

Plant Genomes

Thursday, March 15—7:30 PM

KEYNOTE SPEAKERS

- 1 J. Chory, "A model linking multiple hormone pathways to light-regulated growth"
- 2 J.R. Yates, "Mass spectrometry driven biological discovery"

Session 1 NETWORKS I: DEVELOPMENT

FRIDAY 3/16/2007, 9:00 AM

J. Chory

#	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
3	Kim	Genome-wide views of aging gene networks	25
4	Baurle	A widespread role for the flowering time regulators <i>FCA</i> and <i>FLP</i> in small RNA-mediated silencing	12
5	Vaughn	Epigenetic variation in <i>A. thaliana</i>	12
6	Kakutani	Bonsai—Loss-of-function epigenetic mutation induced in the <i>DDM1</i> (decrease in DNA methylation) background	15
7	Benfey	Root systems biology	25
8	Gifford	A cell-specific N-responsive gene network controls <i>Arabidopsis</i> developmental plasticity	12
9	Pandey	Genomic analysis of guard cell specificity and signaling	12
10	Kryvych	Searching for the genes involved in development of <i>A. thaliana</i> trichomes on the single cell level	12
11	Paponov	Elucidation of auxin signaling network by chemical genetics	12

Session 2 COMPARATIVE GENOMICS

FRIDAY 3/16/2007, 2:00 PM

K. Frazer

#	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
12	Frazer	A genome-wide map of eight million SNPs in the laboratory mouse genome	25
13	Weigel	Hybrid necrosis—Autoimmunity as a common barrier to gene flow in plants	25
14	Purugganan	The nature of selection in plant genomes—Lessons from rice	25
15	Schwartz	Identification of a QTL in the FT upstream region using a new powerful RIL population	12
16	Town	Variations in gene expression across homologous regions of a triplicated region of the genome in different morphotypes of <i>B. oleracea</i>	12
17	Rokhsar	Reconstructing 150 million years of angiosperm genome evolution	12

Session 3 POSTER SESSION and WINE & CHEESE PARTY

FRIDAY 3/16/2007, 4:30 PM

#	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
18	Lightfoot	Leucine rich repeat domains expressed, purified and refolded from <i>E. coli</i> allow functional analysis of the LRR interactome in plants	
19	Koltai	Cross-species microarray hybridizations—A developing tool for studying diversity of plant species	

20	Canaran	Generic software tools for displaying molecular diversity data on the web
21	Carson	Characterizing novel abiotic stress associated genes in <i>A. thaliana</i> using a systems biology approach
22	Rabinowicz	Rough draft sequence of the castor bean genome
23	Chakraborty	Monitoring co-expression patterns of grass pea proteome under high salt, abscisic acid and cold stress
24	Morgante	Insights into the structure and evolution of the large gymnosperm genomes—Genomic DNA sequencing and analysis in Norway spruce (<i>P. abies</i>) and Ginkgo (<i>G. biloba</i>)
25	Dicto	Exploring the defense-related genes in <i>P. colubrinum</i> by cDNA subtraction
26	Rafalski	Distribution of genes, recombination, and repetitive elements in the maize genome
27	FU	An ultra-conserved exon-skipping event in plant transcription factor IIIA gene suggests the regulation of 5S rRNA transcription via alternative splicing
28	Gao	A novel protein is required for RNA-directed DNA methylation and transcriptional gene silencing in <i>Arabidopsis</i>
29	Gehring	Genomic analysis of gene regulation by transposable elements
30	Hunt	Phylogenetic analysis of NAC domain proteins in <i>Arabidopsis</i> , poplar and rice
31	Hurwitz	Cross-species analysis between wild rice and cultivated rice (<i>O. sativa</i>) in the OMAP project
32	Husaini	Overexpression of tobacco osmotin gene leads to salt stress tolerance in strawberry (<i>F. x ananassa</i> Duch.) plants
33	Ichikawa	The FOX hunting system—An alternative gain-of-function gene hunting technique
34	Itoh	Annotation, analysis and database of the rice genome
35	Jeong	FRO7, a chloroplast ferric chelate reductase in <i>Arabidopsis</i>
36	Grosse	Distribution of haplotypes of the barley eIF4E gene
37	Kim	The <i>Arabidopsis</i> VIT1 controls iron homeostasis in plants
38	Liang	Gramene, a grass comparative genome resource
39	Hong-bo	Microalgal genomic resources for comparative genomics
40	Michael	Diurnal and circadian transcript profiling defines functionally conserved noncoding elements between <i>Arabidopsis</i> , rice and poplar
41	Miyao	Retrotransposon insertion mutants and database for functional analysis of rice genes
42	Mohanty	A molecular framework for functional genomics in maize using tagged-GFP lines driven by native regulatory elements
43	Mohr	Computational recognition of cis-regulatory elements with variable order Bayesian trees
44	Mohr	Chromatin immunoprecipitation of seed specific transcription factors in <i>A. thaliana</i>
45	Narechania	Using mathematically-defined repeats to annotate plant genomes

46	Chakraborty	Expressed sequence tags and stress responsive transcriptome of chickpea illustrates predicted and unexpected genes and evolutionary perspective
47	Nilsson	<i>Terminal flower2</i> regulates auxin levels and auxin response in <i>A. thaliana</i>
48	Spiller	A cyanobacterial unorthodox phytochrome-like protein from <i>T. elongatus</i> BP-1 (tlr0924 gene product) is blue-green photoreversible
49	Orsi	Comparative genomics for the cloning of the major seed size gene in tomato—Identification of microsyntenic blocks and correlation with <i>Arabidopsis</i> seed size QTLs
50	Pasternak	The Maize Genome Sequence Browser
51	Popescu	<i>Arabidopsis</i> protein microarrays—A platform for the large scale functional analysis of proteins
52	Grosse	Computational recognition of cis-regulatory elements using VOMBAT
53	Morgante	Characterization of autonomous helitrons in monocots
54	Ren	RiceCyc—A metabolic pathway database for rice
55	Rushton	A genome-wide analysis of transcription factor families in tobacco
56	Sheridan	Compound B-A-A maize chromosome translocations and the segmental analysis of the maize genome
57	Hsing	Transcriptome and proteome analysis of soybean endosperm
58	Meisel	The Chilean gene hunt—A functional genomics approach towards identifying candidate genes associated with peach/nectarine fruit quality
59	Spooner	The Gramene Genome Browser—Visualization of annotation on plant genomes
60	Stein	Analysis of microsynteny in an orthologous region of rice, maize, and sorghum
61	Swarbreck	Gene annotation, a never ending quest
62	Li	The Cowpea Genespace Knowledge Base (CGKB)—A resource for molecular marker development and functional genomics
63	Town	Web services for <i>Arabidopsis</i> data integration
64	Tsugane	Epigenetic regulation of an active DNA transposon <i>nDart</i> and its application for gene tagging in rice
65	Tuskan	The <i>Populous</i> genome provides insights into genome evolution and function
66	Wu	Random-shear BAC library construction and genome gap closing molecular tools
67	Wulff	<i>LRA5</i> —An epigenetic component of <i>Arabidopsis</i> disease resistance
68	Yoshizumi	Gene trapping of the <i>Arabidopsis</i> genome with a firefly luciferase reporter
69	Ming	Recent origin of the papaya sex chromosomes
70	Yuan	Comparative functional genomics study of genes involved in low temperature germinability
71	Zhang	Annotation of cereal microRNA genes
72	Zhao	Annotation of the castor bean genome

73 Zhao Maize-rice synteny analysis and insights into the evolution of the two genomes

Session 4 NETWORKS II: RESPONSE TO ENVIRONMENT

FRIDAY 3/16/2007, 7:30 PM

J. Dangl

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
74	Dangl	Intracellular disease resistance pathways in <i>Arabidopsis</i>	25
75	Provart	Raising the bar for <i>Arabidopsis</i> research—Using large-scale data sets for hypothesis generation	12
76	Wildermuth	Selection for monofunctional isochorismate synthases in plants—Implications for salicylic acid biosynthesis	12
77	Michelmore	Comparative genomics of plant-pathogen specificity	25
78	Sederoff	Transcriptional and translational regulation of gravitropism in maize	12
79	Klink	Analysis of the infection process of <i>G. max</i> (soybean) by the plant pathogen <i>H. glycines</i> , (soybean cyst nematode) using microarrays and laser capture microdissection (LCM)	12

Session 5 PROTEOMICS AND METABOLOMICS

SATURDAY 3/17/2007, 9:00 AM

M.L. Guerinot

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
80	Willmitzer	Small molecules, genes and complex traits	25
81	Guerinot	Metals, mutants and mayhem—What we have learned from ionomics	25
82	Gerstein	Understanding protein function on a genome-scale using networks	25
83	Dinesh-Kumar	High-density <i>Arabidopsis</i> protein microarrays to study protein-protein interactions	25
84	Briggs	High-throughput quantitative proteomics of plant tissue	12
85	Van Wijk	Large scale comparative proteome analyses to study leaf development and cellular differentiation in <i>Arabidopsis</i> and maize	12
86	Murray	Proteomic analysis of peripheral membrane proteins in the <i>A. thaliana</i> genome	12

Session 6 NEW TECHNOLOGIES

SATURDAY 3/17/2007, 1:30 PM

K. Birnbaum

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
87	Hughes	Cracking the second genetic code—Building a vocabulary of DNA-protein interactions specificities	25
88	Birnbaum	A functional genomics system to address genetic redundancy	25
89	Jackson	Fluorescent protein tagged maize lines for cell biology and genomics applications	25
90	Schwab	Gene silencing with an artificial microRNA library covering the <i>Arabidopsis</i> genome	12

Session 7 WORKSHOP: RESOURCES

SATURDAY 3/17/2007, 3:45 PM

J. Ecker / M. Snyder

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
91	Scholl	The <i>Arabidopsis</i> Biological Resource Center—Current acquisitions and activities	12
92	Katari	VirtualPlant—A software platform to support systems biology research in the post-genomic era	12
93	Lam	Chromatin charting—Identification and characterization of position effect loci in the <i>Arabidopsis</i> genome	12

Saturday, March 17—5:30 pm**KEYNOTE SPEAKER**

94 D. Baulcombe, “Short silencing RNA networks”

Session 8 TRANSLATIONAL GENOMICS

SUNDAY 3/18/2007, 9:00 AM

J. Leach

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
95	Leach	Approaches to broad-spectrum durable resistance in rice	25
96	Deng	Global identification and characterization of transcriptionally active regions in the rice genome	25
97	Chen	An integrated study of indirect defense against insects in rice—From ecology to metabolomics to transcriptomics to responsible genes	12
98	Belo	Natural allelic variant of fatty acid desaturase detected by whole genome scan increases oleic level by 35% in maize	12
99	Lightfoot	Use of the Soybean Genome Database (SoyGD) for whole genome annotation—A tool for integrated legume biology	12