Confronting emerging pathogens: A genomics empowered approach to protecting forest health

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Abstract: Invasive microbes, causing diseases such as sudden oak death and chestnut blight, negatively impact forest health, affecting ecosystems and economies around the world. Approaches for managing introduced diseases typically rely on breeding programs that can take decades to identify and deploy resistant plants. To demonstrate how this process can be accelerated to rapidly identify host genes associated with resistance to emerging pathogens, we challenged ca. 1000 re-sequenced *Populus trichocarpa* genotypes with *Sphaerulina musiva*, an invasive fungal pathogen in western North America. We used genome-wide association mapping to identify three loci associated with resistance and one locus associated with susceptibility to S. musiva. Whole transcriptome analysis supported these results with consistent patterns of differential expression with the mapping results. A population-wide characterization of these loci found a disproportionately high number of detrimental mutations in the genes encoding resistance receptors compared to the highly conserved susceptibility locus. Functional characterization of these loci is currently underway. The approach used herein demonstrates the power of population-wide re-sequencing of undomesticated, non-model plant species to rapidly identify loci that could be used to help mitigate long-term impacts of emerging diseases in native ecosystems.

Bio: Dr LeBoldus is an Assistant Professor in Forest Pathology and researches the genetics of host-pathogen interactions in forest trees. His current projects focus on using genomic tools to understand the relationship between genes in the host and pathogen, how they impact virulence and pathogenicity, and how this information may be scaled to elucidate landscape level patterns of pest and disease occurrence. Dr. LeBoldus received a B.Sc. (2003) in Forest Science from the University of British Columbia. He received his M.Sc. (2006) and Ph.D. (2010) from the University of Alberta.