



Geographic Distribution and Environmental Factors Contributing to Genetic Variation in Mountain Pine Beetle Populations in Western North America

Marianne E. Blackburn, Edwina J. Dowle, Gregory J. Ragland



INTRODUCTION

In North America, millions of forest acres have been impacted by *Dendroctonus ponderosae*, the mountain pine beetle (MPB), which normally exists at low population sizes and serves a beneficial role in forest health. The MPB tends to target old, weak trees and by killing them, helps future forest regeneration.¹ However, favorable environmental conditions can lead to exponential population growth, resulting in potential epidemic population outbreaks.

Here, we use GIS data to 1) test the effects of host availability on genetic connectivity among populations, and 2) apply a correlational analysis to identify genetic markers associated with environmental differences across the geographic distribution of MPB. The goal is to understand populations connectivity, and to identify genetic markers that may predict important population metrics such as phenology and growth rate.

Previously, Dowle *et al.* (in review) used 19,904 genetic loci (ddRADseq) to identify three distinct genetic clusters (Y chromosome haplogroups) that correspond with post-glacial expansion from three distinct refugia (Fig. 1b). There is restricted autosomal gene flow among Y haplogroups (Fig. 1a), suggesting partial reproductive isolation, and that different loci may be associated with adaptation to the same environmental factors in different geographic regions.²

METHODS

Spatial Analysis of Tree Cover

We used Geographic Information Systems (ArcGIS 10.2) to examine tree cover around and between populations:

- Raster spatial analysis from global tree canopy cover data³
- Mean tree cover in 1 km radius around each sample for environmental association analysis (Fig. 2)
- Mean tree cover in 1km-wide corridor between sample populations for connectivity analysis (Fig. 3)

Statistical Analysis of Genetic and Environmental Factors

We used principal components analysis (PCA) of 30-year normals for 14 climatic factors (Figure 6):

- Bayesian (Bayenv2) and Latent Factor Mixed Model (LFMM) analysis associating genetic variants with tree canopy cover and climatic principal components (PC1 and PC2)
- Conducted range-wide, and within two genetic clusters (Eastern, and Western, insufficient data for central)

RESULTS

Population Structure and Gene Flow

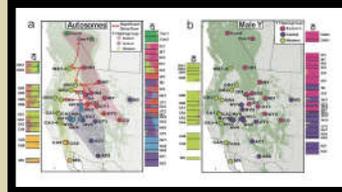


Figure 1. Adapted from Dowle *et al.*, NgADMM results for autosomal (male and female combined) (a), and male Y (b). Sample names follow the state where samples were collected. Samples on the map are color-coded by the majority haplogroup found in each sample. On the autosomal panel red arrows indicate significant autosomal gene flow; tests were only run when crossing Y haplogroup boundaries identified by background color.

GIS Connectivity Analysis

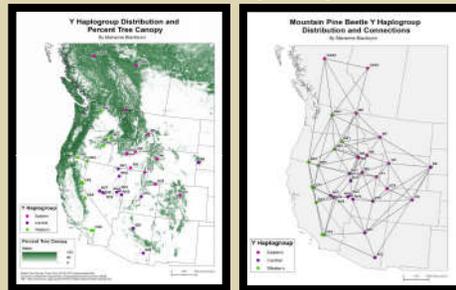


Figure 2. Tree canopy percentage across the MPR range. Samples sites on the map are color-coded by majority haplogroup found in each sample.



Figure 3. Polyline constructed between populations. Sample sites on the map are color-coded by majority haplogroup found in each sample.

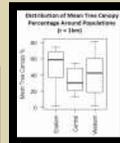


Figure 4. Distribution of mean tree canopy percentage around populations (n = 38).

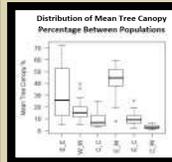


Figure 5. Distribution of mean tree canopy percentage in connections between populations, calculated with a one kilometer buffer around each polyline.

- Median tree canopy percentage:
 - was lowest around populations in the central genetic cluster (Fig. 4)
 - was highest between eastern and western genetic clusters (Fig. 5)
- Low tree canopy coverage associates with lack of gene flow between some geographically proximal populations (e.g., lack of red arrows between NV7 and CA3) (Fig. 1a)

Environmental Association Analysis

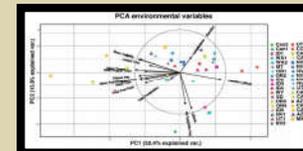


Figure 6. Adapted from Dowle *et al.*, PCA for all 24 climatic variables with loadings.

Haplogroup & Variable	Significant loci that overlap Eastern Y	Significant loci that overlap Eastern Y Range-Wide	Significant loci that overlap Eastern Y PC1	Significant loci that overlap Eastern Y PC2	Significant loci that overlap Western Y	Significant loci that overlap Western Y PC1	Significant loci that overlap Western Y PC2	Significant loci that overlap Tree Canopy
Significant loci that overlap Western Y	154							141
Significant loci that overlap Eastern Y	14	184		37	245		17	175
Significant loci that overlap Range-Wide	77	50	143	100	89	219	37	46
	(p < 0.001)	(p < 0.001)		(p < 0.002)	(p < 0.001)		(p < 0.001)	(p < 0.001)

Table 1. Adapted from Dowle *et al.*, Numbers of loci significantly associated (PDR < 0.05, LFMM; Z > 0.40, Bayenv2) with PC1, PC2 and Tree Canopy in both LFMM and Bayenv2 models in three analyses: 1) including only samples from the western haplogroup, 2) including only samples from the eastern haplogroup, and 3) including samples from across the MPR range. Figure 1 indicates Y haplogroup affiliation of each geographic population. P-values indicate whether the number of overlapping loci was significantly different from chance (fisher exact test).

Candidate loci associated with adaptation to tree availability and climate:

- 100's of loci associated with tree canopy, and significant overlap of associated loci between western and eastern genetic clusters (Table 1)
- Similar results for PC1/PC2 of climatic factors, though much lower overlap between regions for PC1

Despite overlap of associated loci, most putatively adaptive loci were specific to the eastern or western genetic clusters

DISCUSSION

Genetic structure is well predicted by tree density between populations. Gene flow between Y haplogroups is likely restricted by both the patchy distributions of trees and genetic factors (i.e., reproductive incompatibility among Y haplogroups). Environmental association analysis identifies loci that may be related to local adaptation.

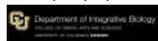
- Analyses within genetic clusters identified a proportion of loci that were not identified in range-wide analysis
- This result likely reflects independent evolution in separate genetic clusters
- This illustrates why knowledge of population structure may be critical in identifying adaptive genetic variants
- **Future prospects:** candidate loci may now be screened for associations with phenotypes, such as development rate, that may be used to predict population dynamics

REFERENCES

1. Safarynik, L. and A.L. Carroll. 2005. The biology and epidemiology of the mountain pine beetle in lodgepole pine forests. P. 3-66 in *The mountain pine beetle: A synthesis of biology, management, and impacts on lodgepole pine*, Safarynik, L. and W.R. Wilson (eds.). Natural Resources Canada, Canadian Forest Service, Pacific Forestry Centre, Victoria, BC, Canada.
2. Dowle, E. D., Bracewell, R. R., Pfrender, M. E., Mock, K. E., Bentz, B. J., Ragland, G. J. (in review). Reproductive isolation and environmental adaptation shape the phylogeography of mountain pine beetle (*Dendroctonus ponderosae*). *Molecular Ecology*.
3. Hansen, M. C., Potapov, P. V., Moore, R., Hancher, M., Turubanova, S. A., Tyukavina, A., Thau, D., Stehman, S.V., Goetz, S.J., Loveland, T.R., Kommareddy, A., Egrow, A., Chini, L., Justice, C.O., and Townshend, J.R.G. (2013). High-resolution global maps of 21st-century forest cover change. *Science*, 342(6160), 850-853.
4. **Photos in header:** Dan West, Colorado State Forest Service: 1) Adult MPB, 2) MPB galleries, live and dead larvae, 3) MPB pitched out of tree, 4) Blue stain fungus in wood of cut stump



Figure 7. Pitch tube caused by MPB attack photo: Marianne Blackburn



For more information, please contact: marianne.blackburn@ucdenver.edu