A forest of information:
The effectiveness of genomic data for managing adaptation
in a changing climate

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Abstract:

Genomic tools are now widely available and becoming a cost-effective option for assessing the strength and nature of local adaptation in natural populations. Genotype-environment association tests can rapidly characterize climatic drivers of population differentiation, and can identify loci that may play a role in local adaptation. Genome-wide association studies can identify loci associated with climate-related phenotypes such as cold or drought hardiness, then the spatial distribution of alleles for these loci can be used to characterize local adaptation. To what extent do these genomic approaches produce signals of local adaptation that are similar to those from short- or long-term provenance trials, i.e., can they be used to inform reforestation decisions in a changing climate? We compared genomic to phenotypic and climatic data for 281 provenances of lodgepole pine (*Pinus contorta*) from across western Canada to assess their effectiveness in characterizing the climatic drivers and spatial scale of local adaptation in this species. We found that genomic and climate data are nearly equivalent for describing local adaptation in seedling traits, particularly those related to cold hardiness. There is also strong agreement between the climate variables associated with genomic variation and with results from a long-term provenance trial, suggesting that genomic data is a viable option for identifying important climate drivers of local adaptation where phenotypic data are unavailable. This talk will also include results from recent studies of genetic and demographic factors limiting species range shifts, the role of hybridization and introgression in climate adaptation, and somatic mutations as a source of genetic diversity in conifers.