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Comparative co-expression network analysis of abiotic stress response in boreal conifers

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Academic dissertation

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Abstract

Gene co-expression networks (GCNs) are a powerful approach for exploring transcriptional regulation by identifying functionally related genes through their expression patterns across various conditions. The inference of GCNs can be achieved by various computational algorithms, each with distinct merits and limitations. The choice of algorithm can influence the network structure and the biological interpretation derived from it. By using a combination of different methods, biases can be minimised providing more robust and complementary insights. These methodologies are particularly valuable for non-model species, a challenge exemplified by Norway spruce and Scots pine. With ongoing climate change, drought and cold stresses are becoming increasingly important factors shaping the survival of these boreal conifers. Boreal regions are experiencing more frequent and prolonged drought periods, alongside greater variability in early spring, including sudden freeze-thaw events and episodes of extreme cold. Understanding the genetic regulation through which species such as Norway spruce and Scots pine, perceive, respond to, and potentially recover from drought and cold is therefore of high importance.

In this thesis I have used an extensive collection of transcriptomic data generated from boreal tree species under abiotic stress conditions to infer GCNs to reveal coordinated patterns of gene expression responses to environmental challenges. In addition, comparative analyses of GCNs enabled the systematic assessment of conservation and divergence of co-expression among these species, identifying both shared regulatory circuits and species-specific adaptations. Analyses uncovered down-regulated modules of developmental processes, up-regulated modules of abiotic stress response, and several candidate transcription factors directly connected to these stress-responsive pathways. Comparison with boreal angiosperms revealed divergent responses in core cold-regulatory processes, most notably in the regulation and representation of C- repeat Binding Factor (CBF) transcription factors. The abiotic stress response patterns of both cold and drought were largely shared between the two conifer species, indicating a high degree of conservation in their transcriptional responses. This conservation extended to the organisation of topologically associated domains, where a subset of highly conserved co-expressed orthologs were found at the same location in the genomes of these conifers.

Together, these analyses demonstrated the utility of comparative co-expression networks as a tool for understanding both conserved and diverged regulatory mechanisms, while offering new perspectives on the resilience of conifers in the context of environmental change.

Keywords: Norway spruce, Scots pine, abiotic stress response, co-expression networks, comparative genomics

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