

CURRICULUM VITAE

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Research Interest			
<p>RICE</p> <p>Plant cell wall is an important structure for the cell morphology, plant development, mechanical strength and stress resistance. Rice is one of major food crops and model grass species, however, its mechanism of metabolic regulation of secondary cell wall synthesis remains largely unknown. We want to established a draft cell wall biosynthesis network, identified some key factors associations with the cell wall components biosynthesis and modification, map-based cloning the genes of stem mutants and characterized their biological roles in cell wall biosynthesis, investigated the regulatory pathway of rice cell wall. Our project will be helpful to a systematic understanding of molecular biological mechanism of cell wall synthesis and remodeling, to genetic improvement of straw strength, and will greatly accelerate the industrial use of the cereal crops straw.</p> <p>1)We integrated transcriptomic associations and cell wall metabolism and found that five certain co-expressed gene modules are positively correlated with distinct cell wall characteristics. The project initially created a weighted gene co-expression network using the expression data downloaded from CREP database, and then established a comprehensive cell wall dataset by determining cell wall compositions of 29 tissues that almost cover the whole life cycle of rice. We subsequently confirmed the five co-expressed modules that strongly correlated with primary and secondary wall cellulose biosynthesis modules, re-organization of the secondary cell walls and with modifications and degradation of hemicellulosic structures and the production of G-rich lignification. It can be used as a draft map for the selection of the candidate genes for further functional study and particular purpose.</p> <p>2)Currently we are characterising some candidate genes from the modules, such as hemicelluloses genes, by identified its T-DNA mutants and construction of its RNAi and overexpressed lines. We also characterized 27 the lignin pathway genes of rice using an integrated approach comprised of phylogeny, transcriptional profiling and co-expression analyses. These investigations revealed very useful clues on the major roles of these genes in lignin monomers biosynthesis pathway. The transformation of the RNAi and overexpression vectors based on gateway systems and editing the genes of interesting by CRISPR are undergoing.</p> <p>3)We selected some brittle culm mutants from T-DNA insertion and physicochemical (Co60 and EMS) mutant pools and map-based cloning the genes of mutants are under going. GUS staining and RT-PCR expression, subcellular localization, genetic complementation, RNAi and overexpression analysis, cell wall composition and</p>			



structural components and stem strength properties measurements were carried out to clarify their roles in cell wall biosynthesis. The agricultural performance, grain qualities, stem mechanical strength, enzymatic digestibility and disease resistance of these mutants were also investigated. Some of genes now have been cloned and functionally analysed by means of interaction analysis (yeast two-hybrid screening and the Chip-seq), as well as the analysis of the gene global expression profiles of the mutants.

WHEAT

China is the largest wheat producer and one of the diversity centers in the world, producing approximately 90 million Mg of lignocellulose from the wheat residues each year, which can be used as feedstock for biofuel purposes. Wheat culm strength, is an agronomic important trait that tightly associated with grain yield and stress resistance. Investigation of the genetic mechanism of the cell wall biosynthesis and modification in crops is one of the prerequisites for cultivation of new germplasms with higher lodging resistance and straw conversion efficiency. However, little information is available regarding the variation in cell wall composition of the wheat straw and how it relates to lodging resistance and enzymatic digestibility. Very little is known about the biochemical and genetic basis of physicochemical properties of wheat straw. During the past four years, we have established the plant cell wall and straw digestibility analysis procedures, collected the wheat germplasms, screened the EMS mutants and given them a preliminary survey.

1) We want to conduct a systematic investigation of the agronomic traits, grain quality, major cell wall components, mechanical strength, lodging resistance, to analyse the sugar yield of wheat straw after diluted alkali pretreatment and subsequent enzymatic digestion by cellulase systems, and to reveal their correlations. Furthermore, we will use the high-throughput screening platform such as HTDP, GENPLAT and electron microscopes to analyse the digestibility and cell wall composition, to conduct a high-resolution measurement of the fine structure of cell walls in order to further reveal their correlation.

2) We will also use the four classes of wheat straw mutants (nine lines) and their populations to observe the changes in the cell wall profiles and the digestibility, to find the key cell wall factors affecting the digestibility and mechanical strength, to map and to clone the genetic loci controlling these cell wall related traits. The research is essential in order to characterize wheat germplasm resources, to understand the genetic mechanism contributing to cell wall formation and remodeling in wheat, to discover valuable genetic materials for energy crop breeding and to develop the strategies for biomass conversion.

Professional Memberships

Vice president member of the council of prataculture
Member of The Chinese Society for Plant Biology (CSPB)

Other Roles

The reviewer for BMC plant biology, BMC Notes, Plant science et al.

Education & Working Experience

Education:

2001-2007 Ph.D., Biochemistry and Molecular Biology,
College of Life Science and Technology,
Huazhong Agricultural University

1998-2001 M.S., Crop Genetics and Breeding, Department of Agronomy,
Huazhong Agricultural University

1993-1997 B.S., Crop Genetics and Breeding, Department of Agronomy,
Huazhong Agricultural University

Professional Appointments:

Research Associate (Post-Doctoral Fellow), Biomass and Bioenergy Research Centre,
Huazhong Agricultural University 2007-2010

Visiting scholar, PRL GLBRC, Michigan State University, USA, 2012-2013

Associate Professor, College of plant sciences and technology, Huazhong Agricultural
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Publications

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3. Wu ZL, Hao HH, Zahoor, Tu YY, Hu Z, Wei F, Liu YY, Zhou YX, Wang YT, Xie GS, Gao CB, Cai XW, Peng LC and Wang LQ*. Diverse Cell Wall Composition and Varied Biomass Digestibility in Wheat Straw for Bioenergy Feedstock. Biomass and Bioenergy, 2014 (Accepted, 5-Year Impact Factor: 4.164) (*通讯作者)
4. 刘扬洋, 马 丽, 周玉霞, 刘雪琴, 王令强*. 2,4-D, Dicamba 和 KT 对小麦成熟胚离体培养的影响. 麦类作物学报, 34 (8): 1044-1048, 2014 (*通讯作者)
5. Peng B, Wang LQ*, Fan CC, Jiang GH, Luo LJ, Li YB and He YQ*. Comparative mapping of chalkiness components in rice using five populations across two environments. BMC Genetics, 15:49, 2014 (*共同通讯作者)
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8. Xie G, Yang B, Xu Z, Li F, Guo K, Xu Z, Li FC, Guo K, Zhang ML, Wang LQ, Zou WF, Wang YT, Peng LC*. Global Identification of Multiple OsGH9 Family Members and Their Involvement in Cellulose

- Crystallinity Modification in Rice. PLoS ONE 8(1): e50171. doi:10.1371/journal.pone.0050171, 2013
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