

White Paper Topic:

## **Plant Molecular Biology and Biotechnology**

### **1. General description of the area**

It is now technically feasible to isolate and chemically modify existing genetic information present in crops, or indeed from any organism, and return or transfer it to a recipient crop, such as rice or cotton. A multitude of improvements to these, and other crops, is envisaged. Enhancements include the development of plants resistant to insects, nematodes, fungal, bacterial and viral pathogens, plants having higher tolerance to abiotic factors such as heat, cold, salinity, and beneficial characters such as seed of increased nutritional quality or cotton with improved fiber characteristics. While there are those that oppose the use of recombinant DNA technologies for crop improvement, in reality the dangers are few and no alternative strategy has the potential to provide for the burgeoning world population, projected to grow by some 70 million per year over the next 50 years, reaching a total of 9 billion. The need for increased supplies of food and fiber is especially acute in China, which has a quarter of the world's population but only 7% of the world's farmland. Indeed, the availability of farmland and water for crop production is globally challenged.

### **2. Benefits of SINO-US collaboration**

Texas A&M has leading researchers in the areas of genomics and biotechnology of rice and cotton and many interactions already exist with Chinese scientists and laboratories. Expansion of these activities through new funding opportunities would be very beneficial to both Chinese and U.S. scientists. Complementation on research expertise and biological resources would save much time and money if the research could be collaboratively conducted.

Chinese scientists have been very active in genomic sequencing of rice and are active members of the International Cotton Genome Initiative (ICGI), for which Drs. Stelly and Kohel are chair and co-chair, respectively. Campus experts in these areas include John Yu, Hongbin Zhang and Jeff Chen, along with other faculty listed above. It has been documented that genomics research is essential to ensure continued crop genetic improvement. China has recognized the practical opportunities of biotechnology and is a world leader in the range of transgenic crops being adopted. Since biotechnology offers unique opportunities for conferral of pest and disease resistance there is mutual interest in basic molecular biology and improvements in plant transformation and stability of gene expression. TAMU scientists Tim Hall, Terry Thomas, Keerti Rathore, Dan Ebbole, Jean Gould and others are recognized experts in these areas.

Importantly, the biotechnological knowledge at TAMU is complemented by faculty such as Lee Tarpley, Bill Park, Marvin Harris, Ted Wilson and Yubin Yang, who have expertise in many facets of practical agriculture and biocontrol.

A stellar group of Chinese scientists participated in the Plant Molecular Biology and Biotechnology roundtable and minisymposium associated with the China-U.S. Conference, sponsored by the Bush School at Texas A&M University in November, 2003. Complementing the talents of these Chinese experts with U.S. scientists at TAMU can be predicted to be synergistic in advancing fundamental knowledge and in the practical application of new technologies derived from the proposed interactions.

The proposed collaborations will also augment diversity and cultural interactions, advancing educational levels. Input and advice from the TAMU International Program (Emily Ashworth) would be very welcome.

### **3. Existing success stories of TAMU-China collaborations**

#### **(a) Research Roundtable on Plant Molecular Biology and Biotechnology (PMBB)**

This Roundtable discussion and associated Minisymposium, held as part of the prestigious China-U.S. Relations: Past, Present and Future Conference at the Leonore and Walter Annenberg Presidential Conference Center at Texas A&M (November 5-8, 2003), was a great success. Co-chaired by Drs. Tim Hall and John Yu, it provided a unique opportunity to share the latest developments in crop biotechnology in Chinese Labs, and in U.S. labs at TAMU and elsewhere.

Many distinguished Chinese and U.S. scientists including Nobel Laureate Dr. Norman Borlaug participated in the entire event. There were 57 participants in the PMBB Roundtable and over 100 in the Minisymposium. Short talks and open discussions stimulated excellent ideas to expand bilateral collaboration on PMBB. All feedback and comments received so far on the meetings have been very positive. Active communication has continued since the PMBB meetings and collaborators from both countries are eager to take action on collaborative research projects that will be of mutually interest and benefit.

#### **(b) Identification and manipulations of fiber genes in cotton germplasm**

Russell Kohel and John Yu, Research Geneticists, USDA-ARS and Texas A&M University; Thea Wilkins, Professor, University of California, Davis; Jinfa Zhang, Associate Professor, New Mexico State University; Tianzhen Zhang and Wangzhen Guo, Professors, Nanjing Agricultural University, China; Shuxun Yu and Youlu Yuan, Cotton Breeders, China National Cotton Research Institute; Xuede Wang and Shujin Zhu, Professors, Zhejiang University, Hangzhou

Dr. Russell Kohel initiated cotton genetic research collaboration with Chinese Colleagues when a group of Chinese cotton scientists visited his lab early 1980's and the collaboration with China National Cotton Research Institute (CRI) and Nanjing Agricultural University over the past two decades has been very positive. The collaboration has expanded to other Chinese cotton programs including Zhejiang University, Peking University, and Huazhong Agricultural University. Numerous exchanges on scientific visits and cotton germplasm have been conducted and research on identification and manipulations of fiber genes was published jointly. In June 2002, an International Cotton Genome Initiative Workshop was held in Nanjing where Drs. Tianzhen Zhang and John Yu were co-chairs. In January 2004, Director of CRI (Dr. Shuxun Yu) and one of his associates (Dr. Youlu Yuan) visited Drs. Kohel, Yu, Percival, Wilkins, and Jinfa Zhang of the three U.S. institutes and signed comprehensive agreements that formalize the collaborative activities including exchanges of genetic resources, scientific visits, and trainees. A grant proposal on cotton molecular breeding was submitted to China's Ministry of Science and Technology.

**(c) Sino-U.S. Center on Plant Stress Biology**

David Ow, Renee Sung, and Sheng Luan, faculty members of UC-Berkeley; Xiaoya Chen, Director of Shanghai Institute of Plant Physiology & Ecology (SIPPE)

Drs. Ow, Sung and Luan visited Dr. Chen's Institute on December 17-18, 2003 and they established the Sino-U.S. Center on Plant Stress Biology. A collaboration agreement was signed at the level of Vice Chancellor of UC-Berkeley and the Chinese counterpart. The Shanghai-based Center will provide a common platform for research, education, and other scientific collaboration. Dr. Ow met with Mr. Ross Kreamer, Agricultural Attache of the U.S. Consulate General and indicated that the U.S. Consul General would attend the signing ceremony in May 2004.

**(d) Molecular mechanisms of heterosis and polyploidy in wheat**

Jeff Chen, Assistant Professor, Texas A&M University; Qixin Sun, Professor and Vice President, China Agricultural University, Beijing

Dr. Sun visited Dr. Chen's lab exchanged visits and they initiated bilateral collaboration in research and graduate education. A proposal will be submitted to China NFS for funding in March 2004.

**(e) Biotic Defense Genomics in Cotton and Functional and Comparative Genomics in Rice**

Hongbin Zhang, Associate Professor, Texas A&M University; Daqun Liu, Professor and President, Agricultural University of Hebei, Hebei; Bo Yan, Professor and Director, Institute for Plant Biotechnology, Agricultural Academy of Yunnan, Kunming

Dr. Bo Yan visited Dr. Zhang's lab for two years and one scientist from Dr. Liu's lab visited Zhang's lab for three years and they initiated bilateral collaboration in research and graduate education.

**(f) Comparative Genomics in Rice and Related Species**

Hongbin Zhang, Associate Professor, Texas A&M University; Bin Liu, Professor, Beijing Genomics Institute, Chinese Academy of Sciences, Beijing

Dr. Bin Liu visited Dr. Zhang's lab twice and they initiated bilateral collaboration in research and graduate education.

#### **4. Collaborative projects for near-term focus**

##### **(a) Elucidation of epigenetic phenomena towards reliable transgene expression in crops**

Potential collaborators: Tim Hall, Texas A&M; Zhang Qifa, Professor and Director of National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan; Cheng Jia-An, Professor and Vice President of Zhejiang University, Hangzhou

Stable expression of transgenes is vital if crops modified by recombinant DNA engineering are to be widely accepted. Several components of transcriptional and post-transcriptional gene silencing have now been identified. These include changes in acetylation and methylation status of histones, with the loss of acetylation corresponding with heterochromatinization and silencing. These changes may be accompanied by DNA methylation and further establishment of gene silencing. One natural role of gene silencing is to provide a defense mechanism against pathogens; it appears that the introduction of a transgene is recognized as an invasion by alien DNA, triggering silencing. Transcription of transgenes also triggers silencing through RNA interference (RNAi) pathways.

The Hall lab has investigated many cases of silencing and has identified some of the ways in which transgenes signal their presence, providing insight to ways by which this signaling can be avoided. The involvement of miniature inverted repeat elements (MITEs) in both silencing and elevated expression from transgene promoters has been demonstrated. The location within the genome also appears to affect transgene expression levels and The Hall group has developed novel approaches for determining the locus at which transgenes are inserted.

##### **(b) Biotechnological approaches to rice water weevil resistance**

Potential collaborators: Tim Hall, Texas A&M; Zhang Qifa, Professor and Director of National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan; Cheng Jia-An, Professor and Vice President of Zhejiang University, Hangzhou

The rice water weevil is a worldwide pest. Treatment with chemical insecticides is harmful to wildlife and carbofuran, previously used in the U.S. is now banned. If a *Bacillus thuringiensis* protein toxic to the RWW could be identified and expressed in the roots of transgenic rice plants, this would be an ecologically effective control method. The Hall lab has isolated two promoters from rice that are strongly expressed in roots and very suitable for driving the potential toxin. Additionally, a new microspore-based transformation technique has been established that gives high numbers of transformants that are homozygous, greatly facilitating the identification of gene function. Hall is invited to China in July 2004 as a member of the Scientific Advisory Board to the National Institute of Biological Sciences in Beijing and plans to meet with potential collaborators there and in Shanghai.

##### **(c) Hickory arthropods**

Potential collaborators: Marvin Harris, Texas A&M; Jiaan Cheng, Zhejiang University

The collaborators have been in continuous contact since the conference on numerous

matters. They are planning joint collaboration/research on hickory arthropods and exploring granting opportunities and student exchange. Harris intends visiting the Chinese institution to meet colleagues/students and examine field sites this summer as part of this effort to increase our knowledge and share information in this area.

**(d) Reproductive heat tolerance; nitrogen metabolism**

Potential collaborators: Tarpley, Wilson, Park, and Yang with: 1. Qifa Zhang and colleagues of the National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan, China in the areas of rice physiology and functional genomics of a) reproductive heat tolerance, and b) nitrogen metabolism; 2. Hualing Mi and Xiaoya Chen of the Institute of Plant Physiology and Ecology of the Shanghai Institutes for Biological Sciences, CAS in the area of rice physiology and biochemistry relevant to global climate change.

Rice grain set is decreased by high day or night temperatures that occur in China and the US in some years, resulting in poor regional grain yields. These years of excessive temperature are expected to occur more frequently because of global warming. The development of heat-tolerant rice is needed now to diminish instabilities in regional food supply. Rice yield in China and the US is often limited by nitrogen fertility, yet the rice plant is inefficient in its use of organic or inorganic nitrogen fertilizer. Increasing the rice plant's nitrogen use efficiency will decrease farmer's costs and diminish nitrogen run-off. Cooperative research in rice physiology, functional genomics, and biochemistry is needed in study to improve reproductive heat tolerance, nitrogen metabolism, and response to global climate change.

**(e) Development of open genomic resources for cotton improvement**

Potential collaborators: Russell Kohel and John Yu of USDA-ARS and Texas A&M; Hongbin Zhang, David Stelly, Jeff Chen, Jean Gould, Keerti Rathore, Wayne Smith, Peggy Thaxton, Dan Ebbole, and Zhanyou Xu of Texas A&M; David Ow of USDA-ARS and UC-Berkeley; Jinfa Zhang of New Mexico State University; Thea Wilkins of UC-Davis; John Killmer of Monsanto; Tianzhen Zhang and Wangzhen Guo of Nanjing Agricultural University, Shuxun Yu and Youlu Yuan of China National Cotton Research Institute; Xuede Wang, Shujin Zhu, and Jun Zhu of Zhejiang University; Yuxian Zhu of Peking University; Xianlong Zhang of Huazhong Agricultural University; Lijun Luo of Shanghai Agrobiological Gene Center; Xiaoya Chen of Shanghai Institute of Plant Physiology & Ecology

China and the U.S. are the two countries with the largest volumes of cotton research and production activities. They are among the major players of 32-nation, 360-member International Cotton Genome Initiative (ICGI) for which Drs. Stelly and Kohel are chair and co-chair, respectively. Cotton genomics has not been supported at the level of other major crops and it is not at the level of its economic importance in the world economy. International collaboration on cotton genomics research is needed to expedite the development of open resources for cotton improvement. Such resources include portable DNA markers, integrated genome map, and gene tags for fiber and other important traits that are very essential for basic and applied research as being conducted in other crops. Continued collaboration between China and the U.S. on this platform building will complement each other's capacity and natural resources and will expedite

the urgently needed research to benefit the global cotton community. Training on students and junior scientists will continue to be achieved through exchanges of visits, workshops, seminars, and joint publications on the collaborative research.

**(f) Improved nutrition of cottonseed & improvement of transformation methods for cotton**

Potential collaborators: Jean Gould, Texas A&M; Dr. Chen Xiaoya (cotton functional genomics), Professor and Director of Shanghai Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences; Dr. Yu Shuxun (cotton breeding and transformation), Professor and Director of China National Cotton Research Institute, Anyang, Henan; Dr. Yuan Youlu (cotton molecular breeding), Professor and Head of Cotton Molecular Breeding Program, China National Cotton Research Institute, Anyang.

Cotton can be transformed using *Agrobacterium* and through the pollen pathway, but both process are inefficient. Drs. Shuxun, Youlu and Gould will collaborate on improving transformation. Cottonseed is as nutritious as soybean, yet cannot be used in feed for non-ruminant animals or as food for humans due to the presence of toxic gossypol, contained in glands, in the cotyledons of the embryo. Dr. Chen will advise Gould. The most urgent of these issues is cotton transformation.

**(g) Functional genomics of cotton fiber development**

Potential collaborators: Jeff Chen, Assistant Professor, Texas A&M University; Xiao-Ya Chen, Professor and Director, Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai; Tianzhen Zhang, Professor, Nanjing Agricultural University, Nanjing; Xuede Wang, Professor, Zhejiang University, Hangzhou

**(h) Comparative and Functional Genomics in Rice and Related Species**

Potential collaborators: Hongbin Zhang, Associate Professor, Texas A&M University; Dr. Bin Liu, Professor, Beijing Genomics Institute, Chinese Academy of Sciences, Beijing; and Dr. Bo Yan, Professor and Director, Institute for Plant Biotechnology, Agricultural Academy of Yunnan, Kunming

Rice has been used as a model species for genome and molecular research of cereals and the genome of japonica rice (*Oryza sativa* ssp. *japonica* cv. Nipponbare) will be completely sequenced soon. Functional analysis of the genomic sequence and determination of the functions of each of its genes is becoming the centerpiece of rice genomics research. Comparative genomics of rice and related species such as indica rice, African rice and their wild species will greatly facilitate determination of functions of the rice genes and related elements. In turn, the genome results of rice will greatly promote the genomics and molecular research of other cereal crops such as maize, wheat and sorghum.

**(i) Rice Blast Disease**

Potential Collaborators: Dan Ebbole, Terry Thomas, TAMU; PRC collaborators, ????

Rice is a major food staple for nearly one-half of the global population. Rice blast disease is caused by the fungus *Magnaporthe grisea*, and it is one of the most economically detrimental cereal diseases world-wide, causing yield losses of up to 50%. This represents a loss of more than 150 million tons of rice. Rice blast is controlled using resistant cultivars or by application of fungicides, although problems are associated with both forms of management. Disease occurrence and severity are variable by year and location and depend primarily on environmental conditions and agricultural practices. Development of *M. grisea* resistant rice would have a major impact on the cultivation of this most important grain. The availability of genome sequences for rice and the rice blast fungus and additional genomic resources will facilitate a functional genomics approach to develop blast resistant rice cultivars more rapidly and to identify targets for more effective fungicides.