

The systems biology of aspen wood development

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Black cottonwood (*Populus trichocarpa*) is the model organism for tree biology in general and wood development in particular. Umeå Plant Science Centre (UPSC) is currently undertaking *de novo* genome assembly of Aspen (*Populus tremula*) as well as a large-scale RNA-Seq transcriptomics study of Aspen wood development. We employ systems biology methods to reverse-engineer the regulatory network of wood development and use this network to describe gene interactions underlying complex emergent phenotypes in wood and to identify central regulators of wood development.

We have used next generation sequencing (RNA-Seq) to quantify mRNA and sRNA across developing wood (30 samples) in five aspens. The data is part of a larger study where metabolomics and proteomics data are also being generated. We are using the inferred network to describe wood-related phenotypes in transgenic trees by combining transcriptomics, proteomics and metabolomics profiling. The aim is to iteratively use data from perturbation experiments to improve the wood-network and to use the improved wood-network to identify target genes for future transgenic collections.

To support biologists in applying systems biology methods, we have updated the Pop Genie (*Populus* Genome Integrative Explorer) resource with integrated tools for exploring gene networks and patterns of gene expression in transcriptomics studies.

Biography

Torgeir R. Hvidsten was born in Oslo, Norway, in 1975. He received his M.S. degree in computer science from the Norwegian University of Science and Technology, Trondheim, Norway, in 2000, and his Ph.D. degree in bioinformatics from the Linnaeus Center of Bioinformatics, Uppsala University, Sweden, in 2004. Since 2008, he is an Assistant Professor at Umeå Plant Science Center, Umeå University, Umeå, Sweden. He is mainly interested in gene regulation in a systems biology context, inference of regulatory networks, integration of transcriptomics, proteomics, and metabolomics data and comparison of networks across species.