

**Report of IUFRO Unit 2.04.10 – Genomics
2011**

Coordinator: Carl Douglas

Deputies: Stephen DiFazio, Patricia Favre

The primary activity of this unit is to meet annually for a one-day workshop hosted at the Plant and Animal Genome (PAG) meeting in January of each year.

The 2011 annual meeting was held on January 16, 2011 at PAG XIX in San Diego, CA, USA.

Twenty-two talks were presented at the Workshop, selected from submitted abstracts. The agenda of the Workshop is attached or can be viewed at <http://www.intl-pag.org/19/19-foresttree.html>)

Abstracts of talks presented were published by PAG XIX on-line, and may be viewed at <http://www.intl-pag.org/19/abstracts/>. Forest Tree Workshop abstracts are W226 through W247 at this site.

The 2012 meeting will be held as the Forest Tree Workshop at PAG XX, January 15, 2012, San Diego CA.

Unfortunately, a photo of the 2011 meeting is not available.

Sunday - All day, 16 January 2011 --- 8:00 am - 6:00 pm



Forest Trees Workshop - Sunrise Room

Organizers: [Carl Douglas](#), University of British Columbia

(cdouglas@interchange.ubc.ca)

and

[Stephen DiFazio](#), West Virginia University

(stephen.difazio@mail.wvu.edu)

and

[Patricia Faivre](#), INRA

(faivre@evry.inra.fr)

(This workshop is also the annual meeting of the International Union of Forestry Research Organizations): (<http://iufro.boku.ac.at/iufro/iufro.net/d2/hp20410.htm>)

Speakers:

8:00-8:10

[Carl Douglas](#), University of British Columbia (carl.douglas@ubc.ca)

"Opening Remarks and Announcements"

8:10-8:30

[Alexander Myburg](#), University of Pretoria (zander.myburg@up.ac.za)

"Assembly and Annotation of the Eucalyptus Genome Sequence"

8:30-8:50

[Martin Ranik](#), Oregon State University (martin.ranik@oregonstate.edu)

"Transcriptomic analysis of floral development in Eucalyptus grandis by mRNA sequencing"

8:50-9:10

[John Carlson](#), Pennsylvania State University (jec16@psu.edu)

"Sequencing the genome of Chinese chestnut (Castanea mollissima)"

9:10-9:30

[Ting Li](#), Oak Ridge National Laboratory (lit1@ornl.gov)

"Discovery of non-classical signatures in small proteins in Populus, Vitis, Arabidopsis, and Glycine"

9:30-9:50

[Christina Quinn](#), State University of New York (crquinn@gmail.com)

"The roles of novel and differentially expressed microRNAs in loblolly pine pollen germination"

10:10-10:30

[Ujwal Ranjit Bagal](#), The University of Georgia (bujwal@uga.edu)

"Phylogenomics of the phenylalanine ammonia lyase gene family in Pinus taeda and other conifers"

10:30-11:00

[Jim Mattsson](#), Simon Fraser University (jmattss@sfu.ca)

"A genomics approach to gene discovery related to ungulate browsing resistance in western red cedar (Thuja plicata)"

11:00-11:20

[Juan Jesus Molina-Rueda](#), Rutgers University (jjmolina@andromeda.rutgers.edu)

"The drought stress response in GS poplars involves alterations in expression of the superoxide dismutase gene family"

11:20-11:40

[Andrew Groover](#), USDA Forest Service (agroover@fs.fed.us)

"Characterization of Class III HD ZIP transcription factors that regulate cell differentiation and tissue polarity during secondary growth"

13:00-13:20

[Dario Grattapaglia](#), EMBRAPA (dario@cenargen.embrapa.br)

"High realized accuracies of genomic selection for volume growth and wood density in Eucalyptus breeding populations with contrasting effective sizes"

13:20-13:40

[Márcio Resende Jr](#), University of Florida (mresende@ufl.edu)

"Genomic selection and next-generation genotyping to hyper-accelerate pine breeding "

13:40-14:00

[Jaime Zapata-Valenzuela](#), North Carolina State University (jazapata@ncsu.edu)

"Genomic selection in a cloned population of loblolly pine "

14:00-14:20

[Vikram Chhatre](#), Texas A&M University (crypticlineage@gmail.com)

"High-density SNP genotyping of east-Texas loblolly pine (Pinus taeda)" 

14:40-15:00

[Jill Wegrzyn](#), University of California, Davis (jlwegrzyn@ucdavis.edu)

"Bioinformatic solutions for data storage, analysis, and interpretation in forest genomics: overview of the tools and resources from the Dendrome project"

15:00-15:20

[Nathalie Pavy](#), Université Laval (nathalie.pavy@sbf.ulaval.ca)

"How SNPs are distributed across 19,000 expressed genes in the gymnosperm white spruce"

15:20-15:40

[Brian J. Knaus](#), USDA Forest Service (bknaus@fs.fed.us)

"Another step for conifer genomics: A Douglas-fir transcriptome"

15:40-16:00

[Jeff Dean](#), University of Georgia (jfddean@gmail.com)

"The Pinus taeda BAC Browser"

16:20-16:40

[Leandro Gomide Neves](#), University of Florida (gomide@ufl.edu)

"Whole-exome sequencing and genotyping in the loblolly pine (Pinus taeda) megagenome"

16:40-17:00

[Sara Pinosio](#), Università di Udine (pinosio@appliedgenomics.org)

"Genome-wide structural variation in poplar "

17:00-17:20

[Stefania Giacomello](#), Università di Udine (giacomello@appliedgenomics.org)

"Sequence and polymorphism map of the Populus nigra genome from a de novo assembly approach"

17:20-17:40

[Hua Bao](#), University of British Columbia (baohua100@hotmail.com)

"Xylem transcriptome analysis of SNP diversity and alternative splicing variation in Populus trichocarpa "

17:40-18:00

[Nathaniel Street](#), Umeå University (nathaniel.street@plantphys.umu.se)

"Sequencing and annotating the genome of Populus tremula to facilitate genome-wide association mapping in the Swedish aspen collection"

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