**12th International Symposium on Rice Functional Genomics: Concurrent Session Speakers**

*Monday (11/17) 2:00-3:40*

Concurrent Session 3: Functional Genomics – Molecular Genetics

1) Fabio Fornara (University of Milan, Italy) - Genetic architecture of rice flowering in Mediterranean Europe

2) Jorge Gomez-Ariza (University of Milan, Italy) - Florigen-independent responses to photoperiod during floral transition at the shoot apical meristem of rice

3) Hiroyuki Tsuji (Nara Inst. of Science & Technology, Japan) - Coordination of flowering and gene expression by rice Hd3a florigen

4) Wanqi Liang (Shanghai Jiao Tong University, PRC) - The role of paralogous bHLH proteins in rice anther development

5) William Marande (CNRGV Plant Genomic Center, France) - Efficient genome locus identification using a non-gridded BAC library strategy

*Monday (11/17) 2:00-3:40*

Concurrent Session 4: Stress Biology – Mutants, Submergence & Oxidative Stress

1) Yue-ie Hsing (Academia Sinica, Taiwan) - Why the tagging efficiency is very low in rice insertion mutants?

2) Antonio Costa de Oliveira (Federal University of Pelotas, Brazil) - Evolution of the Sub1 locus in wild rice genomes

3) Narottam Dey (Visva-Bharati University, India) - Allelic Diversity study for linked SSRs and Sub1 loci in rice for submergence tolerance

4) Michael Frei (University of Bonn, Germany) Using functional genomics to study adaptation of rice to oxidative stress

5) Pallavi Singh (Natl. Inst. of Plant Genome Research, India) – The submergence tolerance gene – Sub1a1 – is regulated by a mitogen activated protein kinase during inundation in rice

*Monday (11/17) 2:00-3:40*

Concurrent Session 5: Evolutionary Biology

1) Derrick Zwickl (University of Arizona, USA) - Phylogenomic analysis of single-copy nuclear genes across the *Oryza*

2) Josh Stein (Cold Spring Harbor Laboratory, USA) – Creation and evaluation of an integrated phylogenomics resource for the *Oryza*

3) Pankaj Jaiswal (Oregon State University, USA) - Reference Rice Phylogeny

4) Jorge Duitama (International Center for Tropical Agriculture, Colombia) - Whole genome sequencing of elite rice cultivars reveals recurrent copy number variation, diversity patterns, and variety specific introgression events in *Oryza sativa* spp. *japonica* and *indica*

5) Francois Sabot (Institut de Recherche pour le Développement, France) - An extensive analysis of the African rice genetic diversity through a global genotyping and prospective massive sequencing

*Monday (11/17) 4:10-6:10*

Concurrent Session 6: Functional Genomics – High Throughput Genetics

1) Ki-Hong Jung (Kyung Hee University, South Korea) - Genome-wide identification and phenomic analyses of late pollen preferred genes conserved in *japonica* and *indica* cultivars

2) Paul Tanger (Colorado State University, USA) – Traditional and field scale high throughput phenotyping reveal multiple QTL from a large mapping population

3) Lizhong Xiong (Huazhong Agricultural University, PRC) - Combining high-throughput phenotyping and genome-wide association studies to unlock the genetic architecture of agronomical traits in rice

4) Christopher Heffelfinger (Yale University, USA) - Flexible and scalable genotyping-by-sequencing for rice population genomics

5) Mathias Lorieux (International Center for Tropical Agriculture, Colombia) - Nested-Association Mapping population of rice: first genotyping-by-sequencing results

6) Shizhong Xu (University of California - Riverside, USA) - Genomic hybrid breeding in rice

*Monday (11/17) 4:10-6:10*

Concurrent Session 7: Stress Biology - Drought

1) Sophia Henry (CIRAD, France) - OsSHR1 & OsSHR2 functions in rice root cortex formation

2) Daisuke Ogawa (NIAS/CREST, Japan) - Studies on the mechanism of drought tolerance *via* acetic acid

3) Chien-Ru Lin (Academia Sinica, Taiwan) - Negative regulators modulate the nutrient starvation signaling sensor SnRK1 in source-sink communication under abiotic stresses

4) Gunjan Sharma (National Inst. for Plant Genome Res., India) - Rice *OsiSAP7* negatively regulates ABA and water-deficit stress signalling

5) Su-May Yu (Academia Sinica, Taiwan) - A protein regulated by a stress-inducible promoter enhances root growth and abiotic stress tolerance in rice without a yield penalty

6) Hiroaki Tamaki (University of California - Davis, USA) - Control of rice grain yield by plant hormone inhibitors

*Monday (11/17) 4:10-6:10*

Concurrent Session 8: Evolutionary Biology

1) Jo Messing (Rutgers University, USA) - The for-ever-young genetic blueprint of *Spirodela polyrhiza*

2) Hajime Ohyanagi (Nat. Inst. of Genetics, Japan) - Deciphering the *Oryza officinals* genome sequence & construction of genomic information infrastructure for *Oryza* wild accessions

3) Tatiana V Tatarinova (University of Southern California, USA) - Analysis and prediction of gene-body DNA methylation in rice

4) Francis Quetier (University of Evry, France) – Scouting for the rice of the future

5) Guotian Li (University of California - Davis, USA) - Comparisons of two model rice varieties, *Kitaake* and *Nipponbare*

6) Jianwei Zhang (University of Arizona, USA) - Platinum standard reference genome sequencing: We can do it!

*Wednesday (11/19) 2:30-3:50*

Concurrent Session 13 – Functional Genomics: Rice & Bioenergy

1) Laura Bartley (University of Oklahoma, USA) - Functional genomics reveals enzymes that incorporate hydroxycinnamates into rice cell walls

2) Bettina Broeckling (Colorado State University, USA) - Identifying rice genes that control plant biomass

3) Li-Fen Huang (Yuan Ze University, PRC) - Manipulation of transitory starch accumulation increases bioethanol production from rice straw

4) Kangmei Zhao (University of Oklahoma, USA) - Exploring the regulation of grass secondary cell wall biosynthesis *via* gene network analysis in rice

*Wednesday (11/19) 2:30-3:50*

Concurrent Session 14 – Genome Biology – Repetitive Elements

1) Dario Copetti (University of Arizona, USA) – Comparative repeat and transposable element analysis in genomes assemblies and raw unassembled reads of closely-related *Oryza* species and the out group *Leersia perrieri*

2) Ning Jiang (Michigan State University, USA) – Genetic and epigenetic impact of mutator-like

elements in rice

3) Scott Jackson (University of Georgia, USA) - Identification and evolutionary analysis of TRIM transposons in 11 *Oryza* genomes

4) Rudie Antonise (KeyGene, Netherlands) - Molecular mutagenesis in rice for trait improvement

*Wednesday (11/19) 2:30-3:50*

Concurrent Session 15 – Functional Genomics & Genome Biology

1) Pankaj Jaiswal (Oregon State University, USA) - Plant Reactome: A reference resource for analyzing plant metabolic and regulatory pathways

2) Joseph Edwards (University of California - Davis, USA) - The microbiome of cultivated rice: Structure, variation and assembly of root-associated microbiota

3) Nidhi Dwivedi (Natl. Inst. of Plant Genome Res., India) - Functional study of MED15 in Rice

4) Zhi-Chang Chen (Okayama University, USA) - Characterization of a gene controlling root growth in rice