

**SECOND ANNUAL
INTERNATIONAL SCIENTIFIC WORKSHOP**

**Organismal-level population genomics
Pinus contorta, *P. banksiana*, & hybrids**

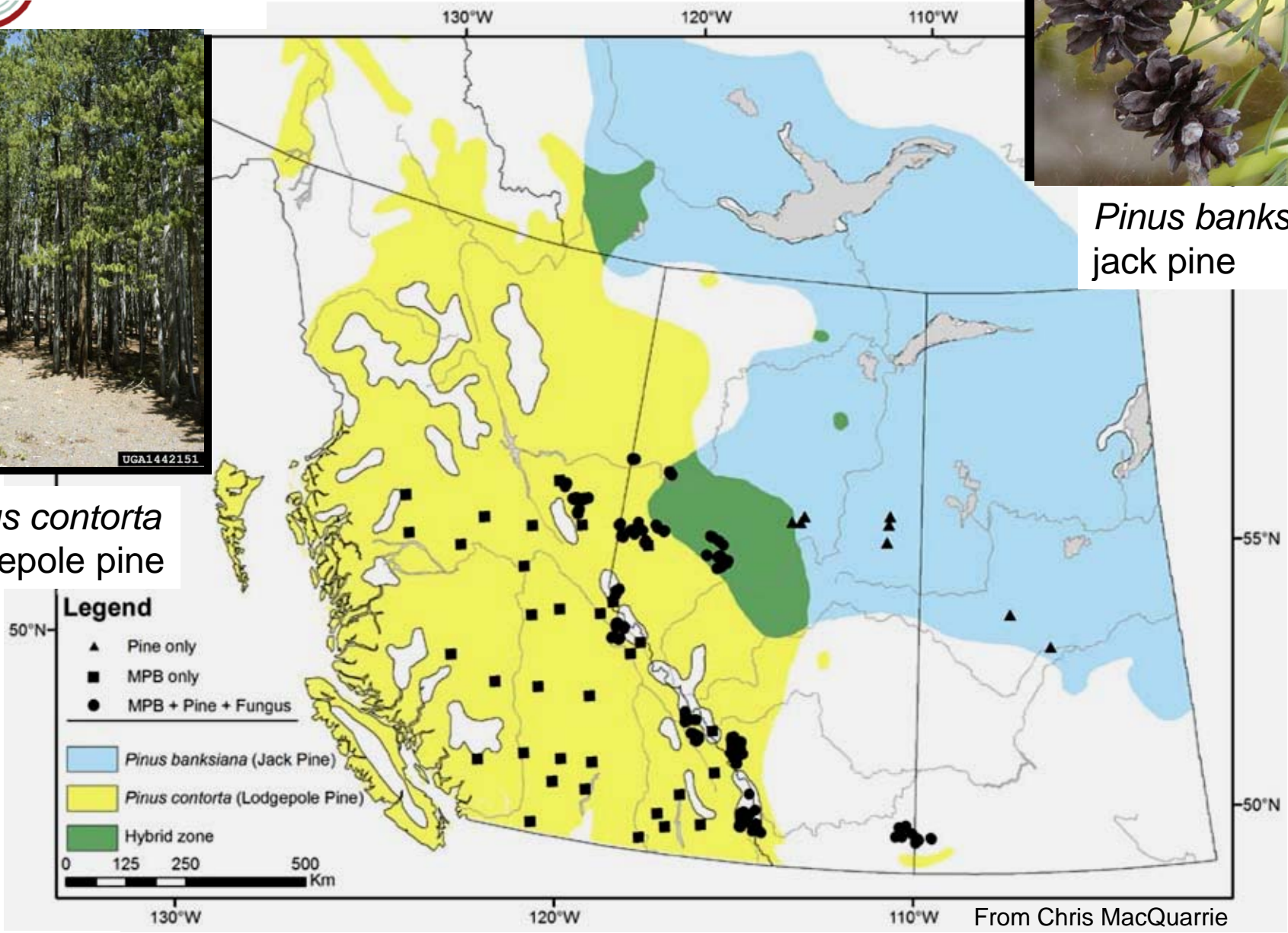
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Corey Davis, Bill Clark, Sophie Dang**



Pinus contorta
lodgepole pine



Pinus banksiana
jack pine



Pine population structure and diagnostics

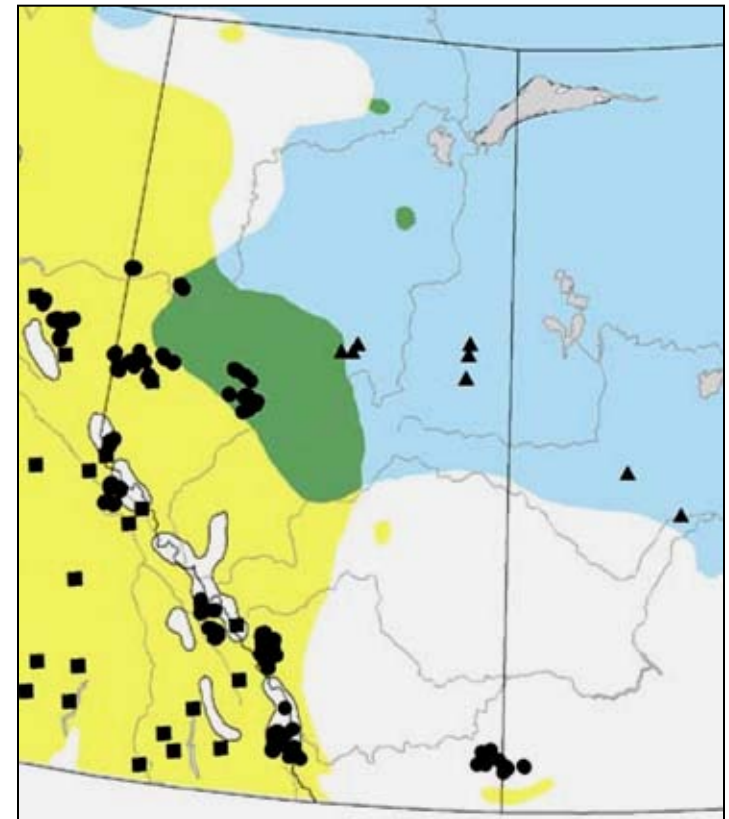
- **Obtain microsatellite allele frequency** from populations of lodgepole pine, jack pine, and putative hybrids
- **Identify population structuring** within two pine species and extent of hybrid zone in Alberta and BC
- **Assess diagnostic potential** of msats in addition to chloroplast, mitochondrial, and nuclear markers

Pine Microsatellites

- Constructed a genomic library from *P. contorta* needle tissue
- Screened 25 newly developed genomic-based msats as well as 23 previously published msats
- Screened against *P. contorta* and *P. banksiana* simultaneously

| Source | Screened | Worked | Rate |
|-----------------|-----------|-----------|------------|
| Genomic | 27 | 5 | 19% |
| EST | 7 | 2 | 29% |
| Low-copy | 9 | 6 | 67% |
| Undermethylated | 5 | 2 | 40% |
| Total | 48 | 15 | 32% |

Sampled: 694 *P. contorta*
483 *P. banksiana*
348 Putative hybrids
Total: 1525 trees surveyed



From Chris MacQuarrie

Marker assessment and genotyping still underway...

Pine Diagnostics

- Identifying potentially diagnostic msats
- Screening additional molecular markers
 - chloroplast regions - paternal inheritance
 - 5 regions with variability between two species
 - Corresponds to regions proposed by plant barcoding initiative
 - mtDNA region - maternal inheritance
 - Large insertion species-specific
 - Nuclear markers
 - Based on previously published orthologous regions
 - e.g. Pelgas *et al.* 2004



Pinus contorta



Pinus banksiana

Pine genomics - Future Directions -

- Deep sequencing of pools from both pine species
- SNP detection
 - in collaboration with N. Isabel
 - candidate gene approach
 - processes that influence tree fitness and resistance
 - potential to use white spruce as a reference
 - ****re-sequencing to confirm SNPs****
- Diagnostic SNPs
 - identify SNPs to separate species and hybrids
 - characterize hybrid zone and levels of interspecific gene flow
- Data management
 - customize the database developed by Arborea to manage genotypic data and re-sequencing