

# **International Conference on Polyploidy, Heterosis, and Epigenetics 2007**

Beijing, China  
May 21-23, 2007

## **Sponsored By**

**China Agricultural University**  
**National Science Foundation of USA**  
**Chinese Academy of Sciences**

## **Assisted By**

**Institute of Genetics and Developmental Biology, CAS**  
**National Natural Science Foundation of China**

## **Supported By**

**LiuHeTong Biotechnology Company**  
**Monsanto Company**  
**Aoke Biotechnology Comany**

**International Conference on Polyploidy,  
Heterosis, and Epigenetics 2007**

**May 21-23, 2007  
JinMa Hotel, Beijing, China**

**Monday, May 21**

- 7:30 am - 8:30 am**      **Breakfast**
- 8:30 am - 8:45 am**      **Welcome / Introductory Comments by the Organizing Committee**  
**Organizers:**  
**Qixin Sun**, China Agricultural University, China  
**Z. Jeffrey Chen**, The University of Texas at Austin, USA  
**Xiaofeng Cao**, Chinese Academy of Sciences, China  
**Luca Comai**, University of California-Davis, USA
- 8:45 am – 9:25 am**      **Keynote Lecture**  
**Vicki Chandler**  
University of Arizona, USA  
Title: Tandem Repeats Mediate Heritable Chromatin Changes Through an RNA- Directed Mechanism
- 9:25 am – 9:45 am**      **Coffee/Tea Break**
- Session 1 – Heterosis: Hypotheses, Models, and Methods**
- Chair: Qixin Sun, China Agricultural University, China**
- 9:45 am – 10:15 am**      **James Birchler**  
University of Missouri, USA  
Title: Studies on heterosis in maize
- 10:15 am – 10:40 am**      **Patrick Schnable**  
Iowa State University, USA  
Title: Heterosis in maize: new tools and complexities

**10:40 am – 11:05 am      Mei Guo,**  
Pioneer Hi-Bred International, Johnston, Iowa  
Title: *Cis*- and *trans*-effects on allele expression and the roles in  
hybrid performance

**11:05 am – 11:30 pm      Jinshui Yang**  
Fudan University , China  
Title: Haplotype variation in structure and expression of a gene  
cluster associated with a yield QTL in rice

**11:30 am - 11:55 am      Z. Jeffrey Chen**  
University of Texas at Austin, USA  
Title: A mechanism for hybrid performance in *Arabidopsis*  
allopolyploids

**11:55 am – 12: 30 pm      Group photo**

**12:30 pm - 1:30 pm      Lunch**

**Session 2 – Polyploidy: Evolutionary Consequences**

**Chair: Zhukuan Cheng, Chinese Academy of Sciences, China**

**1:30 pm – 2:00 pm      Jonathan Wendel**  
Iowa State University, USA  
Title: Polyploidy, domestication, and fiber evolution in  
*Gossypium*

**2:00 pm – 2:25 pm      Jeff Doyle**  
Cornell University, USA  
Title: Evolution of homoeologous regions including a major  
R-gene cluster in soybean and allies

**2:25 pm – 2:50 pm      Barbara Mable**  
University of Glasgow, UK  
Title: Polyploidy and self-incompatibility in *Arabidopsis lyrata*

**2:50 pm – 3:15 pm      Reiner Veitia**  
Université Paris, France  
Title: The fate of paralogs in polyploids: facts and thoughts

## Program **ICPHE 2007**

**3:15 pm – 3:40 pm**      **Scott Jackson**  
Purdue University, USA  
Title:Paleopolyploidy in the Soybean Genome

**3:40 pm – 4:00 pm**      **Coffee/Tea Break**

### **Session 3 – Epigenetics: Small RNA Biogenesis and Chromatin**

**Chair: Jiayang Li, Chinese Academy of Sciences**

**4:00 pm – 4:30 pm**      **Rob Martienssen**  
Cold Spring Harbor Laboratory, USA  
Title:Epigenetic Natural Variation in *Arabidopsis thaliana*

**4:30 pm – 4:55 pm**      **Blake Meyers**  
University of Delaware, USA  
Title:Deep transcriptional profiling of plant small RNAs

**4:55 pm – 5:20 pm**      **Rebecca Doerge**  
Purdue University, USA  
Title:Statistical Issues in the Analysis of Polyploid and Epigenetic Data

**5:20 pm – 5:45 pm**      **Xuemei Chen**  
University of California-Riverside, USA  
Title:microRNA biogenesis in *Arabidopsis*

**5:45 pm – 6:05 pm**      **Selected from abstracts**  
**Xiu-Jie Wang**  
Institute of Genetics and Developmental Biology, CAS, Beijing  
China  
Title:Computational Identification of Natural Antisense Transcripts in *Arabidopsis thaliana*

## **Tuesday, May 22**

**7:30 am – 8:30 am**      **Breakfast**

### **Session 4 – Heterosis: From Theories and Models to Applications**

**Chair: Luca Comai, University of California-Davis, USA**

## Program ICPHE 2007

- 8:30 am - 9:00 am**      **Qixin Sun**  
China Agricultural University, China  
Title: Genetic and molecular basis of heterosis in crop plants—A summary report of heterosis project in China
- 9:00 am – 9:25 am**      **Jinling Meng**  
Huazhong Agricultural University, China  
Title: Exploring fixed and intersubgenomic heterosis assisted with an introgressive genetic map of *Brassica napus*
- 9:25 am – 9:50 am**      **Daniel Zamir**  
Hebrew University of Jerusalem, Israel  
Title: Overdominant QTL and Heterosis in Tomato Interspecific Introgression Lines
- 9:50am – 10:10 am**      **Coffee/Tea Break**
- Session 5 – Polyploidy: Old Events, New Themes and Future Perspectives 1**
- Chair: Xiaofeng Cao, Chinese Academy of Sciences, China**
- 10:10 am – 10:35 am**      **Malika Ainouche**  
Universite de Rennes, France  
Title: Evolutionary consequences of recurrent hybridization and polyploidy in invasive *Spartina* species (Poaceae)
- 10:35 am – 11:10 am**      **J. Chris Pires**  
University of Missouri, USA  
Title: Ancient and recent polyploidy in *Brassica*
- 11:10 am – 11:35 am**      **Brian Dilkes**  
University of California-Davis, USA  
Title: The ploidy hybridization barrier is controlled by a genetic network in *A. thaliana*
- 11:35 am – 1:30 am**      **Poster Session**
- 12:00 am – 1:30 pm**      **Lunch**

**Session 6 – Polyploidy and Speciation: Advantages and Disadvantages**

**Chair: Rob Martienssen, Cold Spring Harbor Laboratory, USA**

- 1:30 pm – 2:00 pm**      **Luca Comai**  
University of California-Davis, USA  
Title: Genetics and molecular mechanisms affecting polyploidy-dependent speciation
- 2:00 pm – 2:25 pm**      **Rod Scott**  
University of Bath, UK  
Title: Triploid block in *Arabidopsis thaliana*
- 2:25 pm – 2:50 pm**      **Bikram Gill**  
Kansas State University, USA  
Title: What have we learned from genetic, cytogenomic and evolutionary analysis of allopolyploid wheat
- 2:50 pm – 3:15 pm**      **Bao Liu**  
Northeast Normal University, China  
Title: Transcriptome analysis in newly synthesized allohexaploid wheat
- 3:15 pm – 3:35 pm**      **Coffee/Tea Break**

**Session 7– Epigenetics: DNA Methylation and Transcriptional Silencing**

**Chair: Chuanyou Li, Chinese Academy of Sciences, China**

- 3:35 pm – 4:05 pm**      **Hugh Dickinson**  
University of Oxford, UK  
Title: Epigenetic Maternal Control of Early Endosperm Development in Maize
- 4:05 pm – 4:30 pm**      **Zhizhong Gong**  
China Agricultural University, Beijing, China  
Title: Transcriptional gene silencing and heterochromatin spreading in *Arabidopsis*

## Program ICPHE 2007

- 4:30 pm – 4:55 pm**      **Jiming Jiang**  
University of Wisconsin, USA  
Title: Transcription of centromeric DNA sequences in rice
- 4:55 pm – 5:20 pm**      **Ming Bo Wang**  
CSIRO Plant Industry, Australia  
Title: The effect of plant ploidy on transgene-induced silencing
- 5:20 pm – 5:40 pm**      **Selected from abstracts**  
**Naoki Kishimoto**  
Division of Plant Sciences, Japan  
Title: Gene dosage effect in primary trisomics: Transcriptome analysis of rice trisomic lines carrying a different extra chromosome
- 5:40 pm – 7:00 pm**      **Dinner**
- Session 8 – Epigenetics:  
Small RNA, histone modifications and Development**
- Chair: Qi Xie, Chinese Academy of Sciences, China**
- 7:00 pm – 7:30 pm**      **Xiaoya Chen**  
Chinese Academy of Sciences, China  
Title: Up-regulation of Transmethylation Pathway in Cotton Fiber Cells
- 7:30 pm – 7:55 pm**      **Xiaofeng Cao**  
Chinese Academy of Sciences, China  
Title: *Oryza sativa* DICER-LIKE Proteins Reveal a Key Role for RNA Silencing and Plant Development
- 7:55 pm – 8:20 pm**      **Yijun Qi**  
National Institute of Biological Sciences, Beijing  
Title: A Complex System of Small RNAs in the Unicellular Green Alga *Chlamydomonas reinhardtii*
- 8:20 pm – 8:45 pm**      **Yuehui He**  
University of Singapore, Singapore  
Title: Epigenetic Regulation of Flowering Time in Arabidopsis
- 8:45 pm – 9:30 pm**      **Poster session**

**Wednesday, May 23**

**7:30 am - 8:30 am      Breakfast**

**Session 9 – Polyploidy: Genetic and Epigenetic Effects**

**Chair: MingSheng Chen, Chinese Academy of Sciences, China**

**8:30 am – 9:00 am      Marjori Matzke**  
Gregor Mendel Institute of Molecular Plant Biology, Austria  
Title: Effects of aneuploidy on chromosome structure,  
expression, and interphase organization in *Arabidopsis thaliana*

**9:00 am - 9:25 am      Ortrun Mittelsten Scheid**  
Gregor Mendel Institute of Molecular Plant Biology, Austria  
Title: Crosstalk between epialleles in polyploid *Arabidopsis*

**9:25 am - 9:50 am      Andrew Leitch**  
Queen Mary, University of London, UK  
Title: Evolution of allopolyploids in the genus *Nicotiana*

**9:50 am – 10:05 am      Coffee/Tea Break**

**Session 10 – Polyploidy: Old Events, New Themes & Future Perspectives 2**

**Chair: James Birchler, University of Missouri, USA**

**10:05 am – 10:35am      Michael Freeling**  
University of California-Berkeley, USA  
Title: Tetraploidy, the fractionation mechanism, large genes and  
trends in plant evolution

**10:35 am - 11:00 am      Boulos Chalhouh**  
INRA/CNRS - URGV, France  
Title: Genetic and transcriptome modifications induced by  
polyploidy in the wheat species (*Triticum* and *Aegilops*) model

**11:00 am – 11:25 am      Pamela Soltis**  
University of Florida, USA  
Title: Gene Loss in Recent Allotetraploid Species of  
*Tragopogon* (Compositae)

## Program ICPHE 2007

- 11:25 am – 11:50 am**      **Closing remarks**  
**Z. Jeffrey Chen**, The University of Texas at Austin, USA
- 11:50 am – 12:50 am**      **Lunch**
- 1:00 pm – 6:00 pm**      **City Tour (The Summer Palace)**
- 6:30 pm – 8:00 pm**      **Dinner**

## Thursday - Sunday, May 24 - 27

### Post-conference Tours:

**Full day Beijing City tour (May 24, 2007): the Great Wall and Ming Tombs**

**Beijing - Xi'an tour (May 25-27, 2007)**

#### Itinerary:

- May 25**      **Fly to Xi'an.**  
**Sightseeing in Xi'an: the Big Wild Goose Pagoda**
- May 26**      **Sightseeing in Xi'an: Terra-Cotta Warriors and Horses, Huaqing Hot Springs**
- May 27**      **Sightseeing in Xi'an: the Ancient City Wall, and the Provincial Museum.**  
**Fly back to Beijing**

## Speaker List ICPHE 2007

### **Malika Ainouche**

Evolutionary Ecology  
Institute/Organization of University of  
Rennes 1 (France), UMR CNRS 6553  
Bat. 14A Campus de Beaulieu  
Rennes 35 042 Cedex France  
Phone: 33-2-23-23-51-11  
[malika.ainouche@univ-rennes1.fr](mailto:malika.ainouche@univ-rennes1.fr)

### **Xiaofeng Cao**

Institute of Genetics and  
Developmental Biology, Chinese  
Academy of Sciences  
5# Datun Road, Chaoyang District  
Beijing 100101 China  
Phone: 86-01-6486-9203  
[xfcao@genetics.ac.cn](mailto:xfcao@genetics.ac.cn)

### **Vicki Chandler**

University of Arizona  
TW Keating Bioresearch Building  
POB 210240, Tucson AZ 85721 USA  
Phone: 1-520-626-2632  
[Chandler@ag.arizona.edu](mailto:Chandler@ag.arizona.edu)

### **Xuemei Chen**

Department of Botany and Plant  
Sciences, University of California,  
Riverside, CA 92521 USA  
Phone: 1-951-827-3988  
[xuemei.chen@ucr.edu](mailto:xuemei.chen@ucr.edu)

### **Luca Comai**

Plant Biology and Genome Center  
451 E. Health Sciences Drive  
UC Davis, CA 95616 USA  
Phone: 530-752-8485  
[lcomai@ucdavis.edu](mailto:lcomai@ucdavis.edu)

### **James Birchler**

Division of Biological Sciences  
University of Missouri, Tucker Hall  
Columbia, Missouri 65211 USA  
Phone: 1-573-882-4905  
[BirchlerJ@Missouri.edu](mailto:BirchlerJ@Missouri.edu)

### **Boulos Chalhoub**

Department of Genetics, URGV  
(INRA-CNRS), 2 rue Gaston  
Crémieux  
Evry F91057 France  
Phone: 33-1-60-87-45-03  
[chalhoub@evry.inra.fr](mailto:chalhoub@evry.inra.fr)

### **Xiaoya Chen**

Institute of Plant Physiology & Ecology  
Shanghai Institutes for Biological  
Sciences Chinese Academy of Sciences  
300 Fenglin Avenue, Shanghai 200032  
China  
Phone: 86-021-54924033  
[xychen@sibs.ac.cn](mailto:xychen@sibs.ac.cn)

### **Z. Jeffrey Chen**

Section of Molecular Cell and  
Developmental Biology, University of  
Texas, 2506 Speedway, NMS 3.122  
Austin, Texas 78712 USA  
Phone: 1-512-475-9327  
[zjchen@mail.utexas.edu](mailto:zjchen@mail.utexas.edu)

### **Hugh Dickinson**

Department of Plant Sciences  
University of Oxford  
South Parks Rd, Oxford  
Oxfordshire OX1 3RB UK  
Phone: 44-01-865-275-800  
[hugh.dickinson@plants.ox.ac.uk](mailto:hugh.dickinson@plants.ox.ac.uk)

## Speaker List ICPHE 2007

### **Brian Dilkes**

Section of Plant Biology and  
the UC Davis Genome Center  
451 E. Health Sciences Drive  
Davis, CA 95616  
Phone: 1-206-714 4307  
[bdilkes@ucdavis.edu](mailto:bdilkes@ucdavis.edu)

### **Jeff Doyle**

Department of Plant Biology  
Cornell University  
228 Plant Science Building, Ithaca  
NY 14853 USA  
Phone: 1-607 255-7972  
[jjd5@cornell.edu](mailto:jjd5@cornell.edu)

### **Bikram Gill**

Wheat Genetics Resource Center  
Plant Pathology Department  
Throckmorton Hall Kansas State  
University  
Manhattan KS 66506-5502 USA  
Phone: 1-785-532-1391  
[bsgill@ksu.edu](mailto:bsgill@ksu.edu)

### **Mei Guo**

Agronomic Traits, Pioneer Hi-Bred  
International, Inc. 7300 NW 62nd Ave,  
Johnston, IA 50131 USA  
Phone: 1- 515-253-2146  
[mei.guo@pioneer.com](mailto:mei.guo@pioneer.com)

### **Scott Jackson**

Department of Agronomy  
Purdue University  
915 W State Street, West Lafayette  
Indiana 47907 USA  
Phone: 1- 765-496-3621  
[sjackson@purdue.edu](mailto:sjackson@purdue.edu)

### **Rebecca Doerge**

Department of Statistics  
Purdue University  
150 North University Street  
West Lafayette, IN 47907 USA  
Phone: 1-765-494-6030  
[doerge@purdue.edu](mailto:doerge@purdue.edu)

### **Michael Freeling**

Department of Plant and Microbial  
Biology, 111 Koshland Hall  
University of California- Berkeley  
Berkeley CA 94720, USA  
Phone: 1-510-642-8058  
[freeling@nature.berkeley.edu](mailto:freeling@nature.berkeley.edu)

### **Zhizhong Gong**

College of Biological Sciences, China  
Agricultural University, Yuanmingyuan  
Xilu 2, Haidian District, Beijing  
100094 China  
Phone: 86-13701187082  
[gongzz@cau.edu.cn](mailto:gongzz@cau.edu.cn)

### **Yuehui He**

Department of Biological Sciences  
National University of Singapore  
Science Drive 4 , 117543 Singapore  
Phone: 65-6872-7978  
[dbshy@nus.edu.sg](mailto:dbshy@nus.edu.sg)

### **Jiming Jiang**

Department of Horticulture, University  
of Wisconsin-Madison, 1575 Linden  
Drive, Madison, Wisconsin 53706 ,  
USA  
Phone: 1- 608-262-1878  
[jjiang1@wisc.edu](mailto:jjiang1@wisc.edu)

## Speaker List ICPHE 2007

### **Naoki Kishimoto**

Plant Genetic Engineering Research  
Unit  
Division of Plant Sciences  
2-1-2 Kannondai, Tsukuba  
Ibaraki 305-8602 Japan  
Phone: 81-29-838-7442  
[naoki@nias.affrc.go.jp](mailto:naoki@nias.affrc.go.jp)

### **Bao Liu**

Northeast Normal University  
5268 Renmin Road  
Changchun 130024 China  
Phone: 86-0431-85099822  
[baoliu@nenu.edu.cn](mailto:baoliu@nenu.edu.cn)

### **Andreas Madlung**

Department of Biology, University of  
Puget Sound, 1500 N Warner St, CMB  
1088, Tacoma, Washington 98416  
USA  
Phone: 1-253-879-2712  
[amadlung@ups.edu](mailto:amadlung@ups.edu)

### **Marjori Matzke**

Gregor Mendel Institute  
Austrian Academy of Sciences  
Dr. Bohr-Gasse 3  
Vienna A-1030 Austria  
Phone: 43-1-79044-9810  
[marjori.matzke@gmi.oeaw.ac.at](mailto:marjori.matzke@gmi.oeaw.ac.at)

### **Blake Meyers**

Dept. of Plant & Soil Sciences,  
University of Delaware, Delaware  
Biotechnology Institute, 15 Innovation  
Way, Newark, DE 19711 USA  
Phone: 1-302-831-3418  
[meyers@dbi.udel.edu](mailto:meyers@dbi.udel.edu)

### **Andrew Leitch**

School of Biological and Chemical  
Sciences, Queen Mary University of  
London, Mile End Road, London E1  
4NS UK  
Phone: 44-207-882-5294  
[A.R.Leitch@qmul.ac.uk](mailto:A.R.Leitch@qmul.ac.uk)

### **Barbara Mable**

Division of Environmental and  
Evolutionary Biology, University of  
Glasgow, Deeb, Graham Kerr Building,  
University of Glasgow, Scotland G12  
8QQ, UK  
Phone: 44-141-330-3532  
[b.mable@bio.gla.ac.uk](mailto:b.mable@bio.gla.ac.uk)

### **Rob Martienssen**

Department of Plant Biology, Cold  
Spring Harbor Laboratory, 1 Bungtown  
Road, Cold Spring Harbor, New York  
11724 USA  
Phone: 1-516-367-8322  
[martiens@csHL.edu](mailto:martiens@csHL.edu)

### **Jinling Meng**

Huazhong Agricultural University  
Wuhan 430070 China  
Phone: 86-027-87282457  
[jmeng@mail.hzau.edu.cn](mailto:jmeng@mail.hzau.edu.cn)

### **J. Chris Pires**

Department of Biological Sciences  
University of Missouri  
1201 Rollins Street  
Bond Life Sciences Center  
Columbia, Missouri 65211-7310 USA  
Phone: 1-573-882-0619  
[piresjc@missouri.edu](mailto:piresjc@missouri.edu)

**Yijun Qi**

National Institute of Biological  
Sciences No.7 Science Park Road  
Zhongguancun Life Science Park  
Beijing 102206, China  
Phone: 86-01-80727837  
[qiyijun@nibs.ac.cn](mailto:qiyijun@nibs.ac.cn)

**Patrick Schnable**

Plant Sciences Institute of Iowa State  
University, 2035B Roy J. Carver  
Co-Laboratory, Ames, IA  
50011-3650 USA  
Phone: 1-515-294-0975515-2  
[schnable@iastate.edu](mailto:schnable@iastate.edu)

**Pamela Soltis**

Florida Museum of Natural History,  
University of Florida, Dickinson Hall,  
Gainesville, FL 32611-7800 USA  
Phone: 1-352-392-1721 ext. 217  
[psoltis@flmnh.ufl.edu](mailto:psoltis@flmnh.ufl.edu)

**Reiner Veitia**

Department of Biology of University  
Denis DIDEROT/Paris VII, Equipe  
21. Institut Cochin. Faculté de  
Médecine. 24 rue du Faubourg Saint  
Jacques  
Paris 75014 France  
Phone: 33-1-4441-2317  
[veitia@cochin.inserm.fr](mailto:veitia@cochin.inserm.fr)

**Xiujie Wang**

Institute of Genetics and  
Developmental Biology, Chinese  
Academy of Sciences  
5# Datun Road, Chaoyang District  
Beijing 100101 China  
Phone: 86-10-64840941  
[xjwang@genetics.ac.cn](mailto:xjwang@genetics.ac.cn)

**Ortrun Mittelsten Scheid**

Gregor Mendel Institute of Molecular  
Plant Biology  
Dr. Bohr-Gasse 3, Vienna A-1030  
Austria  
Phone: 43-1-79044 9830  
[ortrun.mittelsten\\_scheid@gmi.oeaw.ac.at](mailto:ortrun.mittelsten_scheid@gmi.oeaw.ac.at)

**Rod Scott**

Biology & Biochemistry  
Institute/Organization of University of  
Bath, Claverton Down, Bath,  
Somerset BA2 7AY UK  
Phone: 44-1-22538 3437  
[bssrjs@bath.ac.uk](mailto:bssrjs@bath.ac.uk)

**Qixin Sun**

China Agricultural University  
Yuanmingyuan Xilu 2  
Haidian District  
Beijing 100094, China  
Phone: 86-10-62733426  
[qxsun62@public.bta.net.cn](mailto:qxsun62@public.bta.net.cn)

**MingBo Wang**

Division of Plant Industry  
Commonwealth Scientific & Industrial  
Research Organisation (CSIRO)  
PO Box 1600, Clunies Ross Street,  
Canberra, ACT 2601 Australia  
Phone: 61-2-6246 5197  
[Ming-bo.wang@csiro.au](mailto:Ming-bo.wang@csiro.au)

**Jonathan F. Wendel**

EEOB Department, Iowa State  
University, Bessey Hall, Iowa State  
University, Ames, Iowa 50011 USA  
Phone: 1-515-294-7172  
[jfw@iastate.edu](mailto:jfw@iastate.edu)

## Speaker List ICPHE 2007

### **Jinshui Yang**

Institute of Genetics, School of Life  
Science, Fudan University  
200 Handan Road  
Shanghai 200433 China  
Phone: 86-021-65643715  
[Jsyang@fudan.edu.cn](mailto:Jsyang@fudan.edu.cn)

### **Daniel Zamir**

Department of Plant Sciences  
The Hebrew University of Jerusalem  
Faculty of Agriculture  
Hertzel St., P.O. Box 12  
Rehovot 76100 Israel  
Phone: 972-8-9489092  
[zamir@agri.huji.ac.il](mailto:zamir@agri.huji.ac.il)

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

### Keynote Lecture

<b>Contact Person:</b>	Vicki L. Chandler
<b>Email:</b>	<a href="mailto:chandler@ag.arizona.edu">chandler@ag.arizona.edu</a>
<b>Authors:</b>	Vicki L. Chandler
<b>Affiliations:</b>	University of Arizona, Tucson, AZ USA
<b>Abstract Title:</b>	Tandem Repeats Mediate Heritable Chromatin Changes Through an RNA-Directed Mechanism

#### Abstract Text:

Paramutation is an allele dependent transfer of epigenetic information. Paramutation at the *b1* locus in maize is mediated by unique tandem repeats that are necessary and sufficient to communicate in *trans* to establish and maintain meiotically heritable chromatin states. The *mop1* gene (*mediator of paramutation1*) is required for paramutation, *Mutator* transposon silencing, and *mop1* mutants exhibit pleiotropic developmental phenotypes. Map-based cloning of *mop1* has revealed it encodes an RNA dependent RNA polymerase gene (RDRP), most similar to *RDR2*, the RDRP in plants that is associated with production of siRNA (short interfering RNA) molecules targeting heterochromatin. Nuclear run-on assays reveal that the tandem repeats required for *b1* paramutation are transcribed from both strands. In addition, the presence of tandem repeat siRNAs depends on *mop1-1*, yet they are observed in all genotypes, even those that do not undergo paramutation. These data suggest siRNAs are involved, but are not sufficient. We hypothesize that the *mop1* RDRP is required to maintain a threshold level of repeat RNA, which functions in *cis* to regulate transcription of *b1* and in *trans* to establish and maintain the heritable chromatin states associated with paramutation.

#### Session Notes:

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session I –Heterosis: Hypotheses, Models, and Methods

<b>Contact Person:</b>	James A. Birchler
<b>Email:</b>	<a href="mailto:BirchlerJ@Missouri.edu">BirchlerJ@Missouri.edu</a>
<b>Authors:</b>	James A. Birchler
<b>Affiliations:</b>	University of Missouri, Columbia, Missouri USA
<b>Abstract Title:</b>	Studies on heterosis in maize
<b>Abstract Text:</b>	
<p>The genetic and molecular basis of heterosis has eluded a consensus explanation for nearly a century. One common explanation is that slightly deleterious mutations that differ between parents are complemented in the hybrid to produce superior characteristics. However, several lines of evidence from comparing diploid, triploid and tetraploid responses to the hybrid state suggest that a dosage component is involved and that complementation alone is inadequate to explain heterosis fully. In triploid maize, there can be two types of hybrids (AAB and BBA) resulting from two parental genotypes. The magnitude of the heterotic response in these two types of hybrids is not equivalent, despite the fact that reciprocal diploid hybrids produced from the identical lines exhibit indistinguishable heterosis. This finding suggests that heterosis is affected by the dosage of different alleles rather than complementation of recessives by dominant ones. Secondly, single cross hybrid tetraploids derived from two different parental genotypes exhibit heterosis but double cross hybrids with a quadruplex genotype that have the potential for four different alleles per locus in the hybrid exhibit progressive heterosis that is superior to the single cross hybrid tetraploids. Because progressive heterosis has been found with several different combinations of tetraploid genotypes, it seems unlikely that each different genome would always provide superior alleles for a particular characteristic without introducing inferior alleles at other loci that would reduce the cumulative effect. Also, inbreeding depression in tetraploid maize proceeds at a nearly comparable pace to that of diploids of otherwise identical genotype in contrast to the widely different predicted rate of homozygosis of alleles at the two ploidy levels. This observation might also be interpreted to suggest that the dosage of alleles has an impact on the heterotic response. The molecular elucidation of many quantitative trait loci has indicated that many are transcription factors or members of signal transduction cascades. Their action is often dosage dependent. In parallel, genes that typically exhibit a haplo-insufficiency are composed of the same two classes of genes and appear to exhibit a dosage effect as a consequence of an altered stoichiometry of members of regulatory complexes. If heterosis is viewed as a quantitative trait, the question arises whether regulatory gene dosage interactions might play a role. Questions also arise as to whether heterosis is a reflection of cellular biochemical interactions, of cell proliferation effects, of regulatory gene interactions or of other possibilities. A systemic falsification of various hypotheses might narrow the potential explanations.</p>	

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session I – Heterosis: Hypotheses, Models, and Methods

<b>Contact Person:</b>	Patrick S. Schnable
<b>Email:</b>	<a href="mailto:schnable@iastate.edu">schnable@iastate.edu</a>
<b>Authors:</b>	Patrick S. Schnable, Ruth A. Swanson-Wagner, Yi Jia, Rhonda DeCook, Pengcheng Lu, Xuefeng Zhao, Dan Nettleton
<b>Affiliations:</b>	Iowa State University, Ames, IA USA
<b>Abstract Title:</b>	Heterosis in maize: new tools and complexities

### Abstract Text:

Heterosis is the phenomenon whereby the progeny of particular inbred lines have enhanced agronomic performance relative to both parents. Although several hypotheses have been proposed to explain this fundamental biological phenomenon, the responsible molecular mechanisms have not been determined. The maize inbred lines B73 and Mo17 produce a heterotic F<sub>1</sub> hybrid that is being used as a model to study heterosis.

The regulation of gene expression levels in hybrid combinations can be studied via eQTL mapping, a combination of traditional QTL mapping and global expression profiling. The maize IBM population of recombinant inbred lines (RILs) was developed from a cross between the inbred lines B73 and Mo17. Each RIL is mosaic and homozygous for either the B73 or the Mo17 allele at each locus. A genetic map based on the IBM RILs containing over 9,000 markers (ISU\_IBM Map7) was used in conjunction with eQTL analyses to gain insight into the regulation and mechanisms related to heterosis. As a first step, 30 IBM RILs were crossed onto both B73 and Mo17. In combination with the RILs *per se*, the resulting cross-types provide a contrast of gene expression for the heterozygous genotype and both homozygous genotypes across all loci polymorphic between B73 and Mo17.

Four replications of each RIL, B73xRIL, and Mo17xRIL genotype were hybridized to a custom cDNA microarray using a loop design that included all pair-wise comparisons between each RIL and its crosses with B73 and Mo17. In each cross-type hundreds of significant associations were identified between genetic markers and gene expression levels. Although many of these eQTLs exhibit additive gene action, large numbers exhibit dominant gene action. Substantial numbers of the eQTLs act *in trans*.

Natural Antisense Transcripts (NATs) can regulate gene expression by virtue of their ability to form double-stranded RNA duplexes. Both sense and antisense transcripts accumulate to detectable levels for over 70% of a random set of maize genes. Significantly, these sense and antisense transcripts exhibit significantly different expression patterns between the B73 and Mo17 inbreds. To investigate the genetic mechanisms that regulate the accumulation of antisense transcripts, two replications of each of the 90 genotypes (30 RILs, 30 B73xRIL, and 30 Mo17xRIL) described above were hybridized to a custom, strand-specific, oligonucleotide microarray. Many eQTLs

that regulate both the absolute levels of sense and antisense transcripts as well as those that regulate the *ratios* of complementary sense and antisense transcripts were identified. We hypothesize that the complex genetic interactions identified in this study contribute to heterosis.

**Session Notes:**

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session I – Heterosis: Hypotheses, Models, and Methods

<b>Contact Person:</b>	Mei Guo
<b>Email:</b>	<a href="mailto:mei.guo@pioneer.com">mei.guo@pioneer.com</a>
<b>Authors:</b>	Mei Guo, Sean Yang, Mary Rupe, David Bickel, Lane Arthur, and Oscar Smith
<b>Affiliations:</b>	Pioneer Hi-Bred International, Inc., Johnston, USA
<b>Abstract Title:</b>	<i>Cis-</i> and <i>trans</i> -effects on allele expression and the roles in hybrid performance

**Abstract Text:**

Allelic expression differences in regulatory regions are important genetic factors contributing to quantitative trait variation in various organisms. Despite its biological role, the extent of allelic expression variation on a genome scale in plants has not been well characterized. In this study we characterize genome-wide allele-specific expression in a maize hybrid and its inbred parents in the very specific tissue type of developing meristems. We developed an allele-specific expression analysis methodology by utilizing Massively Parallel Signature Sequencing (MPSS™), an open ended RNA profiling technology, to identify signature tag pairs corresponding to the two alleles of genes expressed in the hybrid. Summarization of data from nearly 400 pairs of allelic signature tags we found that approximately 60% of the genes in the hybrid meristems showed differential allelic expression. Because both alleles are subjected to the same trans-acting factors in the hybrid, the data suggest the abundance of cis-regulatory differences in the genome. When comparing allele expression in a hybrid versus its inbred parents, we found that approximately 40% of the genes showed an expression difference between genotypes, suggesting different trans-acting effects present in the hybrid versus the inbred parents. Such trans-acting effects may result in gene expression different from allelic additive expression in the hybrid. The global view of allele-specific expression, as compared to measuring total transcript level, provided a different level of understanding of hybrid gene regulation and a relationship to the molecular basis of heterosis.

**Session Notes:**

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session I – Heterosis: Hypotheses, Models, and Methods

<b>Contact Person:</b>	Jinshui Yang
<b>Email:</b>	<a href="mailto:Jsyang@fudan.edu.cn">Jsyang@fudan.edu.cn</a>
<b>Authors:</b>	Guangming He, Xiaojin Luo, Feng Tian, Kegui Li, Zuofeng Zhu, Wei Su, Xiaoyin Qian, Xiangkun Wang, Chuangqing Sun and Jinshui Yang
<b>Affiliations:</b>	Fudan University, Shanghai, China
<b>Abstract Title:</b>	Haplotype variation in structure and expression of a gene cluster associated with a yield QTL in rice

### Abstract Text:

By constructing nearly isogenic lines (NILs) that differ only at a single quantitative trait locus (QTL), we fine mapped the yield-improving QTL *qGY2-1* to a 102.9-kb region on rice chromosome 2. Comparison analysis of the genomic sequences in the mapped QTL region between the donor (Dongxiang wild rice, *Oryza rufipogon* Griff.) and recurrent (Guichao2, *Oryza sativa* ssp. *indica*) parents used for the development of NILs identified the haplotypes of a leucine-rich-repeat receptor kinase (LRK) gene cluster, which showed extensive allelic variation. We found that the *LRK* gene cluster consists of 7 or 8 *LRK* gene copies arranged in a tandem fashion throughout orthologous genomic region in Guichao2 and Dongxiang wild rice, respectively, thus formed two haplotypes. The sequences between genes in the cluster had a very high rate of divergence. More important, the genes themselves also differed between two haplotypes: only 92% identity was observed for one allele, and another allele was found to have completely lost its allelic counterpart in Guichao2. The other 6 shared genes all showed >98% identity, and 4 of these exhibited obvious regulatory variation. The same haplotype segments also differed in length (43.9-kb in Guichao2 vs. 52.6-kb in Dongxiang wild rice). Such extensive sequence variation was also observed between orthologous regions of *indica* (cv. 93-11) and *japonica* (cv. Nipponbare) subspecies of *Oryza sativa*. Different rates of sequence divergence within the cluster have resulted in haplotype variability in 13 rice accessions, thus providing an unprecedented opportunity for analyzing genomic evolution and for investigating the origin of cultivated rice. Furthermore, we also performed transgenic research with the candidate genes for QTL.

We also detected allelic expression variation in this gene cluster, in which some genes gave unequal expression of alleles in hybrids, ranged from unequal expression of the two alleles simultaneously to expression of a single allele regardless of the parent-of-origin, and both dominance complementation and some overdominance of allelic expression within the cluster occurred. The fact that allele-specific transcript accumulation of *LRK6* in hybrids suggested that the differences in gene expression may be result from *cis*-regulatory variation. These allelic variations in structure and expression suggest that the *LRK* gene cluster identified in our study should be a particularly good candidate for the source of the yield QTL, thus help us understand the molecular basis of

QTL and heterosis. We also identified 278 *OsLRK* genes in rice subspecies *japonica* (cv. Nipponbare) using a genome-wide search strategy, and then investigated their distribution on chromosomes. Comparison between *indica* and *japonica* revealed sequences variation in regulatory regions and coding regions of 102 and 64 *OsLRKs* genes, respectively. Allelic variation of these *OsLRK* genes provided a clue to understand the differentiation of two rice subspecies.

**Session Notes:**

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session I – Heterosis: Hypotheses, Models, and Methods

<b>Contact Person:</b>	Z. Jeffrey Chen
<b>Email:</b>	<a href="mailto:zichen@mail.utexas.edu">zichen@mail.utexas.edu</a>
<b>Authors:</b>	Zhongfu Ni, Yirong Zhang, Eun-Deok Kim, Lu Tian, Misook Ha, and Z. Jeffrey Chen*
<b>Affiliations:</b>	University of Texas at Austin, USA
<b>Abstract Title:</b>	A molecular basis for hybrid performance in Arabidopsis allotetraploids

### Abstract Text:

Interspecific hybrids and stable allopolyploids display hybrid vigor, but the underlying mechanisms remain unknown. Genome-wide transcriptome changes in resynthesized Arabidopsis allotetraploids modulate various regulatory networks, including circadian-mediated pathways that increase photosynthesis and fitness in the progenitors. Here we report that epigenetic modulation of *CIRCADIAN CLOCK ASSOCIATED 1* (*CCA1*) and *LATE ELONGATED HYPOCOTYL* (*LHY*) and their reciprocal regulators *GIGANTEA* (*GI*) and *TIMING OF CAB EXPRESSION 1* (*TOC1*) mediates gene expression changes in downstream pathways in Arabidopsis allotetraploids. *CCA1* and *LHY* were epigenetically repressed from noon to dusk in the allotetraploids, which correlates with upregulation of *TOC1* and *GI* and downstream genes in chlorophyll and starch metabolic pathways. The allotetraploids contain more chlorophyll, produce more starch, and grow larger than the parents under the same environment. This may explain why allopolyploid plants gain advantage from the control of circadian-mediated physiological and metabolic pathways.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session 2 - Polyploidy: Evolutionary Consequences

<b>Contact Person:</b>	Jonathan F. Wendel
<b>Email:</b>	<a href="mailto:jfw@iastate.edu">jfw@iastate.edu</a>
<b>Authors:</b>	Jonathan F. Wendel, Ryan Rapp, Lex Flagel, and Ran Hovav
<b>Affiliations:</b>	Iowa State University, Ames, Iowa USA
<b>Abstract Title:</b>	Polyploidy, domestication, and fiber evolution in <i>Gossypium</i>
<b>Abstract Text:</b>	<p>The cotton genus includes approximately 50 species distributed globally in seasonally arid regions of the subtropics. One notable aspect of this diversity is that four different species, two each in Africa-Asia (<i>G. arboreum</i> and <i>G. herbaceum</i>) and the Americas (<i>G. barbadense</i> and <i>G. hirsutum</i>), were independently domesticated for their extraordinary single-celled, epidermal seed trichomes ("fiber"). <i>Gossypium</i> species exhibit remarkable morphological diversity, ranging from herbaceous perennials to small trees and displaying a great variety of floral and vegetative features. A parallel level of cytogenetic and genomic diversity evolved during the global radiation of the genus, with the eight diploid (all <math>n = 13</math>) genome groups varying 3.5-fold in genome size. Phylogenetic analysis and molecular clock calculations suggest that the genus originated 5 - 10 million years ago, and that the major genome groups arose in rapid succession following formation of the genus. This evolutionary history has included multiple episodes of trans-oceanic dispersal and invasion of new ecological niches. A chance biological reunion among divergent diploid lineages from different hemispheres led to the monophyletic origin, approximately 1-2 million years ago, of American polyploid cottons, which subsequently radiated into lineages represented by five extant species. This remarkable history has led to a spectrum of novel genomic interactions, a high frequency of gene silencing, and possible functional differentiation among homoeologues. Comparisons among synthetic and natural allopolyploids are helping generate an understanding of the scope of epigenetic silencing that arises concomitant with polyploid formation as well as the pace of subsequent expression evolution. The cotton fiber transcriptome is extraordinarily complex, apparently expressing a major fraction of the genes in the genome. Comparative expression profiling is being used to explore the genetic basis of cotton fiber evolution and domestication, using an evolutionary-developmental framework combined with high throughput technologies for gene discovery.</p>
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session 2 - Polyploidy: Evolutionary Consequences

<b>Contact Person:</b>	Jeff J. Doyle
<b>Email:</b>	<a href="mailto:jjd5@cornell.edu">jjd5@cornell.edu</a>
<b>Authors:</b>	Jeff J. Doyle
<b>Affiliations:</b>	Cornell University, Ithaca, NY USA
<b>Abstract Title:</b>	Evolution of homoeologous regions including a major R-gene cluster in soybean and allies

### Abstract Text:

The soybean (*Glycine max*) genome is known to have been shaped by two rounds of polyploidy. The older event is shared, minimally, by other model papilionoid legumes (*Lotus japonicus* and *Medicago truncatula*). The more recent event led to an increase in chromosome number from  $2n = 20-22$  to  $2n = 40$ . In addition, the perennial subgenus of *Glycine* includes numerous species that are the products of very recent allopolyploidy, leading to chromosome numbers of  $2n = 78$  or  $80$ . The NSF PGRP-funded project "Comparative Analysis of Legume Genome Evolution" (<http://www.bio.indiana.edu/~nsflegume/>) is studying the evolution of an approximately 1 Mbp region containing a cluster of disease resistance genes (NBS-LRR R-genes) in soybean (*Glycine max*), by comparing homoeologous regions in two soybean varieties, two perennial *Glycine* species ( $2n = 40$  and  $2n = 80$ ), the diploid sister genus to *Glycine* (*Teramnus*), another phaseoloid (*Phaseolus*), and the legume models *Medicago* and *Lotus*. Comparison of the two homoeologous soybean regions derived from the more recent polyploidy event reveal many differences, in contrast to shorter homoeologous regions described from elsewhere in the genome. Transposable elements are far more common on one homoeologue than on the other, with R-genes showing the opposite pattern. Both transposon insertion and R-gene birth/death are more recent than the polyploid event, however, making it difficult to determine to what extent changes have been driven by polyploidy and suggesting that this evolutionarily labile region may be informative for more recent polyploid events. Comparisons among soybean and genomes of  $2n = 40$  perennial *Glycine* species indicate that the region has undergone continual change in gene content. Initial comparisons of homoeologous regions between a  $2n = 80$  species and its diploid progenitor also reveal numerous changes, including R-gene loss and transposable element insertion, that could be driven by recent polyploidy.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session 2 - Polyploidy: Evolutionary Consequences

<b>Contact Person:</b>	Barbara Mable
<b>Email:</b>	<a href="mailto:b.mable@bio.gla.ac.uk">b.mable@bio.gla.ac.uk</a>
<b>Authors:</b>	Barbara K. Mable
<b>Affiliations:</b>	University of Glasgow, Scotland UK
<b>Abstract Title:</b>	Polyploidy and self-incompatibility in <i>Arabidopsis lyrata</i>
<b>Abstract Text:</b>	
<p>There has been an overwhelming view in the literature that polyploidy is difficult to establish at the species level, due to initial problems with finding a mating partner of the same ploidy level when the progenitor ploidy is more abundant (minority cytotype exclusion principle) and the sterility of odd ploidies that result from interploidy crosses (triploid sterility). As a result, it has been predicted that polyploidy should be more common when outcrossing is not required, so that new polyploid lineages can be propagated through self-fertilization. Under this view, where selfing is prevented through intrinsic self-incompatibility (SI) mechanisms, loss of SI is expected to be frequent in polyploid species or populations. However, there are a lot of confounding variables to consider when this hypothesis is examined across a broad phylogenetic context and the fact remains that there are a lot of polyploid species that are strongly self-incompatible. This is particularly true for the type of SI system exhibited in the Brassicaceae (sporophytic SI). This talk will review what is known about polyploidy and SI in the Brassicaceae and will discuss in detail the inheritance and dominance of SI in polyploid populations of the <i>Arabidopsis lyrata</i> species group.</p>	
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session 2 - Polyploidy: Evolutionary Consequences

<b>Contact Person:</b>	Reiner A. Veitia
<b>Email:</b>	<a href="mailto:veitia@cochin.inserm.fr">veitia@cochin.inserm.fr</a>
<b>Authors:</b>	Reiner A. Veitia
<b>Affiliations:</b>	Université Paris Denis Diderot, Paris France
<b>Abstract Title:</b>	The fate of paralogs in polyploids: facts and thoughts
<b>Abstract Text:</b>	
<p>Plants are remarkable with regard to their capability to go beyond diploidy and remain in seemingly stable polyploid states. It is estimated that more than 50% of flowering plants are polyploids. Theory predicts that most gene duplicates tend to degenerate and disappear, so the high level of paralog retention in plants is puzzling. The extent of paralog survival is so important that protein diversity in plants is thought to be generated primarily through gene duplication rather than by alternative splicing. The fate of gene duplicates has been explored once and again. I will reassess this question from the perspective of dosage effects. Moreover, there is mounting evidence of altered gene expression in allopolyploids and hybrids (non additivity). Indeed, expression of the paralogs can vary among tissues, organs or can be developmentally regulated. Sometimes new tissue specificity appears. Interestingly, the expression patterns in synthetic polyploids may recapitulate those found in the naturally occurring plants. This suggests that certain patterns of expression appear just after a polyploidization event and persist in the long run. Classical epigenetic mechanisms such as altered DNA methylation or chromatin structure have been proposed to explain this phenomenon. Inheritable changes such as deletions have also been documented. Alternatively, sudden changes in gene expression can be due to a regulatory mismatch arising from imbalances among the effectors and their target genes contributed by the merging genomes. I will try to show how this mismatch can arise from the divergence of the relevant regulatory mechanisms in the parents and/or from global effects of the genome on gene regulation.</p>	
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session 2 - Polyploidy: Evolutionary Consequences

<b>Contact Person:</b>	Scott Jackson
<b>Email:</b>	<a href="mailto:sjackson@purdue.edu">sjackson@purdue.edu</a>
<b>Authors:</b>	Jer-Young Lin, Navdeep Gill, Jianxin Ma, Jason Walling, Jeff Doyle, Scott Jackson
<b>Affiliations:</b>	Purdue University, West Lafayette, Indiana USA
<b>Abstract Title:</b>	Paleopolyploidy in the Soybean Genome

### Abstract Text:

Soybean has experienced multiple genome duplications in its evolutionary past as evidenced by cytogenetic analysis, RFLP genetic linkage map, and divergence analysis of paired EST sequences. To shed light on the nature and timing of these duplication events, we have been recently characterizing centromeric components and sequencing a number of large duplicated regions of soybean. We have found two centromeric satellite sequences that mark subsets of chromosomes by FISH. Comparative sequence analysis reveals extensive gene colinearity between most of the duplicated regions. We hypothesize that the centromeric satellite sequences are remnants of an allopolyploidy event that occurred recently and that the regions of extensive gene for gene colinearity also derive from this event. Highly diverged duplicated regions are also seen, which are often masked by extensive chromosomal rearrangements, suggestive of more ancient duplication event. *Phaseolus vulgaris*, also known as common bean, is a close relative of soybean and has proven useful as a more 'diploid-like' outgroup to derive putative ancestral chromosome states that preceded the duplications within the soybean genome.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session 3 - Epigenetics: Small RNA Biogenesis and Chromatin

<b>Contact Person:</b>	Rob Martienssen
<b>Email:</b>	<a href="mailto:martiens@cshl.edu">martiens@cshl.edu</a>
<b>Authors:</b>	Matthew W. Vaughn, Milos Tanurdzic, Zachary Lippman, Hongmei Jiang, Robert Carrasquillo, Pablo D. Rabinowicz, Neilay Dedhia, W. Richard McCombie, Nicolas Agier, Agnès Bulski, Vincent Colot, Rebecca W. Doerge, Robert A. Martienssen
<b>Affiliations:</b>	Cold Spring Harbor Laboratory, New York USA
<b>Abstract Title:</b>	Epigenetic Natural Variation in <i>Arabidopsis thaliana</i>
<b>Abstract Text:</b>	<p>Cytosine methylation of repetitive sequences is widespread in plant genomes, occurring in both symmetric (CpG and CpNpG) as well as asymmetric sequence contexts. We used the methylation-dependent restriction enzyme McrBC to profile methylated DNA using tiling microarrays of <i>Arabidopsis</i> Chromosome 4 in two distinct ecotypes, Columbia and Landsberg <i>erecta</i>. We also used comparative genome hybridization to profile copy number polymorphisms. Repeated sequences and transposable elements (TEs), especially long terminal repeatretrotransposons, are densely methylated, but one third of genes also have low but detectable methylation in their transcribed regions. While TEs are almost always methylated, genic methylation is highly polymorphic, with half of all methylated genes being methylated in only one of the two ecotypes. A survey of loci in 96 <i>Arabidopsis</i> accessions revealed a similar degree of methylation polymorphism. Within-gene methylation is heritable, but is lost at a high frequency in segregating <math>F_2</math> families. Promoter methylation is rare, and gene expression is not generally affected by differences in DNA methylation. Small interfering RNA are preferentially associated with methylated TEs, but not with methylated genes, indicating that most genic methylation is not guided by small interfering RNA. This may account for the instability of gene methylation, if occasional failure of maintenance methylation cannot be easily restored.</p>
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session 3 - Epigenetics: Small RNA Biogenesis and Chromatin

<b>Contact Person:</b>	Blake C. Meyers
<b>Email:</b>	<a href="mailto:meyers@dbi.udel.edu">meyers@dbi.udel.edu</a>
<b>Authors:</b>	Blake C. Meyers, Kan Nobuta, Cheng Lu, Manoj Pillay, Roli Shrivastava, Dong-Hoon Jeong, Amit Hetawal, Mario Arteaga-Vazquez, Vicki Chandler, Pamela Green
<b>Affiliations:</b>	University of Delaware, Newark USA
<b>Abstract Title:</b>	Deep transcriptional profiling of plant small RNAs
<b>Abstract Text:</b>	<p>Small RNAs such as miRNAs and siRNAs are a powerful regulatory force in most eukaryotes because they can function to shut off genes at multiple levels. Deep sequencing of the small RNA component of the transcriptome is an important step toward elucidating the impact of small RNAs on individual genes and the genome as a whole. We have developed and applied small RNA profiling methods based on novel parallel sequencing technologies, including massively parallel signature sequencing (MPSS), 454 Life Science's pyrosequencing technology (454) and Illumina's "sequencing-by-synthesis" (SBS). Using these approaches, we have identified more than 75,000 different small RNA sequences from Arabidopsis (<a href="http://mpss.udel.edu/at">http://mpss.udel.edu/at</a>). By analyzing an <i>rdi2</i> loss-of-function mutant using MPSS and 454, we characterized the complement of miRNAs expressed in Arabidopsis inflorescence to considerable depth. Nearly all known miRNAs were enriched in this mutant and we identified new miRNAs. More recently, we have been analyzing the small RNA component of grass species, particularly rice (<a href="http://mpss.udel.edu/rice">http://mpss.udel.edu/rice</a>) but also in maize. In maize, we've examined the small RNA complement of wildtype and a mutant of the <i>mop1</i> (mediator of paramutation1) gene, and these data are providing insights into the small RNA populations present in complex plant genomes.</p>
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session 3 - Epigenetics: Small RNA Biogenesis and Chromatin

<b>Contact Person:</b>	Rebecca W. Doerge
<b>Email:</b>	<a href="mailto:doerge@purdue.edu">doerge@purdue.edu</a>
<b>Authors:</b>	R.W. Doerge
<b>Affiliations:</b>	Purdue University, West Lafayette USA
<b>Abstract Title:</b>	Statistical Issues in the Analysis of Epigenetic Data
<b>Abstract Text:</b>	<p>Epigenomic changes have been studied in the model plant organism Arabidopsis using DNA microarray technology. Proof of concept for this approach was established analytically using statistical methods based on linear models that test hypotheses of both methylation changes and histone modifications (ChIP-Chip) between two Arabidopsis mutants known to be different in their heterochromatic structure. Although there are similarities (e.g., array, dye, treatment effects) in the statistical models that are used to test differential (gene) expression changes, testing for epigenomic modifications is quite different, and is a good example of when testing the incorrect hypothesis will lead to the wrong conclusion. The statistical issues surrounding the identification of statistically significant epigenomic changes will be discussed for the purpose of illustrating the differences between testing differential gene expression and epigenomic modifications.</p>
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session 3 - Epigenetics: Small RNA Biogenesis and Chromatin

<b>Contact Person:</b>	Xuemei Chen
<b>Email:</b>	<a href="mailto:xuemei.chen@ucr.edu">xuemei.chen@ucr.edu</a>
<b>Authors:</b>	Xuemei Chen
<b>Affiliations:</b>	University of California, Riverside, CA USA
<b>Abstract Title:</b>	microRNA biogenesis in Arabidopsis
<b>Abstract Text:</b>	<p>We are interested in how microRNAs (miRNAs) are produced, modified, and degraded in plants. We have previously demonstrated that plant miRNAs are methylated on the 2' OH of the 3' terminal ribose by the methyltransferase protein HEN1. The methyl group protects miRNAs from an uridylation activity and an exonuclease activity that target the 3' OH. From a genetic suppressor screen using the weak <i>hen1-2</i> allele, we isolated mutations in the largest and second largest subunits of pol IVa that restore miRNA methylation in the <i>hen1-2</i> background. I will present evidence that HEN1 and pol IVa have antagonistic activities in miRNA biogenesis and that one role of methylation is to protect miRNAs from the activities of pol IVa.</p>
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Monday, May 21, 2007

Session 3 - Epigenetics: Small RNA Biogenesis and Chromatin

<b>Contact Person:</b>	Xiujie Wang
<b>Email:</b>	<a href="mailto:xiwang@genetics.ac.cn">xiwang@genetics.ac.cn</a>
<b>Authors:</b>	Xiujie Wang
<b>Affiliations:</b>	Institute of Genetics and Developmental Biology, CAS, China
<b>Abstract Title:</b>	Computational Identification of Natural Antisense Transcripts in <i>Arabidopsis thaliana</i>

### Abstract Text:

Natural antisense transcripts (NATs) are endogenous RNA molecules with sequence complementarity to other RNAs (sense transcripts). Natural antisense transcripts can be classified into *cis*-NATs and *trans*-NATs according to their genomic origins. Emerging lines of evidence have shown that NATs play important roles in the regulation of many gene expression processes, such as transcriptional exclusion, RNA interference, alternative splicing, DNA methylation, RNA editing and X-chromosome inactivation. There are also reports that malfunctions of antisense transcripts can cause some human diseases. Genome-wide studies using computational and experimental methods have shown that about 5% - 10% of genes' products in mammals and plants have *cis*-NATs, with the information of *trans*-NATs unavailable yet.

Using computational methods to analyze the available genome sequence and full-length cDNAs, we have identified over 1,300 *cis*- and *trans*-NAT pairs in *Arabidopsis thaliana*, respectively. The antisense relationships of some NAT pairs were confirmed using RNA secondary structure prediction and gene expression data. We also explored the potential roles of natural antisense transcripts in regulating RNA interference, gene imprinting and alternative splicing. The interlaced relationships observed in some *cis*- and *trans*- NAT pairs suggest that antisense transcripts could be involved in complex regulatory networks in eukaryotes.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

### Session 4- Heterosis: From Theories and Models to Applications

<b>Contact Person:</b>	Qixin Sun
<b>Email:</b>	<a href="mailto:qxsun62@public.bta.net.cn">qxsun62@public.bta.net.cn</a>
<b>Authors:</b>	Qixin Sun
<b>Affiliations:</b>	China Agricultural University, Beijing China
<b>Abstract Title:</b>	Genetic and molecular basis of heterosis in crop plants—A summary report of heterosis project in China

#### Abstract Text:

Hybrid cultivars have been used commercially in many crop plants, and have made significant contributions to the world food supply (Duvick, 1997), however, the genetic and molecular basis of heterosis remains to be revealed. A national heterosis project was initiated in China in 2001 aiming to understand genetic and molecular basis of heterosis. The genetic basis of heterosis of an elite rice hybrid was investigated by using an 'immortalized F<sub>2</sub>' population. The analyses were conducted making use of a linkage map comprising 231 segregating molecular marker loci covering the entire rice genome. Heterotic effects were detected at 33 loci for the four traits with modified composite interval mapping. The heterotic loci showed little overlap with quantitative trait loci for trait performance, suggesting that heterosis and trait performance may be conditioned by different sets of loci. Large numbers of digenic interactions were resolved by using two-way ANOVA and confirmed by randomization tests. All kinds of genetic effects, including partial-, full-, and overdominance at single-locus level and all three forms of digenic interactions (additive by additive, additive by dominance, and dominance by dominance), contributed to heterosis in the immortalized F<sub>2</sub> population, indicating that these genetic components were not mutually exclusive in the genetic basis of heterosis. Heterotic effects at the single-locus level, in combination with the marginal advantages of double heterozygotes caused by dominance by dominance interaction at the two-locus level could adequately explain the genetic basis of heterosis in Shanyou 63.

Although all the genes in hybrid are inherited from its two parental inbreds, hybrid performance or phenotype can be quite different from its parents, or demonstrating heterosis. Therefore, it is reasonable to speculate that changes in gene expression may occur in hybrids as compared to its parental inbreds, and such changes, if any, should be responsible for the heterosis observed in the F<sub>1</sub> hybrid. Differential gene expression patterns were observed between hybrids and their parental inbreds, and by using diallel crosses, our studies indicated that the differential gene expression patterns in leaves were correlated with heterosis for agronomic traits in rice and wheat, which suggested that these differentially expressed genes could play important roles in heterosis. Large scale identification and characterization indicated the differentially expressed genes are involved in diverse biological processes, including carbohydrate metabolism, lipid metabolism, energy metabolism, amino acid metabolism, translation, protein degradation, cellular information processing,, transcription, signal transduction, plant defense and transportation. By constructing nearly isogenic lines (NILs) that differ only at

a single quantitative trait locus (QTL), a yield-improving QTL *qGY2-1* in rice was mapped to a 102.9-kb region on rice chromosome 2. Comparison analysis of the genomic sequences in the mapped QTL region between the donor (Dongxiang wild rice, *Oryza rufipogon* Griff.) and recurrent (Guichao2, *Oryza sativa* ssp. *indica*) parents identified the haplotypes of a leucine-rich repeat receptor kinase gene cluster, which showed extensive allelic variation. More importantly, allelic expression variations were detected in this gene cluster, in which some genes gave unequal expression of alleles in rice hybrids. Further functional characterization of these differentially expressed genes, in combination of elucidating the regulatory mechanisms of the differential gene expression should shed lights on understanding of the molecular basis of heterosis in crop plants.

**Session Notes:**

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

Session 4-Heterosis: From Theories and Models to Applications

<b>Contact Person:</b>	Jinling Meng
<b>Email:</b>	<a href="mailto:jmeng@mail.hzau.edu.cn">jmeng@mail.hzau.edu.cn</a>
<b>Authors:</b>	Donghui Fu, Wei Qian, Jun Zoiu, Chunyu Zhang
<b>Affiliations:</b>	Huazhong Agricultural University, Wuhan, China, 430070
<b>Abstract Title:</b>	Exploring fixed and intersubgenomic heterosis assisted with an A <sup>r</sup> introgressive genetic map of <i>Brassica napus</i>

### Abstract Text:

*Brassica rapa* (A<sup>r</sup>A<sup>r</sup>, 2n = 20) plays an important role in widening germplasm of *B. napus* (A<sup>n</sup>A<sup>n</sup>C<sup>n</sup>C<sup>n</sup>, 2n = 38) and exploiting intersubgenomic heterosis between natural *B. napus* and new-typed *B. napus* created by introgressing component of A<sup>r</sup> genome from *B. rapa*. A RIL population of new-typed *B. napus*, consisting of 138 lines, was developed by successive selfing a F<sub>2</sub> plant of backcrossing, (*B. napus* × *B. rapa*) × *B. rapa*. A linkage map was constructed with 410 SSR markers which were grouped into 24 linkage groups (LGs) and 17 of them were identical with the international reference map of *B. napus*. Two third of recombination events was found between A<sup>r</sup>/A<sup>n</sup> subgenomes and one third of recombination events was occurred among homoeologous chromosomes between A<sup>n</sup>/C<sup>n</sup> genomes. To test the phenotypic contribution of A<sup>r</sup>-allele introgression, RIL population was grown in the field for two years for the yield trait evaluation. Eleven QTL were detected from each year explaining 8-21% and 6-20% of phenotypic variation, respectively. Thirty percent of QTL with positive contribution to phenotypic variation from A<sup>r</sup>-allele could be fixed and heritable, which are helpful to further analysis the "fixed heterosis". Lines from the RIL population were also back-crossed to the parent of *B. napus* resulting a backcrossed (BC) population. Intersubgenomic heterosis in seed yield and biomass yield were observed from the BC population with a two-year's field trail compared with RIL population. Six and seven main-effected QTL for seed yield were detected from BC population explaining phenotypic variation from 9% to 18% and 7% to 10% in two years respectively. In addition, much more QTL with small phenotypic effect were repeatedly detected in the two years. The relationship of heterosis QTL/changed genome fragment/ genes underneath will be discussed in the meeting.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

### Session 4- Heterosis: From Theories and Models to Applications

<b>Contact Person:</b>	Daniel Zamir
<b>Email:</b>	<a href="mailto:zamir@agri.huji.ac.il">zamir@agri.huji.ac.il</a>
<b>Authors:</b>	Semel Y, Krieger U, Gur A, Lippman Z, Zamir D
<b>Affiliations:</b>	The Hebrew University of Jerusalem, Rehovot Israel
<b>Abstract Title:</b>	Overdominant QTL and Heterosis in Tomato Interspecific Introgression Lines

#### Abstract Text:

Agricultural heterosis was observed nearly 100 years ago when hybrid plants out yielded their inbred parents and today this “hybrid vigor” is a major provider for global food production. The genetic basis of heterosis has been debated with respect to the relative importance of dominant, overdominance and epistasis where one of the problems has been the use of whole genome segregating populations where interactions often mask the effects of individual quantitative trait loci (QTL). To partition heterosis into its mode of inheritance components we employed a population of tomato (*Solanum lycopersicum*) introgression lines (ILs), which carry single marker-defined chromosome segments from the distantly related wild species *S. pennellii*. Combined quantitative genetic and phenomic analysis of ILs, which is largely devoid of epistasis, revealed 841 QTL for 35 diverse traits that were measured in the field on homozygous and heterozygous plants. The mode of inheritance of genomic regions associated with greater reproductive fitness was characterized by the prevalence of overdominance, which was virtually absent for the non-reproductive traits. We show that the alliance of overdominance with improved reproductive fitness is a general attribute of sexually reproducing organisms and propose that this naturally selected association is the ancestral basis for heterosis for improved agricultural yields.

#### Session Notes:

## Speaker Abstracts ICPHE 2007

Wednesday, May 23, 2007

Session 5 – Polyploidy: Old Events, New Themes and Future Perspectives 1

<b>Contact Person:</b>	Malika L. Ainouche
<b>Email:</b>	<a href="mailto:malika.ainouche@univ-rennes1.fr">malika.ainouche@univ-rennes1.fr</a>
<b>Authors:</b>	Malika L. Ainouche
<b>Affiliations:</b>	University of Rennes 1 CNRS UMR France
<b>Abstract Title:</b>	Evolutionary consequences of recurrent hybridization and polyploidy in invasive <i>Spartina</i> species (Poaceae)

### Abstract Text:

Genus *Spartina* (Chloridoideae, Poaceae) offers particular opportunities to investigate the consequences of hybridization and genome duplication (allopolyploidy) at different evolutionary time scales in natural populations. This genus exhibits various ploidy levels (from tetraploid to dodecaploid), and several examples of reticulate evolution with important ecological and evolutionary consequences, such as invasive hybrids or the recent formation of the salt marsh allopolyploid species *Spartina anglica* that displays larger ecological amplitude than its parental species and that has rapidly expanded in range (western Europe, America, China, Australia). As genome duplication results in functional redundancy, differential selective pressures may act on the duplicated gene copies that are critical for the subsequent variation, retention, or loss of the duplicated copies. We use the *Spartina* system to explore the evolutionary dynamics of genes duplicated by polyploidy in the short term and the long term of evolutionary time scale at different ploidy levels and to investigate the genetic and epigenetic consequences of allopolyploidy in newly formed species.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Wednesday, May 23, 2007

Session 5 – Polyploidy: Old Events, New Themes and Future Perspectives 1

<b>Contact Person:</b>	Joseph Chris Pires
<b>Email:</b>	<a href="mailto:piresjc@missouri.edu">piresjc@missouri.edu</a>
<b>Authors:</b>	J. Chris Pires
<b>Affiliations:</b>	University of Missouri, Columbia, Missouri USA
<b>Abstract Title:</b>	Ancient and recent polyploidy in <i>Brassica</i>
<b>Abstract Text:</b>	<p>Crops of the Brassicaceae family display an amazing diversity of plant architectures; <i>Brassica oleracea</i> alone includes several morphotypes: broccoli, cabbage, cauliflower, kale, and brussel sprouts. The diploid Brassicas have genomes that contain ancient duplication event(s) that occurred after the divergence of the Brassica and Arabidopsis lineages around 14-20 million years ago. Genome duplications, diploidization, and subsequent functional diversification in diploid Brassicas have been recognized as the substrate leading to the phenotypic diversity exhibited by <i>Brassica oleracea</i>. We have examined homeologous duplicated regions of the <i>B. oleracea</i> genome using real time RT-PCR in different tissues across diverse <i>B. oleracea</i> morphotypes and found variation in gene expression levels among the various morphotypes. In a second study, we investigated recent polyploidy events by analyzing nearly 50 independently derived and genetically identical resynthesized <i>B. napus</i> allopolyploids generated by hybridization of doubled haploid <i>B. rapa</i> and <i>B. oleracea</i> parents. The allopolyploid lines were analyzed, along with parental lines, at both the S<sub>0</sub> and S<sub>5</sub> generations for changes in genome structure, gene expression, and phenotype. An analysis of this scale had not been previously performed on such a large collection of polyploids derived from one set of parents. Results from analysis of the S<sub>5</sub> generation show that genetic changes occur among the lines as they are advanced, and these changes are correlated with the loss of gene transcripts and increased phenotypic variation. Specific genome regions appear to be predisposed to genetic change, and our evidence suggests that many of the genetic changes are due to non-reciprocal transpositions between specific pairs of homoeologs. This type of genome change has occurred also in natural <i>B. napus</i>; and thus, it may be an important cause of phenotypic variation within this species.</p>
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Wednesday, May 23, 2007

Session 5 – Polyploidy: Old Events, New Themes and Future Perspectives 1

<b>Contact Person:</b>	Brian Dilkes
<b>Email:</b>	<a href="mailto:bdilkes@ucdavis.edu">bdilkes@ucdavis.edu</a>
<b>Authors:</b>	Brian Dilkes, Caroline Josefsson, Isabelle Henry, Luca Comai
<b>Affiliations:</b>	University of California at Davis, USA
<b>Abstract Title:</b>	The ploidy hybridization barrier is controlled by a genetic network in <i>A. thaliana</i>

### Abstract Text:

Polyploidy is frequently associated with plant speciation and domestication. Indeed, shifts in ploidy can result in reproductive isolation via postzygotic lethality and permit divergence of the two isolated populations. Using *Arabidopsis thaliana* natural variation and genomic resources we have determined the genetic basis of variation in interploidy crossing success. Remarkably, polyploid derivatives of different ecotypes of *A. thaliana* vary many-fold in their degree of reproductive isolation from diploids. Dissection of the genetic architecture of this variability via QTL analyses has identified both maternally and paternally derived genetic controls. The genes that underlie QTL on both sides are dosage-sensitive regulators of seed viability. Work to determine the identity of genes involved in the maternal control of the ploidy barrier has identified a genetic pathway controlling seed development as a critical regulator of interploidy seed failure. Some of the genes appear to control survival of seeds via the maternal sporophytic tissues, while others affect survival via gametic or post-fertilization expression. Consistent with some expectations, the genes affecting interploidy lethality also influence the species barrier. Thus, both interploidy and interspecies barriers can be sensitive to the doses of the same factors.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

Session 6- Polyploidy and Speciation: Advantages and Disadvantages

<b>Contact Person:</b>	Luca Comai
<b>Email:</b>	<a href="mailto:icomai@ucdavis.edu">icomai@ucdavis.edu</a>
<b>Authors:</b>	Luca Comai, Brian Dilkes, Caroline Josefsson, Isabelle Henry, Harkamal Walia, and Margaret Woodhouse
<b>Affiliations:</b>	451 E. Health Sciences Drive UC Davis, CA USA
<b>Abstract Title:</b>	Genetics and molecular mechanisms affecting polyploidy-dependent speciation

### Abstract Text:

Genome-wide duplication events are thought to have contributed to diversification of plants. We study incipient and recent polyploidization to understand the molecular mechanisms involved. Using the *Arabidopsis* system we analyze the genetic components that lead to successful hybridization and establishment of polyploids. I will describe loci that affect dosage-sensitive responses important in the success of interploidy and interspecific crosses. These loci are consistent with the involvement of both chromatin regulation in the hybrid endosperm and maternal contribution to seed development. I will also describe a genetic experiment to map loci responsible for adaptation in the establishment of the extant allopolyploid *Arabidopsis suecica*. The elucidation of mechanisms critical for polyploidization will contribute to a better understanding of the factors critical to this evolutionary path.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

Session 6- Polyploidy and Speciation: Advantages and Disadvantages

<b>Contact Person:</b>	Rod J. Scott
<b>Email:</b>	<a href="mailto:bssrjs@bath.ac.uk">bssrjs@bath.ac.uk</a>
<b>Authors:</b>	Melissa Spielman, Brian Dilkes, Luca Comai, Dan Ashfield and Rod Scott
<b>Affiliations:</b>	University of Bath, Claverton Down, Bath UK
<b>Abstract Title:</b>	Triploid block in <i>Arabidopsis thaliana</i>
<b>Abstract Text:</b>	<p>The transfer of desirable traits from wild relatives to crop plants is often complicated by operation of hybridization barriers. Post-fertilization barriers are frequently associated with abnormal development of the endosperm, which leads to seed abortion. In <i>Arabidopsis</i> species this type of barrier is due to genomic imprinting (Scott et al., 1998; Bushell et al., 2000). It has been proposed that imprinting also accounts for 'triploid block' in which crosses between diploid (2x) and tetraploid (4x) plants of the same or closely related species fail due to abnormal endosperm development (Haig and Westoby, 1991). We established that in <i>Arabidopsis thaliana</i>, several accessions including Ler produce viable seed when diploids and tetraploids are crossed, although crosses between diploids and hexaploids fail. In contrast, the widely used Col-0 accession operates triploid block in crosses between 2x seed parents and 4x pollen parents. Strikingly, however, seed abortion is largely rescued when a 2x Ler seed parent is substituted for Col-0. Exploiting this difference in crossing behaviour we have mapped a modifier of the triploid block response to a region on chromosome 2 which contains the <i>TRANSPARENT TESTA GLABRA 2 (TTG2)</i> locus. The <i>ttg2-1</i> mutation is known to affect seed development (Johnson et al., 2002; Garcia et al., 2005) and we have found that <i>ttg2</i> mutations in the Ler and the Col backgrounds improve seed viability in crosses with 4x Col-0 pollen parents.</p> <p>Tests with 2x seed parents in other accessions show Col seed parent is not unique in failure to overcome triploid block. For example Bur-0 and Perm behave as Col. Here we will also report the results of an investigation of the relationship between the behaviour of these and several other accessions in crosses with the Col 4x pollen parent (inter-accession interploidy crosses) and their behaviour in intra-accession interploidy (2xX4x) crosses.</p> <p>The various strands of investigation will be brought together in an attempt to explain the related phenomena of triploid block, genomic imprinting, and Endosperm Balance Number.</p>
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

Session 7- Polyploidy and Speciation: Advantages and Disadvantages

<b>Contact Person:</b>	Bikram Gill
<b>Email:</b>	<a href="mailto:bsgill@ksu.edu">bsgill@ksu.edu</a>
<b>Authors:</b>	BS Gill, L. Huang, WL Li, JD Faris
<b>Affiliations:</b>	Kansas State University, Fargo, ND USA
<b>Abstract Title:</b>	What have we learned from genetic, cytogenomic and evolutionary analysis of allopolyploid wheat?

### Abstract Text:

The A, B/G and D diploid donors of tetraploid (*Triticum turgidum* (AABB), and *T. timopheevii* (AAGG) and hexaploid wheats (*T. aestivum* (AABBDD) and *T. zhukovskyi* (A<sup>m</sup>A<sup>m</sup>AAGG) diverged from a common ancestor ca 3 millions years ago. The A and B diploid donors hybridized in nature to produce tetraploid wheat ca 0.3 million years ago. Hexaploid *T. aestivum* arose from hybridization of cultivated tetraploid wheat *T. turgidum* and wild diploid *Aegilops tauschii* (DD) growing as a weed in the crop under domestication ca 8,000 years ago. Hexaploid *T. zhukovskyi* arose from hybridization of *T. timopheevii* and *T. monococcum* (A<sup>m</sup>A<sup>m</sup>) during the past hundred years under cultivation. The natural populations of wild tetraploid wheat exhibit extensive chromosomal polymorphisms over the geographic range of the species in the fertile crescent and Transcausia. These genotypes are evolving in response to local environmental conditions. However, they also display a species-specific chromosomal rearrangement marking a bottleneck in polyploid wheat speciation. Recently several genes have been cloned in wheat and new data are emerging on the comparative structure and expression of homoeoloci as modulated by polyploidy. These results will be discussed in the context of polyploidy-driven gene and genome evolution and speciation.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

### Session 7- Polyploidy and Speciation: Advantages and Disadvantages

<b>Contact Person:</b>	Bao Liu
<b>Email:</b>	<a href="mailto:baoliu@nenu.edu.cn">baoliu@nenu.edu.cn</a>
<b>Authors:</b>	Bao Qi, Jinsong Pang, Moshe Feldman and Bao Liu
<b>Affiliations:</b>	Northeast Normal University, Changchun China
<b>Abstract Title:</b>	Transcriptome analysis in newly synthesized allohexaploid wheat
<b>Abstract Text:</b>	<p>Common wheat, <i>Triticum aestivum</i> L. (genome AABBDD), being a recently formed allohexaploid species (ca. 8500 year-old), is a staple food crop as well as a textbook example of speciation via allopolyploidy. Accumulated recent evidence indicates that allopolyploidy in wheat is accompanied by an array of genomic instability, epigenetic modification and alterations in gene expression, which often occur at the onset of allopolyploid formation. To further study gene expression changes associated with allopolyploidy in wheat from a global perspective, we employed the wheat Affymetrix Microarray system to analyze possible transcriptome changes in leaf tissue of three synthetic allohexaploid wheat lines (genome AABBDD, analogous to common wheat) that were previously shown to have undergone rapid elimination of non-coding and chromosome- or genome-specific sequences (Ozkan et al. 2001). We found that compared with the calculated midparent values or parental mixtures, all three synthetic wheat lines exhibited transcripts that are deviated from parental additive gene expression, which ranged from 3-7% across the three lines. Both up- and down-regulated transcripts were detected, with the latter being slightly more than the former. Most of the non-additive transcripts were those that showed expression divergence between the parental lines, an observation in line with previous findings in <i>Arabidopsis</i> (Wang et al. 2004). An interesting observation is that the proportions of non-additive transcripts that were shared between any two synthetic allohexaploid lines is very small (&lt;10%), nonetheless, the frequencies are significantly higher than expected on a random basis, thus suggesting a strong effect of genetic context on differential expression of parental transcripts in an allopolyploid genome. A preliminary gene orthology analysis indicates that of the annotated genes that showed non-additive expression in the allohexaploid lines, diverse biological functions were involved such as cellular physiological processes and metabolism, stress response, disease resistance and pathogenesis, among others. Although the number of these genes differ among the three lines, their proportions are very similar, suggesting that the majority of the non-additive expressions in the allohexaploid lines are likely non-stochastic. Physical allocation based on Blast analysis against mapped wheat ESTs indicated that the transcripts exhibiting non-additive expressions distributed throughout the wheat genome. Implications of expression alterations in allohexaploid wheat relative to its parents in the context of functional genome evolution in polyploid will be discussed.</p>

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

### Session 7- Epigenetics: DNA Methylation and Transcriptional Silencing

<b>Contact Person:</b>	Hugh G. Dickinson
<b>Email:</b>	<a href="mailto:hugh.dickinson@plants.ox.ac.uk">hugh.dickinson@plants.ox.ac.uk</a>
<b>Authors:</b>	L.M. Costa, Hugh G. Dickinson, M.S. Evans and J.F. Gutiérrez-Marcos
<b>Affiliations:</b>	University of Oxford, Oxford, Oxfordshire UK
<b>Abstract Title:</b>	Differential epigenetic control of imprinted gene expression in maize endosperm

#### Abstract Text:

A combination of gene dosage and genomic imprinting in the endosperm results in a strong maternal control over early seed development in maize. The recently duplicated *Fie1* and *Fie2* sequences, which encode Polycomb Group transcription factors and both expressed solely from the maternal alleles early in development. Reporter constructs, which behave in an imprinted manner, reveal that monoallelic expression is likely to be regulated by differentially methylated regions (DMRs) upstream of the coding regions. Demethylation of this DMR at other points in the plant life history results in gene expression, confirming this role for the DMR in gene regulation. While the DMRs of *Fie1* receive their asymmetric methylation in the gametes, differential methylation of these regions in *Fie2* only takes place in the primary endosperm cells, after fertilisation. The male and female alleles must thus be differentially 'marked', such that only the male is methylated post fertilisation. The nature of this mark, and the reason which these two *Fie* genes have different imprinting systems, will be discussed.

#### Session Notes:

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

### Session 7- Epigenetics: DNA Methylation and Transcriptional Silencing

<b>Contact Person:</b>	Zhizhong Gong
<b>Email:</b>	<a href="mailto:gongzz@cau.edu.cn">gongzz@cau.edu.cn</a>
<b>Authors:</b>	Zhizhong Gong
<b>Affiliations:</b>	China Agricultural University, Beijing China
<b>Abstract Title:</b>	Transcriptional gene silencing and heterochromatin spreading in <i>Arabidopsis</i>

#### Abstract Text:

Mutations in the DNA demethylation protein ROS1 cause hypermethylation of the RD29A promoter and transcriptional gene silencing of the *RD29A-Luciferase (LUC)* transgene. The heterochromatin might spread to cover the linked transgene *35-NPTII* and result in its silencing in *Arabidopsis thaliana*. In order to find out whether the gene silencing mechanisms are same or not between silenced RD29A-LUC and silenced 35S-NPTII, we screened for suppressors of *ros1* using the silenced 35S-NPTII and RD29A-LUC as markers and identified several *ror* mutants (suppressor of *ros1*). The isolated genes can be divided into three different groups: (1) The mutations only reactivate the silenced 35S-NPTII gene but not the RD29A-LUC in the *ros1* mutant. (2) The mutations reactivate both the silenced 35S-NPTII gene and the RD29A-LUC in the *ros1* mutant. (3) The mutations only reactivate the silenced RD29A-LUC but not silenced 35S-NPTII gene. Most mutants also show hypersensitive to DNA damage reagents, and suggesting that the corresponding genes might be involved in DNA repair. Our work suggests that the gene silencing mechanisms in RD29A-LUC and 35S-NPTII loci are different.

#### Session Notes:

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

### Session 7- Epigenetics: DNA Methylation and Transcriptional Silencing

<b>Contact Person:</b>	Jiming Jiang_
<b>Email:</b>	jjiang1@wisc.edu
<b>Authors:</b>	Jiming Jiang
<b>Affiliations:</b>	University of Wisconsin-Madison, Madison, Wisconsin USA
<b>Abstract Title:</b>	Transcription of centromeric DNA sequences in rice
<b>Abstract Text:</b>	
<p>The centromeres in most model eukaryotes are composed of highly repetitive DNA sequences. We have recently demonstrated that several rice centromeres are composed of complex DNA, including both centromere-specific retrotransposons (CRR elements) and satellite repeats (CentO satellite), as well as single copy sequences. Active genes were found in the functional domains of the centromeres of rice chromosomes 3 and 8. These active genes are expressed in several rice tissues and display histone modification patterns similar to those located in rice euchromatin. The CentO satellite repeats and the CRR elements are also transcribed. However, the overall transcription levels of these centromere-specific repetitive DNA elements are low and the transcripts appear to be derived from relatively few loci. Small RNA derived from CentO and specific CRR subfamilies were detected, suggesting that these repeats may play a role in formation and maintenance of centromeric chromatin. These results are parallel to several recent reports in animal species that centromeric chromatin accommodates normal transcription and shows characteristics typical to euchromatin.</p>	
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

### Session 7- Epigenetics: DNA Methylation and Transcriptional Silencing

<b>Contact Person:</b>	Ming-Bo Wang
<b>Email:</b>	<a href="mailto:ming-bo.wang@csiro.au">ming-bo.wang@csiro.au</a>
<b>Authors:</b>	David Smolilo, Lei Wang, Thomas Finn, Jing Chen, Shaun Curtin, Limin Wu, Abed Chaudhury, Peter Waterhouse, Liz Dennis and Ming-Bo Wang
<b>Affiliations:</b>	CSIRO Division of Plant Industry, Canberra, ACT Australia
<b>Abstract Title:</b>	The effect of plant ploidy on transgene-induced silencing
<b>Abstract Text:</b>	
<p>Polyploidization is a naturally occurring phenomenon and plays an important role in genome evolution and speciation of plants. Recent studies have revealed that polyploidization is associated with epigenetic modifications that can result in changes in gene expression. The objective of this project was to examine if polyploidization affects the efficiency of transgene-induced silencing in plants. Diploid (2N) and tetraploid (4N) Arabidopsis were transformed with sense, antisense and hpRNA constructs. Analysis of a large number of transgenic lines showed that transgene-induced silencing was significantly less efficient in the 4N background than in the 2N background. Expression analysis of the transgenic populations revealed that the level of transgene expression was generally lower in 4N than in 2N plants. Also, transgenes from the 2N plants were consistently down-regulated when crossed into wild-type 4N plants, and the silencing induced by the transgenes was significantly released. These results suggest that the reduced gene silencing in the 4N plants was due to decreased expression of the silencing inducer RNAs from the transgenes. The transgenes in the 4N background showed more widespread methylation than those in the 2N background. Consistent with the increased transgene methylation, an RT-PCR analysis revealed that several of the key factors known to be involved in RNA-directed DNA methylation were up-regulated in the 4N background. Taken together, our results suggest that transgenes are more likely to be methylated when introduced into polyploid plants, resulting in more frequent transcriptional repression and, in the case of silencing inducer transgenes, less efficient silencing of target genes.</p>	
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

### Session 7- Epigenetics: DNA Methylation and Transcriptional Silencing

<b>Contact Person:</b>	Naoki Kishimoto
<b>Email:</b>	<a href="mailto:naoki@nias.affrc.go.jp">naoki@nias.affrc.go.jp</a>
<b>Authors:</b>	Naoki Kishimoto, Fumiko Fujii, Hideshi Yasui, Kazuyuki Doi, Atsushi Yoshimura, Kazuko Toyoshima, Keiko Takeuchi, Zenpei Shimatani, Akiko Hashimoto, Yuko Nagata, Kanako Shimbo, Jianzhong Wu, Koji Suzuki, Keiichi Kojima, Masahiro Ishikawa, Junshi Yazaki, Takuji Sasaki <sup>1</sup> and Shoshi Kikuchi
<b>Affiliations:</b>	Division of Plant Sciences, Tsukuba, Ibaraki Japan
<b>Abstract Title:</b>	Gene dosage effect in primary trisomics: Transcriptome analysis of rice trisomic lines carrying a different extra chromosome

#### Abstract Text:

A type of aneuploidy, trisomy, in which cells have an abnormal number of chromosomes ( $2n = 2x+1$ ), results in significant morbidity and mortality. The mechanisms by which the abnormal number (1.5 times) of normal genes located on the chromosome leads to cellular dysfunction and the specific features of various trisomic syndromes are not well understood. Primary trisomy ( $2n = 2x+1$ ) results in significant physiological and morphological abnormalities. In rice (*Oryza sativa*;  $2n = 2x = 24$ ), different primary trisomic individuals carrying a different chromosome as the extra chromosome show different chromosome-specific abnormalities. The mechanisms by which the abnormal number (1.5 times) of normal genes located on the trisomic chromosome causes such abnormalities are not known. Also, only trisomy 11 (trisomy of rice chromosome 11) shows four distinctive phenotypes, unlike the other trisomic types. These phenotypic features shown by each of the 4 types of trisomy 11 are basically heritable; for instance, self-pollination of a 'Pseudo-normal' plant usually produces 'Pseudo-normal' progeny and rarely produces progeny showing other epigenetic types. From primary trisomic lines of rice, we have analyzed nine lines carrying a different chromosome as the extra chromosome with our cDNA microarray system containing 8987 independent EST clones. The following lines were analyzed: trisomy 4 (shows spread tillers); trisomy 6 (shows awned spikelets); trisomy 7 (shows rolled leaves); trisomy 8 (shows erect leaves); trisomy 10 (shows small grains); four types of trisomy 11 ('Pseudo-normal' [normal-diploid-like]; 'Late heading' [extremely late flowering]; 'Coarse' [Coarse grains]; 'Spotted leaf' [brown spotted leaves]).

We compared the microarray data between trisomic ( $2x+1$ ) and disomic ( $2x$ ) sibling plants. In all of the tested lines, most (>90%) of the misregulated genes (>1.5-fold difference from disomic expression) were not located on the trisomic chromosomes. The expression profile analyses revealed clear differences among the tested trisomic lines, even among the four types of trisomy 11. On the contrary, the average levels of transcription of genes on the trisomic chromosomes in trisomic lines were increased less than 1.5-fold (<1.3-fold) compared with disomic lines. We conclude that the dosage effects for the average transcriptional levels result from the 'less than 1.5-fold increase' of

transcriptional level on the trisomic chromosomes. In addition, consistent differences in the relative expression levels among all 12 chromosomes were detected, suggesting that mechanism controlling the expression level at the genome level may act over large distances.

**Session Notes:**

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

Session 8 – Epigenetics: Small RNA, histone modifications and Development

<b>Contact Person:</b>	Xiao-Ya Chen
<b>Email:</b>	<a href="mailto:xychen@sibs.ac.cn">xychen@sibs.ac.cn</a>
<b>Authors:</b>	Xiao-Ya Chen
<b>Affiliations:</b>	Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, CAS, Shanghai China
<b>Abstract Title:</b>	Up-regulation of Transmethylation Pathway in Cotton Fiber Cells
<b>Abstract Text:</b>	<p>Cell sizes are correlated with endopolyploidy, in the sense that cells containing higher quantity of DNA appear larger. Cotton fibers undergo endoduplication and their cellular DNA content is increasing at the early stage of development. We found that global DNA methylation status is much higher in cotton fiber cells than in other types of cells. Consistently, transmethylation pathway genes <i>GhSAHH1</i> and <i>GhADK1</i>, encoding S-Adenosyl-L-homocystein hydrolas and adenosine kinase, respectively, are up-regulated in developing fiber cells, providing abundant methyl groups for DNA methylation. We further analyzed the Arabidopsis <i>SAHH</i> genes (<i>AtSAHH1</i> and <i>AtSAHH2</i>). We found that cytokinins positively regulate the expression of <i>AtSAHH1</i> and <i>AtADK1</i>, and this regulation involves the cytokinin signaling pathway, but not the purine structure. Unlike adenine and adenosine which are SAHH inhibitors, the adenine-type cytokinins have no effect on SAHH activity at protein level. Our data demonstrate a cross-talk between the SAM-dependent transmethylation and the phytohormone cytokinin.</p>
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

Session 8 – Epigenetics: Small RNA, histone modifications and Development

<b>Contact Person:</b>	Xiaofeng Cao
<b>Email:</b>	<a href="mailto:xfcao@genetics.ac.cn">xfcao@genetics.ac.cn</a>
<b>Authors:</b>	Bin Liu, XiaoFeng Cao
<b>Affiliations:</b>	Institute of Genetics and Developmental Biology, CAS, Beijing China
<b>Abstract Title:</b>	Oryza sativa DICER-LIKE Proteins Reveal a Key Role for RNA Silencing and Plant Developmen

### Abstract Text:

MicroRNAs (miRNAs) and small interfering RNAs (siRNAs) are two classes of small regulatory RNAs derived from different types of precursors processed by distinct Dicer or Dicer-like (DCL) proteins. During evolution, four Arabidopsis DCLs and six rice (*Oryza sativa*) DCLs (OsDCLs) appear to have acquired specialized functions. The Arabidopsis DCLs are well characterized, but those in rice remain largely unclear. Here we show that both knock-down and loss-of-function of rice OsDCL4, the rice homolog of Arabidopsis DCL4, led to vegetative growth abnormalities and severe developmental defects in spikelet identity. Those phenotypic alterations appeared distinct from that observed for Arabidopsis *dcl4* mutants, which only exhibited an accelerated vegetative phase-change. This phenotypic variation conferred by loss of function of DCL4 between rice and Arabidopsis suggests that siRNA processing by OsDCL4 has a wider role in plant development than that in Arabidopsis. Biochemical and genetic analysis indicated that OsDCL4 is the major dicer responsible for the 21nt siRNAs associated with inverted repeat transgenes and ta-siRNA biogenesis from endogenous *OstAS3*. We show that the biogenesis mechanism of *TAS3* ta-siRNAs is conserved but putative direct targets of OsDCL4 appear to be differentially regulated between monocots and dicots. Our results reveal a critical role of OsDCL4-mediated ta-siRNA in plant development.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

Session 8 – Epigenetics: Small RNA, histone modifications and Development

<b>Contact Person:</b>	Yijun Qi
<b>Email:</b>	<a href="mailto:qiyijun@nibs.ac.cn">qiyijun@nibs.ac.cn</a>
<b>Authors:</b>	Tao Zhao, Guanglin Li, Shijun Mi, Shan Li, Gregory J.Hannon, Xiu-Jie Wang, and Yijun Qi
<b>Affiliations:</b>	National Institute of Biological Sciences, Beijing China
<b>Abstract Title:</b>	A Complex System of Small RNAs in the Unicellular Green Alga <i>Chlamydomonas reinhardtii</i>
<b>Abstract Text:</b>	<p>Endogenous small RNAs function in RNA interference (RNAi) pathways to control gene expression through mRNA cleavage, translational repression, or chromatin modification. Plants and animals contain many microRNAs (miRNAs) that play vital roles in development, including helping to specify cell type and tissue identity. To date, no miRNAs have been reported in unicellular organisms. Here we show that <i>Chlamydomonas reinhardtii</i>, a unicellular green alga, encodes many miRNAs. We also show that a <i>Chlamydomonas</i> miRNA can direct the cleavage of its target mRNA <i>in vivo</i> and <i>in vitro</i>. We further show that the expression of some miRNAs/Candidates increases or decreases during <i>Chlamydomonas</i> gametogenesis. In addition to miRNAs, <i>Chlamydomonas</i> harbors other types of small RNAs including phased siRNAs that are reminiscent of plant trans-acting siRNAs, as well as siRNAs originating from protein coding genes and transposons. Our findings suggest that the miRNA pathway and some siRNA pathways are ancient mechanisms of gene regulation that evolved prior to the emergence of multicellularity.</p>
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Tuesday, May 22, 2007

Session 8 – Epigenetics: Small RNA, histone modifications and Development

<b>Contact Person:</b>	Yuehui He
<b>Email:</b>	<a href="mailto:yuehui@tll.org.sg">yuehui@tll.org.sg</a>
<b>Authors:</b>	Yuehui He
<b>Affiliations:</b>	National University of Singapore
<b>Abstract Title:</b>	Epigenetic regulation of flowering time in Arabidopsis
<b>Abstract Text:</b>	
<p>The developmental transition from a vegetative to a reproductive phase (<i>i.e.</i> flowering) is perhaps the most critical event in the plant life cycle. In <i>Arabidopsis thaliana</i>, several pathways form a regulatory network that integrates the endogenous development state of the plant and environmental cues (<i>e.g.</i> day length and temperature) to control the timing of the initiation of flowering. A key component in this regulatory network is FLC, a MADS box transcription factor which blocks the floral transition. Recent studies have revealed that chromatin modification plays an important role in regulating <i>FLC</i> expression. Histone H3 lysine-4 (H3K4) trimethylation and histone acetylation are associated with active <i>FLC</i> transcription, whereas histone deacetylation and histone H3 methylation at lysines 9 and 27 are associated with <i>FLC</i> repression. Previously we found that autonomous regulator <i>FLD</i> is required for deacetylation of <i>FLC</i> chromatin and represses <i>FLC</i> expression to promote floral transition, and that activation of <i>FLC</i> expression and the associated increase in H3K4 trimethylation requires the PAF1 (RNA Polymerase II Associated Factor 1)-like complex. In this talk, our recent findings on flowering-time control via regulating the H3K4 methylation state on chromatin of <i>FLC</i> and other floral repressors will be presented.</p>	
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Wednesday, May 23, 2007

Session 9 – Polyploidy: Genetic and Epigenetic Effects

<b>Contact Person:</b>	Marjori Matzke
<b>Email:</b>	<a href="mailto:marjori.matzke@gmi.oeaw.ac.at">marjori.matzke@gmi.oeaw.ac.at</a>
<b>Authors:</b>	Marjori Matzke, Bruno Huettel, Antonius J.M. Matzke
<b>Affiliations:</b>	Gregor Mendel Institute of Molecular Plant Biology, Austrian Academy of Sciences, Vienna, Austria
<b>Abstract Title:</b>	Effects of aneuploidy on chromosome structure, expression, and interphase organization in <i>Arabidopsis thaliana</i>
<b>Abstract Text:</b>	<p>Aneuploidy, defined as losses or gains of individual chromosomes to the karyotype, has a greater impact on the phenotype than whole genome duplications (polyploidy) (1). This difference can be largely explained by imbalances in dosage-sensitive regulatory genes in aneuploids. Evidence from plants and mammals also indicates that aneuploid genomes - perhaps as a consequence of the regulatory gene imbalances - are intrinsically unstable, not only numerically but also structurally and epigenetically. The reasons for this inherent instability of aneuploid genomes are poorly understood, but they are relevant for aneuploid syndromes and human cancers. Plants generally tolerate aneuploidy better than animals and provide good systems for investigating the basis of aneuploid genome instability. For this purpose, we are using <i>Arabidopsis thaliana</i> to study the effects of aneuploidy on chromosome structure, expression and interphase chromosome organization. Results of recent experiments on these topics will be presented.</p> <p>(1) Birchler, JA, Veitia RA (2007) Plant Cell 19: 395-402.</p>
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Wednesday, May 23, 2007

Session 9 – Polyploidy: Genetic and Epigenetic Effects

<b>Contact Person:</b>	Ortrun Mittelsten Scheid
<b>Email:</b>	ortrun.mittelsten_scheid@gmi.oeaw.ac.at
<b>Authors:</b>	Mittelsten Scheid, O., Baubec, T., Berlinger, M., Förster, A.M., Hetzl, J., Hödl, M., Milos, M., Pecinka, A., Wohlrab, B.
<b>Affiliations:</b>	Gregor Mendel Institute of Molecular Plant Biology, Austrian Academy of Sciences, Vienna Austria
<b>Abstract Title:</b>	Crosstalk between epialleles in polyploid Arabidopsis
<b>Abstract Text:</b>	<p>Polyploid formation is connected with rapid genomic changes and /or with epigenetic changes in gene expression patterns. While polyploidy-induced deletions, inversions and transpositions are usually irreversible and represent true genetic changes, epigenetic modifications are potentially reversible and can create epialleles that are indistinguishable at the level of DNA sequence but different with respect to gene expression and chromatin features. Epialleles can contribute significantly to epigenetic diversity and therefore likely to the adaptation potential.</p> <p>Epialleles of a transgenic selectable marker gene conferring hygromycin resistance were observed in several lines of tetraploid <i>Arabidopsis thaliana</i> derived from the same diploid progenitor. The inactive epiallele had undergone transcriptional gene silencing (TGS) while the active version was stably expressed. Both states could be stably inherited to tetraploid and diploid progeny upon selfing, but inactive epialleles reduced the expression of active epialleles in the F2 generation of crosses combining both versions in the same tetraploid (but not in a diploid) genome [1]. We study the molecular mechanisms involved in polyploidy-associated gene silencing and in the epiallelic interaction. Results from forward and reverse genetic approaches, cytological assays and analysis of chromatin features like DNA methylation [2] and histone modifications will be presented.</p> <p>References</p> <p>[1] Mittelsten Scheid, O., Afsar, K., Paszkowski, J 2003. Formation of stable epialleles and their paramutation-like interaction in tetraploid <i>Arabidopsis thaliana</i>. <i>Nat Genet.</i> 34: 450-454.</p> <p>[2] Hetzl, J., Förster, A.M., Raidl, G., Mittelsten Scheid, O. 2007. CyMATE: a new tool for methylation analysis of plant genomic DNA after bisulfite sequencing. <i>Plant J</i>, in press.</p>
<b>Session Notes:</b>	

## Speaker Abstracts ICPHE 2007

Wednesday, May 23, 2007

Session 9 – Polyploidy: Genetic and Epigenetic Effects

<b>Contact Person:</b>	Andrew Leitch
<b>Email:</b>	<a href="mailto:a.r.leitch@qmul.ac.uk">a.r.leitch@qmul.ac.uk</a>
<b>Authors:</b>	Andrew R. Leitch , K. Yoong Lim, Ales Kovarik, Roman Matyasek, Kamila Skalicka, Mark W. Chase, James J. Clarkson, Ilia Leitch, Sandy Knapp and Grandbastien MA
<b>Affiliations:</b>	Queen Mary University of London, London UK.
<b>Abstract Title:</b>	Evolution of allopolyploids in the genus <i>Nicotiana</i>

### Abstract Text:

Recent genome studies have revealed angiosperm evolution proceeds in cycles of polyploidy and diploidisation; e.g. *Arabidopsis thaliana* shows evidence of several polyploidy events in its ancestry (within ~150 my), *Oryza sativa* shows two polyploidy events (~45 Mya and ~70 Mya), and *Zea mays* one polyploidy event in ~20 My. The genus *Nicotiana* includes c. 75 species, c. 35 of which are recent allopolyploids. Using dated phylogenetic trees of *Nicotiana* (calibrated using endemics on volcanic oceanic islands of known geological age), we can estimate ages of allopolyploid species formation. To study the process of genome diploidisation, we examined synthetic allopolyploids and natural allopolyploids of varying ages.

In some synthetic tobacco allopolyploids, we observed genetic change (rDNA amplification and homogenisation, deletion of retroelements and tandem repeats from the paternally derived genome, genome translocations) perhaps stimulated by the “genomic shock” of allopolyploidy. After <0.2 my in natural tobacco, in which rDNA locus number is additive (as expected), there is more evidence of degradation of the paternally derived genome, near complete rDNA homogenisation and fixation of some translocations.

Genome diploidisation proceeds in older allopolyploids (~1 My, species of section *Polydicleae*) with loss of many rDNA loci, evolution of new satellites and parental genome homogenisation. After even longer time-frames (~5 My, species of section *Repandae*) there is considerable to near complete turnover of repeated elements within these genomes. These changes occur without change in chromosome number, but some species of the allopolyploid section *Suaveolentes* (> 10 my) have lower chromosome numbers, perhaps representing a further stage of diploidisation.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Wednesday, May 23, 2007

Session 10 – Polyploidy: Old Events, New Themes & Future Perspectives 2

<b>Contact Person:</b>	Boulos Chalhoub
<b>Email:</b>	<a href="mailto:chalhoub@evry.inra.fr">chalhoub@evry.inra.fr</a>
<b>Authors:</b>	Chagué V., Mestiri I, Charles M., Belcram H., Tanguy A-M., Coriton O., Gomes D. , Huneau C. , Boudet N. , Jahier J. and Chalhoub Boulos
<b>Affiliations:</b>	URGV (INRA-CNRS), Evry-France
<b>Abstract Title:</b>	Genetic and transcriptome modifications induced by polyploidy in the wheat species ( <i>Triticum</i> and <i>Aegilops</i> ) model

### Abstract Text:

Allopolyploidy has played a prominent role in wheat species (*Triticum* and *Aegilops*) evolution and domestication. Our objective is to precise and uncover molecular mechanisms of 'short and long-term' genomic and epigenetic changes that accompanied wheat allopolyploid formation. For this purpose, natural and newly-synthesized wheat allopolyploids are characterized using complementary approaches of genetics, cytogenetics, genomics, transcriptomics and evolution. Genome stability, meiotic behavior and structural changes, such as chromosome number variations, small or large deletions, translocations, and homoeologous recombination, were shown to be variable, depending on the combination of the genomes in the wheat allopolyploids. Large-scale transcriptome analysis show different classes of gene expression changes (up-regulated, down-regulated, silenced, activated...) and an overall higher number of expressed transcripts in the natural or synthetic wheat allopolyploids, as compared to their progenitors. These structural and functional changes as well as analysis of transposable elements activation and their possible role in genomic rearrangements will be discussed.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Wednesday, May 23, 2007

Session 10 – Polyploidy: Old Events, New Themes & Future Perspectives 2

<b>Contact Person:</b>	Pamela S. Soltis
<b>Email:</b>	<a href="mailto:psoltis@flmnh.ufl.edu">psoltis@flmnh.ufl.edu</a>
<b>Authors:</b>	Pamela S. Soltis, Douglas E. Soltis, Jennifer A. Tate, V. Vaughan Symonds, Andrew Doust, Evgeny Mavrodiev, Jin Koh, Alexandra Bigger and Kerry A. Soltis
<b>Affiliations:</b>	University of Florida, Gainesville, FL USA
<b>Abstract Title:</b>	Gene Loss in Recent Allotetraploid Species of <i>Tragopogon</i> (Compositae)

### Abstract Text:

Most extant plant lineages show evidence of at least one round of whole genome duplication. Such large-scale duplications can act as a primary source of genes for new functions and can thus be a major force in evolution. But how do allopolyploids contend with having multiple genomic copies? We are examining the fate of genes duplicated by polyploidy in recent and independently formed natural populations of *Tragopogon miscellus* and *T. mirus* (Compositae). These species have each formed multiple times during the last century in a small geographic area of the northwestern United States. Genomic and cDNA CAPS analyses of individuals from reciprocally formed populations of *T. miscellus* reveal that homeolog loss is random among individuals, but loss of the *T. dubius* copy occurs more frequently. Examination of four additional short-liguled populations of *T. miscellus* shows that loss of parental homeologs occurs for some of the same loci. In fact, many of the same loci show similar homeolog loss in *T. mirus* as well. Furthermore, "duplication-resistant" loci identified in analyses of fully sequenced model organisms show evidence of gene loss in some individuals of *T. miscellus* and of down regulation in others. In contrast, F1 hybrids are additive of their parental genomes, suggesting that polyploidization or later-generation processes are responsible for gene loss. The recent creation of synthetic polyploids allows us to determine at what stage in polyploid evolution these losses occur and provides additional opportunities to investigate the earliest stages of polyploid genome evolution.

### Session Notes:

## Speaker Abstracts ICPHE 2007

Wednesday, May 23, 2007

Session 10 – Polyploidy: Old Events, New Themes & Future Perspectives 2

<b>Contact Person:</b>	Michael Freeling
<b>Email:</b>	<a href="mailto:freeling@nature.berkeley.edu">freeling@nature.berkeley.edu</a>
<b>Authors:</b>	Freeling, M., Lyons, E., Pederson, B., Rapaka, L. and Thomas, B,C.
<b>Affiliations:</b>	University of California, Berkeley, CA. USA 94720
<b>Abstract Title:</b>	Tetraploidy, the fractionation mechanism, large genes and trends in plant evolution

### Abstract Text:

Among mutational-type saltations, tetraploidy is particularly important to evolutionary theory because the massive gene loss mechanism following tetraploidy (or any other sort of duplication) —fractionation—has the potential to remove some sorts of genes and not others. The consequence of this sort of bias is to “drive” evolution in biological directions that naturally follow increases in particular sorts of gene families or family combinations. Several research groups have shown that those genes retained following the most recent tetraploidy in the *Arabidopsis* lineage are biased toward developmental/transcriptional regulatory genes and genes that participate in multiple subunit-subunit interactions. We will show that rice, poplar and *Arabidopsis* have all retained approximately the same sorts of genes following either local or whole-genome duplication. Further, we will show that retention post-tetraploidy is often in clusters, with special genes residing in these clusters, and that clusters are expected when one homeologous chromosome is significantly more fractionated than the other; clusters emerge on the over-fractionated homeolog. Using papaya (order Brassicales) as a diploid outgroup to the *Arabidopsis* fractionated tetraploid makes it clear that the fractionation mechanism sometimes involves long deletions. This work required a special graphic tool (SynView) able to align and compare three sequences, two homeologs and the outgroup.----Subfunctionalization of cis-acting regulatory chromosome is, or recently was, the most popular explanation of over-retention of genes post tetraploidy. We use conserved noncoding sequences (CNSs) to define subfunctionalizable gene space, and then evaluate subfunctionalization critically. We show that subfunctionalization happens AFTER retention, but it is NOT likely a prominent retention mechanism. Recent work of others has shown that *Arabidopsis* genes involved in environmental response are particularly subfunctionalizable. We show that these same genes have large, CNS-rich genespaces. CNS-richness has much to do with subfunctionalizability, but little or nothing to do with whether or not a gene is retained post-tetraploidy.---- The much-reviled saltation ideas of R.B. Goldschmidt, generally rejected as “anti-population genetics” rants in the 1940’s and thereafter, will be revisited in light of comparative gene content data. References: Freeling et al. 2007, The Plant Cell, in press for April / May, and references therein.

## Poster List ICPHE 2007

No	Contact Person	Title
1.	Baige Zhao	Effects of Water-stress on Ascorbate and Glutathione in Transgenic and Non-transgenic Wheat
2.	Bing Wang	Cloning and genetic transformation of a novel rice male sterility gene OsAPT2
3.	K. Yoong Lim	Polyploid-Diploid Cycle in the genus <i>Nicotiana</i>
4.	Andrey B. Shcherban	45S rDNA evolution in a synthetic amphiploid <i>Aegilops sharonensis</i> x <i>Ae.umbellulata</i>
5.	Zujun Yang	Sequence variation of cytoplasm gene occurred in some polyploidy species of Triticeae
6.	Yong Zhang and ZhengLong Ren	Analysis of DNA methylation variation in wheat genetic background after alien chromatin introduction based on methylation-sensitive amplification polymorphism (MSAP)
7.	Zhang Yong and REN Zheng-Long	Fingerprinting Analysis of the Introgressed Lines from <i>Gossypium hirsutum</i> L. x <i>Gossypium barbadense</i> L based on AFLP Markers
8.	Milos Tanurdzic	Epigenomic profiling in diploid and tetraploid <i>Arabidopsis thaliana</i>
9.	Fateme Fadaie	A new polyploidy level for two species, <i>B. sericeous</i> Drobov. and <i>B.fasciculatus</i> Presl. in meiotic study from Iran.
10.	Zhu Jing	Acetylation modification mechanism of MSCs differentiating in vitro
11.	Yang Zujun	Genomic relationship between <i>Dasypyrum</i> and <i>Thinopyrum</i> : evidence from chromosomal distribution of LTR retrotransposon Sabrina
12.	Yang Zujun	A small chromosomal segment translocation emerge in the stable early partial amphiploid of triticale
13.	Song Weining	Homologs of LFY gene in various wheats

## Poster List ICPHE 2007

No	Contact Person	Title
14.	Weiwei Deng/Chunyan Liu	Involvement of the Histone Acetyltransferase AtHAC1 in the Regulation of Flowering Time via Repression of <i>FLOWERING LOCUS C</i> in Arabidopsis
15.	Lifang Niu/Falong Lu	Mutations in the Type II protein arginine methyltransferase AtPRMT5 result in pleiotropic developmental defects in <i>Arabidopsis thaliana</i>
16.	Bin Liu/Pingchuan Li	Loss of Function of <i>OsDCL1</i> Affects MicroRNA Accumulation and Causes Developmental Defects in Rice
17.	Bin Liu	<i>Oryza sativa</i> <i>DICER-LIKE 4</i> Reveals a Key Role for siRNA Silencing in Plant
18.	Jixian Zhai	Small RNA-Directed Epigenetic Natural Variation between Arabidopsis Ecotypes
19.	J.F. Gutiérrez-Marcos	Epigenetic Maternal Control of Early Endosperm Development in Maize

## Poster Abstract ICPHE 2007

<b>Poster # :</b>	1
<b>Contact Person:</b>	Baige Zhao
<b>Email:</b>	<a href="mailto:zbaige@okstate.edu">zbaige@okstate.edu</a>
<b>Authors:</b>	Baige Zhao, Bjorn Martin, Sathya Elavarthi, Shraddha Vadvalkar and Kristel Green
<b>Affiliations:</b>	Oklahoma State University, Stillwater, USA
<b>Abstract Title:</b>	Effects of Water-stress on Ascorbate and Glutathione in Transgenic and Non-transgenic Wheat

### Abstract Text:

Water stress often induces accumulation of reactive oxygen species (ROS) that are deleterious to plant growth. The soluble antioxidants glutathione and ascorbate play a very important role in the metabolism of these drought induced oxidants and in the protection from damage. The gene from *E. coli* encoding mannitol-1-dehydrogenase was previously transformed into the spring wheat cultivar Bobwhite in our laboratory with the intent to cause mannitol accumulation and the hope of improving the drought tolerance. In this study to understand the mechanism of drought tolerance five transgenic wheat lines pTA2-110, pTA2-115, pTA2-118, pTA5-104 and pTA5-108 were used. The pTA2 lines accumulate mannitol in the cytosol, whereas the pTA5 lines accumulate mannitol in the plastids. Bobwhite and pAHC20, which contain the selectable *bar* transgene only, were used as controls. The greenhouse experiment was a randomized complete block design with four replications. After three weeks of establishment, half the plants were exposed to moderate stress by reduced watering, whereas the remaining plants were well watered. Leaf samples were collected at three times two weeks apart starting at the beginning of the stress treatment. Total glutathione (GSH+GSSH), oxidized glutathione (GSSH), reduced glutathione (GSH), total ascorbate (TASA), reduced ascorbate (REDASA), and dehydroascorbate (DHA) were measured spectrophotometrically. There were significant differences in TASA, REDASA, DHA, GSH+GSSG, GSH, and GSSH among transgenic lines, but the differences between transgenic and non-transgenic lines were not significant. Except for pAHC20 and pTA2-115 all lines had similar levels of TASA, REDASA and DHA. GSH+GSSG, GSH did not differ among the lines, but, the GSSG concentrations of Bobwhite, pTA5-108 and pAHC20 were significantly different from pTA5-104. The duration of exposure to water stress seems to trigger diverse changes in the antioxidant concentrations. TAST tended to decrease with the duration of stress, but the difference was not significant. GSH+GSSG initially increased, but remained similar after 15 and 30 days of stress. REDASA increased 33.9% by 15 days of stress, but then decreased to 36.3 % of the initial level after 30 days of stress. DHA, GSSG and GSH showed the same pattern of increasing concentrations in response to water stress. The results indicate that the mechanism of drought tolerance of our transgenic wheat does not involve alteration of the regular antioxidant system and that drought can be managed by the constitutive TASA and GSH+GSSG. As the different lines did show different antioxidant concentrations, we conclude that, the location of the genome into which the transgene is

integrated may decide the expression. Future work to reveal the mechanism of drought tolerance of transgenic wheat may need to include gene copy number and gene location.

**Session Notes:**

<b>Poster # :</b>	2
<b>Contact Person:</b>	Bin Wang
<b>Email:</b>	<a href="mailto:bwang@genetics.ac.cn">bwang@genetics.ac.cn</a>
<b>Authors:</b>	Manli Weng, Li Wang, Lixian Qiao, Chunjiang Zhou, Jun Li and Bin Wang
<b>Affiliations:</b>	Institute of Genetics and Developmental Biology, CAS, Beijing China
<b>Abstract Title:</b>	Cloning and genetic transformation of a novel rice male sterility gene <i>OsAPT2</i>
<b>Abstract Text:</b>	
<p>In plants, adenine phosphoribosyl transferase (APRT, EC 2.4.2.7) is the key enzyme that converts adenine into adenosine-3'-phosphate (AMP), the precursor of energy supplier ATP, in salvage metabolism pathway (SMP), by which to provide enough necessary energy for normal growth development or survival. SMP is usually only put into action when plants are in key reproductive growing stages or in severe stress conditions.</p> <p>In this presentation, a novel rice gene <i>OsAPT2</i>, which encodes a putative adenine phosphoribosyl transferase (APRT), was cloned. Its full-length cDNA is 1125bp, composing an ORF encoding 212 amino acid residues and a stop codon, a 5' UTR of 123 bp and a 3' UTR of 363 bp. The deduced amino acid sequence of <i>OsAPT2</i> is highly homologous to those of previously reported APRTs. The genomic <i>OsAPT2</i> gene contains 7 exons and 6 introns. Its total length is 4758 bp. Then, a pollen specific expression vector of the antisense of the full-length <i>OsAPT2</i> cDNA was constructed and transformed into rice variety Taibei309 by <i>Agrobacterium tumefaciens</i> mediated transformation method. In total, 650 T0 transgenic plants were obtained based on both antibiotic screening and specific PCR identification. From those 11 male sterile lines of T2 generation with seed-setting rate in the range 0-5% in bagged spike were obtained, which were originally come from 5 different T0 transgenic plants. Southern blotting results revealed that they were really transformed by the antisense <i>OsAPT2</i>. Phenotype observation revealed that 10 of the 11 T2 male sterile lines are constitutive, but one is temperature sensitive, its seed-setting rate restored to about 10% in low temperature conditions, and that 4 T2 male sterile lines coming from T0 transgenic plant TA29-247 have no awns, while the other 7 T2 male sterile lines coming from other 4 T0 transgenic plants (TA29-445, TA29-450, TA29-458, TA29-459) all have short awns.</p> <p>Comparative expression pattern analysis between the untransformed parent Taibei309 and obtained male sterile line by both RT-PCR and reverse Northern revealed that the expression of <i>OsAPT2</i> in spikes of male sterile line was down regulated obviously, but keep normal in leaf, stem and root. This result strongly supports one hypothesis of male sterility that the disorder between supplement and requirement in spike during pollen development stage lead to male sterility.</p>	

## Poster Abstract ICPHE 2007

<b>Poster # :</b>	3
<b>Contact Person:</b>	K. Yoong Lim
<b>Email:</b>	<a href="mailto:Y.K.Lim@qmul.ac.uk">Y.K.Lim@qmul.ac.uk</a>
<b>Authors:</b>	K. Yoong Lim, Ales Kovarik, Roman Matyasek, Kamila Skalicka, Mark W. Chase, James J. Clarkson, Ilia Leitch, Sandy Knapp, Grandbastien MA and Andrew R. Leitch
<b>Affiliations:</b>	Queen Mary University of London, UK
<b>Abstract Title:</b>	Polyploid-Diploid Cycle in the Genus <i>Nicotiana</i>
<b>Abstract Text:</b>	<p>Allopolyploids are ideally suited to study genome evolution because patterns of divergence can be measured from a point in evolution when the allopolyploid formed. Recent genome studies have revealed angiosperm evolution proceeds in cycles of polyploidy and diploidisation. We are studying allopolyploid evolution in the genus <i>Nicotiana</i>, which has c. 75 species of which c. 35 species are allopolyploids formed over widely different timescales. Using these allopolyploids we show the process of genetic events following allopolyploidy. In synthetic allopolyploids of tobacco, our analysis reveals genetic change (rDNA amplification and homogenisation, deletion of retroelements and tandem repeats from the paternally derived genome, genome translocations) perhaps stimulated by the “genomic shock” of allopolyploidy. After &lt;0.2 my in natural tobacco, in which rDNA locus number is additive (as expected), there is more evidence of degradation of the paternally derived genome, near complete rDNA homogenisation and fixation of some translocations. Genome diploidisation proceeds in older allopolyploids (~1 My, species of section <i>Polydicleae</i>) with loss of many rDNA loci, evolution of new satellites and parental genome homogenisation. After even longer time-frames (~5 My, species of section <i>Repandae</i>) there is considerable to near complete turnover of repeated elements within these genomes. These changes occur without change in chromosome number, but some species of the allopolyploid section <i>Suaveolentes</i> (&gt; 10 my) have lower chromosome numbers, perhaps representing a further stage of diploidisation.</p>
<b>Session Notes:</b>	

<b>Poster # :</b>	4
<b>Contact Person:</b>	Shcherban A.B.
<b>Email:</b>	<a href="mailto:atos@bionet.nsc.ru">atos@bionet.nsc.ru</a>
<b>Authors:</b>	Shcherban A.B., Badaeva E.D., Adonina I.G., Salina E.A.
<b>Affiliations:</b>	Institute of Cytology and Genetics, Novosibirsk Russia
<b>Abstract Title:</b>	45S rDNA evolution in a synthetic amphiploid <i>Aegilops sharonensis</i> x <i>Ae.umbellulata</i>

**Abstract Text:**

We used synthetic amphiploid *Aegilops sharonensis* x *Ae. umbellulata* as a model system to study genetical and epigenetical changes associated with differential activity of 45S rRNA genes in allopolyploids. The suppression of NOR (nucleolar organizing region) loci inherited from *Ae. sharonensis* was revealed in the amphiploid by AgNOR-staining. As the following PCR and restriction analysis showed, all studied S<sub>2</sub>, S<sub>3</sub> amphiploid plants demonstrate an additive pattern of ETS (external transcribed spacer) sequences of rDNA compared to respective parental species. Only some reduction of the *Ae. sharonensis*-derived restriction fragments was observed. The primary sequence analysis confirmed structural conservation of these sequences at the early stages of amphiploid formation. However, using gCAPS (genomic-cleaved amplified polymorphic sequence) assay we found the new ETS sequence with specific for *Ae. umbellulata* *Msp*AI1 restriction site (s) and close by the length to the ETS of *Ae. sharonensis*. It is not known yet whether this sequence was produced *de novo* within amphiploid, or by amplification of a rare rDNA unit that was originally present in one of the parental genomes. To study epigenetic changes (DNA methylation) we conducted PCR amplification of the short region within ETS after *Hpa*II/*Msp*I digestion of genomic DNA. The intensity of the *Ae. umbellulata*-derived PCR fragment was reduced in all amphiploid plants as a result of probable demethylation of the ETS sequence of *Ae. umbellulata*, or (and) methylation of that of *Ae. sharonensis*. Using FISH we revealed polymorphism in intensity of the NOR sites located on 6S<sup>sh</sup> chromosome among amphiploid plants of S<sub>3</sub>-S<sub>4</sub> generations. Two S<sub>3</sub> plants showed deleted NOR site on one of the two homologous 6S<sup>sh</sup> chromosomes, while the rest of plants had both sites with either unchanged or reduced intensity. Thus, our findings show that in the synthetic amphiploid *Ae. sharonensis* x *Ae. umbellulata* the suppression of the *Ae. sharonensis* 45S rRNA genes is associated with their partial elimination in certain chromosomal loci. Along with epigenetic changes in methylation pattern, these genetic alterations occurred rapidly during few generations after crossing and were stably inherited in the subsequent generations studied. The biased locus-specific elimination of rDNA is consistent with rDNA evolution observed in natural allotetraploids with similar genomic constitution.





## Poster Abstract ICPHE 2007

<b>Poster # :</b>	7
<b>Contact Person:</b>	Yong Zhang and ZhengLong Ren
<b>Email:</b>	<a href="mailto:zhangyong916@126.com">zhangyong916@126.com</a>
<b>Authors:</b>	LIU Zhao-hui, Zhang Yong, YANG Zu-Jun, Li Guang-rong, REN Zheng-Long
<b>Affiliations:</b>	University of Electronic Science and Technology of China, Chengdu China
<b>Abstract Title:</b>	Fingerprinting Analysis of the Introgressed Lines from <i>Gossypium hirsutum L.</i> × <i>Gossypium barbadense L</i> based on AFLP Markers
<b>Abstract Text:</b>	
<p>The main cultivated varieties belonged to the species of Upland cotton (<i>Gossypium hirsutum L.</i>) in the world and their genetic background is very narrow. However, the wild species and race in the genus of <i>Gossypium</i> have abundant genetic diversity and possess lots of excellent genes with potential high yield, fine and strength fiber, disease and insect resistance, drought and coldness resistance, male sterility and so on. The interspecific hybridization for utilizing the benefit genes from these wild tetraploid species had been widely carried out for 20 years in China. It has huge practical and theoretical value to conduct the analyses of the cotton introgression lines of interspecific hybridization toward upland cotton, which help to successfully develop the introgressed lines resistant to the carmine spider mite (<i>Tetranychus cinnabarinus</i>) and to the cotton aphid (<i>Aphis gossypii</i>) in Sichuan. In this paper, the genetic background and phylogeny of 9 introgression lines from same interspecific hybridization of <i>Gossypium hirsutum L.</i> × <i>Gossypium barbadense L</i> and 2 relative lines based on AFLP analysis. The results indicated that AFLP was an efficient technique to distinguish the different cultivars by their unique AFLP fingerprint patterns. Farther more, some unique AFLP markers were detected for 9 cotton lines, which could be used to develop specific probes for identification purposes. Based on 16 pairs AFLP primers, 672 bands altogether were amplified and the percent of polymorphic bands was 91.2 %. Average paired similarity coefficient among germplasm was 0.6147, ranged from 0.464~1.000. The AFLP cluster dendrogram of 11 lines of cotton was constructed with 3 groups: TM-1, the cotton lines resistant to red spider and the lines resistant to aphid. The result of AFLP cluster analysis fitted basically with that of their pedigrees and morphological traits.</p>	
<b>Session Notes:</b>	

<b>Poster # :</b>	8
<b>Contact Person:</b>	Milos Tanurdzic
<b>Email:</b>	<a href="mailto:milos@cshl.edu">milos@cshl.edu</a>
<b>Authors:</b>	Milos Tanurdzic, Matthew Vaughn, Zach Lippman, Hongmei Jiang, Suk-Young Yoo, Brian Dilkes, Luca Comai, RW Doerge and Robert Martienssen
<b>Affiliations:</b>	Cold Spring Harbor, NY USA
<b>Abstract Title:</b>	Epigenomic profiling in diploid and tetraploid <i>Arabidopsis thaliana</i>
<b>Abstract Text:</b>	
<p>DNA methylation and covalent histone modifications are crucial components of genome regulation, including transposon silencing. To better understand these epigenetic phenomena that occur in diploid and autotetraploid <i>Arabidopsis thaliana</i>, we profiled the chromosomal distribution of cytosine and various histone H3 lysine residues methylation patterns using a tiling DNA microarray of chromosome 4. Repeated sequences and transposable elements (TEs), especially LTR retrotransposons, are densely methylated in the diploid <i>A. thaliana</i> and their DNA is associated with H3Lys9me2, but one third of genes also have low but detectable methylation in their transcribed regions, associated with H3Lys4me2. Promoter methylation is rare, and gene expression is not generally affected by differences in DNA methylation. Small interfering RNA (siRNA) are preferentially associated with methylated TEs, but not with methylated genes, indicating that most genic methylation is not guided by siRNA. Upon neo-polyploidization significant redistribution of DNA methylation, sometimes associated with changes in histone modifications, and often associated with specific TEs was observed.</p>	
<b>Session Notes:</b>	
Empty space for session notes	

<b>Poster # :</b>	9
<b>Contact Person:</b>	Fateme Fadaie
<b>Email:</b>	<a href="mailto:fadaie572@yahoo.com">fadaie572@yahoo.com</a>
<b>Authors:</b>	Fateme Fadaie and Masoud Sheidai
<b>Affiliations:</b>	Shahid Beheshty University, Gorgan, Golestan Iran
<b>Abstract Title:</b>	A new polyploidy level for two species, <i>B. sericeus</i> Drobov. and <i>B. fasciculatus</i> Presl. in meiotic study from Iran.

**Abstract Text:**

The genus *Bromus* L., is among the most important forage plants of Iran distributed widely in different regions of the country. The genus *Bromus* comprises several annual as well as perennial grass species. The section *Genea* Dum. is among annual *Bromus* grasses. meiotic analysis revealed the presence of  $2n=14(2x)$  and  $2n= 28(4x)$  chromosome number among the species and populations studied. The two populations of *B.sericeus* studied differed in their ploidy level. The Iranshahr population possessed  $n=14(2n=4x=28)$  chromosome number, while the Khash population possessed  $n=7(2n=2x=14)$ . The earlier study on this species reports the somatic chromosome number of  $2n=14$  (Bolk-ovskikh et al. 1969).Therefore, this is the first report on among-population variation in ploidy level of *B.sericeus*. Iranshahr population of *B.sericeus* which is tetraploid, formed only bivalent in metaphase-I. This is considered to be a cytogenetic characteristic of true allopolyploids, however at present we are not sure if it is a true allopolyploid or the formation of only bivalent is due to presence of a diploidizing mechanism as present in other grasses (Sybenga 1992). The only population of *B.fasciculatus* studied showed the presence of  $n=14(2n=4x=28)$  chromosome number. The only report previously available for this species shows the present of  $2n=2x=14$ (Napoli and Zizza 1984). Therefore, the present study report a new ploidy level (4x) for *B. fasciculatus*. Bivalents and quadrivalent were formed in metaphase and diakinesis stages of meiosis-I in this species.

**Session Notes:**

--

<b>Poster # :</b>	10
<b>Contact Person:</b>	Zhu Jing
<b>Email:</b>	zhujing310@yahoo.com.cn
<b>Authors:</b>	Zhu Jing, Feng Chuan, Deng Bing and Zhang Xiaoping
<b>Affiliations:</b>	Children's Hospital of Chongqing Medical University, Chongqing
<b>Abstract Title:</b>	China Acetylation modification mechanism of MSCs differentiating in vitro

**Abstract Text:**

Constructing recombinant plasmid that can obstruct acetyltransferase Gcn5 expression through RNA interference mechanism and transfecting it into MSCs induced by 5-aza. Then observing whether it can block the MSCs cardiac-specific differentiation process or not by detecting cardiac special proteins myosin heavy chain (MHC) and Cx43. On the other hand the roles of acetylases in the process of MSCs differentiation was analysed.

**Methods and materials:** Firstly, established a recombinant plasmid vector involving a small interference RNA of Gcn5 and identified it by restriction enzymes and DNA sequencing. Secondly, MSCs were isolated from bilateral thighbones and tibias of Wistar rats, purified by adhesive-screening method, then treated with 10 $\mu$ mol/L 5-azacytidine for 24 hours and were maintained for eight weeks. Specimens were obtained at the certain time respectively after 5-aza treatment. Then gene GATA4 and Nkx2.5 were detected by RT-PCR. Thirdly, Gcn5 shRNA recombinant plasmid vector were transfected into MSCs induced with 5-aza and observed the expression of Gcn5, MHC and Cx43 by western-blotting while Gcn5, GATA4 and Nkx2.5 genes were investigated by RT-PCR.

**Results:** 1. After enzyme-cutting and DNA sequencing, the recombinant plasmid was identified to be constructed successfully. 2. GATA4 and Nkx2.5 were expressed significant at 1 week after induced. This was the point of RNA interference. 3. Expression of Gcn5, Cx43 and MHC decreased significant after Gcn5 shRNA recombinant plasmid transfected into MSCs induced by 5-aza. Their silent ratio were 86%, 58% and 67%.

**Conclusions:** The Gcn5 shRNA plasmids constructed in our study could block acetylation during the process of MSCs differentiated into cardiomyocytes. Acetylation played a very important role in the regulation of MSCs differentiated.

**Session Notes:**

--

<b>Poster # :</b>	11
<b>Contact Person:</b>	Yang Zujun
<b>Email:</b>	<a href="mailto:yangzujun@uestc.edu.cn">yangzujun@uestc.edu.cn</a>
<b>Authors:</b>	Liu Cheng, Yang Zujun, Li Guangrong, Zhang Yong, Zhou Jianping, Ren Zhenglong
<b>Affiliations:</b>	University of Electronic Science and Technology of China, Chengdu China
<b>Abstract Title:</b>	Genomic relationship between <i>Dasypyrum</i> and <i>Thinopyrum</i> : evidence from chromosomal distribution of LTR retrotransposon Sabrina

**Abstract Text:**

The wild wheatgrass, *Thinopyrum intermedium*, in tribe Triticeae, has been widely hybridized extensively with wheat and proved to be a valuable source of agronomically important genes. However, the genomic constitution of *Thinopyrum intermedium* was reported as either E<sub>1</sub>E<sub>2</sub>St or JsJsSt genome, therefore it needed to be further studied. In this study, a new Sabrina-like LTR retrotransposon DNA sequence, named pDbH12, was isolated from V<sup>b</sup> genome of *Dasypyrum breviaristatum*. Based on the sequence of pDbH12, a pair of specific primers was designed and PCR amplification was performed on genus in the tribe Triticeae, such as *D. breviaristat* (V<sup>b</sup>), *Thinopyrum intermedium* (EEST), *Secale cereale* cv Jingzhou (R), *Aegilops ventricosa* (DM), *Aegilops tauschii* (DD), *Elymus grandiglumis* (StYP) and *Triticum aestivum* cv Chinese Spring (ABD). The result showed that the target DNA band merely existed in *D. breviaristatum* and *Th. intermedium*. Using pDbH12 as probe, Fluorescence *in situ* hybridization (FISH) was carried out on metaphase chromosomes of the foregoing materials. The result suggested that no hybridization signal was detected on genome R, DM, DD, StYP and ABD, but the strong signals were distributed in all *D. breviaristatum* chromosomes and 14 chromosomes of *Th. intermedium*, where the strong signals were throughout their chromosomes except for the terminal and centromeric regions. Moreover, *Th. intermedium* was analyzed by Genomic *in situ* hybridization (GISH) with the probe of total genomic DNA of *D. breviaristatum*, and the result showed that only terminals of fourteen St chromosomes, indicating the V<sup>b</sup> genome was distant from St genome in *Th. intermedium*. At the same time, Octoploid trititrigia 78784 was analyzed by Genomic *in situ* hybridization (GISH) by using the probe of total genomic DNA of *D. villosum*, we observed that the hybridization signals were throughout five chromosomes arms except for the terminal and centromeric regions. Based on the chromosomal distribution of hybrid pattern of GISH and FISH, it was implied the *Th. intermedium* may contain a V related genome, and the close relationship between V<sup>b</sup> genome of *D. breviaristatum* and the genome of *Th. intermedium*, may due to the amplification of the specific repetitive sequences, like the unique Sabrina-like LTR retrotransposon. We also demonstrated that the probe of pDbH12 would be useful to characterize specific genomic introgression from *Th. intermedium* to wheat.

<b>Poster # :</b>	12
<b>Contact Person:</b>	Yang Zujun
<b>Email:</b>	<a href="mailto:yangzujun@uestc.edu.cn">yangzujun@uestc.edu.cn</a>
<b>Authors:</b>	Zhou Jianping, Yang Zujun, Zhang Huaiyu, Liu Cheng, Li Guangrong, Ren Zhenglong
<b>Affiliations:</b>	University of Electronic Science and Technology of China, Chengdu, Sichuan China
<b>Abstract Title:</b>	A small chromosomal segment translocation emerge in the stable early partial amphiploid of triticale

**Abstract Text:**

As a man-made crop, triticale was regarded as a new potential crop that combined the resistance to environmental stress of rye and the quality of common wheat. In the study, we developed a new triticale, named Z5-3-3, derived from the cross between wheat and octoploid triticale, in which its rye chromatin originated from Chinese landrace Weining Rye. Morphologically, the plant height (80-85cm) of Z5-3-3 is closer to that of the wheat parent MY15, than to that of the rye parent. Genetically, Z5-3-3 has stable fertility and immunity to wheat powdery mildew and stripe rust, under both inoculated and natural conditions in all growth stages. Somatic chromosome counts and pollen mother cells (PMCs) observation show that Z5-3-3 gave its chromosome composition of  $2n=6x=42$  and were mainly 21 II, respectively. Genomic in situ hybridization (GISH) using genomic DNA of rye as probe revealed that Z5-3-3 possessed 14 pairs of wheat chromosomes, 6 pairs of rye chromosomes and 1 pair of wheat-rye small segment translocation chromosomes. The translocated chromosomes contained a small rye fragments located on the terminals of one pair of wheat chromosomes. The above results suggest that Z5-3-3 is a new stable secondary hexaploid triticale which can be use in triticale breeding directly, and it could be a valuable source for the introgression of small rye chromatin to wheat.

**Session Notes:**

## Poster Abstract ICPHE 2007

<b>Poster # :</b>	13
<b>Contact Person:</b>	Song Weining
<b>Email:</b>	<a href="mailto:sweining2002@yahoo.com">sweining2002@yahoo.com</a>
<b>Authors:</b>	Yang Jiantao, Du Xianghong, Song Weining
<b>Affiliations:</b>	Northwest A&F University, Yangling, Shaanxi China
<b>Abstract Title:</b>	Homologs of LFY gene in various wheats
<b>Abstract Text:</b>	
<p>Homologs of LFY gene encode plant-specific transcription factors which play an important role in flower development. A wheat FLORICAULA/LEAFY ortholog, WFL, was reported to be associated with spikelet formation as lateral branch of the inflorescence meristem (Shitsukawa et al., 2006). Bread wheat is derived from a cross between emmer and <i>Aegilops tauschii</i> which took place some 8000 years ago. A better understanding of WFL's role from genetic and genomic perspectives will shed light on its natural evolution and its history under domestication.</p> <p>We designed primers based on WFL sequences and PCR amplified genomic DNAs from a number of wheat lines and their relatives: Chinese Spring (bread wheat cultivar, <i>Triticum aestivum</i>), Jinwheat (bread wheat cultivar), Mt Hemon96 (wild emmer wheat, <i>T. dicoccoides</i>), Coerulescens AC03-1002494 (durum wheat cultivar, <i>T. durum</i>) and 2-4 (<i>Aegilops tauschii</i>) respectively. Individual amplified fragments were cloned and sequenced from both ends. All of these sequences showed at least 95% homology with WFL in the Genbank. Multiple sequence alignments of these sequences showed high similarity with each other. A phylogenetic tree illustrated that the relationship based on these sequences largely corresponds to our current understanding with the evolution of various wheats and its ancestors, although some discrepancies are still to be investigated further.</p>	
<b>Session Notes:</b>	

<b>Poster # :</b>	14
<b>Contact Person:</b>	Lifang Niu, Falong Lu
<b>Email:</b>	<a href="mailto:lfniu@genetics.ac.cn">lfniu@genetics.ac.cn</a> ; <a href="mailto:flu@genetics.ac.cn">flu@genetics.ac.cn</a>
<b>Authors:</b>	LiFang Niu, FaLong Lu, ChunYan Liu, YanXi Pei, JiXian Zhai, XiangFeng Kong and XiaoFeng Cao
<b>Affiliations:</b>	Institute of Genetics and Biological Development, CAS, China
<b>Abstract Title:</b>	Mutations in the Type II protein arginine methyltransferase AtPRMT5 result in pleiotropic developmental defects in <i>Arabidopsis thaliana</i>

**Abstract Text:**

Human protein arginine methyltransferase 5 encodes a type II protein arginine methyltransferase and its orthologs in animals and yeast have been shown to play important roles in the regulation of RNA processing, signal transduction and gene expression. However, PRMT5 homologs in higher plants have not yet been reported and biological significance of these proteins in plant development remains elusive. Here, using conventional biochemical approach, we purified a plant histone arginine methyltransferase from cauliflower that was nearly identical to AtPRMT5, an Arabidopsis homolog of human PRMT5. AtPRMT5 symmetrically di-methylated histone H4R3, H2A and myelin basic protein (MBP) in vitro. Mutations in AtPRMT5 caused pleiotropic developmental defects, including growth retardation, dark green and curled leaves, and *FLC*-dependent delayed flowering, which demonstrates that the type II protein arginine methyltransferase is involved in repression of vegetative growth and *FLC*-dependent flowering time regulation in *Arabidopsis*.

**Session Notes:**

## Poster Abstract ICPHE 2007

<b>Poster # :</b> <b>Contact Person:</b> <b>Email:</b> <b>Authors:</b> <b>Affiliations:</b> <b>Abstract Title:</b>	15 Weiwei Deng, Chunyan Liu <a href="mailto:wwdeng@genetics.ac.cn">wwdeng@genetics.ac.cn</a> ; <a href="mailto:cylu@genetics.ac.cn">cylu@genetics.ac.cn</a> WeiWei Deng, ChunYan Liu, YanXi Pei, Xian Deng, LiFang Niu, and XiaoFeng Cao* Institute of Genetics and Biological Development, CAS, China Involvement of the Histone Acetyltransferase AtHAC1 in the Regulation of Flowering Time via Repression of <i>FLOWERING LOCUS C</i> in Arabidopsis
<b>Abstract Text:</b>  <p>Histone acetylation is an important posttranslational modification correlated with gene activation. In Arabidopsis, the histone acetyltransferase AtHAC1 is homologous to animal p300/CREB (cAMP-responsive element-binding protein)-binding proteins, which are the main histone acetyltransferases participating in many physiological processes, including proliferation, differentiation, and apoptosis. The functions of p300/CBP in animals are well characterized, whereas little is known about the roles of AtHAC1 in developmental control in Arabidopsis. Lesions in AtHAC1 caused pleiotropic developmental defects, including delayed flowering, a shortened primary root, and partially reduced fertility. Analysis of the molecular basis of late flowering in <i>hac1</i> mutants showed that the <i>hac1</i> plants respond normally to day length, gibberellic acid treatment, and vernalization. Furthermore, the expression level of the flowering repressor <i>FLOWERING LOCUS C</i> (<i>FLC</i>) is increased in <i>hac1</i> mutants, indicating that the late-flowering phenotype of <i>hac1</i> mutants is mediated by <i>FLC</i>. Since histone acetylation is usually associated with the activation of gene expression, histone modifications of <i>FLC</i> chromatin are not affected by mutations in <i>HAC1</i> and expression levels of all known autonomous pathway genes are unchanged in <i>hac1</i> plants, we propose that <i>HAC1</i> affects flowering time by epigenetic modification of factors upstream of <i>FLC</i>.</p>	
<b>Session Notes:</b>	
Empty space for session notes	

## Poster Abstract ICPHE 2007

<b>Poster # :</b>	16
<b>Contact Person:</b>	Bin Liu, Pingchuan Li
<b>Email:</b>	<a href="mailto:bliu@genetics.ac.cn">bliu@genetics.ac.cn</a> ; <a href="mailto:lipch@genetics.ac.cn">lipch@genetics.ac.cn</a>
<b>Authors:</b>	Bin Liu, PingChuan Li, Xin Li, ChunYan Liu, ShouYun Cao, ChengCai Chu, and XiaoFeng Cao
<b>Affiliations:</b>	Institute of Genetics and Biological Development, CAS, China
<b>Abstract Title:</b>	Loss of Function of <i>OsDCL1</i> Affects MicroRNA Accumulation and Causes Developmental Defects in Rice

### Abstract Text:

MicroRNAs (miRNAs) and small interfering RNAs (siRNAs) are two types of noncoding RNAs involved in developmental regulation, genome maintenance, and defense in eukaryotes. The activity of Dicer or Dicer-like (DCL) proteins is required for the maturation of miRNAs and siRNAs. In this study, we cloned and sequenced 66 candidate rice (*Oryza sativa*) miRNAs out of 1,650 small RNA sequences (19 to approximately 25 nt), and they could be further grouped into 21 families, 12 of which are newly identified and three of which, OsmiR528, OsmiR529, and OsmiR530, have been confirmed by northern blot. To study the function of rice DCL proteins (*OsDCLs*) in the biogenesis of miRNAs and siRNAs, we searched genome databases and identified six *OsDCLs*. An RNAi approach was applied to knock down two *OsDCLs*, *OsDCL1* and *OsDCL4*, respectively. Strong loss of function of *OsDCL1* gene resulted in developmental arrest at the seedling stage and weak knockdown of *OsDCL1* gene caused pleiotropic developmental defects, which were caused by the disruption of miRNAs biogenesis. Moreover, all miRNAs tested were greatly reduced in *OsDCL1IR* but not *OsDCL4IR* transformants, indicating that *OsDCL1* plays a critical role in miRNA processing in rice.

### Session Notes:

<b>Poster # :</b>	17
<b>Contact Person:</b>	Bin Liu
<b>Email:</b>	<a href="mailto:bliu@genetics.ac.cn">bliu@genetics.ac.cn</a>
<b>Authors:</b>	Bin Liu, ZhiYu Chen, XianWei Song, Xia Cui and XiaoFeng Cao
<b>Affiliations:</b>	Institute of Genetics and Biological Development, CAS, China
<b>Abstract Title:</b>	<i>Oryza sativa</i> DICER-LIKE 4 Reveals a Key Role for siRNA Silencing in Plant Development

**Abstract Text:**

MicroRNAs (miRNAs) and small interfering RNAs (siRNAs) are two classes of small regulatory RNAs derived from different types of precursors processed by distinct Dicer or Dicer-like (DCL) proteins. During evolution, four *Arabidopsis* DCLs and six rice (*Oryza sativa*) DCLs (OsDCLs) appear to have acquired specialized functions. The *Arabidopsis* DCLs are well characterized, but those in rice remain largely unclear. Here we show that both knock-down and loss-of-function of rice *OsDCL4*, the homolog of *Arabidopsis DCL4*, led to vegetative growth abnormalities and severe developmental defects in spikelet identity. Those phenotypic alterations appeared distinct from that observed for *Arabidopsis dcl4* mutants, which only exhibited an accelerated vegetative phase-change. This phenotypic variation conferred by loss-of-function of DCL4 between rice and *Arabidopsis* suggests that siRNA processing by OsDCL4 has a wider role in rice development than that in *Arabidopsis*. Biochemical and genetic analyses indicated that OsDCL4 is the major Dicer responsible for the 21nt siRNAs associated with inverted repeat transgenes and trans-acting siRNA (ta-siRNA) from endogenous *TRANS-ACTING siRNA3* (*OsTAS3*) gene. We show that the biogenesis mechanism of *TAS3* ta-siRNA is conserved but putative direct targets of OsDCL4 appear to be differentially regulated between monocots and dicots. Our results reveal a critical role of OsDCL4-mediated ta-siRNA biogenesis in plant development.

**Session Notes:**

<b>Poster # :</b>	18
<b>Contact Person:</b>	Jixian Zhai
<b>Email:</b>	<a href="mailto:jxzhai@genetics.ac.cn">jxzhai@genetics.ac.cn</a>
<b>Authors:</b>	Jixian Zhai, Jun Liu, PingChuan Li, Blake C. Meyers, Xuemei Chen and Xiaofeng Cao
<b>Affiliations:</b>	Institute of Genetics and Biological Development, CAS, China
<b>Abstract Title:</b>	Small RNA-Directed Epigenetic Natural Variation between Arabidopsis Ecotypes

**Abstract Text:**

Progress in epigenetics has revealed mechanisms which can heritably regulate gene function independent of genetic alternations. Nevertheless, little is known about the role of epigenetics in evolution. This is due in part to scant data on epigenetic variation among natural populations. In plants, small interfering RNA (siRNA) is involved in both the initiation and maintenance of gene silencing by directing heterochromatic modification and/or DNA methylation which could further influence gene expression. Here we report that, in the model plant *Arabidopsis thaliana*, a cluster of ~24 nt siRNAs found at high levels in the ecotype *Landsberg erecta* (Ler) could direct DNA methylation and heterochromatinization at the promoter of *FLOWERING LOCUS C* (FLC), a major repressor of flowering, whereas the same region in ecotype *Columbia* (Col) with almost identical DNA sequence, generates a set of low abundance siRNAs that do not direct these activities. DNA methylation of this region in Ler allele is dependent on genes in known silencing pathways. A genome-wide comparison of Ler and Col small RNAs identified at least 70 loci matched by significant level of ~24 nt siRNAs present specifically in Ler but not Col. These data suggest that there could be substantial small RNA directed epigenetic differences between two closely related *Arabidopsis* ecotypes. This epigenetic variation may play an important role in the evolution of these and other lineages.

**Session Notes:**

## Poster Abstract ICPHE 2007

<b>Submitting # :</b>	19
<b>Contact Person:</b>	J.F. Gutiérrez-Marcos
<b>Email:</b>	<a href="mailto:J.F.Gutierrez-Marcos@warwick.ac.uk">J.F.Gutierrez-Marcos@warwick.ac.uk</a>
<b>Authors:</b>	L.M. Costa, Hugh G. Dickinson, M.S. Evans and J.F. Gutiérrez-Marcos
<b>Affiliations:</b>	University of Warwick, Warwick HRI, Wellesbourne U.K.
<b>Abstract Title:</b>	Epigenetic Maternal Control of Early Endosperm Development in Maize

### Abstract Text:

In angiosperms, double fertilization of an egg cell and a central cell with two sperm cells results in the formation of a seed containing a diploid embryo and a triploid endosperm. The extent to which the embryo sac and/or maternally contributed post-fertilization factors control the development of the seed remains largely unknown. We have identified novel gametophytic maternal-effect maize mutants that exclusively exhibit defects during early endosperm development. In particular, the spatial expression of basal endosperm-specific transcripts (BET) in these mutants is altered during free-nuclear and cellular endosperm development. MEG1, is one such BET imprinted gene that shows preferential maternal expression during the early phases of endosperm development. We show that MEG1 is a small cystein-rich secreted peptide that is necessary for early endosperm development. Further, our data support the view that pre- and post-fertilization maternal factors are equally important for early basal endosperm development.

### Session Notes:

## Submitting Abstract List    ICPHE 2007

1.	Yunliang Jiang	Lower Expression of Thyroid Transcription Factor mRNA in the Lung of SCNT Cow is not Due to the Hypermethylation in the Promoter Region
2.	Li Yun	Study on the multiple traits of chloroplast of triploid <i>Populus tomentosa</i> clones from different hybrid parents
3.	Li Yun	Studies on the Variation of Mature Phenotype and Anlage Differentiation of Floret of Autotetraploid <i>Robinia pseudoacacia</i>
4.	Li Yun	Study on the rescuing technique and the dynamic abortion of Immature Embryo of Tetraploid <i>Robinia pseudoacacia</i>
5.	Li Yun	Parentage Identification of Triploid <i>Populus tomentosa</i> from Doubling female gamete Chromosome by AFLP Marker
6.	Li Yun	Study on Pollen Chromosome Doubling of <i>Ginkgo Biloba</i>
7.	Xiangyang Kang	Triploid induction in <i>Populus alba</i> × <i>P. glandulosa</i> by chromosome doubling of female gametes
8.	Xiangyang Kang	Immunofluorescence and cytological characterization of 2n pollen formation during microsporogenesis in <i>Populus tomentos Carr</i>
9.	Lei Wang	Cloning and characterization of microRNAs from <i>B. napus</i>
10.	Jinling Meng	Exploring fixed and intersubgenomic heterosis assisted with an A <sup>r</sup> introgressive genetic map of <i>Brassica napus</i>
11.	ZENG Qianchun	Dian-type CMS lines and its application for F1 rice hybrids
12.	Yingguo Zhu	Single nucleotide variation of <i>orfH79</i> related to HL-CMS alter the fertility restoring model in AA genome species of genus <i>Oryza</i>

## Submitting Abstract List ICPHE 2007

13.	Zhenlan Liu	Expression partitioning of genes duplicated by polyploidy in response to abiotic stress and during organ development
14.	Shuhui Song and Jun Yu	Differential Gene Expression in an Elite Hybrid Rice Cultivar ( <i>Oryza sativa</i> , L): a Global Transcription Analysis Based on SAGE Data
15.	Liu Xiang-dong	Genetic Analysis on Main Quantitative Traits in Autotetraploid Rice
16.	Liu Xiang-dong	Genetic Effects of Directional Selection on Seed Setting Rate in Hybrid offspring of Autotetraploid Rice
17.	Xiangyang Kang	Cytological Mechanism of Triploid Induction with Colchicine after Pollination in <i>Populus</i>
18.	Qixin Sun	Cloning and Characterization of New Wheat Aquaporins -TaPIP1-2 and TaPIP1-3
19.	Qixin Sun	Wheat ( <i>Triticum aestivum</i> L.) root proteome and differentially expressed root proteins between hybrid and parents
20.	Qixin Sun	Identification of Differentially Expressed Genes in Root between Wheat Hybrid and Its Parental Inbreds Using Barley1 GeneChip
21.	Qixin Sun	Root transcriptome genotyping and expression analysis by using Wheat Genechip® Genome Array
22.	DHONT Angelique	Orthologous comparison in a gene-rich region among grasses reveals stability in the sugarcane polyploid genome.

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	1
<b>Contact Person:</b>	Yunliang Jiang
<b>Email:</b>	<a href="mailto:yljiang723@yahoo.com.cn">yljiang723@yahoo.com.cn</a>
<b>Authors:</b>	Yunliang Jiang
<b>Affiliations:</b>	Shangdong Agricultural University, Taian China
<b>Abstract Title:</b>	Lower Expression of Thyroid Transcription Factor mRNA in the Lung of SCNT Cow is not Due to the Hypermethylation in the Promoter Region

### Abstract Text:

Thyroid transcription factor-1 (TTF-1), a member of NKX2 family, is a homeodomain nuclear transcription factor and plays a pivotal role during lung development and postnatal homeostasis function in mammal. TTF-1 is expressed in mammalian lung, thyroid, and brain tissues, regulate the expression of thyroglobulin and surfactant protein C. The present study obtained the bovine TTF-1 sequence, analyzed its expression in SCNT (somatic cell nuclear transfer) cows, and established the relationship between CpG methylation and TTF-1 expression. By means of RT-PCR, inverse PCR, and degenerate PCR approaches, a DNA fragment of 2498bp of bovine *TTF-1*, including exon1, intron1, partial exon2 and 5'-flanking region (920bp) was obtained. In SCNT cow, a significant lower expression in lung TTF-1 expression was found by real-time fluorescent quantitative RT-PCR. The CpG methylation profiles of three CpG islands in the promoter region spanning 920bp were subsequently analyzed. Both SCNT cow and controls showed hypomethylation at these CpG sites. The results indicated that the lower expression level of TTF-1 in SCNT cow is not due to the hypermethylation in the promoter region.

### Session Notes:

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	2
<b>Contact Person:</b>	Li Yun
<b>Email:</b>	<a href="mailto:yunli63.163.com">yunli63.163.com</a>
<b>Authors:</b>	Cui Binbin, Jiang Jinzhong, Li Yun
<b>Affiliations:</b>	Beijing Forestry University , Beijing China
<b>Abstract Title:</b>	Study on the multiple traits of chloroplast of triploid <i>Populus tomentosa</i> clones from different hybrid parents
<b>Abstract Text:</b>	
<p>The multiple traits of size, amount, DNA content of chloroplast were analyzed with 7 triploid <i>populus tomentasa</i> clones and 3 diploid <i>populus tomentasa</i> clones from different hybrid parents. This study revealed that the most triploid <i>Populus</i> clones are not marked different from their parents on chloroplast size, while their chloroplast number clearly increase with chromosome doubling .For the more, the triploid <i>populus tomentasa</i> clones from female gamete doubling reach the most significant level . Secondly, chloroplast DNA content by volume and by cell in triploid <i>populus tomentasa</i> from male gamete doubling show more significant variation than those from female ones. And then, cpDNA content by volume is direct proportion with ones by cell, while it is no close contact with chloroplast number by volume. To sum up, chloroplast's multiple traits are incompletely increase with increasing of <i>populus tomentasa</i> polyploidy , which their inheritance closely contact with their female parents character.</p>	
<b>Session Notes:</b>	



## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	4
<b>Contact Person:</b>	Li Yun
<b>Email:</b>	<a href="mailto:yunli63.163.com">yunli63.163.com</a>
<b>Authors:</b>	He Jia-yu, Li Yun, Jiang Jin-zhong
<b>Affiliations:</b>	Beijing Forestry University , Beijing China
<b>Abstract Title:</b>	Study on the rescuing technique and the dynamic abortion of Immature Embryo of Tetraploid <i>Robinia pseudoacacia</i>

### Abstract Text:

Tetraploid *Robinia pseudoacacia* is the autotetraploid of diploid *Robinia pseudoacacia*. Because of the abnormal meiosis of autotetraploid, Tetraploid *Robinia pseudoacacia*, most of its young embryos generated by free pollination are dead during embryo development, or even though those young embryos are able to develop into mature seeds embryos, they still can't sprout. The natural bourgeon frequency of seeds of Tetraploid *Robinia pseudoacacia*, which show a 33% average rate of seeds with embryos, is only 1.11%. Based on dissection of these mature seeds, it is proved that most embryos of these seeds are macrocephalic: some are too small or big, some are very dry and thin, some are green or white, some have no hypocotyls and so on. Rate of these macrocephalic embryo that don't sprout in nature is 92.31%. Although these macrocephalic embryos which sprout hardly are harmful for autotetraploid itself, they have great value for genetics and breeding because they are able to afford a lot of variation materials. The abortion of immature embryo of metalloid *Robin pseudoacacia* start from zygote and then goes along with the progress of zygote, in which more and more immature embryos are aborted continuously, till these zygotes develop into mature embryos. At both 10d and 95d after pollination, abortion is more serious than other point with a frequency of 60%-70%. In the period of 30 to 40d after pollination, abortion rate drops to 20%. So the abortion of immature embryo mainly happens during younger and older stage of embryo development. The result of researches on rescuing immature embryo in vitro culture showed that: the best rescuing time is 35d after pollination, the optimal media is Nitsch (pH5.8) supplemented with 6-BA 0.5 mg/l , IBA 2 mg/l , GA 0.5 mg/l, agar 6% and sucrose 6%, with which the topgallant rescuing frequency may be more than 60%; the result of essay rescuing mature embryo in vitro culture showed that 3.8% embryos germinated when rescued with embryo culture in 1/2MS that was thought as best media, but most embryos stopped developing after germinated; that the frequency of embryogenic callus induction reached 70%, the best media is MS (pH5.8) supplemented with 6-BA 0.5mg/l, 2,4-D 2.0 mg/l, agar 6% and sucrose 3%. The keys of our future studies are: to test the best time for sampling, to observe the whole development and anatomic structure of embryo by means of paraffin section examining the changes of both physiological and biochemical characters and the relationship between the characters, and to optimize the rescuing effects of immature and mature embryos of tetraploid *Robinia pseudoacacia* in vitro culture on the basis of referring to above research.



## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	6
<b>Contact Person:</b>	Li Yun
<b>Email:</b>	<a href="mailto:yunli63.163.com">yunli63.163.com</a>
<b>Authors:</b>	Hu Junyan, Li Yun
<b>Affiliations:</b>	Beijing Forestry University , Beijing China
<b>Abstract Title:</b>	Study on Pollen Chromosome Doubling of <i>Ginkgo Biloba</i>
<b>Abstract Text:</b>	
<p><i>Ginkgo biloba</i> is a multiple-use economic tree species in China. Now availabing genetic improvement methods can increase its leaves and timber outputs; however, in terms of its economic, ecological and medical value the professionals are still on the process of discovering. The research mainly focus on the technology using manual treatments to induce 2n pollen, and would establish a base for the triploids breeding by pollinating to female <i>Ginkgo biloba</i> with 2n pollen. During the 2005 to 2006, the large size pollen was obtained from both the buds in the natural and in the cultivated water, however, the percentages were relatively low with the highest among them being 7%. For the two different treatments in the experiment, the concentrations of colchicines in the soaked cotton is 0.6%~1.0%, and in the bottle of colchicines for dipping bud is about 0.6%~0.8%. The volume of large pollen obtained from the experiment is larger than the normal one. The DNA content of large pollen grains induced by colchicine was two times of haploidic pollen by using LSCM. Evidently, the large size pollen we got is unreduced diploid pollen. In order to increase the ratio of unreduced pollen of <i>Ginkgo biloba</i> , we are trying to use different chemical reagent and high temperature to doubling pollen chromosome.</p>	
<b>Session Notes:</b>	

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b> <b>Contact Person:</b> <b>Email:</b> <b>Authors:</b> <b>Affiliations:</b> <b>Abstract Title:</b>	7 Xiangyang Kang <a href="mailto:kangxy@bjfu.edu.cn">kangxy@bjfu.edu.cn</a> Yanhua Li,Xiangyang Kang Beijing Forestry University, Beijing China Triploid induction in <i>Populus alba</i> × <i>P. glandulosa</i> by chromosome doubling of female gametes
<b>Abstract Text:</b>	
<p>Efficient methods for obtaining unreduced female gametes are critical for triploids induction in <i>Populus alba</i> × <i>P. glandulosa</i>. A cytological study of MMCs and PMCs meiosis revealed that there was a close association between MMCs meiotic stage and male bud phenology during development under the same environment conditions. Based on the association, the meiotic stages of MMCs were determined timely by the PMCs meiosis and floral morphological characteristics and the female buds were treated with colchicine solution at the selected meiotic stages. The colchicine treated female buds were pollinated with pollen of <i>P. tomentosa</i>. Triploid poplars were identified among the hybrid progenies from the treatments at every selected stages. The present results demonstrated that the method of assistance for inducing 2n female gametes using the association of MMCs and PMCs appears to be an applicable approach for triploid induction by chromosome doubling of female gametes.</p>	
<b>Session Notes:</b>	

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	8
<b>Contact Person:</b>	Xiangyang Kang
<b>Email:</b>	<a href="mailto:kangxy@bjfu.edu.cn">kangxy@bjfu.edu.cn</a>
<b>Authors:</b>	ZHANG Zheng-Hai, KANG Xiang-Yang
<b>Affiliations:</b>	Beijing Forestry University, Beijing China
<b>Abstract Title:</b>	Immunofluorescence and cytological characterization of 2n pollen formation during microsporogenesis in <i>Populus tomentosa</i> Carr
<b>Abstract Text:</b>	<p>Unreduced gametes, gamete with a somatic chromosomes number, play an important role in plant sexual polyploidization. In the research, microtubules cytoskeleton pattern and cytological aspect of 2n pollen occurrence in <i>Populus tomentosa</i> were illustrated by using indirect immunofluorescence and microscopic examination. There were four mainly types of spindle microtubule during microsporeogenesis, ie. parallel, perpendicular, tripolar and fused. At telophase II, cytokinesis occurred simultaneously among the radial microtubules systems which expand from the sister nuclei and non-sister nuclei. In some meiocytes, abnormal cytokinesis divided the meiocyte into dyad and triad instead of tetrad. The irregular spindle microtubules at metaphase II leading to abnormal cytokinesis, that result in dyad and triad at the tetrad of meiosis. In addition, the triad and dyad released one or two unreduced microspore which undergo microgametogenesis and developed into 2n pollen. The results revealed that the 2n pollen of <i>Populus tomentosa</i> is genetically equivalent to first division restitution (FDR), FDR 2n pollen has a maximum heterozygosity, so it can give a high heterozygous to hybrids in triploid breeding of <i>Populus tomentosa</i>.</p>
<b>Session Notes:</b>	

<b>Submitting # :</b>	9
<b>Contact Person:</b>	Lei Wang
<b>Email:</b>	<a href="mailto:caaswvl@163.com">caaswvl@163.com</a>
<b>Authors:</b>	Lei Wang <sup>1,2</sup> , Ming-Bo Wang <sup>2</sup> , Jin-Xing Tu <sup>3</sup> , Chris Helliwell <sup>2</sup> , Peter Waterhouse <sup>2</sup> , Liz Dennis <sup>2</sup> , Ting-Dong Fu <sup>3</sup> , Yun-Liu Fan <sup>1*</sup>
<b>Affiliations:</b>	Chinese Academy of Agricultural Sciences, Beijing China
<b>Abstract Title:</b>	Cloning and characterization of microRNAs from <i>B. napus</i>
<b>Abstract Text:</b>	
<p>Non-coding small RNAs function to regulate gene expression at both transcriptional and posttranscriptional levels, guiding modification of chromatin and controlling developmental pathways, and are present in diverse eukaryotic organisms. Among these molecules, 21-25 nt small interfering RNAs (siRNAs) and microRNAs (miRNAs) are the two major types, both of which are produced by RNase III-like enzyme called Dicer in plants. MiRNAs originate from "hairpin" precursors transcribed from one strand of distinct genomic loci, which adopts a fold-back structure by complementary base pairing, whereas siRNAs are processed from long double-stranded RNA molecules. miRNAs are known to be involved in diverse functions such as regulation of cell proliferation, development of organisms, differentiation, apoptosis, carcinogenesis and viral infection.</p> <p>In plants, miRNA precursors are transcribed by RNA polymerase II and processed in the nucleus by the DICER-LIKE1(DCL1) protein, giving rise to miRNA duplexes with 2 nt 3' overhangs. Mature miRNAs, generated from the RNA duplex, incorporated into RNA-induced silencing complexes (RISCs), which in turn suppress expression of target genes through mRNA degradation or sometimes translational inhibition. Hundreds of miRNAs have been identified from Arabidopsis, rice, poplar and several other plant species.</p> <p>In <i>B. napus</i>, where the phenomenon of hybrid vigor is used in cropping systems, phenotypic characteristics are strongly influenced by heterozygosity. With the long-term goal of exploring the possible involvement of miRNAs in the hybrid vigor phenomenon, A library containing approximately 50,000 small RNA sequences was constructed for <i>Brassica napus</i>. Analysis of 3025 sequences obtained from this library resulted in the identification of 11 conserved miRNA families, which were validated by secondary structure prediction using surrounding sequences in the related <i>Brassica oleracea</i> genome. Three 21 nt small RNA sequences reside within the arm of pre-miRNA like stem-loop structures, making them likely candidates for novel non-conserved miRNAs in <i>B. napus</i>. Most of the conserved miRNAs were expressed at similar levels in a F1 hybrid <i>B. napus</i> line and its 4 double haploid progeny that showed marked variations in phenotypes, but many were differentially expressed between <i>B. napus</i> and Arabidopsis. The miR169 family was expressed at high levels in young leaves and stems, but was undetectable in roots and mature leaves, suggesting that miR169 expression is developmentally regulated in <i>B. napus</i>.</p>	



## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	11
<b>Contact Person:</b>	ZENG Qianchun
<b>Email:</b>	<a href="mailto:zqch1964@yahoo.com.cn">zqch1964@yahoo.com.cn</a>
<b>Authors:</b>	LUO Qiong, LI Zhengyou, ZENG Qianchun
<b>Affiliations:</b>	Dian-type Hybrid Rice Research Centre of Yunnan Province, Kunming 650201, China
<b>Abstract Title:</b>	Dian-type CMS lines and its application for F1 rice hybrids
<b>Abstract Text:</b>	
<p>Rice grain as the Chinese staple food is very important for the economic development and national food safety. It should be highlighted on the retention of the increase in rice yield and the total rice grain production due largely to the use of F1 rice hybrids along with the increasing of food demanding and in contradiction the shrinking of rice cultivation area. The hybrid combinations of CMS-WA (cytoplasmic <u>m</u>ale <u>s</u>terile line of <u>w</u>ild <u>a</u>bortive) was still the dominant one in terms of three lines F1 <i>indica</i> rice hybrids production, but the planting area of CMS-G, -D as well as CMS-ID etc was going up gradually year by year. For the F1 <i>japonica</i> rice hybrids, the CMS lines derived from both the Dian-type and BT (Chinsurah <u>B</u>oro II/ <u>T</u>aizhong 65). Dian-type CMS line was developed by Professor Li Zhengyou in 1969, and its combination was first released in 1972 in Yunnan Province of China. There are 10 kinds of Dian-type CMS lines, namely Dian-1, Dian-2, ... and Dian-10, in all. The differences among the ten CMS Dian-types lines were the various germplasms. The critical constraints to the extension of <i>japonica</i> hybrid rice was mainly due to the weak heteroses in comparison with the inbred <i>japonica</i> rice. In order to meet the heterosis challenge in japonica rice hybrid, the team of Dian-type hybrid rice has been focusing on the development of strong vigor restorer lines through subspecies cross (<i>japonica</i> × <i>indica</i>) since 1970s. We have obtained a few strong restorer lines of Dian-type CMS lines, such as Nan 29 and Nan 34, over 20 years. Nan 34 was a japonica restorer line with high quality, good rice blast resistance and indica rice germplasm as well. Six rice hybrid combinations inclusion of Dianza 31, Dianza 31, Dianza 33, Dianza 34, Yuza 34 and Dianza 80, comes from restorer Nan 34 were certified for release to commercialization by the Crop Variety Committee of Yunnan Province of China in recent years. For example, the Yuza 34 was one of the released Dian-type japonica hybrid rice combinations, which was bred by Dian-type hybrid rice team of Yunnan Province in 2001. It was developed from Dianyu No.1A, a Dian I-type japonica CMS line with stable male sterility and indica rice germplasm, and Nan 34, There were much significant difference in parental heredity in Yuza 34, in which both the male parent Nan 34 and the female Dianyu No.1A consist of the heredity of both indica and japonica rice. The combination was middle matured rice, with characteristics of erect, slightly rolling, broad but not too wide, long flag leaf, and well-knit tiller, fertilizer and cold tolerance, both rice blast and blight resistance. Its' milled rice reached the Ministry high-quality rice grade 2 according to the rice quality test results. Yuza 34 was the No.1 (mean yield was 10.419 t/hectare) in terms of rice yield among the field trials assessment from 2002 to 2003 in Yunnan Province. Yuza 34 was certified for release to commercialization by the Crop Variety</p>	

Committee of Yunnan Province in December 2004. In addition, Yuza 34 has met the super-rice yield level with mean yield 12.978 t/ hectare among an area of 8.053 hectare at Baoshan, Yunnan Province, China, in 2006. The Dian-type *japonica* F1 hybrid rice area were about  $13.3 \times 10^4$  hectares annually in China recent years. The defects of low quality in spite of the high yield of F1 rice hybrids exposed gradually to us along with the improvement of people's living standard. The quality problem has become the constraints of the production of F1 rice hybrids. With the carrying out of the national projects such as breeding super rice and gene transfer in rice etc, Chinese rice breeding will aim at creating such a novel variety with high yield, good quality as well as multiple resistance in the twenty-first century. Dianza 86, a new Dian-type F1 japonica hybrid combination could be the promising one in the light of its three years' field trials demonstration.

**Session Notes:**

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	12
<b>Contact Person:</b>	Yingguo Zhu
<b>Email:</b>	zhuyg@public.wh.hb.cn
<b>Authors:</b>	Shaoqing Li, Shihua Duan, Cuixiang Wan, Yanping Tan and Yingguo Zhu
<b>Affiliations:</b>	Wuhan University, Wuhan China
<b>Abstract Title:</b>	Single nucleotide variation of <i>orfH79</i> related to HL-CMS alter the fertility restoring model in AA genome species of genus <i>Oryza</i>

### Abstract Text:

Identification of the resource of cytoplasmic male sterility (CMS) in wild rice always attracts the rice breeders for developing alternative CMS lines. *orfH79*, a chimeric gene in mitochondrial genome suggested to be related to HL-type CMS of rice. In this report, characterization of the distribution and single nucleotide polymorphism of *orfH79* related to Honglian CMS in the genus of *Oryza* with AA genome were performed. PCR and Southern blot analysis revealed that 8 out of 42 investigated accessions were identified sharing *orfH79*. Sequence analysis revealed that *orfH79* has different allelic forms, and a total of 9 nucleotide substitutions being detected in the 8 newly identified *orfH79* alleles in wild rice which resulted in the change of 3 amino acids, and the sequence identities ranged from 98 to 100%. Outcrossing demonstrated that the pollen grains of the F1s or sterile plants in BC1F1 populations from crosses between wild rice with *orfH79* and Yuetai B (Honglian maintainer) as parent were partial or completely sterile. After eight round backcrosses, three newly allocytoplasmic CMS lines (w15A, w34A and w46A) with similar abortive characteristic as Honglian CMS lines were developed. Test-cross revealed that w15A and w46A had similar fertility restoring model as that of Yuetai A, and w34A was almost opposite to others. Which means that the single nucleotide variation lead to the change of the restoring and maintenance model.

### Session Notes:

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	13
<b>Contact Person:</b>	Zhenlan Liu
<b>Email:</b>	<a href="mailto:littlep8909@hotmail.com">littlep8909@hotmail.com</a>
<b>Authors:</b>	Zhenlan Liu, Keith Adams
<b>Affiliations:</b>	University of British Columbia, Vancouver, Canada
<b>Abstract Title:</b>	Expression partitioning of genes duplicated by polyploidy in response to abiotic stress and during organ development

### Abstract Text:

Allopolyploidy has been a prominent speciation mechanism and a recurrent process during plant evolution that has contributed greatly to the large number of duplicated genes in plant genomes. Polyploidy often leads to changes in genome organization and gene expression. The expression of genes duplicated by polyploidy, termed homeologs, can be partitioned between the duplicates so that one copy is expressed and functions only in some organs and the other copy is expressed only in other organs, indicative of subfunctionalization. To determine how homeologous gene expression patterns change during organ development and in response to abiotic stress conditions we have examined expression of the alcohol dehydrogenase gene AdhA in allopolyploid cotton (*Gossypium hirsutum*). Expression ratios of the two homeologs vary considerably during the development of organs from seedlings and fruits. Abiotic stress treatments, including cold, dark, and water submersion, altered homeologous gene expression. Most notably, only one copy is expressed in hypocotyls during a water submersion treatment and only the other copy is expressed during cold stress. These results imply that subfunctionalization of genes duplicated by polyploidy has occurred in response to abiotic stress conditions. Partitioning of duplicate gene expression in response to environmental stress could lead to duplicate gene retention during subsequent evolution.

### Session Notes:

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	14
<b>Contact Person:</b>	Shuhui Song, Jun Yu
<b>Email:</b>	<a href="mailto:songsh@genomics.org.cn">songsh@genomics.org.cn</a> ; <a href="mailto:Junyu@genomics.org.cn">Junyu@genomics.org.cn</a>
<b>Authors:</b>	Shuhui Song, Jun Yu
<b>Affiliations:</b>	Beijing Genomics Institute, CAS, Beijing China
<b>Abstract Title:</b>	Differential Gene Expression in an Elite Hybrid Rice Cultivar ( <i>Oryza sativa</i> , L): a Global Transcription Analysis Based on SAGE Data

### Abstract Text:

It has been proposed that differentially-expressed genes, aside from genetic variations affecting protein processing and functioning, between hybrid and its parents provide vital candidates for heterosis or hybrid vigor. Our previous work analyzed the potential effects of gene-expression difference on the heterosis of rice, based on serial analysis of gene expression (SAGE) data annotated with available full-length cDNA from an elite Chinese super-hybrid rice (*LYP9*) and its parental cultivars (*93-11* and *PA64s*) in three major tissue types at three different developmental stages. In this work, by using an improved strategy of tag-to-gene mapping and the two recently annotated genome assemblies (*93-11* and *PA64s*), we extendedly identified 10,268 high-quality tags, reaching a grand total of 20,595 together with the previous results. We further detected 8.5% and 5.9% physically-mapped genes that are differentially expressed among the triad (in at least one of the three stages) at *P*-values less than 0.05 and 0.01, respectively. We observed 406 up-regulated and 469 down-regulated genes ( $P < 0.05$ ) among 12 major gene expression patterns; and functional analyses of these genes highlighted the conclusion that up-regulated genes and enzymes in hybrid are mostly related to enhancing carbon assimilation in leaves and roots. In addition, we newly detected a group of up-regulated genes being related to male sterility and 442 down-regulated genes being related to carbon metabolism, signal transduction, and protein processing. The results provide us an insight on the multiple molecular mechanisms that contribute to heterosis, including variable gene expression patterns.

### Session Notes:



## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	16
<b>Contact Person:</b>	LIU Xiang-dong
<b>Email:</b>	<a href="mailto:xdliu@scau.edu.cn">xdliu@scau.edu.cn</a>
<b>Authors:</b>	LI Ya-juan, FANG San-hu, LU Yong-gen, LI Jin-quan and LIU Xiang-dong
<b>Affiliations:</b>	South China Agricultural University, Guangzhou China
<b>Abstract Title:</b>	Genetic Effects of Directional Selection on Seed Setting Rate in Hybrid offspring of Autotetraploid Rice

### Abstract Text:

Autotetraploid rice bears stronger biological heterosis than diploid rice, while its low seed setting rate has effects on wide utilization in rice breeding. Through studies in several successive years, some autotetraploid rice crosses with high seed setting rate were obtained. To investigate genetics of seed setting rate in autotetraploid rice, genetic effects of directional selection on seed setting rate and correlation between seed setting rate and agronomy traits were studied by analyzing the data of successive F<sub>1</sub>-F<sub>6</sub> offspring, which were derived from autotetraploid hybrids Guanglu'ai 4-4x×L202-4x with high seed setting rate. The results indicated that directional selection for high seed setting rate produced good effects and progenies from plant with high seed setting rate displayed high averaged seed setting rate. Under pressure from manual selection, average seed setting rate of genetic population and percentage of high-seed-setting-rate plants increased gradually with generations increased, positive correlation of seed setting rate was detected between progenitor and progeny populations, and genetic advance was small in directional selection for seed setting rate. It suggested that seed setting rate in autotetraploid rice were controlled by multi genes, frequency of homozygosis increased gradually with generations increased and strong pressure of directional selection were required to obtain stable high seed setting rate for many generations in autotetraploid rice. Correlation analysis indicated that number of panicles, length of flag leaf, width of flag leaf and exsertion of the first internode increased slightly and number of grain per panicle decreased during directional selection for high seed setting rate. It was indicated that directional selection for high seed setting rate coupled with attention to number of panicles, number of grain per panicle and exsertion of the first internode was helpful in improving traits simultaneously and would promote the application in practice of autotetraploid rice.

### Session Notes:

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	17
<b>Contact Person:</b>	Xiangyang Kang
<b>Email:</b>	<a href="mailto:kangxy@bjfu.edu.cn">kangxy@bjfu.edu.cn</a>
<b>Authors:</b>	Jun Wang, Xiangyang Kang, Daili Li and Yanchun Jing
<b>Affiliations:</b>	Beijing Forestry University, Beijing China
<b>Abstract Title:</b>	Cytological Mechanism of Triploid Induction with Colchicine after Pollination in <i>Populus</i>

### Abstract Text:

Using cytological techniques and genome *in situ* hybridization (GISH), mechanism of triploid induction with colchicine after pollination in *Populus* was studied. The results showed, on the basis of mastering the stigma receptivity accurately, 54-66h post-pollination was the optimal period to induce triploid plants in *P. pseudo-simonii* × *P. nigra* var. *lica*, and the highest ratio of obtained triploids was 66.7%. GISH revealed 38 chromosomes (two sets) were from female parent and only one set chromosomes were from male parent. So it could be concluded that 2n eggs were produced. By cytological observation, the effective period was just corresponding to the four-nucleate stage in embryo sac development, and a positive correlation was found between the percentage of four-nucleate embryo sacs and ratio of triploids ( $r = 0.6660$ ,  $P = 0.1024$ ). Compared with another ways for inducing triploids in *Populus*, treating embryo sacs at four-nucleate stage was the best efficient approach to produce 2n eggs. Considering the penetrating time of colchicine, the third mitosis during embryo sac development was the real object treated with colchicine, so it might be more sensitive to outer stimulations (i.e. colchicine). It suggested that the sensitivity of the third mitosis during embryo sac development had important significance to polyploidization and speciation in plant.

### Session Notes:

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	18
<b>Contact Person:</b>	Qixin Sun
<b>Email:</b>	<a href="mailto:qxsun62@public.bta.net.cn">qxsun62@public.bta.net.cn</a>
<b>Authors:</b>	Ramesh N. Pudake, Zhongfu Ni ,Yingyin Yao and Qixin Sun
<b>Affiliations:</b>	China Agricultural University, Beijing China
<b>Abstract Title:</b>	Cloning and Characterization of New Wheat Aquaporins -TaPIP1-2 and TaPIP1-3

### Abstract Text:

The protoplast intrinsic proteins (PIPs) form a large part of Aquaporin family of ancient origin and are found in bacteria, fungi, animals, and plants. PIPs act as channels in membranes to facilitate passive transport of water and some other substrates like CO<sub>2</sub>, glycerol or urea across the cell membrane. However, the majority of PIPs are characterized in rice and Arabidopsis, very few wheat members of the PIP family have been known and many more have to be identified. In earlier microarray experiment, we have identified that TaPIP1 is differentially expressed among the hybrid and its parent in wheat, which was later confirmed by quantitative RT PCR. To determine whether aquaporins have physiological roles during plant development in wheat, we cloned different genes encoding plasma membrane intrinsic proteins (PIPs) in Wheat. The full-length coding sequences of two new genes encoding PIPs were obtained by PCR on cDNA of roots at tillering stage and were named as TaPIP1-2 and TaPIP1-3. Both TaPIP1-2 and TaPIP1-3 were highly homologous with 95.89% identity in amino acid sequence; but the latter was 33 bp shorter than TaPIP1-2 in coding sequence. At cellular level we found more number of TaPIP1-3 transcripts than TaPIP1-2. Comparisons of this new gene sequence with conserved amino acid residues with other PIPs revealed that they have characteristic features of aquaporin. To get idea of possible functional role of these two different aquaporins, we transformed them in Arabidopsis and Yeast, and overexpression studies are underway.

### Session Notes:

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b> <b>Contact Person:</b> <b>Email:</b> <b>Authors:</b> <b>Affiliations:</b> <b>Abstract Title:</b>	19 Qixin Sun <a href="mailto:qxsun62@public.bta.net.cn">qxsun62@public.bta.net.cn</a> Xiao Song , Zhongfu Ni, Zhenxing Li, Haiyan Wu, Yinhong Zhang, Qixin Sun China Agricultural University, Beijing China Wheat ( <i>Triticum aestivum</i> L.) root proteome and differentially expressed root proteins between hybrid and parents
<b>Abstract Text:</b>  <p>To better understand the development of wheat root, a reference map of the major soluble proteins of wheat root was established using a combination of 2-DE and MALDI TOF MS and MS/MS, and a total of 450 protein spots were detected with silver staining in a pH ranges of 4 to 7, in which 285 spots corresponding to 243 proteins were identified. These identified proteins were grouped into diverse functional categories. In comparison with wheat leave proteome, in root, proteins involved in metabolism and transport were overrepresented, whereas proteins involved in energy, disease &amp; defense, transcription and signal transduction were under-represented. To further get an insight into the molecular basis of wheat heterosis, differential proteome analysis between hybrid and parents were performed. A total of 45 differentially expressed protein spots were detected, and both quantitative and qualitative differences could be observed. Moreover, 25 of the 45 differentially expressed protein spots were identified, which were involved in metabolism, signal transduction, energy, cell growth &amp; division, disease &amp; defense, secondary metabolism. These results indicated that hybridization between two parental lines can cause expression differences between wheat hybrid and its parents not only at mRNA levels but also at protein abundances.</p>	
<b>Session Notes:</b>	
Empty space for session notes	

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	20
<b>Contact Person:</b>	Qixin Sun
<b>Email:</b>	<a href="mailto:qxsun62@public.bta.net.cn">qxsun62@public.bta.net.cn</a>
<b>Authors:</b>	Zhang Yinhong Ni Zhongfu Yao Yingyin Zhao Jun Sun Qixin
<b>Affiliations:</b>	China Agricultural University, Beijing China
<b>Abstract Title:</b>	Identification of Differentially Expressed Genes in Root between Wheat Hybrid and Its Parental Inbreds Using Barley1 GeneChip

### Abstract Text:

Heterosis, or hybrid vigor refers to the phenomenon in which hybrids between two inbred varieties or lines exhibit greater than their inbred parents. Heterosis in plants is associated with increases in grain yield, vegetative growth rate, tolerance to pests and environmental stress, accelerated maturity, and many other changes in desirable agronomic characteristics. The phenomenon has been known for centuries, exploited extensively in crop production and has been a powerful force in the evolution of plants, but there is still no consensus as to the genetic basis, and even less is known about the molecular parameters associated with heterosis. It has been suggested that molecular foundation of phenotypic changes could reside in the variability of genome expression. Further analysis indicated that differential gene expression patterns in leaf tissue in rice, maize and wheat were correlated with heterosis. Previous studies detected significant difference in mRNA quantity and expression patterns between hybrids and their parental inbreds. Therefore, it is reasonable to speculate that differential gene expression between hybrids and their parents should be responsible for the observed heterosis. Microarray is a useful technology that offers a high-throughput analysis of differential gene expression. In this study, by using Affymetrix 22K Barley1 GeneChip, we reported the first genome-wide analysis of root transcriptome divergence between wheat hybrid and its parents. In addition, *in silico* and comparative mapping of differentially expressed cDNAs was also analyzed. The result is that a total of 1187 genes displayed expression difference between hybrid 3338/2463 and its parents, and can be clustered into eight differential expression patterns, including hybrid 3338/2463 expression levels greater than the high parent or less than the low parent, almost equal to one parent, only one or two materials expression. Further analysis revealed that among these 1187 genes, 975 genes shown high sequence similarity to the GenBank entries, and represented diverse functional categories, such as metabolism, cell growth and maintenance, signal transduction, response to stress, transcription regulation and others. Fourteen genes were selected for RT-PCR analysis and expression patterns of 9 (64.29%) genes were confirmed. Remarkably, 380 differentially expressed genes could be mapped on the Chinese Spring deletion bins, and with the number of genes in seven homoeologous groups being 158, 148, 121, 140, 132, 94 and 127 respectively. It was concluded that a combination of systematic identification of differentially expressed genes with comparative mapping would provide further insight into understanding of molecular basis

of heterosis

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	21
<b>Contact Person:</b>	Qixin Sun
<b>Email:</b>	<a href="mailto:qxsun62@public.bta.net.cn">qxsun62@public.bta.net.cn</a>
<b>Authors:</b>	Haiyan Wu, Yinhong Zhang, Zhongfu Ni, Zhen Su, Qixin Sun
<b>Affiliations:</b>	China Agricultural University, Beijing China
<b>Abstract Title:</b>	Root transcriptome genotyping and expression analysis by using Wheat Genechip® Genome Array
<b>Abstract Text:</b>	<p>Affymetrix oligonucleotide arrays have provided an important and versatile tool for measuring gene-expression and genotyping in a variety of genomes. Here we report root transcriptome genotyping and expression analysis by using Wheat Genechip® Genome Array, and two genotypes, that is common wheat 3338 and spelt wheat 2463, were used for study. The results indicated that 617 probe sets changed significantly between 3338 and 2463 in roots of seedling germinated after 10 and 20 days. Geneontology analysis revealed that the genes represented by 617 probesets are involved in different biological processes, including transport, nucleic acid binding, protein metabolism and transferase activity <i>et al.</i> MAS5 detection calls summary showed that about 28.52% of these different expressed (DE) probesets only present in one genotype, but absent in the other genotype. According to Affymetrix genechip design, each probeset on the chip, which may present a unique transcript in genome, is typically represented by 11 different 25bp-oligo pairs covering feature of the transcribed region of that transcript. The intensity of each PM probe which belongs to 617 DE probesets were also be analyzed. The results indicated that 76.18% DE probesets have at least 6 PM probes changed significantly. Single-feature polymorphism (SFP) discovery using these expression arrays can be helpful to high-through genotype wheat varieties. Using our self-developed SFP-sig and RPP (robustified projection pursuit) algorithm, we predicted 697 and 1061 probe sets which contain SFP probes. Taken the results of SFP and DE probesets together, there were 165 DE probesets contain SFP probes. In worthy to note that 44 probesets were detected to have differences only in transcript levels, which can be candidates of gene expression markers (GEMs). It can be concluded that SFP probes are not mainly but part source of variation in wheat allele expression diversity by checking SFP contained probesets Our results verified that gene expression measurements from Affymetrix Genechip® microarrays also can be leveraged to identify many types of polymorphism across the genome and can be an efficiently ways to developed markers in larger genetic population.</p>
<b>Session Notes:</b>	

## Submitting Abstract ICPHE 2007

<b>Submitting # :</b>	22
<b>Contact Person:</b>	DHONT Angelique
<b>Email:</b>	<a href="mailto:dhont@cirad.fr">dhont@cirad.fr</a>
<b>Authors:</b>	Nazeema Jannoo, Laurent Grivet, Nathalie Chantret, Olivier Garsmeur, Jean Christophe Glaszmann, Paulo Arruda and Angélique D'Hont
<b>Affiliations:</b>	Universidade Estadual de Campinas, Campinas, SP, Brazil
<b>Abstract Title:</b>	France Orthologous comparison in a gene-rich region among grasses reveals stability in the sugarcane polyploid genome.
<b>Abstract Text:</b>	<p>Sugarcane (<i>Saccharum</i> spp.) is an important grass that contributes 60% of the raw sugar produced worldwide and it has a high biofuel production potential. This non-cereal grass, probably has the most complex of all crop genomes studied to date, mainly due to the very high degree of polyploidy (&gt;10x), together with its interspecific origin. Modern sugarcane cultivars derive from interspecific crosses between the polyploid species <i>S. officinarum</i>, the domesticated sugar-producing species with <math>x=10</math> and <math>2n=8x=80</math>, and <i>S. spontaneum</i>, a vigorous wild species with <math>x=8</math> and <math>2n=5x=40</math> to <math>16x=128</math> and many aneuploid forms. Both species are thought to have an autopolyploid origin. Modern sugarcane are highly polyploid (more than decaploid) and aneuploid, with around 120 chromosomes and a genome size of around 10 000 Mb. Their meiosis mainly involves bivalent pairing and chromosome assortment results from a combination of polysomy and preferential pairing. Molecular cytogenetics and genetic mapping studies have shown that modern cultivars typically display 70 to 80% of chromosomes entirely derived from <i>S. officinarum</i>, 10 to 20% from <i>S. spontaneum</i> and a few chromosomes derived from interspecific recombinations.</p> <p>We investigated genome dynamics in this highly polyploid context by analyzing two homoeologous sequences (97 kb and 126 kb) in a region, bearing <i>Adh1</i> in sorghum, that has been thoroughly studied within the Poaceae family, revealing a complex history of local rearrangement in rice, sorghum and maize. Our findings indicated that the two <i>Saccharum</i> species diverged by 1.5-2 mya from one another and 8-9 mya from sorghum. The two sugarcane homoeologous haplotypes showed perfect colinearity as well as high gene structure conservation. Apart from the insertion of a few retro-transposable elements, high homology was also observed along the non-transcribed regions. Relative to sorghum, the sugarcane sequences displayed colinearity, with the exception of two genes present only in sorghum, and striking homology in most non-coding parts of the genome. The gene distribution highlighted high synteny and colinearity with rice and</p>

partial colinearity with each homoeologous maize region, which became perfect when the sequences were combined. The haplotypes observed in sugarcane may thus closely represent the ancestral Andropogoneae haplotype. This first analysis of sugarcane haplotype organization at the sequence level suggests that the high ploidy in sugarcane did not induce generalized reshaping of its genome, thus challenging the idea that polyploidy quickly induces generalized rearrangement of genomes. These results also consolidate the fact that sorghum is a choice model for sugarcane.

**Session Notes:**

## Attendees List ICPHE 2007

Name	Email	Affiliation
DHONT Angelique	dhont@cirad.fr	CIRAD, Montpellier Cedex 5, France
Xue Bai	baixue@nibs.ac.cn	National Institute of Biological Sciences, Beijing China
Hongwei Chen	Kunta_1979@126.com	Beijing Forestry University, Beijing China
Shanshan Cui		Beijing Forestry University, Beijing China
Xia Cui	xcui@genetics.ac.cn	Institute of Genetics and Developmental Biology, CAS, Beijing China
Weiwei Deng	wwdeng@genetics.ac.cn	Institute of Genetics and Developmental Biology, CAS, Beijing China
Yong Ding	yding@genetics.ac.cn	Institute of Genetics and Developmental Biology, CAS, Beijing China
Yuzhu Dong	yzdong@genetics.ac.cn	Institute of Genetics and Developmental Biology, CAS, Beijing China
Fatemeh Fadaie	fadaie572@yahoo.com	Shahid beheshty street, Research Center of Agricultural and Natural Resources of Gorgan Iran
Mingji Feng	mjfeng@genetics.ac.cn	Institute of Genetics and Developmental Biology, CAS, Beijing China
Donghui Fu	tm@webmail.hzau.edu.cn	Huazhong Agricultural University, Wuhan China
Jianwei Gao	Jianweigao3@yahoo.com	Shandong Academy of Agricultural Sciences, Jinan China
Xiaofeng Gu	Xfgu@sdu.edu.cn	Shandong Agricultural University, Taian China
Biaojian Guo	gbj9999@163.com	Shandong Agricultural University, Taian China
Yonghua Han	hanyh329@163.com	China Agricultural University, Beijing China
Guangming He	heguangming@nibs.ac.cn	National Institute of Biological Sciences, Beijing China
Jiayu He	yunli63@163.com	Beijing Forestry University, Beijing China
Dr. Edward Himelblau	ehimelbl@calpoly.edu	California Polytechnic State University, USA
Junyan Hu		Beijing Forestry University, Beijing China
Zanmin Hu	zmhu@genetics.ac.cn	Institute of Genetics and Developmental Biology, CAS, Beijing China
Jinping Hua	jinpings_hua@cau.edu.cn	China Agricultural University, Beijing China
Jinzhong Jiang	yunli63@163.com	Beijing Forestry University, Beijing China
Yunliang Jiang	yljiang723@yahoo.com.cn	Shandong Agricultural University, Taian China
Weiwei Jin	weiweijin@cau.edu.cn	China Agricultural University, Beijing China
Xiaojie Jin	yunli63@163.com	Beijing Forestry University, Beijing China
Naoki Kishimoto	naoki@nias.affrc.go.jp	Plant Genetic Engineering Research Unit Division of Plant Sciences Japan
Xiangfeng Kong	xfkong@genetics.ac.cn	Institute of Genetics and Developmental Biology, CAS, Beijing China
Jinsheng Lai	jlai@cau.edu.cn	China Agricultural University, Beijing China
Aili Li	liaili@caas.net.cn	Chinese Academy of Agricultural Sciences, Beijing

Daili Li	<a href="mailto:daili_81@126.com">daili_81@126.com</a>	China Beijing Forestry University, Beijing China
Guanglin Li	<a href="mailto:guanglin369@yahoo.com.cn">guanglin369@yahoo.com.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China

## Attendees List ICPHE 2007

Name	Email	Affiliation
Jingrui li	<a href="mailto:Lijingrui@nibs.ac.cn">Lijingrui@nibs.ac.cn</a>	National Institute of Biological Sciences, Beijing China
Libin Li	<a href="mailto:henryleesd@yahoo.com.cn">henryleesd@yahoo.com.cn</a>	Shandong Academy of Agricultural Sciences, China
Pengbo Li	<a href="mailto:lpbmhs@126.com">lpbmhs@126.com</a>	China Agricultural University, Beijing China
Pingchuan Li	<a href="mailto:lipch@genetics.ac.cn">lipch@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Shan Li	<a href="mailto:lishan@nibs.ac.cn">lishan@nibs.ac.cn</a>	National Institute of Biological Sciences, Beijing China
Suoping Li	<a href="mailto:lisp369@163.com">lisp369@163.com</a>	Henan University, Zhengzhou China
Yanhua Li	<a href="mailto:cnliyanhua@163.com">cnliyanhua@163.com</a>	Beijing Forestry University, Beijing China
Yin Li	<a href="mailto:liyirain@yahoo.com.cn">liyirain@yahoo.com.cn</a>	Zhongshan University, Guanzhou China
Yu Li	<a href="mailto:boopa@163.com">boopa@163.com</a>	Beijing Forestry University, Beijing China
Yun Li	<a href="mailto:yunli63@163.com">yunli63@163.com</a>	Beijing Forestry University, Beijing China
Qingzhi Liang		China Agricultural University, Beijing China
K. Yoong Lim	<a href="mailto:Y.K.Lim@qmul.ac.uk">Y.K.Lim@qmul.ac.uk</a>	Queen Mary University of London, UK
Baoshen Liu	<a href="mailto:liubs@sdau.edu.cn">liubs@sdau.edu.cn</a>	Shandong Agricultural University, Taian China
Bin Liu	<a href="mailto:bliu@genetics.ac.cn">bliu@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Chunyan Liu	<a href="mailto:cyliu@genetics.ac.cn">cyliu@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Jun Liu	<a href="mailto:jliu@genetics.ac.cn">jliu@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Man Liu	<a href="mailto:liumanbj@126.com">liumanbj@126.com</a>	Beijing Forestry University, Beijing China
Xiangdong Liu	<a href="mailto:xdliu@scau.edu.cn">xdliu@scau.edu.cn</a>	South China Agricultural University, Guangzhou China
Zhenlan Liu	<a href="mailto:littlep8909@hotmail.com">littlep8909@hotmail.com</a>	University of British Columbia
Zhujun Liu	<a href="mailto:liuzhj@genomics.org.cn">liuzhj@genomics.org.cn</a>	Beijing Genomic Institute, China
Falong Lu	<a href="mailto:FLLu@genetics.ac.cn">FLLu@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Haisheng Lu	<a href="mailto:haisheng.lu@monsanto.com">haisheng.lu@monsanto.com</a>	Monsanto Company, USA
Guangzheng Luo	<a href="mailto:gzluo@genetics.ac.cn">gzluo@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Jianxin Ma	<a href="mailto:maj@purdue.edu">maj@purdue.edu</a>	Purdue University, USA
Rongcai Ma	<a href="mailto:marongcai@baafs.net.cn">marongcai@baafs.net.cn</a>	Beijing Research Center of Agro-Biotechnology, China
Long Mao	<a href="mailto:maolong@caas.net.cn">maolong@caas.net.cn</a>	Chinese Academy of Agricultural Sciences, Beijing China
Lifang Niu	<a href="mailto:lfniu@genetics.ac.cn">lfniu@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Ramesh N. Pudake		China Agricultural University, Beijing
Brian E. Scheffler	<a href="mailto:bscheffler@ars.usda.gov">bscheffler@ars.usda.gov</a>	MSA Genomics Laboratory, USDA-ARS USA
Weixing Shan	<a href="mailto:wxshan@nwsuaf.edu.cn">wxshan@nwsuaf.edu.cn</a>	Northwest A & T University, Yanglin China
Andrey B. Shcherban	<a href="mailto:atos@bionet.nsc.ru">atos@bionet.nsc.ru</a>	Institute of Cytology and Genetics, Russia

Jinfeng Shi		Institute of Genetics and Developmental Biology, CAS, Beijing China
Shuhui Song	songsh@genomics.org.cn	Beijing Genomics Institute, CAS, Beijing China
Weining Song	sweining2002@yahoo.com	Northwest A & F University, Yangling China

## Attendees List ICPHE 2007

Name	Email	Affiliation
Xianwei Song	<a href="mailto:xwsong@genetics.ac.cn">xwsong@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Xiao Song		China Agricultural University, Beijing100094, China
Yi Sui	<a href="mailto:ysui@genetics.ac.cn">ysui@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Yufen Sun	<a href="mailto:yfensun@genetics.ac.cn">yfensun@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
MILOS TANURDZIC	<a href="mailto:milos@cshl.edu">milos@cshl.edu</a>	Cold Spring Harbor Laboratory USA
Bin Wang	<a href="mailto:bwang@genetics.ac.cn">bwang@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Daojie Wang	<a href="mailto:daojiawang@nwsuaf.edu.cn">daojiawang@nwsuaf.edu.cn</a>	Northwest A & T University, Yanglin China
Guixiang Wang	<a href="mailto:guixiangwangcau@sina.com">guixiangwangcau@sina.com</a>	China Agricultural University, Beijing China
Huan Wang	<a href="mailto:hwang@genetics.ac.cn">hwang@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Jun Wang	<a href="mailto:beilin_people@163.com">beilin_people@163.com</a>	Beijing Forestry University, Beijing China
Lei Wang	<a href="mailto:caaswvl@163.com">caaswvl@163.com</a>	Chinese Academy of Agricultural Sciences, Beijing China
Wei Wang	<a href="mailto:wangwei@nibs.ac.cn">wangwei@nibs.ac.cn</a>	National Institute of Biological Sciences, Beijing China
Xiujie Wang	<a href="mailto:xjwang@genetics.ac.cn">xjwang@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Huajun Wu	<a href="mailto:wuhuajun111111@163.com">wuhuajun111111@163.com</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Yufeng Wu	<a href="mailto:yfwu@genetics.ac.cn">yfwu@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Qin Xu	<a href="mailto:xuqin_87375396@163.com">xuqin_87375396@163.com</a>	China Agricultural University, Beijing China
Lu Yang	<a href="mailto:lyang@genetics.ac.cn">lyang@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Zujun Yang	<a href="mailto:yangzujun@uestc.edu.cn">yangzujun@uestc.edu.cn</a>	University of Electronic Science and Technology of China, Chengdu China
Yi Yuan	<a href="mailto:yiyuan@genetics.ac.cn">yiyuan@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Qianchun Zeng	<a href="mailto:Zqch1964@yahoo.com.cn">Zqch1964@yahoo.com.cn</a>	Dian-type Hybrid Rice Research Centre of Yunnan Province, Kunming China
Jixian Zhai	<a href="mailto:jxzhai@genetics.ac.cn">jxzhai@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Hui Zhang	<a href="mailto:zhanghui@nwnu.edu.cn">zhanghui@nwnu.edu.cn</a>	Northwest Normal University, Lanzhou China
Shengli Zhang	<a href="mailto:ysui@genetics.ac.cn">ysui@genetics.ac.cn</a>	Institute of Genetics and Developmental Biology, CAS, Beijing China
Sumei Zhang		Shandong Agricultural University, Taian China

Xi Zhang	zxada@163.com	China Agricultural University, Beijing China
Xueyong Zhang	xueyongz@public.bta.net.cn	Chinese Academy of Agricultural Sciences, Beijing China
Yinhong Zhang		China Agricultural University, Beijing100094, China

## Attendees List **ICPHE 2007**

Name	Email	Affiliation
Yong Zhang	zhangyong@genetics.ac.cn	Institute of Genetics and Developmental Biology, CAS, Beijing China
Yong Zhang	Zhangyong916@126.com	University of Electronic Science and Technology of China, Chengdu China
Yujun Zhang	yujun_zhang@hotmail.com	National Center of Gene Research, CAS China
Zhenghai Zhang	zhangzh2006@126.com	Beijing Forestry University, Beijing China
Baige Zhao	zbaige@oksate.edu	Oklahoma State University, Stillwater USA
Yingtao Zhao	ytzhao@genetics.ac.cn	Institute of Genetics and Developmental Biology, CAS, Beijing China
Qi Zheng	qizheng@genetics.ac.cn	Institute of Genetics and Developmental Biology, CAS, Beijing China
Jing Zhu	zhujing310@yahoo.com.cn	Chongqing Medical University, China
Yingguo Zhu	zhuyg@public.wh.hb.cn	Wuhan University, China