Agricultural Genomics 2015: From Variation to Improved Production
November 15-18, 2015–Shenzhen ManWan Harmona Resort, Shenzhen, China
MEETING PROGRAM

Sunday, November 15

09:00 – 22:00  Conference Registration

12:00 – 13:30  Lunch

18:30 – 20:00  Dinner

Monday, November 16

07:30 – 08:30  Breakfast

09:00 – 14:00  Conference Registration

12:00 – 13:30  Lunch

15:00 – 15:30  Opening Remarks
   Chair: Sanwen Huang

Myles Axton, Chief Editor, Nature Genetics, USA
Xingyuan He, Director General, Northeast Institute of Geography and Agroecology, CAS

15:30 – 18:30  Session I: Agricultural Genomics
   Chair: Weicai Yang

15:30  Can genomics help us meet the targets for future wheat production?
   Peter Langridge, Australian Centre for Plant Functional Genomics, Australia

16:00  Post transcriptional regulation mediated by protein arginine methylation
   Xiaofeng Cao, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

16:30  Harnessing Oryza natural variation to help solve the 10-billion people question
   Rod Wing, University of Arizona, USA
17:00   Genome organization of autotetraploid potato
        Sanwen Huang, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences

17:30   Towards plant pan-genomics
        David Edwards, University of Western Australia, Australia

18:00   Genetic imprinting and endosperm development of maize
        Jinsheng Lai, China Agricultural University

18:30 – 20:00   Dinner

20:00 – 22:30   Session I: Agricultural Genomics
                 Chair: Maarten Koornneef

20:00   Genome sequencing of Triticumurartu – the progenitor of wheat
        A genome
        Hongqing Ling, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

20:30   Sequencing and functional analysis of wheat chromosome 6B
        Jianzhong Wu, National Institute of Agrobiological Sciences, Japan

21:00   Rice genetics: from mechanisms to breeding
        Chengcai Chu, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

21:30   Genes underlying hypoxia adaptation of Tibetan domestic animals and their functional roles in tumorigenesis
        Dongdong Wu, Chinese Academy of Sciences

22:00   The genomic perspective on the invasive biology: exampled by the codling moth, Cydia pomonella
        Fei Li, Zhejiang University

Tuesday, November 17

07:00 – 08:00   Breakfast

08:00 – 10:00   Session II: Development and physiology
                 Chair: Zachary Lippman

08:00   A tale of tails: mechanisms of microRNA turnover in
08:30 Control of seed and organ size in plants
Yunhai Li, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

09:00 Genetic and hormonal control of vascular tissue formation in the Arabidopsis embryo
Dolf Weijers, Wageningen University and Research Centre, Netherlands

09:30 Decipherment of major loci controlling 24 agronomic traits in tomato by genome-wide association study
Xia Cui, Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences

10:00 – 10:30 Shenzhen Moment
Chair: Qian Qian
Shengyuan Gao, Director, Shenzhen Dapeng New District Management Committee
Yihuan Wu, Deputy Mayor, Shenzhen Municipal Government
Jiayang Li, President, Chinese Academy of Agricultural Sciences

10:30 – 11:00 Group Photo, Coffee Break

11:00 – 12:00 Session II: Development and physiology
Chair: Yunhai Li

11:00 Evolutionary novelty and artificial selection of soybean stem architecture
Jianxin Ma, Purdue University, USA

11:30 Returning to domestication to revitalize crop improvement: the florigen revolution
Zachary Lippman, Cold Spring Harbor Laboratory, USA

12:00 – 13:30 Lunch

13:30 – 15:30 Session III: Reproductive biology and heterosis
Chair: Zuhua He

13:30 Dominant gene action accounts for much of the unexplained
phenotypic variance in a maize GWAS and provides insight into heterosis
Patrick Schnable, Iowa State University, USA

14:00 A recently occurring tandem repeats yield NPT super rice by epigenetically releasing position-dependent depression of IPA1
Zuhua He, Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences

14:30 Genomic bases for seed development and heterosis in Arabidopsis, rice and wheat
Z. Jeffrey Chen, University of Texas, Austin, USA

15:00 Genomic study of complex traits in hybrid rice varieties
Xuehui Huang, Shanghai Institutes of Biological Sciences, Chinese Academy of Sciences

15:30 – 16:00 Coffee Break

16:00 – 18:30 Session IV: Stress and disease biology
Chair: Beat Keller

16:00 Molecular diversity of fungal disease resistance genes in cereals and their applications in breeding
Beat Keller, University of Zurich, Switzerland

16:30 Coordinated regulation of nodulation and flowering simultaneously improves N and P use efficiency in soybean
Hong Liao, Fujian Agriculture and Forestry University

17:00 Environmentally-responsive gene regulatory interaction networks in rice
Michael Purugganan, New York University, USA

17:30 Resistance gene identification in Brassica napus: a pan genome approach
Jacqueline Batley, The University of Western Australia, Australia

18:00 Dissecting the genetic basis and signaling network of shade avoidance response in Arabidopsis and maize
Haiyang Wang, Biotechnology Research Institute, Chinese Academy of Agricultural Sciences
18:30 – 20:30  Dinner

20:30 – 22:30  AGIS Night, Talk to me

Wednesday, November 18

07:30 – 08:30  Breakfast

08:30 – 10:00  Session V: Yield and nutritional improvement
   Chair: Peter Langridge

   08:30  New opportunities for G2P analysis in barley facilitated by a map-based genome sequence
   Nils Stein, IPK Gatersleben, Germany

   09:00  Combined genomics and metabolomics for phytochemical research in major crops
   Jie Luo, Huazhong Agricultural University

   09:30  From trait dissection to yield: the phenotype-to-gene route for resilient yields under water limitation
   Vincent Vadez, Consultative Group for International Agricultural Research, India

10:00 – 10:30  Coffee Break

10:30 – 12:00  Session VI: Germplasm, informatics and breeding
   Chair: Sarah Hearne

   10:30  Arabidopsis as model for QTL cloning using multiparent populations
   Maarten Koornneef, Max Planck Institute for Plant Breeding Research, Germany

   11:00  Association mapping for enhancing maize genetic improvement
   Jianbing Yan, Huazhong Agricultural University

   11:30  Saving the babies from the bathwater in genome-wide association studies
   Zhiwu Zhang, Washington State University

12:00 – 13:30  Lunch

13:30 – 15:30  Session VI: Germplasm, informatics and breeding
**Chair: Nils Stein**

13:30 The significance of aboriginal rice accessions on modern rice varieties  
Yue-Ie Hsing, Academia Sinica, Taiwan

14:00 Genomic exploration and use of genebank collections: early insights and experiences from seeds of discovery-maize  
Sarah Hearne, Consultative Group for International Agricultural Research (CGIAR)

14:30 Exploring wild soybean using a genomic approach  
Hon-Ming Lam, Chinese University of Hong Kong, HongKong

15:00 Natural variation of J locus adapts soybean in low latitude  
Fanjiang Kong, Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences

15:30 – 16:00 **Coffee Break**

16:00 – 17:30 **Session VI: Germplasm, informatics and breeding**  
**Chair: Jianbing Yan**

16:00 Multiple de novo genome sequences of hot pepper provide insights into species diversification in *Capsicum spp.*  
Doil Choi, Seoul National University, Korea

16:30 The impact of genome triplication event in Brassica on crop domestication  
Xiaowu Wang, Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences

17:00 Genetic improvement of nitrogen utilization in rice  
Jianru Zuo, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

17:30 – 18:00 **Closing Ceremony**  
**Chair: Rod Wing**

Qian Qian, Director General, Agricultural Genomics Institute at Shenzhen, CAAS  
Myles Axton, Chief Editor, Nature Genetics, USA  
Jiayang Li, President, Chinese Academy of Agricultural Sciences
18:30 – 20:00  Dinner