

ProCoGen final open conference and workshops
Promoting Conifer Genomic Resources
30th November – 4th December 2015
Orléans, France

Centre de Conférences d'Orléans, Orléans, France

Agenda

Monday, November 30 th 2015	
13.00 – 13.40	Opening
<ul style="list-style-type: none"> • María-Teresa Cervera and Carmen Díaz-Sala, INIA-CIFOR and Universidad de Alcalá (Spain) : Introduction to ProCoGen & conference [ProCoGen] • Jean Bousquet, University of Laval (Canada) : Opening conference: current state and future prospects of the conifer genomics [to be confirmed] 	

Monday, November 30 th 2015	
14.00 – 18.00	Session 1. Structural genomics of conifer species Chairman: Pär Ingvarsson (University of Umeå), Yves Van de Peer (Flanders Institute for Biotechnology)
<ul style="list-style-type: none"> • Nathaniel Street, University of Umeå (Sweden) : <i>Picea abies</i> genome sequencing [Invited speaker] • John Mackay, Oxford University (UK) : <i>Picea glauca</i> genome sequencing [to be confirmed] • Jill Wegrzyn, University of Connecticut (USA) : Sequence assembly & annotation in <i>Pinus taeda</i> [Invited speaker] • Pär Ingvarsson, University of Umeå (Sweden) : <i>Pinus sylvestris</i> genome sequencing [ProCoGen] 	
<i>Coffee break</i>	
<ul style="list-style-type: none"> • Outi Savolainen, University of OULU (Finland) : SNP detection [ProCoGen] • Daniel Peterson, Mississippi State University (USA) : Genome sequencing strategies [Invited speaker] • Kostya Krutovsky, University of Göttingen (Germany) : <i>Pinus sibirica</i> and <i>Larix sibirica</i> genome sequencing [Invited speaker] • Jérôme Salse, INRA French National Institute for Agricultural Research (France) : Karyotype and gene order evolution from reconstructed extinct ancestors highlight contrasts in genome plasticity of modern rosid crops [Invited speaker] 	

- Selected oral presentations (x3)

Tuesday, December 1st 2015

8.30 – 14.10

Session 2. Functional Genomics of conifer species

Chairman: Francisco Canovas (University of Malaga), Sara von Arnold (Swedish University of Agricultural Sciences), Luc Harvengt (FCBA)

- Phillip Wilcox, University of Otago (New Zealand) : Genomic and genetic characteristics of the exome capture/transcriptome [Invited speaker]
- Francisco Cánovas, University of Malaga (Spain) : *Pinus pinaster* transcriptome dynamics [ProCoGen]
- Célia Miguel, iTQB (Portugal) : *Pinus pinaster* miRNAs [ProCoGen]
- Carl Gunnar Fossdal, Norwegian Forest and Landscape Institute (Norway) : Functional genomics of *Picea abies*: development and adaptation [ProCoGen]

Coffee break

- Sara von Arnold, Swedish University of Agricultural Sciences (Sweden) : Transcription regulatory networks associated to development and other key processes [ProCoGen]
- Jeffrey Dean, Mississippi State University (USA) : Genetic control of adaptive traits in *P. taeda* [Invited speaker]
- University of British Columbia, (Canada) : Functional genomics in white and Sitka spruce and on conifer defense systems [Invited speaker]
- Luc Harvengt, FCBA Institut Technologique Forêt Cellulose Bois-construction Ameublement (France) : Epigenetic dynamics associated to growth and adaptation [ProCoGen]

Lunch

- Selected oral presentations (x4)

14.30 – 19.00

Session 3. Comparative Genomics of conifer species

Chairman: Maria-Teresa Cervera (INIA-CIFOR), Lieven Sterck (Flanders Institute for Biotechnology)

- Saneyoshi Ueno, Forestry and Forest Products Research Institute (Japan) : *Cryptomeria japonica* [Invited speaker]
- Zander Myburg, University of Pretoria (South Africa) : Angiosperms analysis: Eucalyptus genome [to be confirmed]

- Matias Kirst, University of Florida (USA) : Populus [Invited speaker]
- INRA, (France) : Comparative mapping Pinaceae [ProCoGen]
- Jose Antonio Cabezas, INIA-CIFOR (Spain) : ProCoGen comparative mapping based on exome capture [ProCoGen]

Coffee break

- Pär Ingvarsson on behalf of Amanda de La Torre, Swedish University of Agricultural Sciences (Sweden) : Conifer comparative genome analysis [ProCoGen]
- Nathalie Pavy, Laval University (Canada) : Comparative study of *Picea* species [to be confirmed]
- Flanders Institute for Biotechnology, (Belgium) : ProCoGen Genome portal: Plaza for gymnosperms [ProCoGen]
- Toni Gabaldon, Fundacio Privada Centre de Regulacio Genomica (Spain) : Phylogenomics analysis for the conifer species [ProCoGen]
- Selected oral presentations (x4)

Wednesday, December 2 nd 2015	
8.30 – 14.10	Session 4. Translational Genomics of Conifer species Chairman: Leopoldo Sanchez (INRA), Marco Bink (Wageningen UR)
<ul style="list-style-type: none"> • Stephen Cavers, NERC Centre for Ecology and Hydrology (UK) : Genomic tools and genetic conservation • Jean-Marc Bouvet, CIRAD French agricultural research and international cooperation organization (France) : Multi-trait genomic selection for breeding Eucalyptus hybrids - importance of additive and non-additive effects [Invited speaker] • Marco Bink / Joost van Heerwaarden, Wageningen UR Biometrics (Netherlands) : Optimal uses of genomic information in breeding programs: a simulation study [ProCoGen] • Laurent Bouffier, INRA French National Institute for Agricultural Research (France) : Integration of molecular tools into the maritime pine breeding program in France [ProCoGen] 	
<i>Coffee break</i>	
<ul style="list-style-type: none"> • Santiago Gonzalez-Martinez, INRA French National Institute for Agricultural Research (France) : Back to nature: candidate genes, population genomics and prediction of maladaptation in natural populations [Invited speaker] • Leopoldo Sanchez, INRA French National Institute for Agricultural Research (France) : Genetic diversity in GS [ProCoGen] • John Hickey (UEDIN), University of Edinburgh - Roslin Institute (UK) : Some insights of future developments in GS [to be confirmed] • Luc Harvengt, FCBA Institut Technologique Forêt Cellulose Bois-construction Ameublement (France) : Economic evaluation of GS: Maritime pine and Sitka spruce case studies [ProCoGen] 	
<i>Lunch</i>	

<ul style="list-style-type: none"> • Giovanni Vendramin, CNR Italian National Research Council (Italy) : Designing core collections from natural range distributions [ProCoGen] • John Woolliams, University of Edinburgh - Roslin Institute (UK) : RAD sequencing in Sitka Spruce for Genomic Selection [ProCoGen] • Selected oral presentations (x4) 	
14.20 – 15.00	Session 5. Wrap-up presentation by key-note speaker on take-home messages and prospects
<ul style="list-style-type: none"> • Jean Bousquet, University of Laval (Canada) : Wrap-up [to be confirmed] 	
<i>Coffee break</i>	

ProCoGen internal meeting

Wednesday, December 2nd 2015	
15.15 – 18.00	ProCoGen Meeting [only for members of ProCoGen consortium]
<ul style="list-style-type: none"> • Pending activities & future prospects, dissemination and management • General Assembly Meeting (management) 	
19.30 –	Social dinner [open to all conference attendants]

ProCoGen Training Workshop
Practicalities of marker and genome-assisted selection
3rd December 2015
Orléans, France

Thursday, December 3 rd 2015	
8.00 – 16.00	Practicalities of marker and genome-assisted selection
<ul style="list-style-type: none"> • John Hickey, University of Edinburgh - Roslin Institute (UK) : Data imputation; genomic relationships [to be confirmed] 	
<i>Coffee break</i>	
<ul style="list-style-type: none"> • Marco Bink / Joost van Heerwaarden, Wageningen UR Biometrics (Netherlands) : Association and mapping [ProCoGen] 	
<i>Lunch</i>	
<ul style="list-style-type: none"> • Leopoldo Sanchez, INRA French National Institute for Agricultural Research (France) : GS evaluation and case studies [ProCoGen] 	
<i>Coffee break</i>	

ProCoGen Dissemination Workshop
From our labs to your forests
3rd December 2015
Orléans, France

Thursday, December 3 rd 2015	
8.00 – 16.00	From our labs to your forests
	<ul style="list-style-type: none">• Transcriptomic tools and applicability*
	<i>Coffee break</i>
	<ul style="list-style-type: none">• Comparative genomics*
	<i>Lunch</i>
	<ul style="list-style-type: none">• Breeding, forest practices and dissemination*
	<i>Coffee break</i>

*details to follow soon

ProCoGen Dissemination Workshop
Transfer of genomic tools to breeding programs
4th December 2015
Orléans, France

Thursday, December 3 rd 2015		
16.30 – 18.00	Transfer of genomic tools to breeding programs	
<ul style="list-style-type: none"> • Panorama of breeding programs in Europe [Invited speaker] • How to start from scratch a genomic characterization (genotyping/sequencing) for a species with little or no sequence resources? [ProCoGen] 		
Friday, December 4 th 2015		
8.30 – 12.00	Transfer of genomic tools to breeding programs	
<ul style="list-style-type: none"> • How to build up a core collection from natural ranges, with the aim of compiling a species reference collection, a discovery panel, or a base for breeding? [ProCoGen] • Can genomics simplify current breeding without the cost of a genome-wide approach? [ProCoGen] 		
<i>Coffee break</i>		
<ul style="list-style-type: none"> • Steps to setup a proof-of-concept genomic selection initiative. [ProCoGen] • Why and how to handle genetic diversity in a genomic selection program? [ProCoGen] 		
<i>Lunch</i>		