

**SECOND ANNUAL  
INTERNATIONAL SCIENTIFIC WORKSHOP**

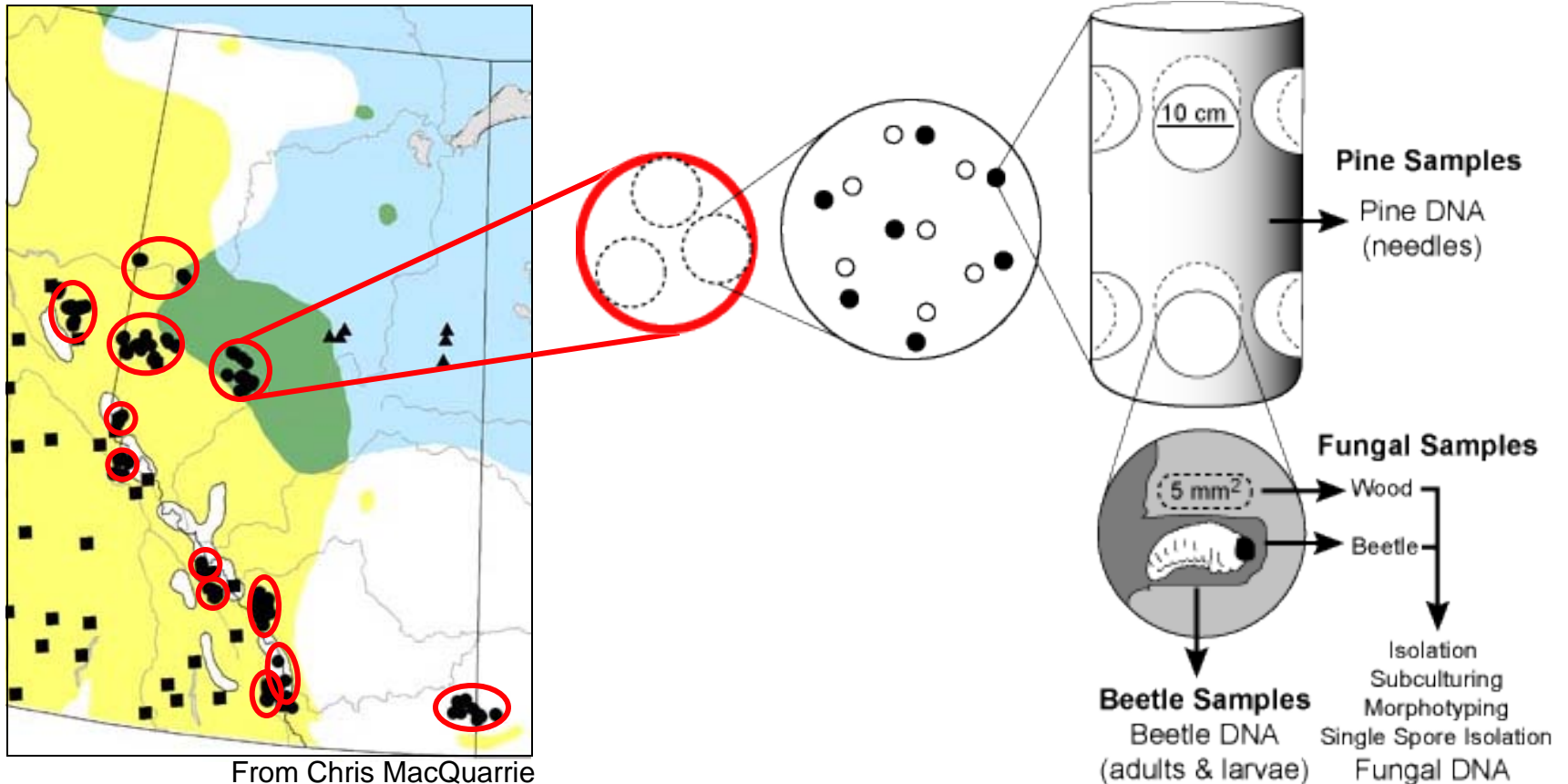
***Organismal-level population genomics  
- Mountain pine beetle -***

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Corey Davis, Stephanie Boychcuk, Sophie Dang**

# Mountain pine beetle phylogeography

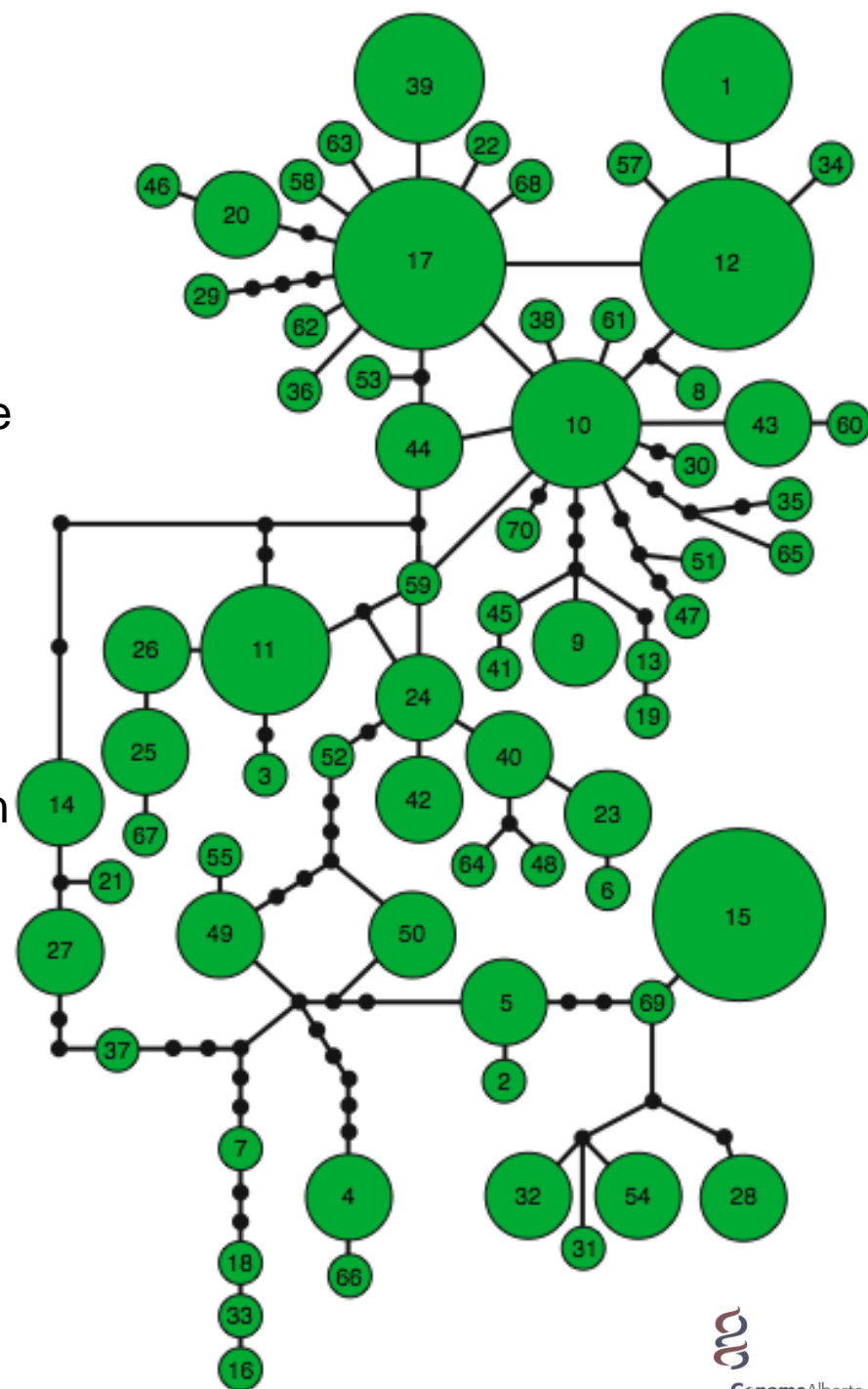
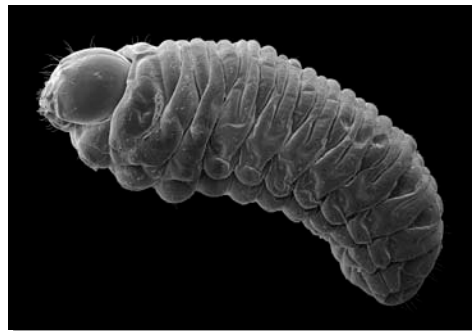
- Obtain mitochondrial DNA sequence data for MPB
- Relate TRIA collected samples to previously surveyed MPB populations - Mock *et al.* 2007
- Compare results with MPB microsatellite derived population genetic structure
- Contribute to DNA barcoding initiative

- 150 beetles samples, with 10-15 individuals per landscape, some landscapes with multiple individuals per tree
- Combined with MPB mtDNA data previously published by Mock *et al.* 2007



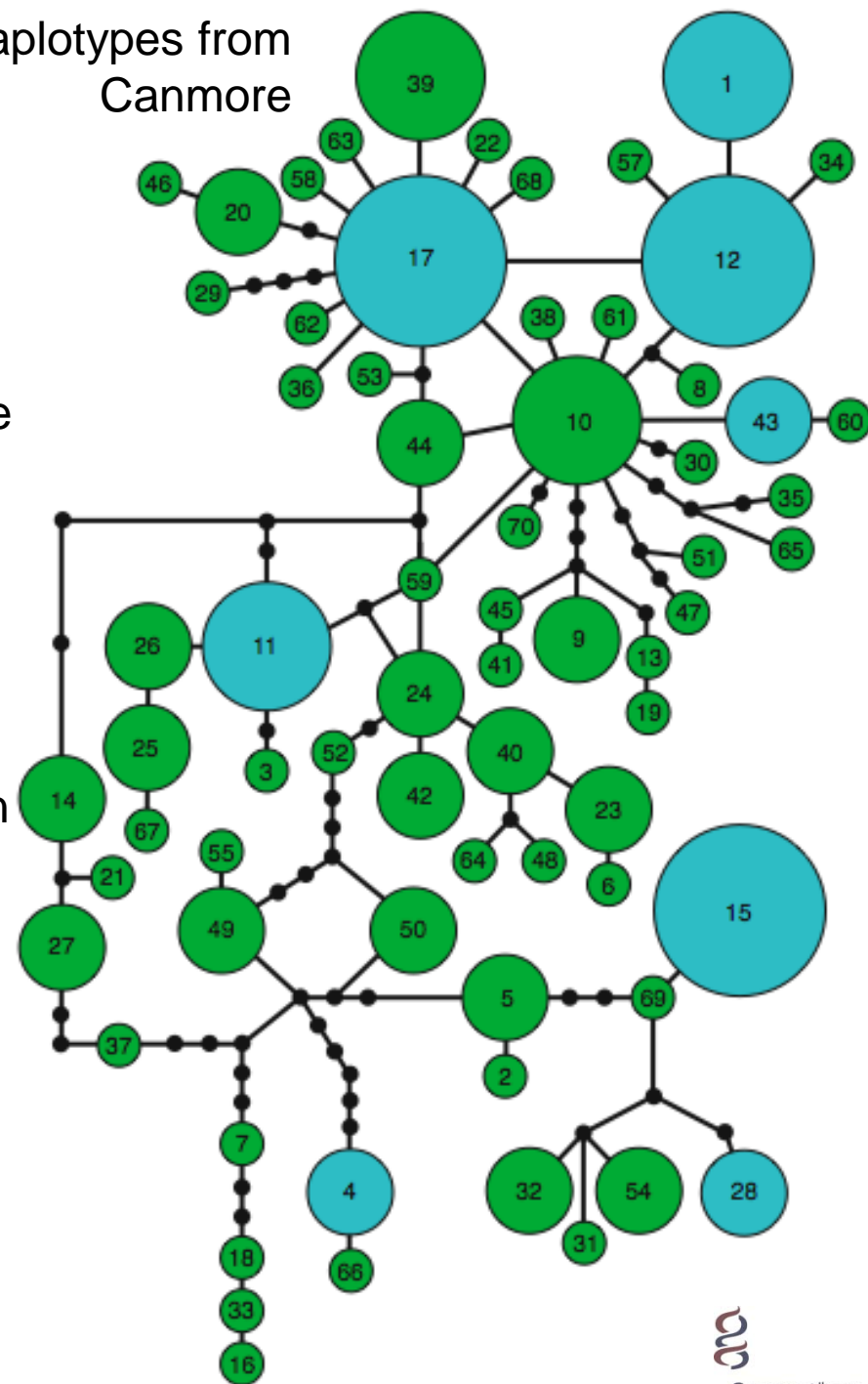
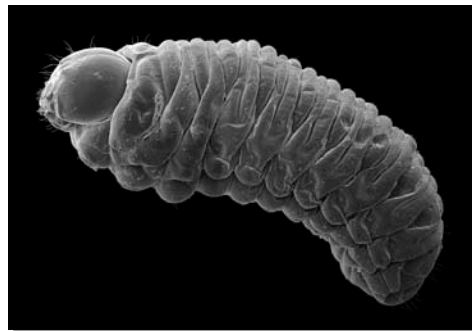
# mtDNA network results

- 70 haplotypes, including mtDNA sequence from Mock *et al.* 2007
- Network structure shows little correspondence to geographic location
- Mock *et al.* haplotypes were located throughout the network, with the exception of some southern USA populations
- Multiple haplotypes within individual trees were detected



## mtDNA network results

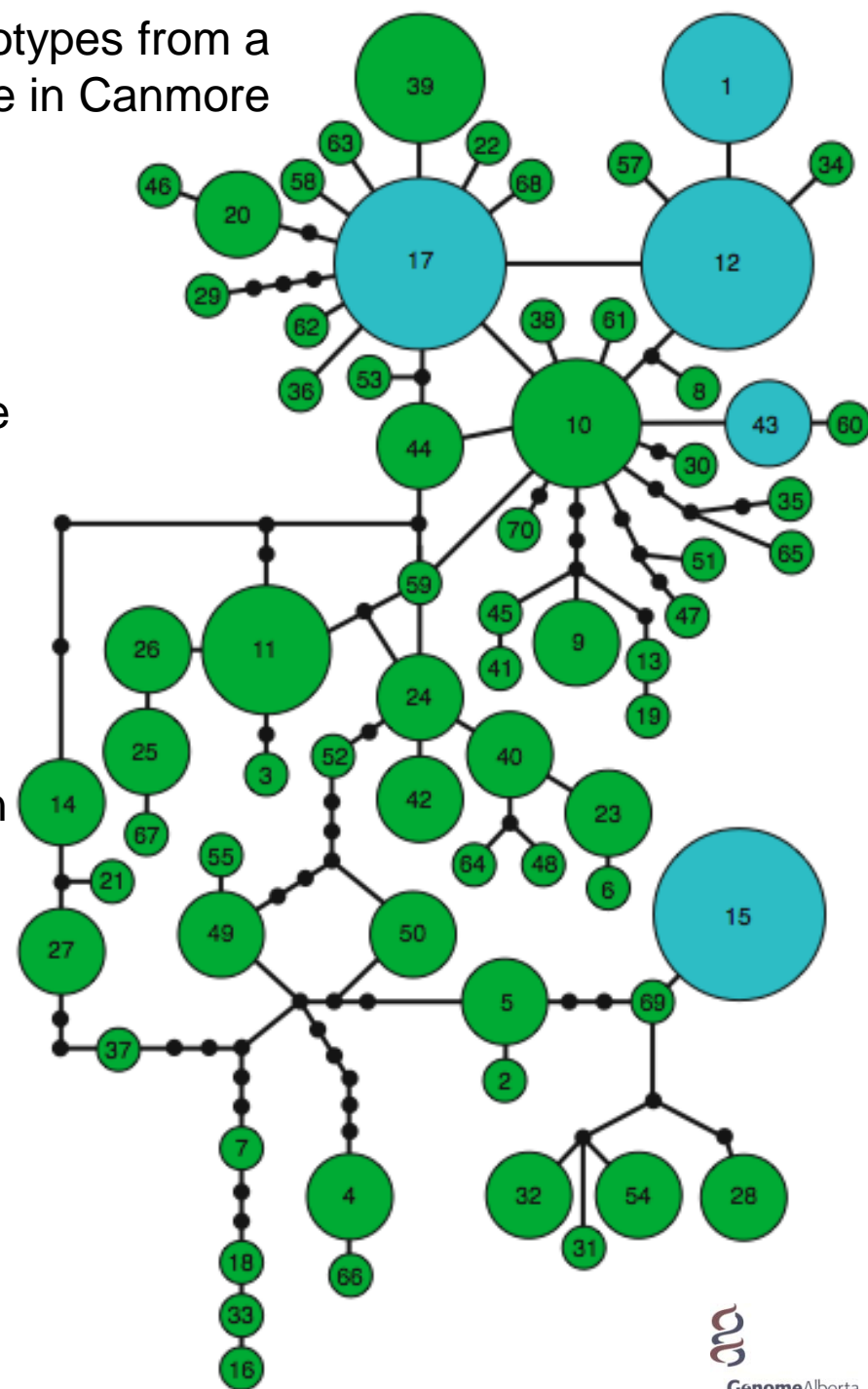
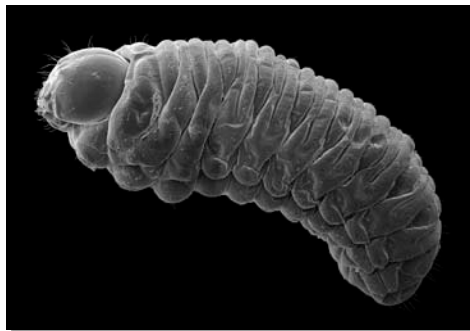
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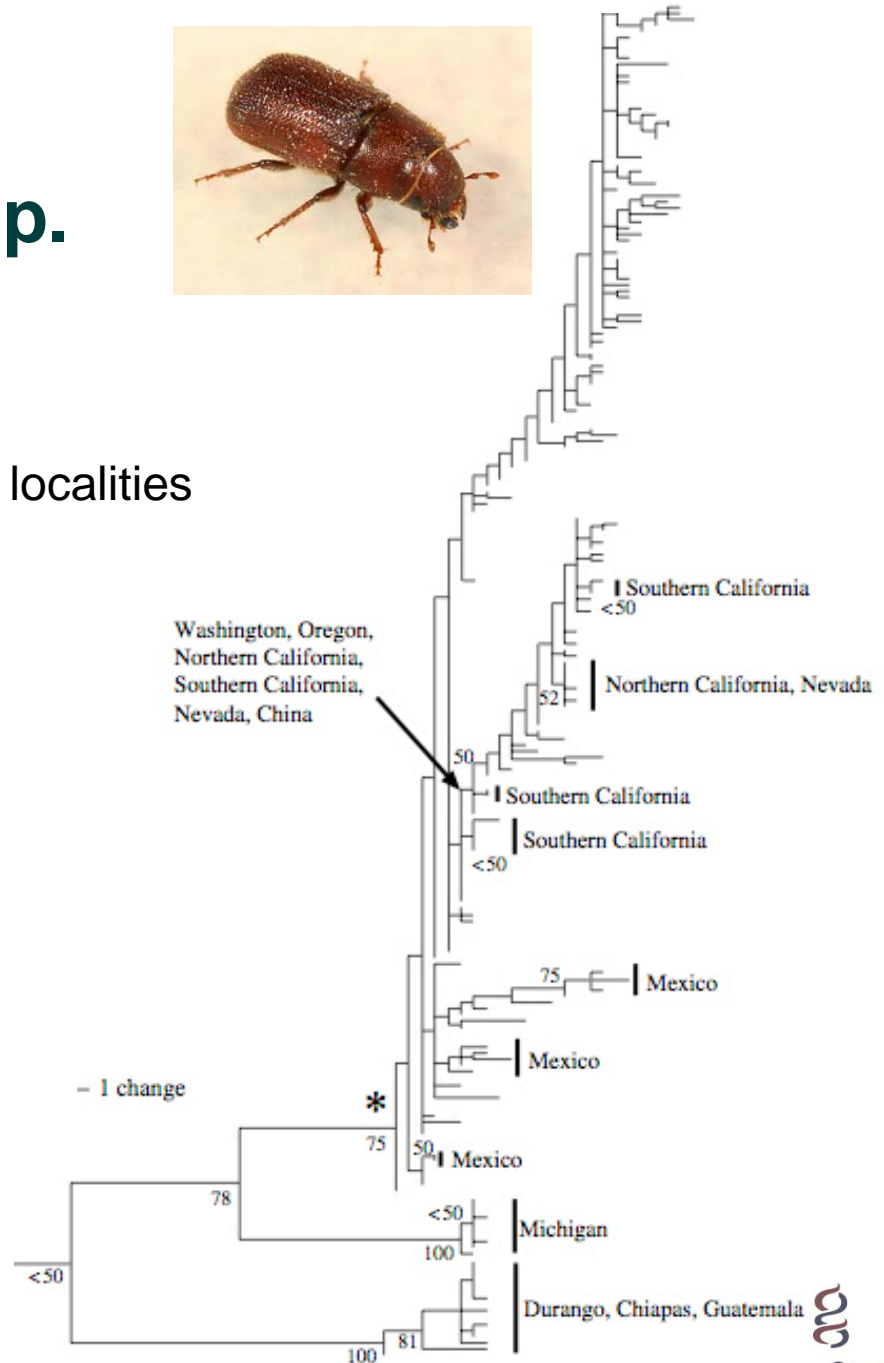
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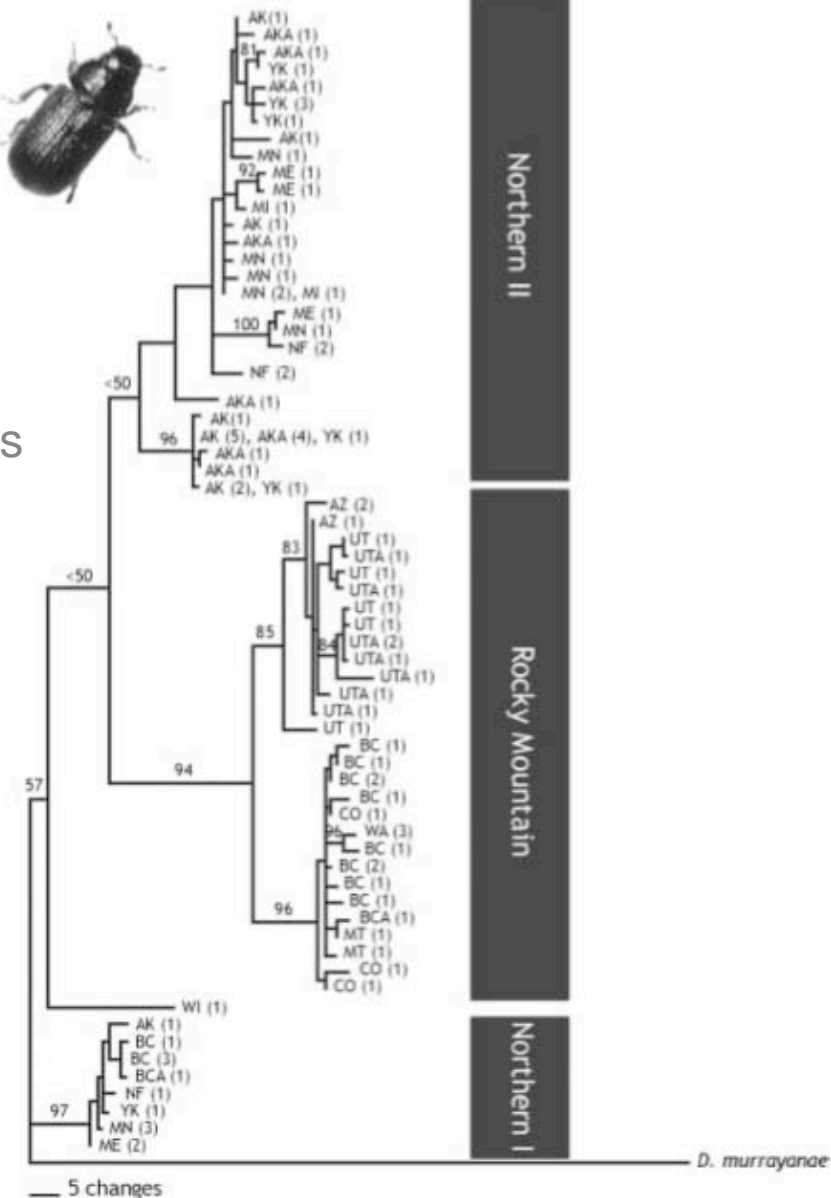
## Other *Dendroctonus* spp.

- *D. valens* (Cognato *et al.* 2005)
- mtDNA (COI) from 218 individuals, 28 localities
- High haplotype diversity, with pairwise divergence up to 16%



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- *D. valens* (Cognato *et al.* 2005)
- mtDNA (COI) from 218 individuals, 28 localities
- High haplotype diversity, with pairwise divergence up to 16%
- *D. rufipennis* (Maroja *et al.* 2007)
- mtDNA (COI) from 93 individuals, 16 localities
- High haplotype diversity
- Over half of the haplotypes were unique





# Mountain pine beetle phylogeography

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# Mountain pine beetle genomics - Future Directions -

- Deep sequencing of pools of individuals from the outbreak zone
- *in silico* SNP detection
  - cDNA libraries developed by C. Keeling
  - deep sequencing
  - in collaboration with N. Isabel
- candidate gene SNP detection
  - processes influencing MPB dynamics
- **\*\*re-sequencing to confirm SNP\*\***
- Data management
  - customize the database developed by Arborea to manage genotypic data and re-sequencing