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Pine genomic signatures of resiliency to mountain pine beetle

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Project Overview

Multiple pine traits such as chemical and physical defenses, drought tolerance, and phloem thickness among others together define the complex trait of host quality. These traits influence the successful detection, attack, and colonization of pines by mountain pine beetle (MPB) and subsequent beetle reproduction. Host quality differs between pines from historic and novel MPB ranges[1], implying spatial variation in pine resilience to MPB. In addition, MPB resistance is a heritable trait in lodgepole and thus it is feasible to breed for improved MPB resistance[2].

As a part of the TRIA-Net project, our preliminary results show that lodgepole pine killed by MPB during BC's hyperepidemic have a genetic signature distinct from survivors. Additionally, lodgepole pine trees that were not attacked in the leading-edge of MPB migration are genetically distinct in comparison to their attacked neighbors. Here, we aim to verify these preliminary results and identify genomic markers contributing to high and low resilience to MPB thus indirectly assessing host quality.

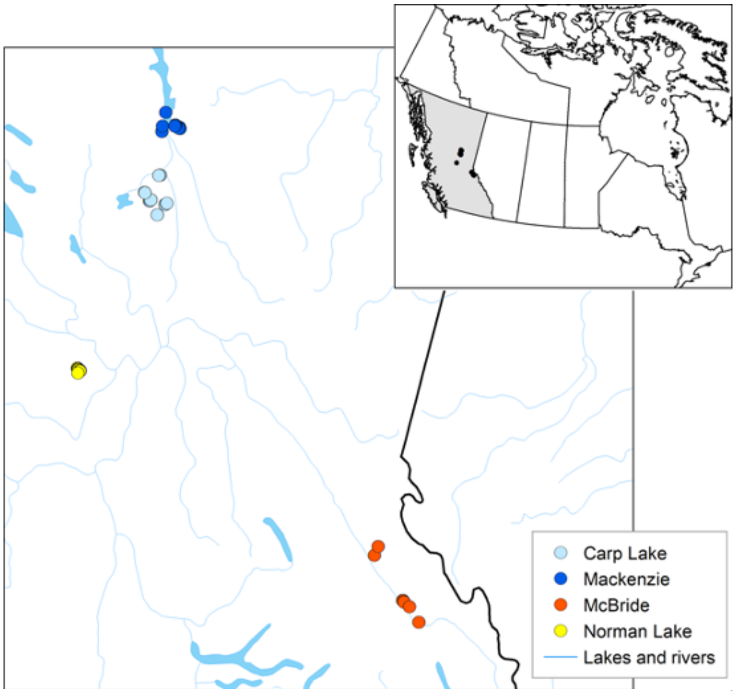

Figure 1. *Sampling locations for the Lindgren Collection. Seedlings grown from cones collected at these four locations have been genotyped to address the hypothesis that survivors of MPB attack are genetically distinct from trees that succumb to attack.*

The Genomics of Host Quality

Previous models of MPB spread risk have used MPB demographic history and climatic variables as predictors. The influence of host genotype is an understudied component of modeling future spread-dynamics. To address this, we assess the genetic component of host quality that will then be applied to models of spread risk.

Our first objective is to determine if lodgepole pines that survived the MPB hyperepidemic in central BC have a genetic makeup that differentiates them from MPB-killed lodgepole pines from the same stands. We have generated "The Lindgren Collection" dataset, which is a collection of lodgepole pine seedlings curated by researchers at the University of Northern British Columbia and is now maintained by BCMFLNRO.. The progeny of MPB casualties or survivors were grown by collecting seed from MPB-killed or surviving trees in four different stands in central BC following the MPB hyperepidemic (Figure 1). The Lindgren Collection has been genotyped, generating ≥ 14k DNA markers that we refer to as single nucleotide polymorphism (SNP) loci.

For more information on this or other Mountain Pine Beetle Ecology Program publication, please contact Keith McClain at kmcclain@friresearch.ca

The second dataset, for our second objective, is the "Paired Sampling Collection," The goal is to determine if there is an underlying genetic component related to MPB attack susceptibility at the leading edge of MPB range expansion. In 16 stands, samples of paired attacked and unattacked trees within a short range of each other were collected.

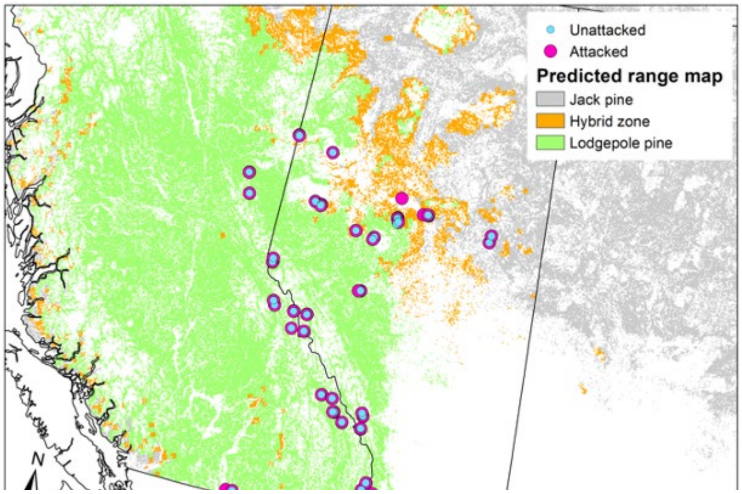

Figure 2. *Sampling locations for replicated, paired sampling of attacked and unattacked trees within British Columbia and Alberta.*

Both the Lindgren Collection and the Paired Sampling Collection will be analyzed using quantitative[3], population[4], and landscape genomic methods to discover DNA markers in the Lindgren Collection that associate with MPB survivorship, and that associate with MPB attack in the Paired Sampling Collection. Collectively, genes containing these DNA markers constitute the genomic signatures of high or low MPB resilience, respectively. The outcomes of these analyses will be used to create spatial genetic maps differentiating pine populations in historic and novel MPB habitats. If there is a spatial pattern of pines harbouring resiliency genes, these stands could be designated as being at lower risk of attack. Knowing which stands are most at risk of MPB infestation is key to planning monitoring and forest management.

Our final objective is to identify genomic signatures that distinguish lodgepole pine in historic and novel MPB habitats. These analyses can tell us whether host genetics might play a role in the different responses to MPB and their fungal associates that have been observed between lodgepole pines from historic and novel habitats. To address this, we have collected lodgepole pine samples throughout the Canadian portion of the species range (Figure 3). Using previous site incidence data together with population, and landscape genomic methods, we will determine if co-evolved trees within the historic range can be differentiated genetically from naïve trees in the expanded MPB range. If we can isolate those differences, we will be able to use these data to differentiate between past and present host distributions and to inform future expansion based on standing genetic variation on the landscape.

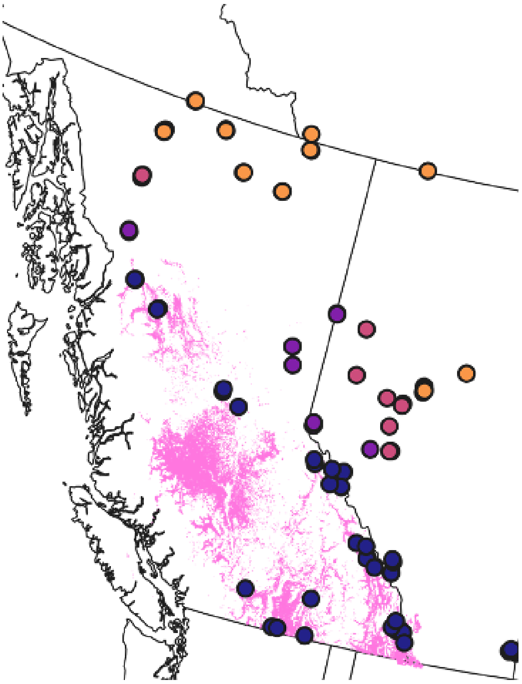

Figure 3. *MPB historic range shaded pink. The color gradient for sampling locations (circles) indicates distance from MPB historic range.*

References

[1] Cudmore et al. 2010. J Appl Ecol 47:1036–1043; Burke et al. 2017. Ecosphere 8:e01778.
[2] Yanchuk et al. 2008. Tree Genet Genomes 4:171–180.
[3] Neale and Kremer. 2011. Nature Rev Genet 12:111–122.
[4] Cullingham et al. 2014. New Phytol. 204:215–229.