UMEÅ UNIVERSITY

What makes a tree a tree?

Regulatory network controlling wood formation in coniferous and angiosperm forest tree species

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Academic dissertation

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Abstract

What makes a tree a tree?
The capacity to form and maintain woody tissue has been key for the ecological success and economic relevance of forest trees. While fundamental cell types and developmental processes are common to most trees, there are significant differences between the two main tree lineages: angiosperms and gymnosperms. Comparative genomic research has dramatically expanded our understanding of plant genome evolution, with several studies demonstrating that the transcriptional programmes underlying xylogenesis are largely conserved between lineages. Modern research suggests that both speciation and intraspecific variation are often the result, not only of coding sequence mutations, but also of shifts in gene expression regulation.
The aim of this thesis was to elucidate how genomic architecture and regulatory programmes govern wood development and secondary growth evolution. By combining comparative genomics with high-resolution spatial transcriptomics across six angiosperm and gymnosperm species, this research establishes a multi-layered regulomic and evolutionary framework for studying wood formation.
The results identified multiple regulatory gene groups linked to wood evolution and development and generated significant genomic resources. In particular, chromosome-scale reference genomes were generated for two conifer species, and an "evo-devo" resource for wood was established using a high-resolution comparative regulomic framework across across wood differentiation layers in six tree species. Furthermore, a modified DNA Affinity Purification sequencing (DAP-seq) protocol was developed and optimised for mature woody tissues.
These resources can facilitate the identification of conserved and lineage-specific regulators, providing a critical blueprint for precision breeding and targeted genome engineering. Ultimately, these findings can contribute to the development of advanced materials and the transition toward a carbon-neutral bioeconomy.

Keywords: Wood formation, Xylogenesis, Comparative genomics, Spatial transcriptomics, Regulatory networks, Cryosectioning, Gymnosperms, Angiosperms, Picea abies, Populus tremula, DAP-seq.

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