

## **Crop Improvement through Biotechnology (CITB)**

Research Roundtable Summary

**Beijing, November 14-17, 2005**

### **I. Session Title: Crop Improvement through Biotechnology (CITB)**

### **II. Co-Chairs (name and affiliation):**

### **III. Participating Collaborators:**



**John Yu (ARS and TAMU), Yuxian Xu (Peking U) and Tim Hall (TAMU),  
Co-organizers of the CITB Research Roundtable**

**1. Dr. Shu-Nong Bai, Peking University**

DNA Acetylation is involved in regulation of Arabidopsis root development

**2. Dr. Roy G. Cantrell, Cotton Incorporated**

Cotton Genomics: A Platform for International Collaboration

**3. Dr. Xiao-Feng Cao, Institute of Genetics and Developmental Biology, CAS**

DNA methylation related epigenetics.

**4. Dr. Xiaoya Chen, Shanghai Institute of Plant Physiology and Ecology, CAS**

Investigation of gossypol biosynthesis.

**5. Dr. Zhi-Zhong Gong, China Agricultural University**

Molecular mechanisms of stress-resistance in Arabidopsis plants

**6. Dr. Jean H. Gould, Texas A&M, Forest Science**

Somaclonal variation in transgenic rice and its impact on agronomic characteristics

**7. Dr. Wangzhen Guo, Nanjing Agricultural University**

Development of EST-SSRs and their use for genomics and MAS breeding in *Gossypium*

**8. Dr. Timothy C. Hall**, Texas A&M, Biology

MITEs contribute positively and negatively to gene expression in rice.

**9. Dr. Russell J. Kohel**, USDA-ARS, Crop Germplasm Research Unit

The international cotton genome initiative and its role in international collaboration

**10. Dr. Zhong-Ping Lin**, Peking University

Molecular mechanisms of drought resistance in higher plants

**11. Dr. Jin-Yuan Liu**, Tsinghua University

Proteomic studies using cotton fiber cell extracts

**12. Dr. Lijun Luo**, Shanghai Agrobiological Gene Center

Progress in improving the drought tolerance of rice

**13. Dr. Yong-Mei Qin**, Peking University

Molecular cloning and functional characterization of KCS/KCR genes from developing cotton fiber cells

**14. Dr. Li-Jia Qu**, Peking University

IAA methyl-transferase activity is involved in Arabidopsis leaf shape development.

**15. Gui-Xian Xia**, Institute of Microbiology, CAS

Cytoskeleton and cotton fiber development

**16. Dr. Wei-Cai Yang**, Institute of Genetics and Developmental Biology, CAS

DNA mismatch repair system and mitochondrial genome stability in higher plants

**17. Dr. Shuxun Yu**, Cotton Research Institute, CAAS

Cotton molecular breeding in China

**20. Dr. Tianzhen Zhang**, Nanjing Agricultural University

Cotton fiber quality improvement through biotechnologies in China

**21. Dr. Xianlong Zhang**, Huazhong Agricultural University

Developing germplasm by cell fusion in cotton

**22. Dr. Shuijin Zhu**, Zhejiang University

The full utilization of cotton production via biotechnology

**23. Dr. Yuxian Zhu**, Peking University

Functional genomic studies on cotton fiber cell elongation

**24. Dr. John Z. Yu**, USDA-ARS, Southern Plains Agricultural Research Center

**IV. Session Summary** (include summary of field of research):

The CITB Roundtable began in the afternoon of November 16, 2005, with 10-minute PowerPoint presentations highlighting individual research areas for collaboration (see above). The Roundtable participants spent the same evening on the campus of Peking University to discuss potential areas for future collaboration. In the morning of November 17, 2005, the Roundtable participants formulated topics and objectives of collaborative proposals, prioritized future needs, and summarized action plans for a draft report to the Conference during the luncheon session. All of the participants expressed their appreciation to CITB for the opportunity to participate in the Roundtable associated with the China-U.S. Relations Conference. Rapid advances in plant molecular biology and biotechnology are playing increasing roles in crop improvement. Since food and fiber are mainstays of economic prosperity, it is essential that Chinese and U.S. researchers are at the cutting-edge of these advances. Texas A&M University and Peking University are among the leaders in the areas of genomics and biotechnology of rice and cotton and many research interactions are already established.

Collaborative projects were conducted with complementary research expertise and biological resources. For example, Chinese scientists have been very active in genomic sequencing of rice and are participating in the International Cotton Genome Initiative (ICGI) for which Russell Kohel and John Yu are current chair and co-chair, respectively.

A new research project was initiated last year to characterize cotton germplasm accessions of the Chinese collection and the U.S. collection at TAMU. Mutual interest exists in basic molecular biology. Improvements in plant transformation and stability of gene expression were demonstrated by TAMU scientists Tim Hall and Jean Gould, and Chinese scientists Lijun Luo and Zhong-Ping Lin. Expansion of these activities through roundtable discussions and subsequent funding opportunities would be very beneficial to both Chinese and US scientists and indeed to the general population.

**V. Findings/Recommendations:**

Among the 35 ICGI nations, China and U.S. are the largest on cotton research and production. Nearly one half of the 495 ICGI researchers are from China and the U.S. that represent a majority of the ICGI Steering Committee including Russell Kohel, John Yu, David Stelly, Tianzhen Zhang, and Xiaoya Chen. There is a clear consensus that the two countries should work together on cotton research so as to provide basic biotechnological information for cotton improvement. The cotton participants identified many collaborative areas and strongly recommended two for funding. The first is to map and sequence the cotton genome and the second is to reconcile many quantitative trait loci (QTL) for value-added fiber and cottonseed production.

Several Chinese groups are making major advances in identifying valuable abiotic traits such as drought and salt tolerance. In addition to annotation of the genes involved, discovery of additional genes through knockout approaches is of interest. U.S. laboratories likely to participate include the Gould and Hall labs and Dr. Wilson's scientists at TAES, Beaumont, TX. Owing to an overlap of schedules for the roundtable event and a major meeting at the International Rice Research Institute (IRRI, Philippines), several major rice laboratories were not present and their interest in participating in future collaborations will be explored by e-mail.

Dr. Lijun Luo gave a very clear and excellently illustrated presentation on his group's development of rice engineered to withstand drought and salt-related stresses. This topic was also covered in the presentation by Dr. Zhong-Ping Lin. Dr. Jean Gould cautioned the group with regard to somaclonal

variation in transgenic rice. Epigenetic impacts on gene expression in rice, as in other plants, were illustrated in basic research conducted by Drs. Xiao-Feng Cao and Timothy Hall. Several potential areas of collaboration exist. However, a major hurdle is how to obtain financial support for more extended initial visits between the laboratories and seed money for collaborative projects.

## **VI. Future Collaborations and Justification:**

1. Integrated mapping and sequencing of the cotton genome: As the world's leading nature fiber crop, cotton is one of the few major crops remaining to be mapped and sequenced. There is a strong interest and consensus from both Chinese and U.S. scientists to collaborate on integrating genetic and physical mapping information and initiating sequencing of the cotton genome. This collaboration has been going on since the last conference and will expand if funding can be obtained. The resources generated from this research will lay a solid foundation for many research applications, including the discovery of all genes for cotton improvement. Prior research collaborations resulted in a draft map of Texas Marker-1, the genetic standard for the world's Upland cotton. Many DNA markers, BAC clones, and EST genes already have been located on each of the 26 cotton chromosomes. This is considered a high-impact project that requires leadership through China-U.S. collaborations.

2. Value-added fiber and cottonseed: Collaborative research has been going on since the last conference to improve cotton fiber and seed by adding productivity- and quality-related values through biotechnology. Many quantitative trait loci (QTL) have been identified for fiber and seed quality and other traits. Collaborative research will help identify common genomic regions for such traits among labs in both countries. This information is needed for cotton breeders to confirm specific DNA markers for selection of value-added traits.

3. Functional analysis of value-added grain quality and stress tolerance: Rice is arguably the most important crop in Asia, including China. Its sequenced genome and ease of *Agrobacterium*-mediated transformation make it attractive for both basic and applied research.

4. Verification and collection of tagged rice lines: A novel post-genomic *in silico* approach for verifying gene location developed for sequenced genomes and experimentally verified for *Arabidopsis* (Yang and Hall, 2005, Bioinformatics in press), is now available and its adaptation to rice would be straightforward. Of those present, the Hall, Gould and Luo groups have substantial interest in this project, with the annotated collection of tagged lines ultimately residing at Dr. Luo's institute in Shanghai.

5. Gene discovery, trait improvement: Several Chinese groups are making major advances in identifying valuable abiotic traits such as drought and salt tolerance (Drs. Luo, Lin). In addition to annotation of the genes involved, discovery of additional genes through knockout approaches is of interest. U.S. laboratories likely to participate include the Gould and Hall labs and Dr. Wilson's scientists at TAES, Beaumont, TX.

6. Epigenetics: The recognition that several epigenetic mechanisms are intrinsic to gene expression was reflected in several exciting presentations. Collaboration between the laboratories of Drs. Cao, Yang and Hall is a natural outcome from the roundtable discussions, especially given the interest and expertise of these groups in transgenic *Arabidopsis* and rice.

## **VII. Other Information:**

U.S. visa and Intellectual Property (IP) continue to be sensitive issues that will affect future China-U.S. research collaboration.