

ProCoGen 2nd Training Workshop

Alcalá de Henares, February 19th – 21st 2014

Conifer Functional Genomics: Analysis of gene networks involved in conifer adaptation

International Conference Room, [University of Alcalá](#), Alcalá de Henares, Spain

The European Commission launched in 2012, under its 7th Framework Programme on Research the project ProCoGen: *Promoting a functional and comparative understanding of the conifer genome, implementing applied aspects for more productive and adapted forests.*

ProCoGen (www.procogen.eu) is an integrated research, development and education outreach-minded project aimed at maintaining / ensuring production services of forest ecosystems in the frame of global change. The main objective of the project is to develop an integrative and multidisciplinary genomic research in conifers to unravel genome organization and to identify genes and gene networks controlling important ecological and economic traits, such as those related to the control and the reduction of climatic change impact in relation to growth, drought or cold stress and, thus, provide tree breeders with tools for precise selection.

Besides the research activities, ProCoGen fosters to provide training to the participants through a set of Training Workshops, whose main goal is providing information on new outcomes as well as to explore, to promote and to strength collaborations.

The second Training Workshop, "Conifer Functional Genomics: analysis of gene networks involved in conifer adaptation", will be focused on genomic-based approaches for the study of the functional regulation of growth and adaptive responses to abiotic stresses.

Agenda

Wednesday February 19th 2014

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| 16.30 – 18.00 | Overview on Functional Genomics |
| <ul style="list-style-type: none"> • Pär Ingvarsson, University of Umeå (Sweden): Conifer Functional Genomics: The case of <i>Picea abies</i> [30'] • Toni Gabaldón, CRG (Spain): Functional and evolutionary implications of gene orthology [30'] | |

Thursday February 20th 2014

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| 09.00 - 10.00 | Session I: Tools in Conifer Functional Genomics |
| <ul style="list-style-type: none"> • Jose Luis García, CIB (Spain): New technologies to sequence complex genomes [30'] • Yves van de Peer, VIB UGent (Belgium): Bioinformatic tools to analyze complex genomes [30'] | |
| <i>10.00 - 10.30 Coffee break</i> | |
| 10.30 - 12.00 | Session I: Tools in Conifer Functional Genomics (cont.) |
| <ul style="list-style-type: none"> • Celia Miguel, iTQB (Portugal): Epigenetics and Epigenomics of complex genomes [30'] • Kermit Ritland, University of British Columbia (Canada): Genetical genomics and gene network reconstruction [30'] • Nathalie Pavy, John Mackay and Jean Bousquet, Université Laval (Canada): The landscape of SNP diversity and relationships with gene function and expression in white spruce [30']. | |
| <i>12:30-14:30 Lunch</i> | |
| 14.30 - 16.30 | Session II: World-Wide Initiatives in Conifer Functional Genomics |
| <ul style="list-style-type: none"> • John Mackay, Université Laval (Canada): Functional Genomics in <i>Picea glauca</i>. [30'] • Jeffrey Dean, University of Georgia (USA): Functional genomics in <i>Pinus taeda</i>. [30'] • Francisco M. Cánovas, Universidad de Málaga (Spain): Functional Genomics in <i>Pinus pinaster</i> [30'] • Harry Wu, SLU (Sweden): Functional Genomics in <i>Pinus radiata</i> [30']. | |
| <i>16.30 - 17.00 Coffee break</i> | |
| 17.00 – 17:30 | Session III: Conifer Functional Genomics case-study |
| <ul style="list-style-type: none"> • Carl Gunnar Fossdal, NFLI (Norway): Functional genomics of development and adaptation in <i>Picea abies</i>. [30'] | |

Friday, February 21st 2014

09.30 - 10.30 Session III: Conifer Functional Genomics case-study (cont.)

- Maite Cervera, INIA-CIFOR (Spain): Functional genomics of drought response in *Pinus pinaster* [30']
- Matias Kirst, University of Florida (USA): Functional Genomics of Plant Evolution: How EVE leads the flowering plants to dominate the world [30']

10.30 - 11.00 Coffee Break

11.00 – 12.00 Final lecture

- Diana Coman, ETH Zurich (Switzerland): Linking the circadian clock to the specialized metabolism using gene co-expression networks