic crop were established, including the simplified and efficient technology for cotton planting, the double cropping mode of oil sunflower. Additionally, many plant varieties with high-quality and salt-tolerant were bred to adapt the saline-alkali soils, including multi-purposed Chinese wolfberry ("Haiqi" and "Yanqi"), cotton (Cangmian 198 and Delinong 5). The products and the precise fertilizing method were developed for the arid saline soils. These technologies can increase the net income by more than 15,000 RMB/ha in the heavy saline land area, and save 1,800 m³/ha of freshwater resource. Moreover, this study was promoted to be accumulated to 1,625 thousand mu in Hebei Province, and it can increase revenue 314 million yuan. Thus, this study promotes agricultural development and improves the ecological environment in the saline plain in Hebei Province. It has achieved remarkable economic and social benefits.

Publications


Email: xjliu@sjziam.ac.cn

Figure: The efficient cotton planting mode.
Molecular Genetics of Plant Defense

Dr. Dongping Lu, Principal Investigator. Ph.D. (2007, University of Hawaii, USA). The research group is mainly interested in molecular genetics of plant defense, focusing on the mechanism of plant immunity to pathogen and how pathogens, especially Magnaporthe oryzae, develop disease in host.

Email: dplu@sjziam.ac.cn

A *Xanthomonas oryzae pv. oryzae* effector, XopR, associates with receptor-like cytoplasmic kinases and suppresses PAMP-triggered stomatal closure

Shuangfeng Wang, Jianhang Sun, Fenggui Fan, Zhaoyun Tan, Yanmin Zou, Dongping Lu

Receptor-like cytoplasmic kinases (RLCKs) play important roles in plant immunity signaling; thus, many are hijacked by pathogen effectors to promote successful pathogenesis. *Xanthomonas oryzae pv. oryzae* (Xoo) is the causal agent of rice leaf blight disease. The strain PXO99A has 18 non-TAL (transcription activation-like) effectors; however, their mechanisms of action and host target proteins remain largely unknown. Although the effector XopR from the Xoo strain MAFF311018 was shown to suppress PAMP-triggered immune responses in *Arabidopsis*, its target has not yet been identified. We found that PXO99A XopR interacts with BIK1 at the plasma membrane. BIK1 is a receptor-like cytoplasmic kinase (RLCK) belonging to the RLK family and mediates PAMP-triggered stomatal immunity. We found that XopR suppresses PAMP-triggered stomatal closure in transgenic *Arabidopsis* expressing XopR (Fig.). In addition, XopR is able to associate with RLCKs other than BIK1. These results suggest that XopR likely suppresses plant immunity by targeting BIK1 and other RLCKs.

Figure: Suppression of PAMP-triggered stomatal closure by XopR.
(A) XopR expression suppresses flg22-induced stomatal closure. (B) Confirmation of XopR-HA expression in the two transgenic lines.

Publication

Transitions in Chinese agriculture resulted in industrial animal production systems, disconnected from crop production. We analyzed side-effects of these transitions on total dissolved nitrogen (TDN) and phosphorus (TDP) inputs to rivers (Fig.). In 2000, when transitions were ongoing, 30%–70% of the manure was directly discharged to rivers (range for sub-basins). Before the transition (1970) this was only 5%. Meanwhile, animal numbers more than doubled. As a result, TDN and TDP inputs to rivers increased 2- to 45-fold (range for sub-basins) during 1970–2000. Direct manure discharge accounts for over two-thirds of nutrients in the northern rivers and for 20%–95% of nutrients in the central and southern rivers. Environmental concern is growing in China. However, in the future, direct manure inputs may increase. Animal production is the largest cause of aquatic eutrophication. Our study is a warning signal and an urgent call for action to recycle animal manure in arable farming.

Figure: A simplified historical overview of farming systems in China. This overview is shown in relation to direct nutrient losses to rivers, and their environmental impacts including harmful algal blooms (HABs). The transition in Chinese agriculture started in the early 1980s.
Agricultural Hydrology and Water Resources

Dr. Yanjun Shen, Principal Investigator, Ph.D. (2004, Chiba University, Japan). The laboratory is mainly interested in eco-hydrological processes, especially the processes related to agricultural water use and ecological conservation. By field observation, route survey, remote sensing, and numerical modeling, we focus on the water cycles at plot, watershed, and regional scales. Currently, we are investigating the water cycle deterioration mechanism owing to human exploitation in Hai River Basin and the recovery possibility. We are also involved in the research on hydrology and water resources change and adaptation to climate warming.

Email: yjshen@sjziam.ac.cn

Agricultural water supply/demand changes under projected future climate change in the arid region of northwestern China

Ying Guo, Yanjun Shen

The water resources in the arid region of northwestern China, which are impacted by climate change, tend to be more unstable, and the environment and ecosystems will suffer from severe water shortage. We predicted potential future climate trends based on CMIP5 simulations and estimate the water availability and agricultural water demand under future climate change scenarios in this region. It is found that the irrigation water demand will increase by 4.27–6.15 billion/m³ in this region over the next 60 years, compared to the demand of 32.75 billion/m³ during 1971–2000. However, the annual runoff will only increase by 4.8–8.5 billion/m³, which is equivalent to or even less than the increased irrigation water demand. In fact, other water demand increases were not considered here. Thus, the water supply/demand contradiction will result in more severe water shortages in the future. According to a comparison with simulated irrigation water demand under three adaptation strategy scenarios, we found it is necessary to take effective measures such as improving the efficiency of irrigation water utilization, reducing crop planting areas and adjusting crop planting structures to alleviate the impacts of future climate changes on the water use. It is found that reducing crop planting areas is the most effective measure for saving water in this region.

Publications

Chen Y., Li Z., Li W., Dong H., Shen Y. Water and ecological security: dealing with hydroclimatic challenges at the heart of China’s Silk Road. Environ. Earth Sci. 2016, 75: 1-10.

Figure: Irrigation water demand change from the historical period of 1971–2000 to future period (2016–2045 and 2046–2075) with irrigation water efficiency as 0.42, 0.48, 0.52, 0.68 and 0.8 without crop type adjusting (crop area as that in 1990, 2000 and 2010 represented by black solid line, red solid line and blue solid line, respectively) and with crop planting types adjusting form the types as that in 2010 to spring maize in Northern Xinjiang and Hexi area and cotton in Southern Xinjiang (crop area as that in 1990, 2000 and 2010 represented by black dotted line, red dotted line and blue dotted line, respectively).
Combination of CFCs and stable isotopes to characterize the interaction of surface water and groundwater in a headwater basin of the North China Plain

Shiqin Wang, Ruiqiang Yuan, Changyuan Tang, Xianfang Song, Matthew Currelle, Zhenglun Yang, Zhuping Sheng

Mountainous areas are characterized by steep slopes and rocky landform, with hydrological conditions varying rapidly from upstream to downstream, creating variable interactions between groundwater and surface water. In this study, surface water–groundwater interaction within a catchment of the North China Plain was assessed along the stream length, and during different seasons using hydrochemical and stable isotope data, and groundwater age-dating with chlorofluorocarbons (CFCs). The river is gaining, due to groundwater discharge in the headwater catchment both in the dry and rainy seasons. This is shown by very similar stable isotopic values in river and groundwater. Mixing fractions calculated using CFCs data reveal that groundwater was mainly recharged by a mixture of old water (recharged before 1950), carried by a regional flow system along the direction of river flow, along with young water (recharged after 1980), which enters the river through local flow systems from hilly areas adjacent to the river valley (particularly during the dry season). The binary mixing model by using CFC12 and CFC-113 showed that the ratio of young water v.s. total groundwater recharge ranged from 0.95 to 0.25 and from 1.0 to 0.73 in the upper and lower reaches, respectively. In the middle reach, river morphology and groundwater extraction in the catchment allows some loss of river water back into the aquifer, leading to decreasing estimates of groundwater age. These data suggest that in this area, the river becomes increasingly losing downstream; the opposite of typical river behavior and what would be expected based on topography. This is explained by declining groundwater levels below the river, due to groundwater extraction in the plains area.
Sustainable Agricultural Water Management

Dr. Yonghui Yang, Principal Investigator, Ph.D. (2002, Chiba University, Japan), Vice Director of Center for Agricultural Resources Research of ICDBG, and Vice Director of the Center for Water Resources Research in Chinese Academy of Sciences. Our group is mainly interested in improving the evaluation of key hydrological elements such as rainfall, ET, and runoff, understanding the key driving forces of water system change including both natural and human forces, Land-Water-Food NEXUS for water sustainability and food security.

Email: yonghui.yang@sjziam.ac.cn

Modification and validation of Priestley–Taylor equation for estimating cotton evapotranspiration under plastic mulch condition

Zhipin Ai, Yonghui Yang

Compared with more comprehensive physical algorithms such as the Penman–Monteith model, the Priestley–Taylor model is widely used in estimating evapotranspiration for its robust ability to capture evapotranspiration and simplicity of use. The key point in successfully using the Priestley–Taylor model is to find a proper Priestley–Taylor coefficient, which is variable under different environmental conditions. Based on evapotranspiration partition and plant physiological limitation, this study developed a new model for estimating the Priestley–Taylor coefficient incorporating the effects of three easily obtainable parameters such as leaf area index (LAI), air temperature, and mulch fraction. Meanwhile, the effects of plastic film on the estimation of net radiation and soil heat flux were fully considered. The reliability of the modified Priestley–Taylor model was testified using observed cotton evapotranspiration from eddy covariance in two growing seasons, with high coefficients of determination of 0.86 and 0.81 in 2013 and 2014, respectively (Fig.). Then, the modified model was further validated by estimating cotton evapotranspiration under three fractions of mulch cover: 0%, 60%, and 100%. The estimated values agreed well with the measured values via water balance analysis. It can be found that seasonal variation of the modified Priestley–Taylor coefficient showed a more reasonable pattern compared with the original coefficient of 1.26. Sensitivity analysis showed that the modified Priestley–Taylor coefficient was more sensitive to LAI than to air temperature. Overall, the modified model has much higher accuracy and could be used for evapotranspiration estimation under plastic mulch condition.

Figure: Comparison of the modified Priestley–Taylor coefficient in cotton plots under three mulch fractions in 2013 (a) and 2014 (b). (c) and (d) are mulching cotton field and Eddy covariance system respectively.

Publications


Mechanisms and Techniques to Improve Farmland Water Use Efficiency

Dr. Xiying Zhang, Principal Investigator. Ph.D. (2006, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan). The research group is interested in crop water relationship. We conducts field experiments on the water transfer and regulation mechanisms in the soil-plant-atmosphere continuum for the purposes of reducing irrigation water use by improving water use efficiency to farmland crops.

Email: xyzhang@sjziam.ac.cn

Publications


Assessing the impact of air pollution on grain yield of winter wheat

Xiuwei Liu, Hongyong Sun, Til Feike, Xiying Zhang, Liwei Shao, Suying Chen

The major wheat production region of China the North China Plain (NCP) is seriously affected by air pollution. In this study, yield of winter wheat (Triticum aestivum L.) was analyzed with respect to the potential impact of air pollution index under conditions of optimal crop management in NCP from 2001 to 2012. Results showed that air pollution was especially serious at the early phase of winter wheat growth. However, no significant correlations were found between final grain yield and the weather factors during the early growth phase. In contrast, significant correlations were found between grain yield and total solar radiation gap, sunshine hour gap, diurnal temperature range and relative humidity during the late growing phase. To disentangle the confounding effects of various weather factors, and test the isolated effect of air pollution-induced changes in incoming global solar radiation on yield under ceteris paribus conditions, crop model based scenario-analysis was conducted. The simulation results of the calibrated Agricultural Production Systems Simulator (APSIM) model indicated that a reduction in radiation by 10% might cause a yield reduction by more than 10%. Increasing incident radiation by 10% would lead to yield increases of (only) 7%, with the effects being much stronger during the late growing phase compared to the early growing phase. However, there is evidence that APSIM overestimates the effect of air pollution induced changes on radiation, as it does not consider the changes in radiative properties of solar insulation, i.e., the relative increase of diffuse over direct radiation, which may partly alleviate the negative effects of reduced total radiation by air pollution. Concluding, the present study could not detect a significantly negative effect of air pollution on wheat yields in the NCP. However, the positive relation of radiation and diurnal temperature range with yield indicated the possible negative effects of air pollution on winter wheat.
Transcriptomic analysis of water stress response of *Triticum urartu*

Hongliang Zhang, Daowen Wang, Zhengbin Zhang

Drought is one of the most serious abiotic stresses negatively affecting wheat distribution and yield. Understanding the transcriptomic response of wheat under drought is significant for elucidating the mechanisms of drought resistance and the genetic improvement of cereal crops, such as wheat. Microarray hybridization is used in this research to analyze the transcriptomic reprogramming of the diploid wild einkorn wheat *Triticum urartu*, which provides A genome to common and durum wheat species, subjected to water deprivation and resupply. The results are as follow: 1) A large number of genes responsive to water stress were identified. A total of 1691 genes were upregulated and 1238 genes were downregulated in the leaves. The genes that were upregulated in both leaves and roots included those encoding dehydrins, late embryogenesis abundant proteins and aldehyde dehydrogenases, etc. 2) Some important metabolic processes were affected by water stress, such as carbohydrate metabolism, photosynthesis, cell wall metabolism, and oxidative phosphorylation. 3) A total of 186 transcription factor (TF) genes distributed in 29 families were responsive to water stress. Among them, eight TF gene families accounted for nearly 70% of the TF genes responsive to water stress. The WRKY and bHLH TF genes were the top two families, each of them accounting for 13% of the total. 4) The targets of some TF proteins were predicted through constructing gene regulatory networks. For example, the key gene for proline synthesis, *P5CS*, may be regulated by two putative TFs, i.e., TRIUR3_35146 (MYB TF) and TRIUR3_05289 (Hox7 TF). These results provide gene and molecular marker resources for the genetic improvement of drought resistance in wheat and related crops.

Figure: The targets of some TF proteins were predicted through constructing gene regulatory networks. (a) The expression profile of TRIUR3_07818, TRIUR3_35146 and TRIUR3_05289. (b) A potential model for regulating *P5CS1* gene expression under water stress.
Center for Core Facility & Advanced Technologies (CCFAT) were organized following the principle that the center should provide technical service for the major projects and tasks of the Country and the Chinese Academy of Sciences, for the development of disciplines and new layout, and for the development of the basic research capacity of the institute. CCFAT owns the facilities and technologies that can strongly support genomics, proteomics, metabolomics, cell biology and mostly the whole life sciences research.

CCFAT is currently composed of seven specialized technical platforms (biotechnology analysis, genome analysis, proteomics analysis, lipidomic analysis, metabolomics analysis, plant hormone analysis, biological imaging analysis), animal experiment center, and isotope laboratory.

Biotechnology Analysis Platform provided the service of the plant genetic transformation and plant genome editing. The platform is devoted to the development of genome editing technology system of important crops and model plants, the establishment of biosafety genome editing and breeding technology, and the innovation of high-quality, high-throughput and precision crop germplasm. A seed innovation system based on crop genome engineering will be established to advance the process of genetic improvement and to provide technical support for ensuring the food security and the sustainable development of agriculture in China.

Genome Analysis Platform meets the demands of functional genomics and molecular breeding and other cutting-edge cross-disciplinary research projects of the institute to provide new genome sequencing and assembly, genome resequencing and polymorphic loci identification, transcription group sequencing and analysis, crop genetics and breeding population analysis, the bioinformatics databases and software development services. The near-term goal of the platform is to create an innovative platform for advanced genomics and bioinformatics analysis that will enable the integration of genomics data outputs, analyses and applications, as well as the development of national and CAS major tasks.

Lipidomic Analysis Platform utilizes advanced mass spectrometry technology and develops efficient lipidomic analysis techniques to achieve high-throughput analysis of thousands of lipid components in plant and animal tissues, and other biological samples, including phospholipids (PC, LPC, PE, LPE, PI, PIP, PIP2, LPI, PS, LPS, PG, LPG, PA, LPA, CL, and monolysocardiolipin), sphingomyelin (Cer, SM, GluCer, Gal-Cer, GM3 ganglioside, sphingosine, and Sph-1-P), glycerolipid (TAG and DAG), ubiquinone, acetyl carnitine, free fatty acid, free cholesterol, and cholesteryl ester, so as to meet the urgent needs of the domestic research in this field.

Metabolomics Analysis Platform integrates a variety of analytical techniques to analyze the small molecule metabolites in various organisms at different levels. The informatics methods are combined with the biochemistry techniques to analyze differences in metabolic fingerprints in different states, such as wild-type and mutant before and after treatments of different growth conditions, thereafter to yield corresponding biomarkers. The platform also identifies unknown metabolic pathways, and understands the metabolite pathways in depth, in order to reveal the whole functional state of the organism at a specific time in a specific environment, and to provide clues and research information for explaining the inherent laws of living bodies. The technical services provided by the platform include: qualitative and quantitative analysis of metabolites of polar and non-polar metabolites, metabolic profile analysis, metabolic profiling of the fatty acids, analysis of the metabolites of the metabolites and metabolites.

Proteome Analysis Platform has established the solution digestion, gelatinase digestion and other sample preparation methods and has optimized for large-scale sample preparation of liquid chromatography separation method in the proteome sample preparation. In the aspect of post-translational modification, the phosphorylated proteomic enrichment and identification techniques have been established. Quantitative and differential proteomics have been
established for SILAC (stable isotope labeling) quantification, iTRAQ marker quantification, and N15 marker quantitative proteomics techniques. A number of post-translational modifications analysis can be provided, including identification of phosphorylation sites in cell lines, identification and quantification of ubiquitination sites, and characterization of acetylated and methylated protein mass spectrometry.

Plant Hormone Analysis Platform has a complete set of chromatography and mass spectrometry equipments and standard analytical chemistry laboratory equipments. Quantitative analysis of plant hormones, including IAA, abscisic acid (ABA), abscisic acid (ABA), etc., and quantitative analysis of phytohormones, such as jasmonic acid (JA), salicylic acid (SA), cytokinin (CKs), gibberellin (GAs), brassinosteroids (BRs) of various tissues in Arabidopsis thaliana, rice, corn and wheat and other plant species are the characteristic technical services of the platform.

Biological imaging Platform is committed to the development of new optical imaging technology and equipment, and to carry out the interaction between cells and biological macromolecules and other disciplines in the process of cross-cutting research. The platform has several sets of advanced optical microscopy systems, including: rotary confocal microscopy, total internal reflection fluorescence microscopy, two-photon microscopy, super-resolution microscopy, which can be performed to observe culture cells and living animal and plant cells and other biological samples. While providing testing services, the platform is also committed to the development of new optical imaging technologies, such as optical tweezers-multi-photon integrated imaging and single-molecule fluorescence imaging.

The Animal Experimental Center can provide model animals (e.g., ICR mice, C57BL/6 mice, BALB/c mice, SD rats, Wistar rats, Xenopus laevis), laboratory animal foster (available in rats, mice, rabbits, guinea pigs, African clawed frogs, zebrafish and tree shrews), resource conservation (preservation of live stock, including sperm, embryos, cells, DNA, etc.), commissioned animal experiments (mouse transgene, embryo transfer and other services) and antibody preparation (monoclonal and polyclonal antibodies, including mice, rabbits and guinea pigs).

The Isotope Laboratory fulfills the needs of the institute's isotope experiment, permitting the use of 14 nuclides.

The above-mentioned professional and technical platforms, with their own characteristics and advantages, provide strong guarantee for the development of our major disciplines and undertake major scientific research tasks of the country and CAS, and realize scientific and technological innovation and serve the social goals. During 2016, the center provided nearly 10,000 samples of testing, and more than 1,200 hours of machine-time service; the center published 13 original research articles and provided technical support and services to 25 articles published by other research groups of the Institute; the center applied 14 patents, 12 of which are from biotechnology platform and 1 from metabolic platform and 1 from biological imaging platform.

In 2016, CCFAT gained excellent results of the evaluation of the CAS into the merit-based support. The animal experimental center of CCFAT obtained a funding support of the Model and Characteristics of Animal Experiment Platform from 2016 to 2018. Chief scientist Caixia Gao of Biotechnology Platform won the 2016 Nature "Chinese Science Star".
State Key Laboratory of Plant Genomics

The State Key Laboratory of Plant Genomics was founded in 2003 by the Ministry of Science and Technology of China. The Laboratory was upgraded from the Key Laboratory of Plant Biotechnology of the Chinese Academy of Sciences founded in 1990. In the nationwide State Key Laboratory evaluation in 2006 and 2011, the Laboratory was twice evaluated as outstanding (Rank A).

The Laboratory uses combined approaches of multidisciplinary life sciences to address fundamental questions in plant growth and development, with an emphasis on the dissection of the molecular mechanisms of complex agronomic traits of crops. An important mission of the Laboratory is to extend knowledge in basic research to crop improvement for superior traits. The Laboratory mainly uses rice and Arabidopsis as model systems to unravel the structure and function of plant genomes, functional genomics of important agronomic traits, phytohormone-regulated plant growth and development, plant-environment and plant-pathogen interactions, and molecular breeding.

**HOME PAGE:** http://www.plantgenomics.genetics.cas.cn  
**DIRECTOR:** Jianru Zuo  
**DEPUTY DIRECTORS:** Chengcai Chu, Xiaofeng Cao, Wei Qian  
**PRINCIPAL INVESTIGATORS:** Mingsheng Chen, Shouyi Chen, Zhukuan Cheng, Rongxiang Fang, Huishan Guo, Yuling Jiao, Zhaosheng Kong, Chuanyou Li, Jiayang Li, Shaoyang Lin, Jun Liu, Dongping Lu, Jinqiong Qiu, Guodong Wang, Xiujie Wang, Yonghong Wang, Guixian Xia, Qi Xie, Shanguo Yao, Jinsong Zhang, Jianmin Zhou, Yihua Zhou, Lihuang Zhu, Zhen Zhu

**SCIENTIFIC STEERING COMMITTEE**  
**CHAIR:** Rongxiang Fang  
**VICE CHAIRS:** Yongbiao Xue, Bin Han  
**MEMBERS:** Xiaofeng Cao, Xiaoya Chen, Kang Chong, Huishan Guo, Jiayang Li, Yaoguang Liu, Hong Ma, Qian Qian, Weihua Wu, Jianmin Zhou, Yuxian Zhu, Jianru Zuo

**SCIENTIFIC ADVISORY BOARD:** Shouyi Chen, Zhihong Xu, Qifa Zhang, Lihuang Zhu, Zhen Zhu

**MAJOR RESEARCH PROGRESSES**

During the past year, scientists in the Laboratory have made important advances in several research fields. In plant genomics studies, Xiaofeng Cao’s group reported that REF6 uses four zinc fingers to directly recognize a CTCTGYTY motif, allowing genome-wide, site-specific demethylation of H3K27me3. These results identify a new targeting mechanism of an H3K27 demethylase to counteract Polycomb-mediated gene silencing (Cui et al., Nat Genet, 2016). The same group also applied genetics, transcriptomics, proteomics and biochemistry to show that AtPRMT5 modulates constitutive and alternative pre-mRNA splicing, uncovering a key process through which arginine methylation impacts diverse developmental processes (Deng et al., PNAS, 2016). Jiayang Li and several other scientists proposed a regulatory framework for precision breeding with "genome-edited crops" (GECs) so that society can fully benefit from the latest advances in plant genetics and genomics, which showed pioneering influence in the application of genome-edited technology (Huang et al., Nat Genet, 2016). Jiayang Li’s group and collaborators successfully carried out efficient intron-mediated site-specific gene replacement through the non-homologous end joining (NHEJ) pathway assisted by the CRISPR/Cas9 system, and these newly developed technology can be generally applied to molecular breeding and analysis of plant genes (Li et al., Nat Plants, 2016). Xiujie Wang’s group and collaborators found that AGO3, and likely AOG4, predominantly bound 24-nt sRNAs to modulate DNA methylation, indicating that AGO3 is a component in the epigenetic pathway (Zhang et al., Nat Plants, 2016).

In functional genomics studies, Jiayang Li’s group identified a defective soluble starch synthase gene (SSIIIa) responsible for resistant starch (RS) production. This discovery holds great promise in improving cooking quality of rice especially
in the *indica* varieties which are dominating in southern Asia (Zhou et al., *PNAS*, 2016). Yonghong Wang and Jiayang Li’s
groups discovered a new molecular mechanism controlling shoot branching. They showed that the MKK7-MPK6 cascade
phosphorylates Ser337 on PIN1, establishing a molecular link between the MAPK cascade and auxin-regulated plant
development (Jia et al., *PLoS Biol*, 2016). Lihuang Zhu’s group and collaborators conducted integrated genetics and omics
analyses in a model two-line rice hybrid system, Liang-you-pei 9 (LYP9) and its parents to identify multiple quantitative trait
loci (QTLs) involved in yield heterosis, and proposed a common mechanism for yield heterosis in the present commercial
hybrid rice (Li et al., *PNAS*, 2016). Chengcai Chu’s group analyzed a newly identified a dominant panicle enclosure mutant
*regulator of eui1* (*ree1-D*) to show that HOX12 acts directly through *EUI1* to regulate panicle exsertion in rice (Gao et al.,
*Plant Cell*, 2016). Zhukuan Cheng’s group showed that P31 is a functional synaptonemal complex (SC) protein and is
essential for double-strand break (DSB) formation and SC installation in rice (Ji et al., *PNAS*, 2016). The same group and
collaborators demonstrated that MS5 participates in progression of meiosis during early prophase I and that its allelic
variants alter fertility in oilseed rape (*Brassica napus* L.), which may provide a promising strategy for pollination control
for heterosis breeding (Xin et al., *Plant Cell*, 2016). Chuanyou Li’s group and collaborators identified DA3 as a negative
regulator of endoreduplication and showed that endoreduplication is linked to cell and organ growth via interaction of
DA3 with key cell-cycle regulators (Xu et al., *Plant Cell*, 2016). Yuling Jiao’s group reported that the initiation of axillary
meristems requires a meristematic cell population continuously expressing the meristem marker *SHOOT MERISTEMLESS*
(*STM*), and proposed a threshold model for axillary meristem initiation (Shi et al., *PLoS Genet*, 2016).

In studying of plant-environment/pathogen interactions, Jian-Min Zhou’s group reported that the *Pseudomonas syringae*
effector HopB1 acts as a protease to cleave immune-activated BAK1, leading to enhanced virulence, but not disease
resistance revealing a virulence strategy by which a pathogen effector attacks the plant immune system with minimal
host perturbation (Li et al., *Cell Host Microbe*, 2016). The same group demonstrated that heterotrimeric G proteins are
directly coupled to the FLS2 receptor complex and regulate immune signaling through both pre-activation and post-
activation mechanisms (Liang et al., *eLife*, 2016). Huishan Guo’s group made several important progresses in the study of
devastating wilt diseases. Their work reported the pathway in which hyphopodium of *Verticillium dahliae* redirect fungal
growth toward host cells to penetrate cotton roots and to colonize the host vascular system (Zhao et al., *PLoS Pathog*,
2016). Further study revealed that in response to infection with *Verticillium dahliae*, cotton plants increase production
of microRNAs and export them to the fungal hyphae for specific silencing of fungal genes, uncovering cross-kingdom
gene silencing as a novel defence strategy of host plants (Zhang et al., *Nat Plants*, 2016). Jinlong Qiu’s group found that
MPK4 interacts with and phosphorylates MYB75 to increase the stability of MYB75 and that this modification is essential
for light-induced anthocyanin accumulation. These findings revealed an important role for a MAPK pathway in light
signal transduction (Li et al., *Plant Cell*, 2016). Qi Xie’s group reported that the two major complexes involved in the ER-
associated protein degradation (ERAD) system closely interact with each other, which is conserved between plants and
mammals (Chen et al., *Nat Plants*, 2016).

**AWARDS AND RECOGNITIONS**

Prof. Xiaofeng Cao was elected as an academician of the Third World Academy of Sciences. Prof. Qi Xie was highlighted in
Thomson Reuters China Citation Laureates. Prof. Chuanyou Li and Prof. Xiujie Wang received Leading Talent Awards from
the Scientific and Technological Innovation Program.
Sate 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: 1) to systematically study the genetic basis of important agronomic traits of major crops and to identify key genes involved; 2) to develop efficient gene transfer strategies in plant utilizing chromosome engineering and molecular breeding tools for designing crop varieties through the assembly elite genes or alleles; and 3) to create novel germplasms and to breed crop varieties with excellent agronomic traits, such as high yield, superior quality, high nutrient efficiency and improved tolerance to biotic and abiotic stresses.

Home Page: http://pcce.genetics.cas.cn
Director: Hongqing Ling
Vice Directors: Xiangdong Fu, Fangpu Han, Dingzhong Tang
Principal Investigators: Huabang Chen, Caixia Gao, Junming Li, Yunhai Li, Zhensheng Li, Cuimin Liu, Xigang Liu, Zhiyong Liu, Qianhua Shen, Yiping Tong, Zhixi Tian, Daowen Wang, Aimin Zhang, Xiangqi Zhang, Baoge Zhu

Scientific Steering Committee
Chair: Weihua Wu
Vice Chair: Daowen Wang
Members: Xiangdong Fu, Zhikang Li, Hongqing Ling, Bao Liu, Xu Liu, Shiping Wang, Yongbiao Xue, Hongquan Yang, Fusuo Zhang, Yuxian Zhu

Scientific Advisory Committee: Rongxiang Fang, Tingyun Kuang, Zhensheng Li

Major Research Progresses

In 2016, PCCE made significant progresses in the research of genomics, genome editing, yield and quality improvement, plant disease resistance, mineral nutrient efficiency, chromosome engineering and molecular design for breeding of new varieties on the major crops such as wheat, rice, corn and soybean. PCCE published 51 papers, authorized 11 patents, applied 6 PCT patents, authorized 6 crop variety protections, and approved 2 new wheat varieties. The varieties of wheat, corn and soybean bred by PCCE were cultivated more than 180,000 ha in 2016. The representative achievements are as follows:

Genomics: Zhixi Tian’s group studied the co-evolution of miRNAs and their target genes during soybean domestication and found that the evolution of miRNAs was faster than that of their target genes (Liu et al., Plant J, 2016).

Genome Editing: Caixia Gao’s group accomplished transgene-free genome editing in wheat through transient expression of CRISPR/Cas9 DNA or RNA (Zhang et al., Nat Commun, 2016). In addition, they also achieved in gene replacement and insertion by intron targeting using CRISPR-Cas9 in rice (Li et al., Nat Plants, 2016).

Crop Yield and Quality Improvement: Yunhai Li’s group confirmed that SAP was an F-box protein forming part of a SKP1/Cullin/F-box E3 ubiquitin ligase complex, and functioned in the control of organ size by promoting the proliferation of meristemoid cells (Wang et al., Nat Commun, 2016). They also illustrated that the OsGRF4 regulated by OsmiR396 was involved in grain size and yield control of rice (Duan et al., Nat Plants, 2016). Xigan Liu’s group demonstrated that FHY3 activated SEP2 via inhibiting CLA3 to regulate meristem determinacy and maintenance (Li et al., PNAS, 2016). Cuimin Liu’s group illustrated the crystal structure of Chlamydomonas chloroplast chaperonin homo-oligomer (CPN60β1), and analyzed the functional partition of Cpn60α and Cpn60β subunits in substrate recognition and cooperation with co-chaperonins (Zhang et al. BMC Biol, 2016; Zhang et al., Mol Plant, 2016). Aimin Zhang’s group constructed a high resolution linkage map of einkorn wheat and characterized QTLs controlling seed size with it (Yu et al., Theor Appl Genet, 2016).
**Plant Disease Resistance:** Qianhua Shen’s group collaborated with Qi Xie’ group identified a new E3 ligase which affected the NLR receptor stability and immunity to powdery mildew (Wang et al., *Plant Physiol*, 2016). Dingzhong Tang’s group revealed that the mutation of glucosinolate biosynthesis enzyme cytochrome P450 83A1 monooxygenase increased camalexin accumulation and powdery mildew resistance (Liu et al., *Front Plant Sci*, 2016). Daowen Wang’s group analyzed coexpression network of the genes regulated by the two types of resistance responses to powdery mildew in wheat (Zhang et al., *Sci Rep*, 2016). Zhiyong Liu’s group fine mapped the spot blotch resistance gene *Sb3* in wheat (Lu et al., *Theor Appl Genet*, 2016).

**Mineral Nutrient Efficiency:** Xiangdong Fu’s group illustrated that the shoot-to-root mobile transcription factor HY5 coordinated plant carbon and nitrogen acquisition (Chen et al., *Curr Biol*, 2016). Yiping Tong’s group proved that knocking out of *TaPHO2-A1* was able to improve phosphate uptake and grain yield under low phosphorus conditions in common wheat (Ouyang et al., *Sci Rep*, 2016). Hong-Qing Ling’s group characterized the *AtSPX3* promoter and elucidated its complex regulation in response to phosphorus deficiency (Li et al., *Plant Cell Physiol*, 2016).

**Chromosome Engineering and breeding of New Varieties:** Fangpu Han’s group demonstrated de novo centromere formation and centromeric sequence expansion in wheat and its wide hybrids (Guo et al., *PLoS Genet*, 2016). Junming Li’s group bred the wheat varieties “Kenong 2009” and “Kenong 2011”, and they have been approved by National variety committee and the variety committee of Hebei province, respectively. Zhensheng Li’s group and Huabang Chen’s group bred the wheat and corn varieties for the Bohai Granary Science and Technology Demonstration Project.
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.

HOME PAGE: http://mdb.genetics.ac.cn
DIRECTOR: Weicai Yang
VICE DIRECTORS: Xun Huang, Jianwu Dai, Fan Chen
PRINCIPAL INVESTIGATORS: Shilai Bao, Yuhang Chen, Zhuo Du, Mei Ding, Weixiang Guo, Yuqiang Jiang, Wei Li, Xiaojiang Li, Jiajia Liu, Runlin Ma, Wenxiang Meng, Guanghou Shui, John R. Speakman, Fangzhen Sun, Ye Tian, Qiang Tu, Yingchun Wang, Zhaohui Wang, Yongbiao Xue, Zhiheng Xu, Chonglin Yang, Jian Zhang, Yongqing Zhang

In 2016, the laboratory published 98 papers. Four eminent scientists spoke at the FORUM on DEVELOPMENT, GENETICS, AND DISEASE. During 2016, the laboratory achieved significant advances in the following fields:

Early Development: Weicai Yang’s group reported the identification of a cell-surface receptor heteromer, MDIS1–MIK, on the pollen tube that perceives the female attractant LURE1 in *Arabidopsis thaliana*. This finding identified the long-puzzled receptor heteromer of the LURE1 attractant and revealed the activation mechanism and will contribute to the full understanding of male-female recognition during plant reproduction. Meanwhile, this study establishes the theory of through inter-species expressing of receptor to break down the reproductive isolation and will shed light in the crop breeding (Wang et al., *Nature*, 2016). In the Solanaceae, Rosaceae and Plantaginaceae, the S-locus encodes a single S-RNase and a cluster of S-locus F-box (SLF) proteins to control the pistil and pollen expression of SI, respectively. Yongbiao Xue’s group revealed that the electrostatic potentials act as a major physical force between cytosolic SLFs and S-RNases, providing a mechanistic insight into the self/non-self-discrimination between cytosolic proteins in angiosperms (Li et al., *Plant J*, 2016). Large numbers of maternal RNAs are deposited in oocytes and are reserved for later development. Jian Zhang’s group reported loss of Zar1 causes markedly upregulation of zona pellucida (ZP) family proteins, while overexpression of ZP proteins in oocytes causes upregulation of stress related activating transcription factor 3 (atf3), arguing that tightly controlled translation of ZP proteins is essential for ER homeostasis during early oogenesis. Furthermore, Zar1 binds to zona pellucida (zp) mRNAs and represses their translation (Miao et al., *Development*, 2016).

Neurodevelopment and Disease: Zhiheng Xu’s group and Guoli Ming’s group at Johns Hopkins University School of Medicine revealed that Crmp2 (collapsing response mediator protein 2), a schizophrenia risk gene, plays a critical role in neural development, circuit integrity and brain function. They provided a valuable mouse model for better understanding the aetiology of schizophrenia and targeted strategies for drug development (Zhang et al., *Nat Commun*, 2016). Xu’s group also demonstrated MEA6 plays a critical role in lipid transportation through the coordinated regulation of the COPII machinery, which provided insight into mechanisms underlying VLDL transportation. More importantly, this mouse model provides a useful tool for potential biomarkers or drug screening related to fatty liver disease (Wang et al., *Cell Res*, 2016). Mei Ding’s group found that the single calponin homology (CH) domain-containing protein CHDP-1 induces the formation of cell protrusions by coupling membrane expansion to Rac1-mediated actin dynamics in *C. elegans* (Guan et al., *PLoS Genet*, 2016). Xiaojing Li’s group revealed age- and cell type-dependent vital functions of Htt (huntingtin, Huntington’s disease protein) and the safety of knocking down neuronal Htt expression in adult brains as a treatment (Wang et al., *PNAS*, 2016; Liu et al., *PLoS Genetics*, 2016). The study of Yongqing Zhang’s group shed new light onto the neuronal
functions of UBE3A (E3 ubiquitin ligase) and provides novel perspectives for understanding the pathogenesis of UBE3A-associated Angelman syndrome and autism (Li et al., *PLoS Genet*, 2016).

**Stem Cell and Tissue Engineering:** Zhiheng Xu’s group gave direct evidence that Zika infection causes microcephaly in a mammalian animal model. They found the virus infected the neural progenitor cells, and infected brains reveal expression of genes related to viral entry, altered immune response, and cell death. Further study showed passive transfer of convalescent serum containing high-titer neutralizing antibodies to pregnant mice can not only suppress ZIKV replication but also inhibit cell death and reduction of neural progenitor cells in infected fetal brains, thus preventing microcephaly (Wang et al., *Cell Res*, 2016). Jianwu Dai’s group screened a functional scaffold, which showed higher endogenous neurogenesis efficiency as well as *in vivo* survival and neuronal differentiation rate of the grafted neural stem cells are observed (Li et al., *Adv Funct Mater*, 2016).

**Lipid Metabolism and Development:** John Speakman’s group demonstrated Thrifty Gene Hypothesis that obesity provided a selective advantage to survive famines may be not correct (Wang et al., *Cell Metab*, 2016). Using state-of-the-art lipidomic approach, Guanghou Shui’s group found a breakdown in DHA esterification into neural membranes may prove more detrimental than a diminished dietary supply of DHA *per se* (Lam et al., *Oncotarget*, 2016).

**Vesicle Trafficking and Development:** Together with Xiaojiang Hao’s group at Kunming Institute of Botany, CAS, Chonglin Yang’s group showed that protein kinase C couples activation of the TFEB transcription factor with inactivation of the ZKSCAN3 transcriptional repressor through two parallel signaling cascades. It revealed that PKC activators are viable treatment options for lysosome-related disorders (Li et al., *Nat Cell Biol*, 2016). Phosphatidylinositol 3-phosphate (PtdIns3P) plays a central role in endosome fusion, recycling, sorting, and early-to-late endosome conversion. Yang’s group identified two new factors, SORF-1 and SORF-2, as essential PtdIns3P regulators in *Caenorhabditis elegans*. These findings revealed a conserved mechanism that controls appropriate PtdIns3P levels in early-to-late endosome conversion (Liu et al., *J Cell Biol*, 2016).
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.

HOME PAGE: http://lc.sjziam.ac.cn
DIRECTOR: Yanjun Shen
VICE DIRECTORS: Zhongmin An, Yisong Cheng
PRINCIPAL INVESTIGATORS: Diaoguo An, Chunsheng Hu, Junming Li, Mengyu Liu, Lin Ma, Yanjun Shen, Shiqin Wang, Xiyang Zhang, Zhenngbin Zhang

SCIENTIFIC STEERING COMMITTEE
CHAIR: Changming Liu
VICE CHAIRS: Qiang Yu, Chunsheng Hu
MEMBERS: Bojie Fu, Tieqing Huang, Baoguo Li, Junming Li, Mengyu Liu, Zhu Ouyang, Tusheng Ren, Shanmin Shen, Yanjun Shen, Guirui Yu, Jiabao Zhang, Lifeng Zhang, Xiyang Zhang

MAIN OUTPUTS
1. Totally, up to 54 papers were published in 2016, 31 of which were on the SCI indexed journals.
2. Four patents were granted in 2016, two of which were invention patents. Six patents, including three inventive, have been applied for certification.
3. Two projects have been awarded the provincial Science and Technology Progress Award and the Natural Science Award.

MAIN RESEARCH PROGRESSES
1. Determined the soil organic/inorganic carbon storage in the soil profile at 0–100 cm depths and the concentration of dissolved inorganic carbon in soil leachate in four kinds of N application treatments (0, 200, 400, and 600 kg N ha\(^{-1}\) y\(^{-1}\)) for 15 years in the North China Plain.
2. Quantified nutrient flows and losses in the whole manure management chain (from animal feeding to manure application to land) in China and potential to reduce nutrient losses and increase the amount of manure applied to crop land and replace fertilizer NPK.
3. Established the nitrification-related pathways (including ammonia oxidation) and heterotrophic denitrification as the most predominant sources of N\(_2\)O emissions from soil ecosystems.
4. Proposed a series of technologies to save irrigation water through altering the sawing date and spaces according to effective rainfall.
5. Rectified ET algorithm using P-T model under a film-mulched farmland and found that the annual water consumption from pear garden is about 70 mm larger than that from croplands.

6. Quantified that water in deep vadose zone moves mainly as a type of matric flow by a rate of ~1.14 m/y with loading large amount of solutions. Denitrification acts as a major factor to reducing nitrate leaching to aquifers in plain region, while dinitrogen is little in mountain aquifers.

7. Clarified the nexus relations among regional cropping pattern, water resources, and grain yield in semiarid NCP, and pointed out that the upper limit of irrigation land should be restrained as much as 4 million ha in the NW arid region. These findings posed great understanding to agricultural water saving practices at the dimension of crop drought resistance physiology, brackish water utilization, efficient water and nitrogen management at field scale, as well as understanding to the agriculture-water-ecology nexus relations or even the appropriate reclamation extent at region scale.

8. Characterized a new \( Pm2 \) allele, \( PmFG \), which confers powdery mildew resistance in the wheat germplasm Line FG-1, and seven closely linked markers were developed for \( PmFG \).

9. The new variety of wheat "Kenong 2011" was certified. In addition, a number of quantitative trait loci (QTLs) for wheat kernel size, quality and tolerance to low-N stress were characterized using a recombinant inbred line population derived from Kenong 9204 × Jing 411.

10. A transcriptomic analysis of the responses to water deprivation and resupply in \( Triticum urartu \) was carried out, which provided gene and molecular marker resources for the genetic improvement of drought resistance in wheat and related crops.
Key Laboratory of Agricultural Water Resources, Chinese Academy of Sciences

Hebei Key Laboratory for Water-Saving Agriculture

Hebei 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.

This two laboratories focus on improving agricultural water use efficiency in individual, field and regional levels, guaranteeing 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.

HOME PAGE: http://lawr.sjziam.ac.cn
DIRECTOR: Yanjun Shen
VICE DIRECTORS: Xiying Zhang, Shiqin Wang
PRINCIPAL INVESTIGATORS: Diaoguo An, Jiansheng Cao, Chunsheng Hu, Xiaofang Li, Binbin Liu, Jintong Liu, Mengyu Liu, Xiaojing Liu, Lin Ma, Yonghui Yang, Wanjun Zhang, Zhengbin Zhang
STRATEGIC COMMITTEE: Zhensheng Li, Changming Liu, Lun Shan, Junliang Tian, Guihai Wang
SCIENTIFIC STEERING COMMITTEE
CHAIR: Dahe Qin
VICE CHAIRS: Bojie Fu, Chunsheng Hu
MEMBERS: Wenjun Ding, Shaozhong Kang, Xiaoyan Li, Xurong Mei, Huijun Wang, Jianhua Wang, Yanfen Wang, Fengchang Wu, Jun Xia, Zhenghui Xie, Yonghui Yang, Zhaoji Zhang

MAIN RESEARCH PROGRESSES:

Substantial progresses in several aspects have been achieved by the key laboratory in 2016. The Director and the Scientific Steering Committee of the key laboratory were changed. A development plan of the laboratory for the 13th Five-Year was made this year. A second class prize of Natural Science Award in Hebei Province was won by the key Lab., and 31 SCI papers were published. Dr. Xiaofang Li was recruited and founded by the CAS Hundred Talents Program. The main achievements of the laboratory in 2016 are as follows:

Crop Physiological and Genetic Basis for High Efficient Water Use: Zhengbin Zhang and his coworkers used microarray hybridization to analyze the transcriptomic reprogramming of the diploid wild einkorn wheat *Triticum urartu*, which provides A genome to common and durum wheat species, subjected to water deprivation and resupply. A large number of genes responsive to water stress were identified, and confirmed that some important metabolic processes were affected by water stress, such as carbohydrate metabolism, photosynthesis, cell wall metabolism, and oxidative phosphorylation. Diaoguo An’s group used a population of 131 F16 RILs derived from a cross 200 “Chuan 35050 × Shannong 483” to investigated under well-watered (WW) and drought stress (DS) environments across 2 years to map quantiative trait loci (QTLs) for yield and physiological traits. A total of 225 QTLs were detected, including 32 non-environment-specific loci that were significant in both DS and WW.

Hydrological Process in Farmland: Xiying Zhang’ group summarized a long-term field experiment (from 1987 to 2015, 28 growing seasons of winter wheat) on the responses of winter wheat to different levels of water stress under the changing background of cultivars, soil fertility and weather conditions at a site in the North China Plain. This research
proved that one irrigation application from recovery to jointing for winter wheat could achieve relative stable yield and a rather high WUE through 28 seasons and should be taken as optimized irrigation scheduling under limited water supply condition. Yonghui Yang’ group developed a new model for estimating the Priestley–Taylor coefficient incorporating the effects of three easily obtainable parameters such as leaf area index, air temperature, and mulch fraction based on evapotranspiration partition and plant physiological limitation. The modified model has a high accuracy and could be used for evapotranspiration estimation under plastic mulch condition.

Optimal Allocation of Regional Agricultural Water Resources: Yanjun Shen and his collaborators predicted potential future climate trends based on CMIP5 simulations and estimated the water availability and agricultural water demand under future climate change scenarios in the arid region of northwestern China. According to a comparison of simulated irrigation water demand under three adaptation strategy scenarios, they found it is necessary to take effective measures such as improving the efficiency of irrigation water utilization, reducing crop planting areas and adjusting crop planting structures to alleviate the impacts of future climate changes on the water use. Shiqin Wang’s group investigated the sources of nitrate contamination in groundwater and its migration law from piedmont area to the North China Plain. A combination of multiple regression and multi-tracer methods were used to confirm that the change of land use in mountain area is the key factor influencing the content of nitrate in groundwater of this area.
Editorial Committee of Annual Report

Chair
Xun Huang

Vice Chair
Xin Yu

Members
Fan Chen       Xiaodong Deng       Xiangdong Fu       Tian Guan
Hong Ji        Hongqing Ling      Chunguang Liu       Xiaoqing Liu
Lei Qi          Guangxing Qiu     Guanghou Shui       Limei Tan
Jing Wang       Xiujie Wang       Yingjiao Zhang      Jianmin Zhou
Jianru Zuo
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.296, Huazhong Road, Shijiazhuang, Hebei 050021, China
MDIS1–MIK mediates the male perception of female attractants in plants
Wang et al., 2016, *Nature*

Zika Virus Disrupts Neural Progenitor Development and Leads to Microcephaly in Mice
Li et al., 2016, *Cell Stem Cell*