

CBI was well represented at Plant and Animal Genome (PAG) XXVII, January 12-16, 2019. San Diego, CA

Talks

1. PanGWAS: GWAS of the pan-genome provides new insights into *P. trichocarpa* phenotypic variation – Jay Chen, Doug Hyatt, Daniel Jacobson, Piet Jones, David Kainer, Wellington Muchero, Manesh Shah, Jared Streich, and Gerald Tuskan (ORNL)
2. The GWAS Times: A time-series aware GWAS to detect natural climate adaptations in Arabidopsis and *Populus* – Dan Jacobson, Jared Streich, Ashley Cliff, and Jonathan Romero (ORNL)
3. Large-scale systems biology approaches to integrated discovery: explainable-AI and supercomputing as the new microscope for complex systems – Dan Jacobson (ORNL)
4. Data science, computational, and AI – Dan Jacobson (ORNL)
5. Expression Quantitative Trait Locus Mapping in *Populus* – Jay Chen (ORNL)
6. Expanding the capabilities for plant genome-editing and synthetic biology – Degao Liu, Henrique De Paoli, Brian Mendoza, Cong Trinh (UT), Gerald Tuskan, and Xiaohan Yang (ORNL)
7. Rhizosphere microbial communities associated with switchgrass grown in marginal soils – Kelly Craven, Malay Saha, and Michael Udvardi (Noble Research Institute)

Posters

1. Your Daily GWATS: A time-series aware GWAS to detect natural climate adaptations in North America *Populus trichocarpa* – Dan Jacobson, David Kainer, Jared Streich, Ashley Cliff, and Jonathan Romero (ORNL)
2. High-resolution expression quantitative trait nucleotide (eQTN) mapping elucidates transcriptional regulation in *Populus trichocarpa* – Zin Zhang, Meng Xie, Yongil, Yang, Lee Gunter, Sara Jawdy, Tim Tschaplinski, Nancy Engle, Gerald Tuskan, Jay Chen, and Wellington Muchero (ORNL)
3. Understanding the epigenomic landscape and transcriptional architecture of switchgrass imposed with single and combinations of drought and heat stress – Malay Saha (Noble Research Institute)
4. The draft nuclear genome assembly of *Eucalyptus pauciflora*: new approaches to comparing de novo assemblies – David Kainer (ORNL)

Session Organizer

Weedy and invasive plant genomics – Neal Stewart, Jr. (UT)

Tools and Resource Session

The *Medicago truncatula* small signaling peptide database – Michael Udvardi and Malay Saha (Noble)

Other Attendees

- 2 Stephen DiFazio (WVU), David Macaya-Sanz (WVU), and Yuhong Tang (NOBLE)

PAG brings together over 3,000 leading genetic scientists and researchers in plant and animal research, and over 130 exhibits, 150 workshops, 1100 posters and over 1800 abstracts.

