



Huazhong Agricultural University & University of California Davis

JOINT SYMPOSIUM

FROM PLANT GROWTH TO BIOMASS PRODUCTS

华中农业大学

加州大学戴维斯分校

植物生物学与生物质利用双边学术会议

2014年9月10-11日

武汉·湖北

September 10-11th, 2014

Wuhan, China



华中农业大学
HUAZHONG AGRICULTURAL UNIVERSITY



加州大学戴维斯分校
UNIVERSITY OF CALIFORNIA DAVIS

植物生物学与生物质利用双边学术会议

2014年9月10-11日 · 华中农业大学

SECTION I (9月10日上午8:30-11:50)

● Progress on biomass and bioenergy research in HZAU

彭良才: 华中农业大学长江学者特聘教授, 作物遗传改良国家重点实验室固定研究员, 生物质与生物能源研究中心主任。研究方向: 生物质与生物能源。

● Plant-based production of enzymes for biofuel applications

Karen McDonald: 美国国家科学基金会首席科学家, 加州大学戴维斯分校工程学系教授、副院长。研究方向: 细胞生物反应器。

● Brassinosteroid signaling network and plant development

王学路: 华中农业大学长江学者特聘教授, 生命科学技术学院院长。研究方向: 植物激素信号转导及逆境下植物生长发育机制。

● High energy biofuel production through conversion of starch to oil

Katayoon Dehesh: 加州大学戴维斯分校植物生物学系教授。研究方向: 生物燃料及植物防御反应机制。

SECTION II (9月10日下午2:00-6:10)

● Genome wide association study in maize

严建兵: 华中农业大学生命科学技术学院教授、副院长, 作物遗传改良国家重点实验室副主任。研究方向: 玉米分子生物学。

● Microtubule-based transport and plant growth

Bo Liu: 加州大学戴维斯分校植物生物学系教授。研究方向: 植物及真菌细胞骨架。

● The role of phospholipase D and phosphatidic acid in regulating plant growth

洪月云: 华中农业大学生命科学技术学院教授, 作物遗传改良国家重点实验室固定研究员。研究方向: 植物类脂物质代谢及信号转导。

● Genomic approaches for understanding biomass production and wood formation in trees using *Populus*

Andrew Groover: 美国农业部森林研究所主任, 加州大学戴维斯分校植物生物学系兼职副教授。研究方向: 树木发育生物学。

● Re-discovery of the traditional Chinese medicine by biomedical techniques

胡学博: 华中农业大学植物科学技术学院教授。研究方向: 药用植物活性物质研究。

● Simulation and comparison of the sugar production by enzymatic hydrolysis of *Eichhornia crassipes* and sugarcane bagasse biomass

周文兵: 华中农业大学资源与环境学院副教授。研究方向: 生物质材料化与能源化利用。

SECTION III (9月11日上午8:30-12:00)

● Chlorophyll synthase is critical for vitamin E tocopherol synthesis and altered expression impacts vitamin E levels and the epigenome of *Arabidopsis*

张椿雨: 华中农业大学植物科学技术学院教授。研究方向: 油菜维生素E及脂肪酸类代谢组学。

● Development of a novel route for fuels and chemicals production from cellulosic biomass

Zhiliang Fan: 加州大学戴维斯分校生物与农业工程系副教授。研究方向: 纤维素材料利用。

● Unravelling polysaccharide transport and deposition into the plant cell wall

Georgia Drakakaki: 加州大学戴维斯分校植物科学系副教授。研究方向: 植物细胞的内源运输。

● *Chalk5* regulates grain chalkiness, a trait affecting quality and head rice yield in rice

李一博: 华中农业大学生命科学技术学院教授。研究方向: 调控水稻粒型及蛋白的分子机制。

● *GbEXPATR*, a truncated α -expansin, enhances cotton fiber elongation through cell wall restructuring

涂礼莉: 华中农业大学植物科学技术学院副教授。研究方向: 棉花纤维发育的分子机制。

会议地点: 作物遗传改良国家重点实验室基因楼129报告厅

主办单位:

华中农业大学作物遗传改良国家重点实验室, 生物质与生物能源研究中心, 国家油菜工程技术研究中心, 植物科学技术学院

学术顾问: 傅廷栋院士, 张启发院士 会议主席: 彭良才教授(中方), Bo Liu教授(美方)

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联系人: 王艳婷, 电话: 027-87281765 电子邮箱: wyt@mail.hzau.edu.cn. 网站: <http://bbrc.hzau.edu.cn>

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ORGANIZERS:

Huazhong Agricultural University (HZAU), China

National Key Laboratory of Crop Genetic Improvement (NKLCGI)

Biomass and Bioenergy Research Center

National Rapeseed Engineering Research Center

College of Plant Sciences and Technology

College of Life Sciences and Technology

College of Resources and Environment

University of California Davis (UCD), USA

Department of Plant Biology

Department of Plant Sciences

Department of Chemical Engineering and Materials Science

Department of Biological and Agricultural Engineering

SPONSORS:

Ministry of Education, China (MOE)

State Administration of Foreign Experts Affairs, China (SAFEA)

SYMPOSIUM CHAIRS:

Dr. Liangcai Peng, Huazhong Agricultural University, China

Dr. Bo Liu, University of California Davis, USA

VENUE:

Lecture Hall 129, Gene Building,

National Key Laboratory of Crop Genetic Improvement,
Huazhong Agricultural University, Wuhan, 430070, P.R. China.

HOTEL:

International Academic Exchanging Hotel,
Huazhong Agricultural University, Wuhan, 430070, P.R. China.

CONTACT:

Web: [http:// bbrc.hzau.edu.cn](http://bbrc.hzau.edu.cn)

Ms. Yanting Wang, Tel: 86-27-87281765,

Email: wyt@mail.hzau.edu.cn

Wednesday 10th September; Hall 129, Gene Building, NKLC*

8:30-8:50 am Opening Remarks

Chair: Liangcai Peng, Professor, College of Plant Science and Technology,
Huazhong Agricultural University (HZAU)

Welcome Address: Vice President, HZAU

8:50-9:30 am Progress on plant cell wall and bioenergy research in BBRC

Liangcai Peng

9:30 -9:50 am Photography & Morning tea (Room 127, Gene Building)

9:50-10:30 am Plant-based production of enzymes for biofuel applications

Karen McDonald, Professor, Department of Chemical Engineering and
Materials Science, University of California Davis (UCD)

10:30-11:10 am Brassinosteroid signaling network and plant development

Xuelu Wang, Professor, College of Life Science and Technology, HZAU

11:10-11:50 am High energy biofuel production through conversion of starch
to oil

Katayoon Dehesh, Professor, Department of Plant Biology, UCD

11:50 am-13: 00 pm Lunch, 2nd Floor, IAEC*

Chair: Guosheng Xie

14:00-14:40 pm Genome wide association study in maize

Jianbing Yan, Professor, College of Life Science and Technology, HZAU

14:40-15:20 pm Microtubule-based transport and plant growth

Bo Liu, Professor, Department of Plant Biology, UCD

15:20-16:00 pm The role of phospholipase D and phosphatidic acid in regulating plant growth

Yueyun Hong, Professor, College of Life Science and Technology, HZAU

16:00-16:20 pm Afternoon tea (Room 127, Gene Building)

Chair: Bo Liu

16:20-17:00 pm Genomic approaches for understanding biomass production and wood formation in trees using *Populus*

Andrew Groover, Adjunct Associate Professor, Department of Plant Biology, UCD

Geneticist and Director, USDA Forest Service, Institute of Forest Genetics

17:00-17:40 pm Re-discovery of the traditional Chinese medicine by biomedical techniques

Xuebo Hu, Professor, College of Plant Science and Technology, HZAU

17:40-18:10 pm Simulation and comparison of the sugar production by enzymatic hydrolysis of *Eichhornia crassipes* and sugarcane bagasse biomass

Wenbing Zhou, Associate Professor, College of Resources and Environment, HZAU

18:10-20:00 pm Dinner at Yue Dan Ge and Yu Ming Ge(月丹阁、玉茗阁),
2nd Floor, IAEC*

Thursday 11th September; Hall 129, Gene Building, NKLC*

Chair: Peng Chen

8:30-9:10 am Chlorophyll synthase is critical for vitamin E tocopherol synthesis and altered expression impacts vitamin E levels and the epigenome of *Arabidopsis*

Chunyu Zhang, Professor, College of Plant Science and Technology, HZAU

9:10-9:50 am Development of a novel route for fuels and chemicals production from cellulosic biomass

Zhiliang Fan, Assistant Professor, Department of Biological and Agricultural Engineering, UCD

9:50-10:10 am Morning Tea (Room 127, Gene Building)

Chair: Tao Xia

10:10-10:50 am Unravelling polysaccharide transport and deposition into the plant cell wall

Georgia Drakakaki, Assistant Professor, Department of Plant Sciences, UCD

10:50-11:30 am *Chalk5* regulates grain chalkiness, a trait affecting quality and head rice yield in rice

Yibo Li, Professor, College of Life Science and Technology, HZAU

11:30-12:00 am *GbEXPATR*, a truncated α -expansin, enhances cotton fiber elongation through cell wall restructuring

Lili Tu, Associate Professor, College of Plant Science and Technology,
HZAU

12:00-12:10 pm Closing Remarks

Liangcai Peng

12:10 am-13:30 pm, Lunch, 2nd Floor, IAEC*

15:00-17:30 pm Campus visit and free talks with HZAU scientists

**18:00-20:00 pm, Dinner at Yue Dan Ge and Yu Ming Ge(月丹阁、玉茗阁),
2nd Floor, IAEC***

***: NKLC—National Key Laboratory of Crop Genetic Improvement;
IAEC---International Academic Exchanging Center**

Progress on plant cell wall and bioenergy research in BBRC

Liangcai Peng*

*National Key Laboratory of Crop Genetic Improvement,
Biomass and Bioenergy Research Centre,
College of Plant Sciences and Technology,
Huazhong Agricultural University, Wuhan, China.*

Since Biomass and Bioenergy Research Centre (BBRC) was found in 2008, our work has focused on three major fields: (1) Upstream-basic research on plant cell wall biosynthesis using cotton, *Arabidopsis* and rice as model plants; (2) Midstream-energy crop selection by germplasm resource collection (*Miscanthus*, rapeseeds), cell wall mutant selection (rice, wheat, sweet sorghum, corn) and genetic manipulation (rice, *Arabidopsis*, corn); (3) Downstream-biomass conversion and biofuel process. We have performed systems biology analyses between cell wall composition/structure and biomass digestibility in 200 representative *Miscanthus* natural-germplasms and 45 typical rice genetic-mutants. Both plant samples displayed a diverse cell wall structure and varied biomass saccharification, suggesting that cell wall structure can fundamentally determine biomass enzymatic digestibility upon various chemical and physical pretreatments. Notably, xylan is a key positive factor on both sugar release and ethanol fermentation by negatively affecting lignocellulose crystallinity, whereas lignin plays dual effects distinctive in different plant species. Analysis of lignocellulosic digestions with three individual cellulase enzymes, together with atomic force microscopic observation *in situ* and *in vitro*, leads to a novel finding about the ditch structure of plant cell walls. Consequentially, three types of nine genes are proposed for the ditch structure formation and modification, suggesting a fundamental model on mechanism of biomass digestion and conversion into biofuels. It also provides insights into biotechnology for bioenergy crop breeding and biofuel process.

1. Xu et al. Hemicelluloses negatively affect lignocellulose crystallinity for high biomass digestibility under NaOH and H₂SO₄ pretreatments in *Miscanthus*. ***Biotechnol Biofuels*** **2012**. 5(1):58-70.
2. Xie et al. Global identification of multiple OsGH9 family members and their involvement in cellulose crystallinity modification in rice. ***PLoS ONE*** **2013**. 8(1): e50171. doi:10.1371/journal.pone.0050171.

3. Zhang et al. Three lignocellulose features that distinctively affect biomass enzymatic digestibility under NaOH and H₂SO₄ pretreatments in *Miscanthus*. *Bioresour Technol* **2013**. 130:30-37.
4. Li et al. Arabinose substitution degree in xylan positively affects lignocellulose enzymatic digestibility after various NaOH/H₂SO₄ pretreatments in *Miscanthus*. *Bioresour Technol* **2013**. 130:629-637.
5. Li et al. An integrative analysis of four CESA isoforms specific for fiber cellulose production between *Gossypium hirsutum* and *Gossypium barbadense*. *Planta* **2013**. 237(6):1585-1597.
6. Wu et al. Biomass digestibility is predominantly affected by three factors of wall polymer features distinctive in wheat accessions and rice mutants. *Biotechnol Biofuels* **2013**. 6:183.
7. Li et al. Distinct biochemical activities and heat shock responses of two UDP-glucose sterol glucosyltransferases in cotton. *Plant Science* **2014**. 219-220: 1-8.
8. Li et al. Sugar-rich sweet sorghum is distinctively affected by wall polymer features for biomass digestibility and ethanol fermentation in bagasse. *Bioresour Technol* **2014**. 167: 14-23.
9. Li et al. Mild alkali-pretreatment effectively extracts guaiacyl-rich lignin for high lignocellulose digestibility coupled with largely diminishing yeast fermentation inhibitors in *Miscanthus*. *Bioresour Technol* **2014**. 447-454.
10. Guo *et al.* An integrated genomic and metabolomic framework for cell wall biology in rice. *BMC Genomics* **2014**. 15: 596.
11. Li et al. The minor wall-networks between monolignols and interlinked-phenolics predominantly affect biomass enzymatic digestibility in *Miscanthus*. *PLoS ONE* **2014**. 9(8): e105115.
12. Wang et al. Research progress in the groove structures of plant cell walls and biomass utilizations. *SCIENTIA SINICA Vitae* **2014**. 44: 766-774.

* E-mail: lpeng@mail.hzau.edu.cn

Plant-based production of enzymes for biofuel applications

Karen McDonald*

*Department of Chemical Engineering and Materials Science,
University of California Davis, CA. USA.*

Plant-based production of recombinant proteins holds enormous promise for energy-efficient and cost-effective production of industrial bioproducts as well as high value products such as vaccines, antibodies and human therapeutic proteins. To meet the accelerating worldwide demand for liquid transportation fuels, conversion of cellulosic biomass into advanced biofuels will require a significant amount of cellulose degrading enzymes at a low cost. Current methods for production of cellulose and hemicellulose degrading enzymes rely primarily on submerged fungal fermentation and are expensive, energy intensive, generate carbon dioxide, and consume cellulosic feedstock for growth of the production microorganisms. Our group is investigating transient production of cellulase enzymes in whole plants and/or harvested plant tissues. Gene constructs containing the genes for thermostable endoglucanase (E1) and xylanase (Xyl) from *Acidothermus cellulolyticus*, beta-glucosidase (BglB) from *Thermatoga martima*, and exoglucanase (CBH1) from *Thermoascus aurantiacus* have been designed, synthesized, and introduced into several binary expression vectors for production using transient agroinfiltration in tobacco and/or sunflower. Crude extracts from tissues could be used as additives to other pretreated biomass, or to initiate self-deconstruction, or a combination of the two, since the spent biomass that produces the enzymes can also serve as a source of cellulose. Advantages of the transient approach over production of enzymes in stably transformed plants are that it is rapid, performed in a contained environment, utilizes wild type (non-transgenic) plant biomass and/or agricultural wastes, allows multiple enzymes to be produced in the same plant tissue using co-infiltration, and decouples the plant growth and enzyme production stages so that they can be separately optimized.

* E-mail: kamcdonald@ucdavis.edu

Brassinosteroid signaling network and plant development

Xuelu Wang*

*National Key Laboratory of Crop Genetic Improvement,
College of Life Science and Technology,
Huazhong Agricultural University, Wuhan, China.*

Unlike animals, plants are sessile and need to constantly regulate their developmental and physiological processes to respond to various internal and external stimuli. Brassinosteroids (BRs) mainly play roles in promoting plant growth and development, while abscisic acid (ABA) is a hormone induced by many stress signals. It is known that BRs and ABA co-regulate hundreds of gene expression. Our previous study demonstrated that ABA inhibits BR primary signaling through BIN2 or upstream unknown components. Recently, we found that BIN2 can interact with and phosphorylate Snf1-related kinase 2s (SnRK2s), SnRK2.2 and SnRK2.3, suggesting that GSK3-like kinases function as positive regulators in ABA signaling. We propose that the signaling cascades of ABA and BRs primarily crosstalk after BR and ABA perception, but before the downstream transcriptional factor BES1, which also explains why a large proportion of BR-responsive genes are also regulated by ABA. Our studies provide significant insight into the molecular mechanisms by which BRs interact with ABA. In addition, we are interested in the underlying mechanism of BR regulating plant development. The Arabidopsis root epidermal cell types Hair cells and Non-hair cells are defined by position in a predictable manner. We systematically examined root hair phenotypes in BR-related mutants, and found that BR signaling inhibits root hair formation through GSK3-like kinases or upstream components. Genetic analysis demonstrated that BR-regulated root epidermal cell patterning is dependent on the WER-GL3/EGL3-TTG1 transcriptional complex. One of the GSK3-like kinases, BIN2, interacted with and phosphorylated EGL3, and EGL3s mutated at phosphorylation sites were retained in hair cell nuclei. BIN2 can also phosphorylate TTG1 to inhibit the activity of the WER-GL3/EGL3-TTG1 complex. Thus, our study explains how BR signaling regulates both the formation and activity of the WER-GL3/EGL3-TTG1 complex through GSK3-like kinases to coordinately regulate root epidermal cell fate specification. (Zhang et al., 2009, *PNAS*; Cai et al., 2014, *PNAS*; Cheng et al., *eLife* 2014; 10.7554/*eLife*. 02525)

* E-mail: xlwang@mail.hzau.edu.cn

High energy biofuel production through conversion of starch to oil

Katayoon Dehesh*

*Department of Plant Biology, College of Biological Science,
University of California Davis, CA. USA.*

Fossil fuel is believed to have derived from sedimented lipid-rich organic material that under high pressure and temperature were transformed into oil. Therefore, plant TAG, the bio-product chemically most similar to fossil oil, offers the greatest potential to replace fossil oil. In fact, plant oil as one of the most energy-rich and abundant form of reduced carbon in nature have been used to generate heat and light since ancient times. Plant oils consist almost entirely of TAGs, an attractive and feasible alternative bio-based energy substitute to petroleum-based diesel fuel. The ecological properties of biodiesel offer numerous additional advantages to conventional petroleum-based diesel. The most notable advantages are: (a) the maintenance of a balanced carbon dioxide cycle through usage of renewable biological materials; (b) combustion of biodiesel reduces emission of carbon monoxide, sulfur, aromatic hydrocarbons and soot particles; (c) biodiesel is non-toxic and completely biodegradable; (d) the biodiesel high flash point translates to low flammability and thus its safe and non-hazardous usage; (e) biodiesel provides good lubrication properties, thereby reducing wear and tear on engines. Moreover, pure biodiesel or biodiesel mixed in with petroleum-based diesel can be used in conventional diesel engines with no, or only marginal, modifications and it can be distributed using the existing infrastructure. Towards production of oil in high biomass, we initiated a research program for identification of the regulatory switch(s) involved in conversion of starch to oil. We specifically employed two closely related oat cultivars that differ in oil content at the expense of starch as determined by several approaches such as carbon flux analysis throughout the developmental stages of seeds in conjunction with metabolic profiling as well as non-invasive NMR studies. These studies in parallel with transcriptome analyses and extensive metabolic profiling identified a number of genes now targeted for conversion of starch to oil.

* E-mail: kdehesh@ucdavis.edu

Genome wide association study in maize

Jianbing Yan*

*National Key Laboratory of Crop Genetic Improvement,
College of Life Science and Technology,
Huazhong Agricultural University, Wuhan, China.*

The rapid development in genome-wide genotyping techniques promises to improve the power of association mapping and significantly refine our understanding of the genetic architecture of complex quantitative traits. We have built up a maize association mapping panel containing more than 500 diverse maize inbred lines which has been genotyped by using Maize 50K SNP chip and deep RNA sequencing technology. Totally, 1.06 million high quality maize SNPs were obtained covering about 60% of the annotated genes in B73 genome (1, 2). Large scale eQTL (1) and QTL mapping including fatty acids (2), flowering time (3) and metabolic traits (4) and so on were performed. Many functional genes and loci were identified and validated that potentially can be used for molecular breeding. A new model called A-D test (5) was also developed that is more powerful and working better especially for rare alleles. In the presentation, we will report the detail and discuss the challenges and opportunities for whole genome wide association studies in plants.

1. Fu et al. RNA sequencing reveals the complex regulatory network in the maize kernel. *Nat Commun* **2013**. 4:2832.
2. Li et al. Genome-wide association study dissects the genetic architecture of oil biosynthesis in maize kernels. *Nat Genet* **2013**. 45: 43-50.
3. Yang et al. CACTA-like transposable element in ZmCCT attenuated photoperiod sensitivity and accelerated the postdomestication spread of maize. *Proc. Natl. Acad. Sci .U.S.A* **2013**. 110: 16969-16974.
4. Wen et al. Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights. *Nat Commu* **2014**. 5: 3438.
5. Yang et al. Genome Wide Association Studies using a new nonparametric model reveal the genetic architecture of 17 agronomic traits in an enlarged maize association panel. *Plos Genet* **2014**. in press.

* E-mail: yjianbing@mail.hzau.edu.cn

Microtubule-based transport and plant growth

Bo Liu*

*Department of Plant Biology,
University of California Davis, CA. USA.*

Plant growth harnesses polarized cell expansion that depends on transport of macromolecules and vesicles along the cortical microtubule track by motors in the kinesin superfamily. Kinesins are mechanochemical ATPase enzymes that use the energy released from ATP hydrolysis to walk along microtubules. We hypothesized that among over 50 different kinesins produced by a single plant, some were exclusively devoted to cell elongation. We used cotton (*Gossypium hirsutum*) fibers that underwent robust elongation to discover such kinesins and found GhKinesin-4A expressed abundantly. The motor was detected by immunofluorescence on vesicle-like structures that were associated with cortical microtubules. In the model plant *Arabidopsis thaliana*, the orthologous AtKinesin-4A (also known as FRA1) protein, previously implicated in cellulose deposition during secondary growth in fiber cells, was examined by live-cell imaging in cells expressing a fluorescently tagged functional protein. The motor decorated vesicle-like particles that exhibited linear movement along cortical microtubules at velocities averaged at 0.89 $\mu\text{m}/\text{min}$, which was significantly different from those linked to cellulose biosynthesis. We also discovered that AtKinesin-4A and the related AtKinesin-4C played redundant roles in cell wall mechanics, cell elongation, and the axial growth of various vegetative and reproductive organs as the loss of AtKinesin-4C greatly enhanced the defects caused by a null mutation at the *Kinesin-4A* locus. The double mutant displayed a lack of cell wall softening at normal stages of rapid cell elongation. Our findings established a connection between the Kinesin-4-based transport of cargoes containing non-cellulosic components along cortical microtubules and cell wall mechanics as well as cell elongation in flowering plants.

* E-mail: bliu@ucdavis.edu

The role of phospholipase D and phosphatidic acid in regulating plant growth

Yueyun Hong*

*National Key Laboratory of Crop Genetic Improvement,
College of Life Science and Technology,
Huazhong Agricultural University, Wuhan, China.*

Increasing evidence showed that phosphatidic acid (PA) functions as a class of important growth mediators involved in various cellular and physiological processes. Rapid activation of phospholipase D (PLD), which hydrolyzes membrane lipids to generate phosphatidic acid (PA), occurs under various stress conditions such as nutrient starvation and osmotic stress conditions. Arabidopsis contains 12 PLDs, whereas rice has 17 putative PLDs. PLDe and its derived PA play a positive role in promoting plant growth. PLDe is mainly associated with the plasma membrane, and is the most permissive of all PLDs tested with respect to its activity requirements. Knockout (KO) of PLDe decreases root growth and biomass accumulation, whereas over-expression (OE) of PLDe enhances root growth and biomass accumulation. The level of PA was higher in OE plants, but lower in KO plants than in wild-type plants, and suppression of PLD mediated PA formation by alcohol alleviated the growth-promoting effect of PLDe. OE and KO of PLDe had opposite effects on lateral root elongation in response to nitrogen. Increased expression of PLDe also promoted root hair elongation and primary root growth under severe nitrogen deprivation. The results suggest that PLDe and PA promote organism growth and play a role in nitrogen signaling. In addition, overexpression of PLDe in *Brassica napus* also enhances biomass. Further study showed that PA binds to ribosomal protein kinase to promote the phosphorylation, thus enhance cell growth. The result suggest PA mediated signaling process may play a role in connecting membrane sensing of nutrient status to increased plant growth and biomass production.

* E-mail: hongyy@mail.hzau.edu.cn

Genomic approaches for understanding biomass production and wood formation in trees using *Populus*

Andrew Groover*

*US Forest Service, Pacific Southwest Research Station,
Department of Plant Biology,
University of California Davis, CA. USA.*

We describe two projects that illustrate approaches for understanding the genes and mechanisms underlying biomass production and wood formation in *Populus*. In the first project, we are collaborating with the Comai lab at UC Davis to create a novel functional genomics germplasm resource for *Populus*. To create this resource, pollen from a *P. deltoides* male was irradiated to induce chromosomal breaks, and used in controlled pollination to a *P. nigra* female. Molecular karyotypes were developed for the resulting F1 seedlings using low-pass Illumina sequencing, which precisely define the locations of both deletions and additions of chromosome segments. Several hundred F1 individuals have been created, with over 50% carrying detectable deletions or insertions. Importantly, the deletions and insertions in these lines create dosage variation whose effects result in measurable phenotypes, and we are currently establishing field trials to identify chromosomal regions and genotypes with bioenergy-related phenotypes including biomass production.

In a second project, we are identifying the mechanisms underlying the development of tension wood in *Populus*. Tension wood forms in response to gravitational stimulus, and acts to pull stems or branches towards an upright position. Of practical significance, tension wood is characterized by altered cell walls that have high cellulose and low lignin that are conducive to biofuels conversion. We have determined the interacting roles of a Class I KNOX transcription factor, auxin, and gibberellin in the induction and development of tension wood.

* E-mail: agroover@fs.fed.us

Re-discovery of the Traditional Chinese Medicine by biomedical techniques

Xuebo Hu*

*College of Plant Sciences and Technology,
Huazhong Agricultural University, Wuhan, China.*

Traditional Chinese Medicine (TCM) is largely represented by a collection of medicinal plants, which has been used for treating diseases for thousands of years in China. TCM is distinct from other folk medicine because of its profound theory and logistic which explains diseases formation and guides the treatments, normally dealing with complicated herbal formula. The criteria of TCM is heavily challenged by modern medical principles and theories. But TCM believers insist that the TCM is unique and it does not need to meet the standards of modern medicine. In the newly established laboratory, we firstly credit TCM on the claim of curing of diseases, however, the claim is investigated by the science and technology of modern medicine. We are mainly looking at two projects: 1. Biochemical foundation of the myth of Lingzhi (*Ganoderma lucidum*), a kind of large mushroom is believed to extend people's live forever. In an effort to understand the mechanism, a T-DNA insertion library mediated by agrobacterium is being made. The yield of triterpene and saccharide of each mutant will be assayed. 2. Anti-inflammation mechanism of Diwu (*Anemone flaccida* Fr. Schmidt), a rare plant grows only in the mountains in central China. The *A. flaccida* is endangered TCM because of extensive harvest, which is believed to have peculiar effect on arthritis. The crude extract of saponin of *A. flaccida* is in phase III clinical trial in China, however, the mechanism behind the phenomenon is largely unknown. We are now looking at the genomics of *A. flaccida* and trying to understand what makes it so special. On the other hand, we will also investigate the target of saponin in the inflammation pathway in the molecular level.

* E-mail: xuebohu@mail.hzau.edu.cn

Simulation and comparison of the sugar production by enzymatic hydrolysis of *Eichhornia crassipes* and sugarcane bagasse biomass

Wenbing Zhou*

College of Resources and Environment,
Huazhong Agricultural University, Wuhan, China.

Production of fermentable sugar from biomass is the critical step in the second generation bio-ethanol production, different plant biomasses show various performance in the process, therefore, screening of suitable feedstock for bio-ethanol production has apparent significance. Cellulose extracted from *Eichhornia crassipes* and sugarcane bagasse, respectively, were mixed with commercial xylose and lignin to compose artificial biomass with different ratio of three components-cellulose, xylose and lignin, the artificial biomass were then subjected to enzymatic hydrolysis, a binary linear-regression equation $y = \beta_1\chi_1 + \beta_2\chi_2$ was established to reflect the relationship between the sugar yield (y) of two kinds of artificial biomass by enzymatic hydrolysis and their cellulose and xylose contents (χ_1, χ_2), the differences of the contribution of cellulose or xylose to the sugar production of their artificial biomass were analyzed. Furthermore, the sugar production of two kinds of practical biomass with “H₂O₂+NaOH” pretreatment were compared with those predicted by the sugar production equation of their artificial biomass. The result indicated, the sugar production contribution of *E. crassipes* cellulose to its artificial biomass is greater than that of sugarcane bagasse’s cellulose to its artificial biomass ($\beta_{1EC} > \beta_{1SC}$), but they are all lower than the sugar production contribution of xylose in two kinds of artificial biomass ($\beta_{1EC} < \beta_{2EC}, \beta_{1SC} < \beta_{2SC}$), meanwhile, the sugar production contribution of xylose in two kinds of artificial biomass are very similar ($\beta_{2EC} \approx \beta_{2SC}$). The physical properties analysis of extracted celluloses showed that, *E. crassipes* cellulose has apparently higher specific surface area (SSA), which may explain why *E. crassipes* artificial biomass can be hydrolyzed faster in the earlier hydrolysis time. The sugar production of the practical biomasses pretreated by “H₂O₂-NaOH” are slightly higher than those predicted by sugar production equation of their artificial biomasses, and show similar rule as those of their artificial biomass, i.e., *E. crassipes* biomass is hydrolyzed faster in the initial hydrolysis stage compared to sugarcane bagasse biomass, however, as a whole, sugarcane bagasse biomass has greater sugar production potential than *E. crassipes* biomass, due to significantly higher cellulose content.

*E-mail: zhouwb@mail.hzau.edu.cn

Chlorophyll synthase is critical for vitamin E tocopherol synthesis and altered expression impacts vitamin E levels and the epigenome of *Arabidopsis*

Chunyu Zhang*

*National Key Laboratory of Crop Genetic Improvement,
College of Plant Sciences and Technology,
Huazhong Agricultural University, Wuhan, China.*

Chlorophyll synthase catalyzes the final step in chlorophyll biosynthesis, the esterification of chlorophyllide with either geranylgeranyl diphosphate (GGDP) or phytyl diphosphate (PDP). Recent studies have pointed to the involvement of chlorophyll-linked reduction of geranylgeraniol via geranylgeranyl reductase (GGR) as a major pathway for the synthesis of the PDP precursor of tocopherols. This indirect pathway of PDP synthesis suggests a key role of chlorophyll synthase in tocopherol production to generate the geranylgeranyl-chlorophyll substrate for GGR. In this study, contributions of chlorophyll synthase to tocopherol formation in *Arabidopsis* were explored by disrupting and altering expression of the corresponding gene *CHLSYN* (At3g53820). Leaves from the *chlsyn* null mutant were nearly devoid of tocopherols, and homozygous *chlsyn* seeds contained only ~ 25% of wild-type tocopherol levels. Leaves of RNAi lines with partial suppression of *CHLSYN* displayed marked reductions in chlorophyll but up to a two-fold increase in tocopherol concentrations. CaMV35S-mediated overexpression of *CHLSYN* unexpectedly yielded an RNAi-like gene suppression phenotype at high frequencies, accompanied by strongly reduced chlorophyll content and increased tocopherol levels. This phenotype and the associated detection of a *CHLSYN*-specific miRNA were reversed with *CHLSYN* overexpression in *rdr6*, which is defective in RNA dependent RNA polymerase 6, a key enzyme in small RNA processing. *CHLSYN*-overexpression in *rdr6* had little effect on chlorophyll content, but resulted in up to a 30% reduction in tocopherol levels in leaves. These findings show that altered *CHLSYN* expression impacts tocopherol levels and also demonstrate strong epigenetic regulation of *CHLSYN* to mediate chlorophyll and tocopherol synthesis.

* E-mail: zhchy@mail.hzau.edu.cn

Development of a novel route for fuels and chemicals production from cellulosic biomass

Zhiliang (Julia) Fan*

*Department of Biological and Agricultural Engineering,
University of California Davis, CA, USA.*

One significant obstacle impeding the large scale production of fuels and chemicals from cellulosic biomass is the lack of a low cost processing technology. The conventional biochemical platform for biorefinery involves five distinct steps: pretreatment, enzymatic hydrolysis, fermentation, and product recovery. Sugars are produced as the reactive intermediate for the subsequent fermentation. Steps involved with overcoming the recalcitrance of cellulosic biomass (pretreatment, cellulase production, and enzymatic hydrolysis) are the three most costly steps in the whole process. Here we propose a novel biochemical platform for fuels and chemical production that will replace the two most costly steps in the conventional platform with a single biological step. Cellulolytic microorganism (s) that can secrete all the enzymes needed to hydrolyze cellulose and hemicellulose will be modified to convert most of the carbohydrate contained in the cellulosic biomass to sugar aldonates. In a second step, sugar aldonates will be utilized as the carbon source to produce ethanol and other products. The new route can potentially lower the cost of cellulosic bioprocessing substantially. Our study has revealed that cellulose can be diverted to sugar aldonates production using a *Neurospora crassa* strain with multiple copies of beta-glucosidase gene knocked out. Over-expression laccase and deletion of cellobionate phosphorylase improved the cellobionate production. Both of the hydrolysis product of cellobionate (glucose and gluconate) can be fermented to ethanol by an engineered *Escherichia coli* strain. Gluconate was utilized even faster than that of glucose. Deletion of the competing pathway in *E. coli* improved the ethanol yield from gluconate.

*E-mail: jzfan@ucdavis.edu

Unravelling polysaccharide transport and deposition into the plant cell wall

Georgia Drakakaki*

*Department of Plant Sciences,
University of California Davis, CA. USA.*

Plant cell walls are composed primarily of structural carbohydrates that can be broken down into sugars, providing energy directly as food/feed, or indirectly as biofuels. A greater understanding of their synthesis and assembly can lead to the development of more nutritious food/feed and more accessible biofuels. While cell wall structure and biosynthesis have been extensively studied, little is known about the transport of polysaccharides into the developing cell wall. The endomembrane system has been implicated in this process, however our mechanistic understanding of the highly regulated membrane and cargo transport mechanisms in relation to polysaccharide deposition is yet very limited.

Our research is focusing on how plant cells direct different polysaccharides, cell-wall biosynthetic enzymes and other components into the developing cell wall. We are employing a highly multidisciplinary approach in our studies that comprises chemical genomics, proteomics and genetics. Chemical genomics circumvents lethality challenges present in conventional genomic approaches and allows us to pursue the study of pathways that were hitherto impossible.

We have identified novel pharmacological inhibitors, which specifically target cell wall deposition during cell division and/or during cell elongation. Among them is, Cestrin a novel inhibitor of cellulose synthase localization. It reduces the cellulose content in plants, and interferes with the interplay of cellulose synthases with microtubules. Its behavior affords the identification of new players involved in the organization of cellulose synthase complexes at the plasma membrane. A further pharmacological inhibitor that we have identified is Endosidin 7. It targets specifically and in a time dependent manner callose synthase activity during late cytokinesis and arrests cell plate maturation. Our data detail the essential role of callose during the late stages of cell plate maturation and establish a model that describes the temporal relationship between vesicles and regulatory proteins at the cell plate assembly matrix during polysaccharide deposition.

In a complementary extension of our studies we used a proteomic approach, to identify components of the endomembrane system that are present in the trans-Golgi Network (TGN), a site of polysaccharide trafficking and recycling of endosomal components. Vesicle isolation affords the most direct dissection of the role vesicles play in stress response and growth. Identification of the SYP61 vesicle proteome revealed the presence of proteins involved in cell wall biosynthesis, modification and in adaptive stress responses. Interestingly cellulose synthases were identified in the SYP61 vesicle proteome, indicating that SYP61 vesicles are involved in the trafficking of the CESA complexes. Based on our cumulative data, we propose that SYP61 mediates trafficking of cell wall and stress response components.

*E-mail: gdrakakaki@ucdavis.edu

Chalk5 regulates grain chalkiness, a trait affecting quality and head rice yield in rice

Yibo Li *

*National Key Laboratory of Crop Genetic Improvement,
College of Life Science and Technology,
Huazhong Agricultural University, Wuhan, China.*

Improving grain quality is one of the most important goals of plant science research. Grain chalkiness in rice, a chalky texture of endosperm, is a highly undesirable trait of the grain for human food that deteriorates milling, cooking, eating and appearance quality, and thus represents a major problem in many rice-producing areas of the world. However, the molecular basis of this trait is still poorly understood. Here, we show that a major quantitative trait locus (QTL), *Chalk5*, regulates grain chalkiness which also affects head rice yield and many other quality traits. *Chalk5* encodes a vacuolar H⁺-translocating pyrophosphatase (V-PPase) with inorganic pyrophosphate (PPi) hydrolysis and H⁺-translocation activity. *Chalk5* functions as a positive regulator of grain chalkiness rate. Elevated expression of *Chalk5* increases chalkiness of the endosperm putatively by disturbing the pH homeostasis of the endomembrane trafficking system in developing seeds, which affects the biogenesis of protein bodies and is coupled with a great increase in small vesicle-like structures, thus forming air spaces among endosperm storage substances and resulting in chalky grain. Introgression of the *Chalk5* allele of non-chalky variety into a chalky variety greatly decreases rice grain chalkiness rate by 80.5% and increases head rice yield by 37.9%, equally increasing the grain yield. Our results indicated that two consensus nucleotide polymorphisms among rice varieties in *Chalk5* promoter may partly account for the difference in *Chalk5* mRNA levels causing natural variation of grain chalkiness. The tight linkage of *Chalk5* for grain chalkiness and quality, and GS5 and qSW5/GW5 for grain size, weight and yield, points to the genetic and molecular evidence for the inconsistency between grain quality and yield during modern breeding. Breaking such linkage by recombination may result in genotypes producing wide grain with low chalk to achieve high yield with good quality in breeding programs of *Indica* rice.

Key words: Rice, Grain chalkiness, QTL, *Chalk5*, Quality, Head rice yield

* E-mail: liyibo@mai.hzau.edu.cn

***GbEXPATR*, a truncated α -expansin, enhances cotton fiber elongation through cell wall restructuring**

Yang Li¹, Lili Tu^{1*}, Filomena A Pettolino², Shengmei Ji¹, Juan Hao¹, Daojun Yuan¹, Fenglin Deng¹, Jiafu Tan¹, Haiyan Hu¹, Qing Wang¹, Danny J. Llewellyn², Xianlong Zhang^{1*}

¹National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan, Hubei 430070, China

²Commonwealth Scientific and Industrial Research Organization (CSIRO), Plant Industry, Canberra, Australia.

Cotton fiber is an ideal single-cell model to study cell elongation, cell wall metabolism and cellulose biosynthesis. Expansin proteins mediate plant cell wall extension and were identified as cell wall-loosening agents. To investigate the biological functions of α -expansins during fiber development, two homoeologous fiber-specific α -expansins from *Gossypium barbadense* were analyzed. *GbEXPA2* (encoded from the DT genome) is a classical α -expansin, while *GbEXPATR* (AT genome) encodes a truncated protein lacking domain 2 of other α -expansins. Silencing EXPA caused shorter fibers with thicker cell walls. *GbEXPA2* over-expression had no effect on mature fiber length, but produced fibers with slightly thicker walls. Interestingly, *GbEXPATR* over-expression resulted in longer, finer and stronger fibers coupled with significantly thinner cell walls, which was associated with lower expression of certain secondary wall-associated genes, especially chitinase-like genes, and walls with lower cellulose levels but higher non-cellulosic polysaccharides indicating that the improved fiber was caused by a delay in the transition to secondary wall synthesis. We conclude that α -expansins play a critical role in fiber development by loosening the cell wall; furthermore, a truncated form, *GbEXPATR*, has a more dramatic effect on fiber elongation and should be a candidate gene for developing *G. hirsutum* cultivars with superior fiber quality.

Key words: cotton fiber, *Gossypium barbadense*(cotton), truncated α -expansin, cell elongation, secondary cell wall

* E-mail: lilitu@mail.hzau.edu.cn

Liangcai Peng

*Professor, Changjiang Scholar,
National Key Laboratory of Crop Genetic Improvement,
College of Plant Science and Technology,
Director of Biomass and Bioenergy Research Center,
Huazhong Agricultural University, Wuhan, China.*



Dr. Liangcai Peng obtained his B. Sci on Agronomy in Huazhong Agricultural University (HZAU), China in 1983, and Ph.D. on Biochemistry and Molecular Biology in Australian National University (ANU), Australia in 1997, working with Dr. Richard Williamson (member of Australian Academy of Science) on cellulose biosynthesis in *Arabidopsis*. He as postdoctoral fellow, continued to work on cellulose biosynthesis with Dr. Debby Delmer (member of American Academy of Science) in University of California Davis. Later, he as Research Scientist, worked on plant and yeast responses to oxidative and abiotic stress, and genetic manipulation for plant stress tolerance at Plant Gene Expression Center of ARS-USDA.

In 2006, Dr. Liangcai Peng was selected as Changjiang Scholar by Ministry of Education of China, and took a full Professor position at College of Plant Science and Technology, Huazhong Agricultural University (HZAU). Since then, he has established Biomass and Bioenergy Research Center in HZAU, working on plant cellulose biosynthesis; cell wall genomics and metabolism; carbon partitioning and biomass production, bioenergy crop breeding, pretreatment and biofuel conversion technology.

Dr. Peng has published two “Science” articles on cellulose biosynthesis, cited with more than 800 times, His recent works have been published in *Biotechnol. Biofuels*, *Bioresour. Technol.*, *BMC Genomics*, *BMC Plant Biol.*, *Planta*, *Plant Sci.*, *JIPB*, *BBRC*. In addition, he as chairs, has organized four International Symposiums on Bioenergy and Biotechnology.

Karen McDonald

*Professor,
Department of Chemical Engineering and Materials Science,
Associate Dean of Engineering,
UC Davis ADVANCE Faculty Director.*



Dr. McDonald leads the UC Davis ADVANCE Program as Faculty Director and provides daily project leadership and management. In collaboration with Chancellor Katehi, Vice Provost Stanton, and Associate Director Shauman, Dr. McDonald is the main point of contact with the External Advisory Board, the Internal Advisory Committee, all initiative committees, Internal and External Evaluators and the NSF ADVANCE Program Officers.

She is also Professor in the Department of Chemical Engineering and Materials Science and served as Associate Dean for Research and Graduate Studies in the College of Engineering at UC Davis for 13 years prior to joining the UC Davis ADVANCE program. In addition, Dr. McDonald is the Principal Investigator of an NSF Integrative Graduate Education and Research Traineeship (IGERT) training program entitled “Collaborative Research and Education in Agricultural Technologies and Engineering (CREATE)”, Co-Director of the NIH Training Program in Biomolecular Technology and Co-Director of NSF RESOURCE Graduate STEM Fellows in K-12 Education Program at UC Davis.

She joined UC Davis in 1985 after completing her PhD in Chemical Engineering at the University of Maryland, College Park, MD, M.S. in Chemical Engineering at the University of California at Berkeley and a B.S. in Chemical Engineering at Stanford University. She was the first female faculty member in the Department of Chemical Engineering and one of the first few in the College of Engineering at UC Davis.

Her research focuses on using techniques in chemical engineering, plant sciences, and molecular biology to optimize the plant cell’s ability to behave as a bioreactor. This research utilizes *Agrobacterium*-mediated gene transfer to create genetically engineered plants and plant cell cultures that are then coaxed into producing proteins of interest. This research has the potential to revolutionize how biofuels, vaccines, and pharmaceuticals are manufactured.

She has authored over 60 journal publications including *BMC Biotechnol*, *BMC Bioinformatics*, *Biotechnol Bioeng*, *Plant Biotechnol J*, *J Environ Manage*, etc.

Xuelu Wang

*Professor, Changjiang Scholar,
National Key Laboratory of Crop Improvement,
College of Life Science and Technology,
Huazhong Agricultural University, Wuhan, China.
E-mail: xlwang@mail.hzau.edu.cn*



Working Experience:

2014-present: Professor and Dean, College of Life Science and Technology, Huazhong Agricultural University.
2007-2014: Professor, School of Life Sciences, Fudan University, Professorship for “Cheung Kong Scholar” 2009.
2001-2007: Postdoctoral fellow of Howard Hughes Medical Institute, The Salk Institute for Biological Studies, La Jolla, CA. Prof. Joanne Chory’s group.
2000-2001: Research associate, Department of Plant Sciences, The University of Arizona, Tucson, AZ. Prof. Brian Larkins’ group.
1992-1995: Research associate, Institute of Crop Genetic Resources, Chinese Academy of Agricultural Sciences, Beijing, China.

Education:

1995-2000: Ph.D., Department of Plant Sciences, The University of Arizona, Tucson, AZ. Prof. Brian Larkins’ group.
1989-1992: M.S., The Graduate School, Chinese Academy of Agricultural Sciences, Beijing, China. Major: Plant Genetics.
1985-1989: B.S., Hebei Agricultural University, Baoding, Hebei, China Major: Plant Genetics.

Selected Publications:

1. Cai et al. GSK3-like kinases positively modulate abscisic acid signaling through phosphorylating subgroup III SnRK2s in Arabidopsis. *Proc. Natl. Acad. Sci. U.S.A* **2014**. 111, 9651–9656.
2. Cheng et al. Brassinosteroids determine root epidermal cell fate via GSK3-like kinases that phosphorylate multiple components of the WER-GL3/EGL3-TTG1 transcriptional complex. *eLife* **2014**.10.7554/eLife.02525
3. Wang et al. Strigolactone/MAX2-induced degradation of brassinosteroid

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Katayoon (Katie) Dehesh

*Professor,
Department of Plant Biology,
College of Biological Science,
University of California Davis, CA, USA.*



Dr. Dehesh received her B. S. in Pahlavi University in 1977, and obtained Ph. D. in Stress Physiology in 1977 from Sussex University in United Kingdom.

Her research focuses on two distinct areas: biofuels and unraveling the mechanisms of plant defense responses. The plant defense projects relate to early stress detection events and the hydroperoxidelyase mediated signaling network. Our biofuels projects include the manipulation of starch to oil conversion in oat endosperm and the engineering of altered fatty acid profiles in the seeds of promising energy crops.

She has authored over 8 patent applications and 50 journal publications including *Cell*, *Plant Cell*, *Plant J*, *Plant Physiol*, *Plant Mol Biol*, *Curr Opin Plant Biol*, etc.

Jianbing Yan

*Professor,
National Key Laboratory of Crop Genetic Improvement,
College of Life Science and Technology,
Huazhong Agricultural University, Wuhan, China.
E-mail: yjianbing@mail.hzau.edu.cn; Tel: 86-27-87280110*



Professional positions:

2010/09-present: Professor, College of Life Science and Technology/National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University.
2009/09-2011/03: Scientist, International Maize and Wheat Improvement Center.
2008/10-2009/08: Associate scientist, International Maize and Wheat Improvement Center.
2006/10–2008/09: Postdoctoral associate, International Maize and Wheat Improvement Center.
2007/01-07, 10-12: Visiting Scientist, Institute Genomic Diversity, Cornell University.
2005/10–2009/07: Associate professor, College of Agronomy and biotechnology, China Agricultural University.
2003/12–2005/09: Assistant professor, College of Agronomy and biotechnology, China Agricultural University.

Education background:

Ph. D. Plant Genetics, Huazhong Agricultural University, China, 1998/9-2003/6
B.S. Biotechnology, Huazhong Agricultural University, China, 1995/9-1999/6

Research Interests:

Genetic basis of quantitative traits especially for quality and yield related traits,
Association mapping and QTL cloning,
Maize genomics and molecular breeding.

Other Roles:

Associate director, National Key Laboratory of Crop Genetic Improvement, HZAU
Associate dean, College of Life Science and Technology, HZAU

Honors:

Japan International Award for Yong Agricultural Researchers 2010
 Dupont Young Professor Award 2011
 Hubei Chutian Scholar Professor, 2011
 New Century Excellent Talents in University, 2011
 Natural Science Foundation for Excellent Youth, 2012
 Organization Department of Youth Talent Support Plan, 2013

Services in editorial boards:

Theoretical and Applied Genetics; Molecular Breeding

Selected Publications:

In total, more than 50 peer-reviewed international articles

1. Yang et al. Genome wide association studies using a new nonparametric model reveal the genetic architecture of 17 agronomic traits in an enlarged maize association panel. *PLoS Genetics*, in press.
2. Wen et al. Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights. *Nat Commun* **2014**. 5: 3438.
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14. Yang et al. Comparison of SSRs and SNPs in assessment of genetic relatedness in maize. *Genetica* **2011**. 139(8):1045-54.
15. Yan et al. Association mapping for enhancing maize genetic improvement. *Crop Science* **2011**. 51: 433-449 (Invited Review).
16. Wei et al. Detection on genetic integrity of conserved maize (*Zea mays* L.) germplasm in genebank using SNP markers. *Genet Resour Crop Ev* **2011**. 58: 189–207.
17. Yan et al. Rare genetic variation at *zea mays crtRB1* increases β -carotene in maize grain. *Nature Genetics* **2010**. 42: 322–327.
18. Yang et al. 2010 Characterization of a global germplasm collection and its potential utilization for analysis of complex quantitative traits in maize. *Molecular Breeding* **2011**.28:511–526.
19. Li et al. Function, relationship, and evolutionary fate of two maize genes orthologous to rice GW2 associated with kernel size and weight. *BMC plant biology* **2010**. 10:143 doi:10.1186/1471-2229-10-143.
20. Yang et al. Genetic analysis and characterization of a new maize association mapping panel for quantitative trait loci dissection. *Theoretical and Applied Genetics* **2010**. 121: 417-431.
21. Yan et al. High-throughput SNP genotyping with the GoldenGate assay in maize. *Molecular breeding* **2010**. 25:441–451 DOI: 10.1007/s11032-009-9343-2.
22. Yan et al. Genetic characterization of a global maize collection using SNP markers. *PLoS ONE* **2009**. 4(12): e8451.
23. Li et al. Cloning and characterization of a putative GS3 ortholog involved in maize kernel development. *Theoretical and Applied Genetics* **2010**. 120:753–763.

Bo Liu

*Professor,
Department of Plant Biology,
University of California Davis, CA, USA.*



Dr. Liu obtained his B. S. and M.S. on Cell Biology in Peking University, and Ph.D. on Botany in University of Georgia. Later he as Research Assistant in University of Georgia and as Postdoctoral Research Fellow in University of Medicine and Dentistry of New Jersey. Since 1998 he moved to University of California Davis.

His lab focuses on cell biology of the cytoskeleton and intracellular motility in plant and fungal cells. The dynamics of microtubules and actin microfilaments during plant cell division and cell growth. Roles of kinesin motor proteins in mitosis and cytokinesis. Molecular mechanisms of cytoskeleton-mediated hyphal growth in filamentous fungi. *Arabidopsis thaliana*, *Oryza sativa* (rice), and *Gossypiumhirsutum* (cotton) as model systems for plant studies, and *Aspergillusnidulans* as a model for fungal studies.

He has authored over 13 research articles in *Plant Cell* and published more than 40 other journal publications including *Plant Physiol*, *Mol Biol Cell*, *Genetics*, *Cytoskeleton*, *Protoplasma*, *PLoS Genet*, *Curr Biol*, *Curr Opin Plant Biol*, etc.

Yueyun Hong

*Professor,
National Key Laboratory of Crop Genetic Improvement,
College of Life Science and Technology,
Huazhong Agricultural University, Wuhan, China.*



Dr. Yueyun Hong received her Ph.D in Cell & Molecular Biology, University of Missouri-St. Louis in 2007. Since 1989 she had worked as assistant principal investigator, and then associate principal investigator in Fujian Academy of Agricultural Science. She moved to Huazhong Agricultural University as a professor in 2008.

Her research focuses on lipid metabolism and lipid signaling involved in crop plant growth, development and abiotic stress response via using a combination of approaches such as molecular, genetic, biochemical, cellular, and metabolic analyses. The specific interests are included as following: 1) To identify the critical enzymes involved in membrane lipid remodeling; 2) To clarify the roles of lipid messengers such as phosphatidic acid, diacylglycerol in plant growth and osmotic stress response; 3) To explore the signal cascade mediated by lipid messengers in physiological effects; 4) To determine the critical enzymes and the regulation network involved in oil accumulation in *Brassica napus*.

She has authored over 20 Journal publications including *Plant Cell*, *Plant Journal*, *Plant Cell & Environment*, *Molecular Plant*, *Plant Biotechnology Journal*, etc.

Andrew Groover

*Adjunct Associate Professor,
Department of Plant Biology,
University of California Davis, CA, USA;
Geneticist and Director,
USDA Forest Service, Institute of Forest Genetics.*



Dr. Andrew Groover received his B. S. and M.S. at University of Georgia Forest Genetic, and obtained Ph.D. in 1997 from University of North Carolina. He then moved to the Cold Spring Harbor Laboratory working as a postdoc. Since 2000 he has worked at USDA and University of California Davis.

His lab studies the developmental biology of forest trees. They also develop molecular genetics and genomic tools for gene discovery and characterization for the model forest trees in the genus *Populus*.

He has authored over 19 journal publications including *Science*, *Plant Physiol*, *New Phytol*, *Plant Mol Biol*, *Trends Plant Sci*, *Curr Opin Plant Biol*, etc.

Xuebo Hu

*Chutian Professor of Institute for Medicinal Plants,
Leader of Medicinal Plants,
College of Plant Science and Technology,
Huazhong Agricultural University, Wuhan, China.*



Before joining the faculty of HZAU at 2012, Dr. Hu worked at Department of Biomedical Engineering, Cornell University firstly as a Postdoc and then research associate, from 2006 to 2012. Dr. Hu's research extensively focused on the protein engineering and antibody discovery at Cornell University. Dr. Hu was a scientist on plant virology in Institute of Microbiology, Chinese Academy of Sciences before he moved to Cornell. Dr. Hu won his PhD degree from Zhejiang University in 2004 and Bachelor degree from HZAU in 1997. Dr. Hu has published nearly 20 papers including *PNAS*, *J Biol Chem*, *PLoS ONE*, etc.

Representative Publications:

1. Zhao et al. Ethanol and Methanol Can Improve Huperzine A Production From Endophytic *Colletotrichum gloeosporioides* ES026. *PLoS ONE* **2013**. 8:e61777.
2. Hu et al. Cell Surface Assembly of HIV gp41 Six-Helix Bundles for Facile, Quantitative Measurements of Hetero-oligomeric Interactions. *J. Am. Chem. Soc* **2012**. 134:14642-14645.
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4. Hu et al. Yeast surface two-hybrid for quantitative in vivo detection of protein-protein interactions via the secretory pathway. *J Biol Chem* **2009**. 12; 284(24):16369.

Wenbing Zhou

*Associate Professor,
College of Resources and Environment,
Huazhong Agricultural University. Wuhan, China.*



Dr. Zhou obtained his B. S. on Chemical Engineering in 1996, and Ph.D. on Plant Nutrition in Huazhong Agricultural University in 2007. Since 1996, he joined Huazhong Agricultural University. In 2006, he visited Waikato University, New Zealand, for 3 months, and in 2011-2012, worked as a visiting scholar in Curtin University, Australia, for one year. In 2014, he was selected into the Wuhan Youth Science and Technology Chenguang Program.

His lab focuses on biomass utilization, including utilization of agricultural wastes and natural plant fiber material, modified cellulose from natural plant straw, for purpose of material and energy application. Recent research interest focuses on the relationship between the structure properties of biomasses or their derived celluloses, their physical or chemical reactivity and their efficiency in material or energy utilization.

He has authored 5 research articles in *Bioresour Technol* and published more than 40 other journal publications including *BioResources*, *Energy & Fuels*, *J Hazard Mater*, *Spectrosc Spect Anal*, *Hydrobiologia*, etc.

Chunyu Zhang

*Professor,
National Key Laboratory of Crop Genetic Improvement,
College of Plant Science and Technology,
Huazhong Agricultural University, Wuhan, China.*



Dr. Zhang obtained his Ph.D. on Plant Developmental Biology in Huazhong Agricultural University in 2005. Since then, he has worked as faculty at the same University. From 2007 to 2010, he worked as Visiting scientist at Danforth Plant Science Center and University of Nebraska Lincoln.

His lab mainly focuses on vitamin E and novel fatty acids metabolomics. Acknowledges obtained from these explorations will be applied into genetic engineering of seed qualities for canola.

He has authored over 10 research articles including *Plant Journal*, *J Exp Bot.*, etc.

Zhiliang (Julia) Fan

*Assistant Professor,
Department of Biological and Agricultural Engineering,
University of California Davis, CA, USA.*

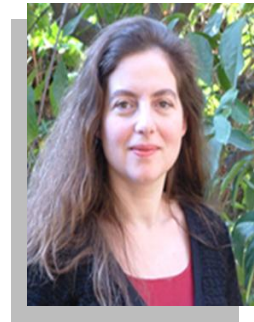


Dr. Fan completed her PhD in 2004 at Dartmouth College. Her primary research interests are in advancing technologies for production of fuels and chemicals from renewable resources, including metabolic engineering and biocatalyst development; fermentation process development and modeling; biological and chemical process design and economic evaluation. Current research is focused on novel processes for ethanol and isobutanol production from cellulosic materials.

She has authored over 16 journal publications including *Bioresource Technol*, *J Microbiol Methods*, *J Biotechnol*, *Enzyme Microb Technol*, etc.

Georgia Drakakaki

*Assistant Professor,
Department of Plant Sciences
University of California Davis, CA, USA.*



Dr. Drakakaki obtained her PhD from John Innes Center (JIC) UK and received her postdoctoral training in the laboratory of Prof. Natasha Raikhel at UC Riverside. She Joined the Department of Plant Sciences in January 2010.

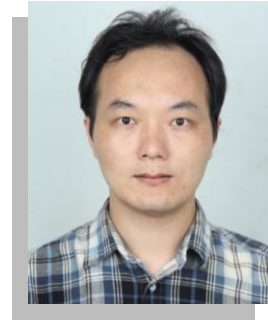
She is a member of Plant Biology (PBG) and the Biochemistry, Molecular, Cellular and Developmental Biology (BMCDB) graduate groups. She is a Designated Emphasis in Biotechnology trainer and member of the UCD Energy Institute.

Her research focuses on endomembrane trafficking in plant cells. A key area is how trafficking pathways control cell wall biosynthesis and polysaccharide deposition. Her group employs multidisciplinary research approaches, including the use of small molecules (chemical genomics), organelle proteomics and genetics.

She has authored over 20 journal publications including *PNAS*, *Cell Research*, *Plant J*, *Plant Physiol*, *Plant Cell*, *Plant Mol Biol*, etc.

Yibo Li

*Professor,
National Key Laboratory of Crop Genetic Improvement,
College of Life Science and Technology,
Huazhong Agricultural University, Wuhan, China.*



He received his B.S. in 2004 at Henan Agricultural University, and obtained Ph.D. in 2011 from Huazhong Agricultural University. He then continued his Research Associate (RA) (Professor) training in the National Key Laboratory of Crop Genetic Improvement at the same university. He joined the College of Life Science and Technology and the National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, from May 2014.

He has been focusing on the molecular mechanisms of regulating both grain size and chalkiness in rice for ten years. We have successfully isolated the first QTL gene for positively regulating rice grain size and 1000-grain weight, *GS5*, and the first QTL gene for rice grain chalkiness, *Chalk5*. Her group has systematically uncovered the molecular, biochemical and cytologic mechanisms for the formation of grain chalkiness based on the results from *Chalk5*. His present researches continue to focus on uncovering the mechanisms underlying both rice seed size and grain chalkiness controls involved in their major genes. He also has been dreaming to solve fundamental questions of seed development in rice based on tools and platforms from rice seed size and grain chalkiness regulations.

He has authored two research articles in *Nature Genetics* and published more than 4 other journal publications including *TAG*, *Plant Breeding* and *BMC Genetics*.

Lili Tu

*Associate professor,
National Key Laboratory of Crop Genetic Improvement,
College of Plant Science and Technology,
Huazhong Agricultural University, Wuhan, China.
Tel: +86-27-87283955, 13377873192
Fax: +86-27-87280016
E-mail: lilitu@mail.hzau.edu.cn, or tulili_66@163.com*



Work Experience:

- Jul 2007 – present: Work in Huazhong Agricultural University as a teacher major in cotton genetics and breeding. Take classes of BIOCHEMISTRY for undergraduate students.
- Jul 2007– present: Work in National Key Laboratory of Crop Genetic Improvement and National Center of Plant Gene Research (Wuhan) as a research fellow major in cotton genetics and breeding.

Education:

- Ph. D. 2001-2007: Huazhong Agricultural University
Major: Crop Genetics and Breeding
Minor: Cotton Genetics and Breeding
- B. Sc. 1997-2001: Huazhong Agricultural University
Major: Agronomy

Research Interests:

Cotton is the most important crop in providing a natural raw textile fiber for humans. Higher quality fiber equates to a more comfortable textile and better productivity in the spinning mill so manipulating fiber developmental processes to improve quality is a common target for breeding and biotechnology. We are focusing on elucidating the mechanism of cotton fiber development and cloning genes related to high quality fiber.

Representative Publications:

1. Liu et al. Small RNA and degradome profiling reveals a role for miRNAs and their

- targets in the developing fibers of *Gossypium barbadense*. *The Plant J* **2014**.doi: 10.1111/tpj.12636.
2. Tu et al. Flavonoid pathway in cotton fiber development. *SCIENTIA SINICA Vitae* **2014**. 44: 758-765.
 3. Han et al. A peptide hormone gene, GhPSK promotes fiber elongation and contributes to longer and finer cotton fiber, *Plant Biotechnol J* **2014**. 12: 861-871.
 4. Tang et al. The calcium sensor GhCaM7 promotes cotton fiber elongation by modulating ROS production, *New Phytol* **2014**. 202: 509-520.
 5. Tan et al. A Genetic and Metabolic Analysis Revealed that Cotton Fiber Cell Development Was Retarded by Flavonoid Naringenin, *Plant Physiol* **2014**. 162: 86-95.
 6. Hao et al. GbTCP, a cotton TCP transcription factor, confers fibre elongation and root hair development by a complex regulating system. *J Exp Bot* **2013**. 63: 6267-6281.
 7. Deng et al. GbPDF1 (Protodermal factor 1) is Involved in Cotton Fiber Initiation via the Core cis-Element HDZIP2ATATHB2. *Plant Physiol* **2012**. 158: 890-904.

