**Introduction**

Pine forests in western North America have been devastated by an unprecedented outbreak of mountain pine beetle-fungal complex. Primarily, lodgepole pine forests in Canada have been affected resulting in economic loss and ecosystem damage. More concerning is the range expansion of the beetle/fungi both north and east resulting in exposure to a new host species, jack pine (Cullingham et al. 2011), a sister species to lodgepole pine. This naive host is distributed throughout the Boreal forest across Canada and into the eastern United States putting an entire ecosystem at risk.


**Questions**

Are there genetic differences within and between lodgepole and jack pine?

Do these genetic differences affect mountain pine beetle colonizing or reproductive success (i.e. spread potential)?

How do environmental factors interact with the host-insect relationship?

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**Methods**

- **Genes of potential importance are expressed in response to the change in environment**
  - Spatially informed
    - MatSAM (Joost et al. 2008)
  - Spatially uninformed
    - BayeSCAN (Foll & Gaggiotti 2008)
    - BayeFST (Balding 2003)
    - Introgress (Gompert & Buerkle 2009)

- **RNA used as a source for high-throughput sequencing**
  - Extract RNA which represents the expressed portion of the genome (transcriptome)
  - Identify loci that deviate from neutral expectations within and between species, “outlier analysis” (Beaumont & Balding 2004)

- **Lodgepole**
  - RNA was generated and processed using a bioinformatic workflow
  - Characterize SNPs in lodgepole, jack pine and their hybrids across naive and non-naive stands
  - Millions of DNA fragments were generated and assembled

- **Jack pine**
  - SNP detection/selection
    - Minimum coverage: 15X
    - MAF: 10%
    - SNP > 100bp Flanking region
  - 1536 SNPs

- **Combined**
  - 1 597 295 fragments
  - 1 558 772 fragments

**Results**

Across data-sets, 136 SNP loci showed patterns of non-neutral inheritance. The majority of which were found when comparing lodgepole and jack pine (“All”). These include transcription factors, protein degradation, growth regulators, synthesis, energy production and water transport.

**Implications**

This research addresses knowledge gaps that exist given the range-expansion of the beetle to novel environments. From here we will assess the function of these candidate loci to identify whether they influence spread potential. We can then use our interpolated surfaces as inputs in spread-risk and economic models to mitigate the impacts of this outbreak, and assess potential future outbreaks.

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**References**


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