

SCIENTIFIC PROGRAM

SESSION LECTURE

No.45

Plant Genetics and Genomics
Room: 303AB

Co-Chairs: Bin Han



June M. Kwak



Day 3 October 29th (Monday) 8:30 – 12:00

Time	Speaker	Title
8:30-9:00	Bin Han <i>Shanghai Institute of Plant Physiology and Ecology, Chinese Academy of Sciences, China</i>	Unlocking genetic basis of complex traits and heterosis in rice
9:00-9:30	June M. Kwak <i>Daegu Gyeongbuk Institute of Science and Technology</i>	Cellular precision for cell surface integrity and cell fate control
9:30-10:00	Kenneth M. Olsen <i>Washington University in St. Louis, USA</i>	De-domestication and Evolutionary Genomics of Weedy Rice
10:00-10:30	Tea Break	
10:30-11:00	Jie Luo <i>Institute of Tropical Agriculture and Forestry, Hainan University, China</i>	Dissection of metabolic diversity in major crops
11:00-11:30	Zhixi Tian <i>Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China</i>	Survey for the key domestication genes in soybean



Bin Han

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Bin Han was elected as an academican of the Chinese academy of sciences in 2013. He is director of National Center for Gene Research, CAS-Center of Excellence for Molecular Plant Sciences, Shanghai Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. Professor Han is focusing on rice genome sequencing and re-sequencing, comparative genome analysis of rice subspecies, and rice functional genomics.



June M. Kwak

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June M. Kwak is interested in understanding how organisms recognize changes in their environment and evoke the necessary responses and adjust the developmental programs to adapt to the changes in their entire life. His research goal is to achieve a detailed understanding of the flexibility of cellular signaling networks and developmental programs using cellular model systems.



Kenneth M. Olsen

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The aims of his research are to understand the molecular basis of adaptation in plants, including genomic changes during crop domestication and the genetics of local climatic adaptation in wild plant species.



Zhixi Tian

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The aims of his research are to identify genes controlling important agronomical traits and to apply them into the soybean breeding through combination of association mapping, QTL mapping, map-based cloning along with comparative genomic approach, as well as construction and utilization of mutant database which will facilitate soybean germplasm enhancement and benefit soybean production.



Jie Luo

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His research group mainly investigates the genetic and biochemical bases of the metabolic diversity in major crops such as rice and maize using combined metabolomics, genomics, genetics, and biochemistry. He is working to integrate quantitative metabolomics into broader surveys of phenotypes and to characterize the link between metabolism and higher order phenotypes with the potential for metabolome-based crop improvement.