

The regulatory landscape of *Populus tremula*

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Populus has become an important model system for trees due to its relatively small genome and fast growth. One member of the genus is *Populus tremula* (aspen), which is a deciduous tree species native to the temperate regions of Europe and Asia and is an important organism in terms of forest biodiversity. We have recently sequenced the *P. tremula* genome, and a draft genome assembly is available (<http://popgenie.org>). In a species such as *P. tremula*, where the long generation time makes it infeasible to perform controlled perturbation experiments for a large number of samples, natural populations are an attractive alternative. We resequenced twelve populations (103 individuals) of *P. tremula* across Sweden and quantified transcript abundances in leaves using RNA-Sequencing (219 samples). With both sequence and gene expression data available, we aim to identify the mechanisms giving rise to natural variation in gene expression and phenotypes such as metabolites and growth. We accomplish this by identifying expression quantitative trait loci (eQTL) and viewing them in the context of a gene co-expression network, and by identifying gene sets with expression profiles explaining phenotypes. We use the results to answer questions such as: Do genes associated with SNPs have special co-expression network characteristics? Are eQTLs a result of local adaptation? What higher order phenotypes can be explained on the basis of eQTLs and co-expression?