

Population genomics of Oregon white oak (*Quercus garryana*)



Jonathan Degner

Centre for Forest Conservation Genetics
University of British Columbia
jcdegner@alumni.ubc.ca

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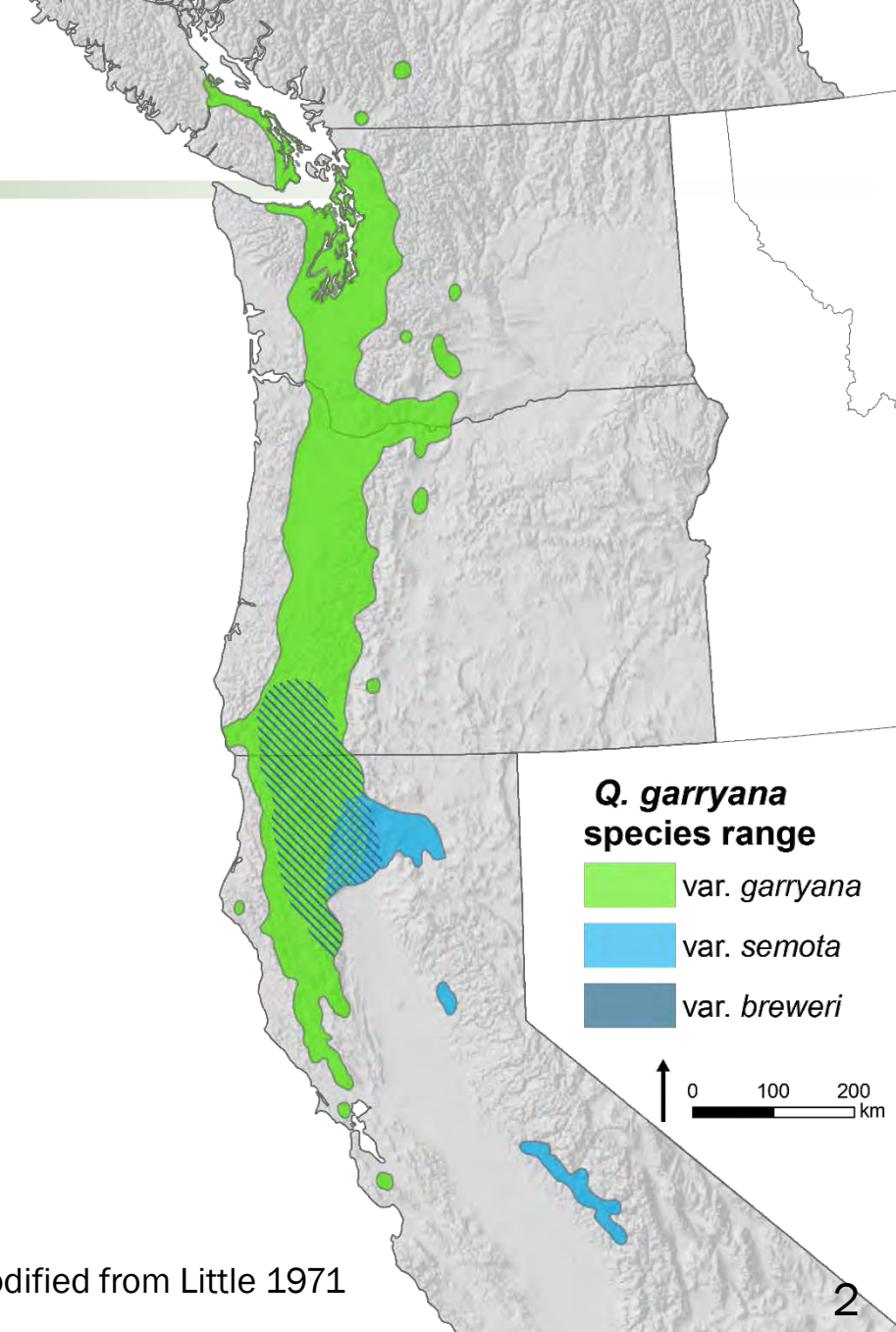
Overview

- Species background
- Methodology
- Population structure
 - Population-level statistics
 - Genetic clustering
- Taxonomic implications



Species background

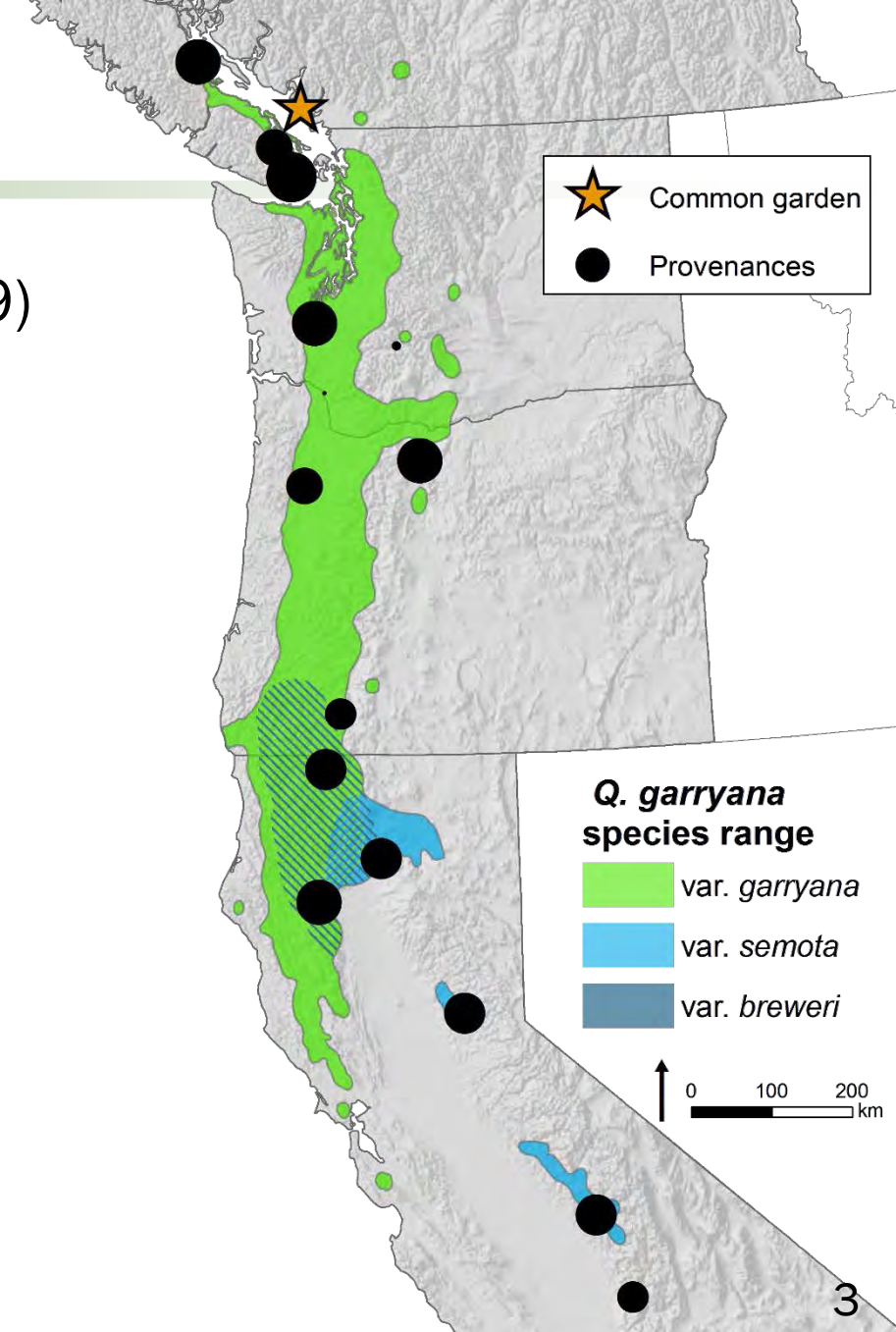
- Submediterranean deciduous angiosperm
- 3 taxonomic varieties
 - *Q. garryana* var. *garryana*: tree up to 25m
 - *Q. garryana* var. *breweri*: shrub up to 5m
 - *Q. garryana* var. *semota*: shrub up to 5m
- Tends to occupy dry, rich sites throughout range
- Broad latitudinal range
- Isolated to high elevations in southern extent



Modified from Little 1971

Sampling design

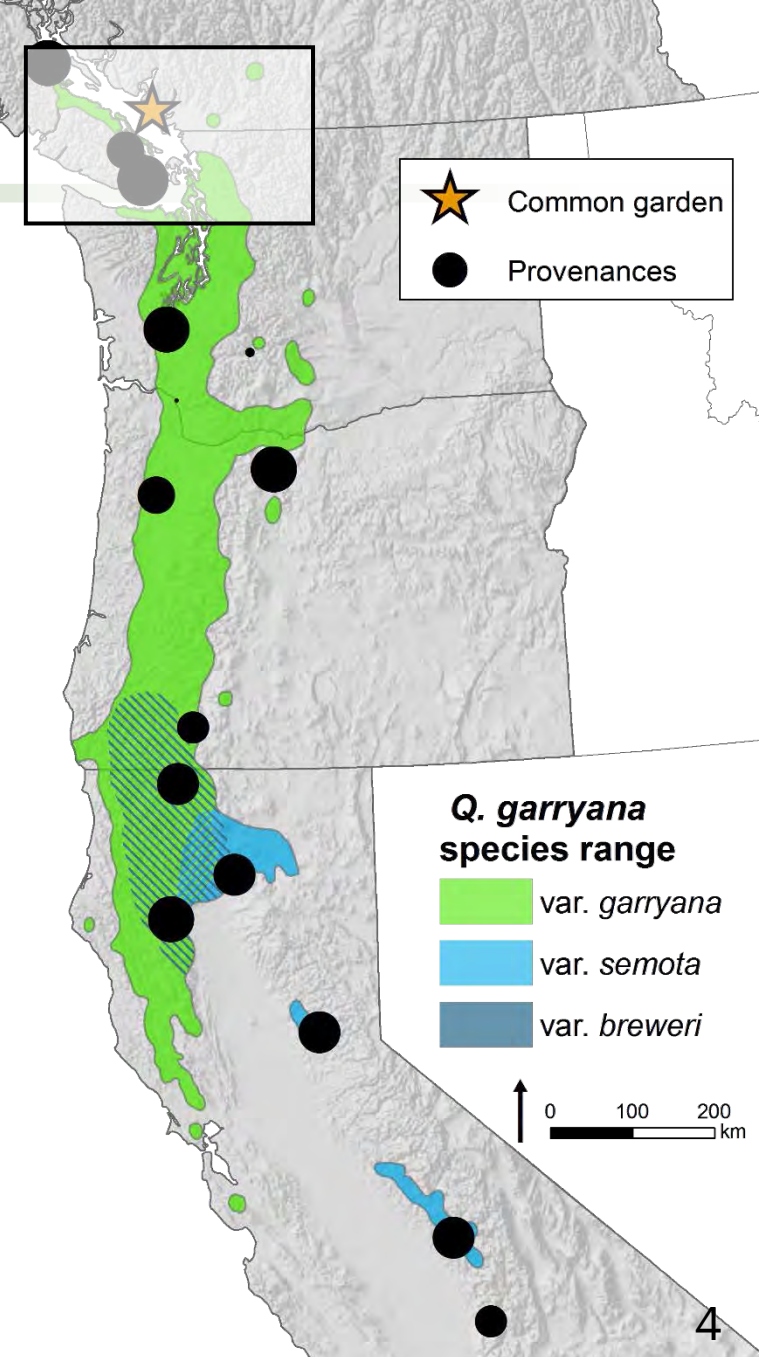
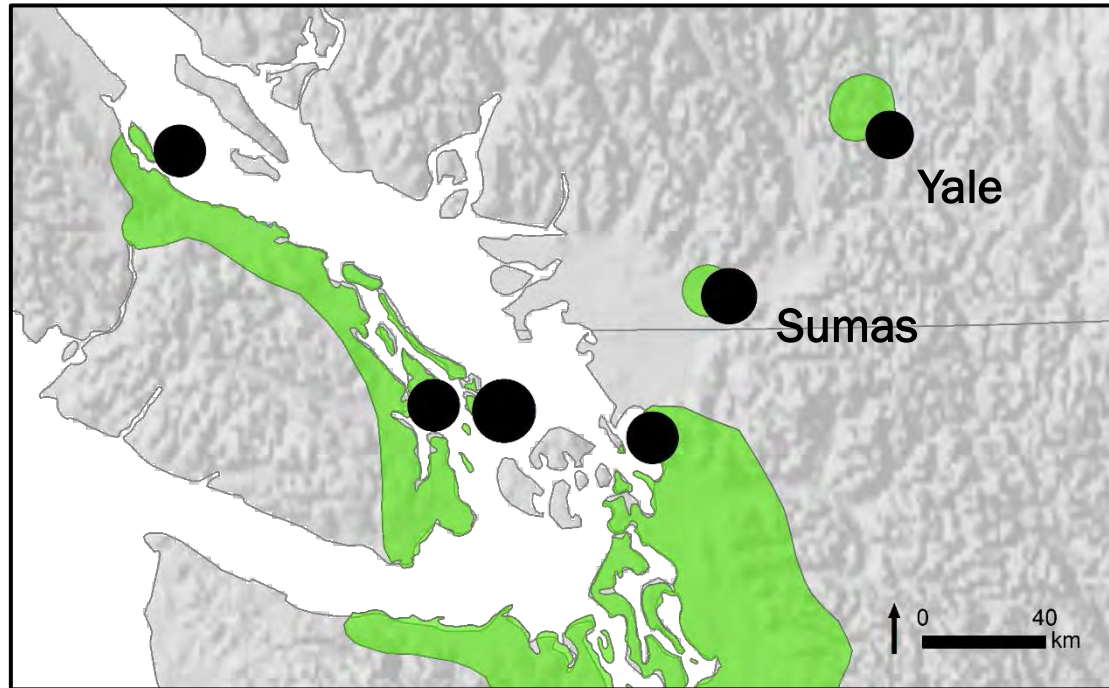
- Common garden established at UBC (Huebert 2009)
- 15 populations from across species range
 - ~10 half-sib families per population
 - 12 replicates
- Sampled for this study:
 - 1 tree per family, 7-11 trees per population
 - 2 populations with very low germination
 - 120 trees successfully sequenced



Sampling design

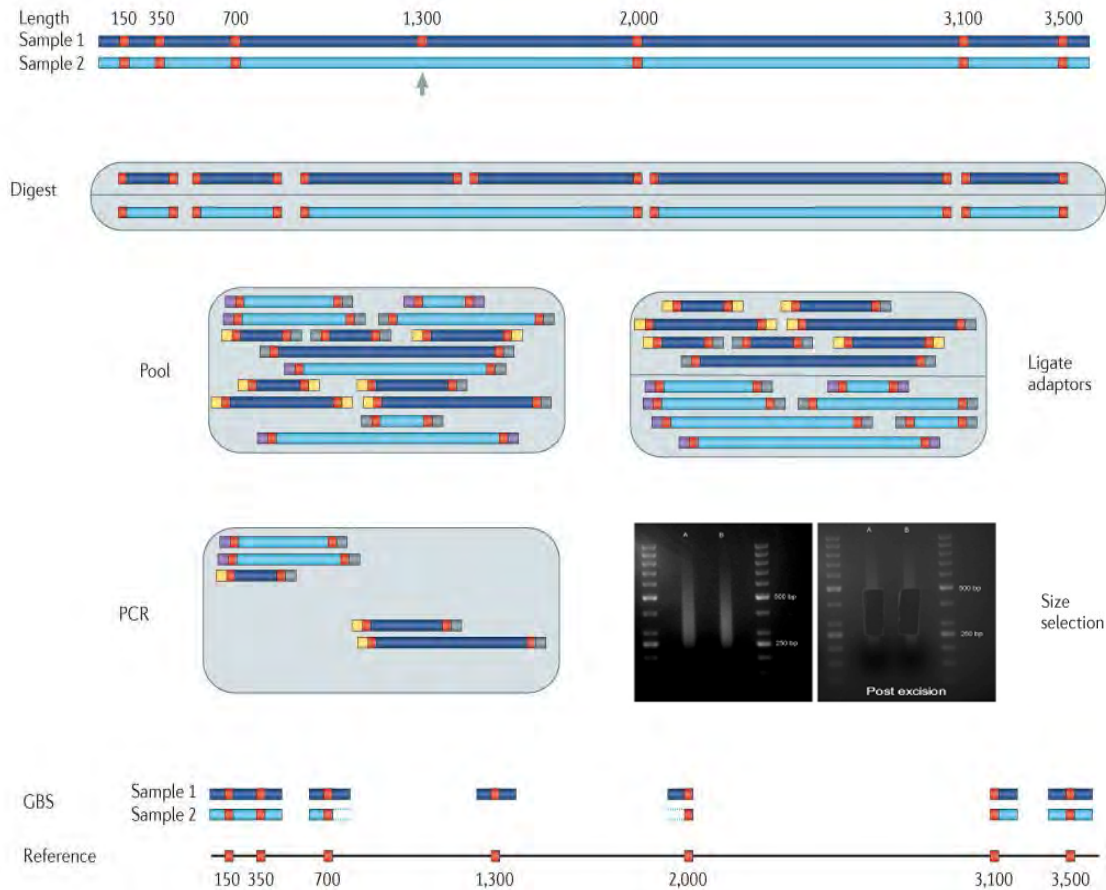
Extended sampling

- 3 Gulf Island populations
- 2 inland BC populations
- Northernmost population on the US mainland
- 13-17 trees per population
- 87 trees successfully sequenced



Genomic library design

Genotyping-by-sequencing (GBS)



- 207 individuals
- 48,641 high quality SNPs called
- 4,855 SNPs used for population genetic analyses

Modified from Davey *et al.* 2011

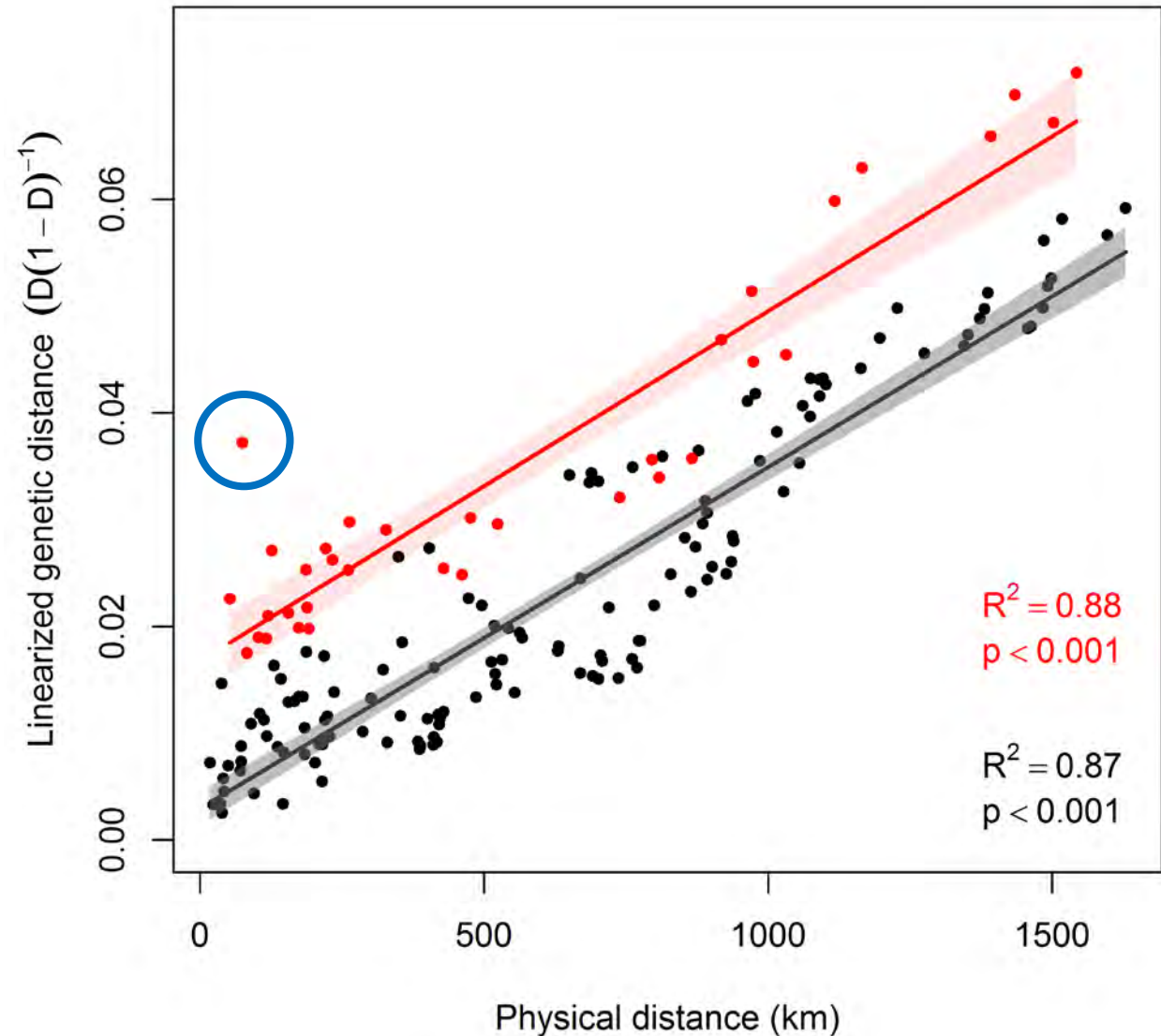
Research questions

- How distinct are populations of *Quercus garryana*?
- Does genetic data support the current taxonomy?
- Can we identify the origin of isolated inland populations in BC?

Population-level statistics

Pairwise genetic distance

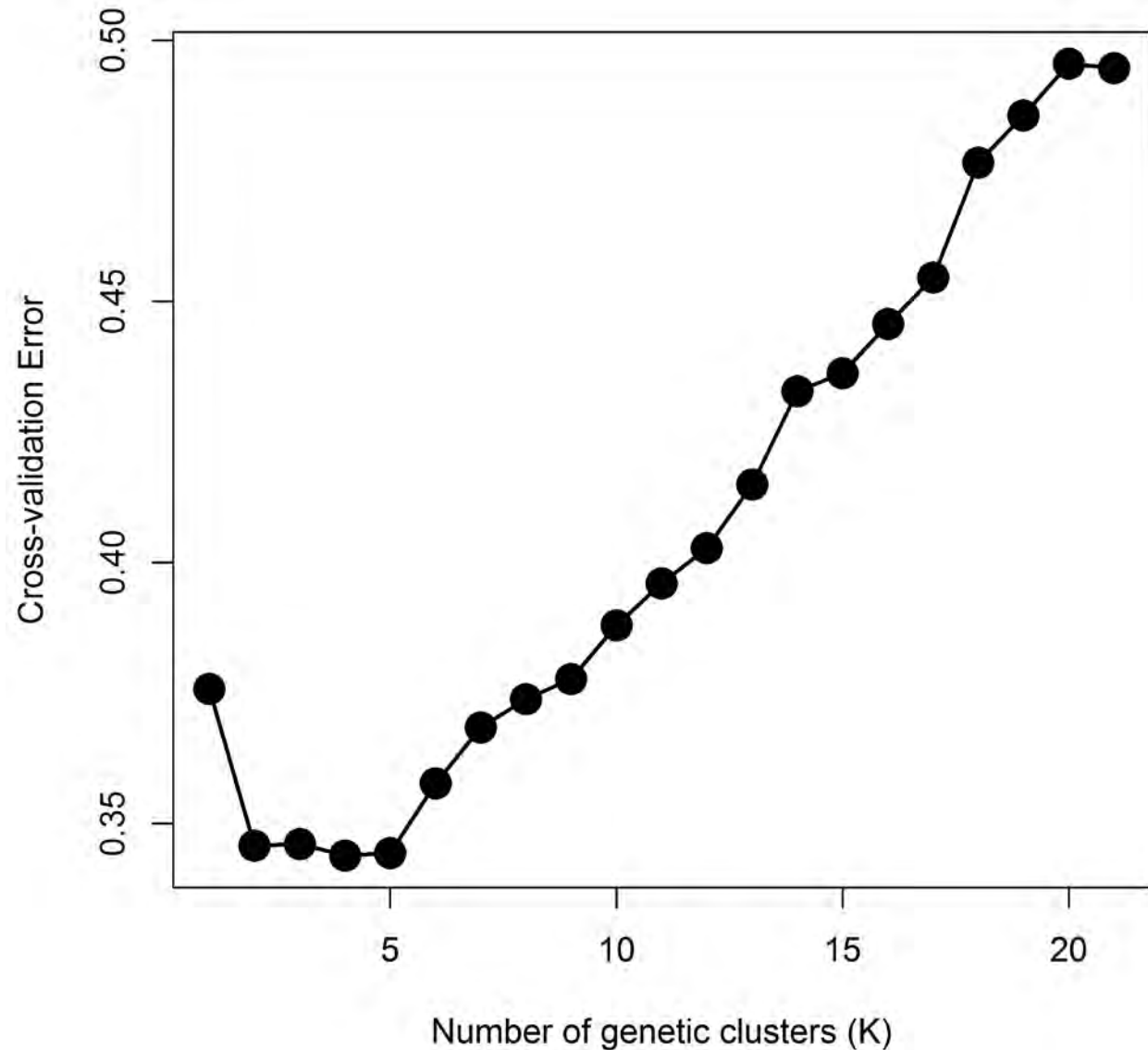
- Jost's D (Jost 2008)
- $\mu = 0.026$
 - $\mu_{Fst} = 0.104$
- $\sim 0.01/300\text{km}$



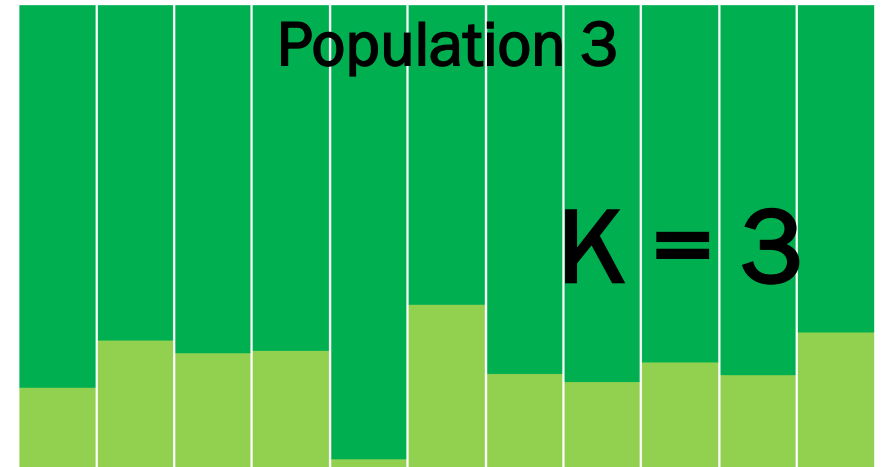
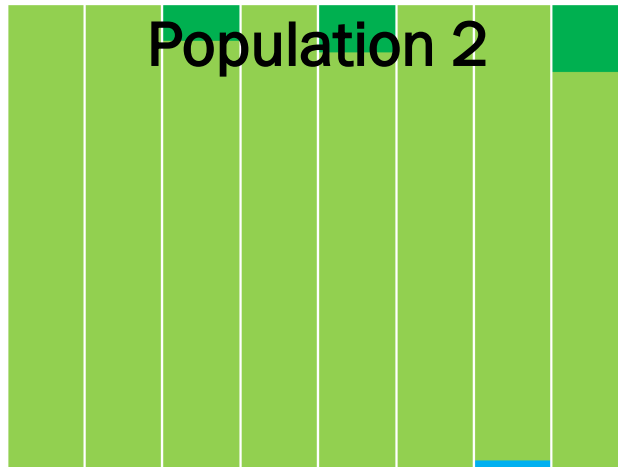
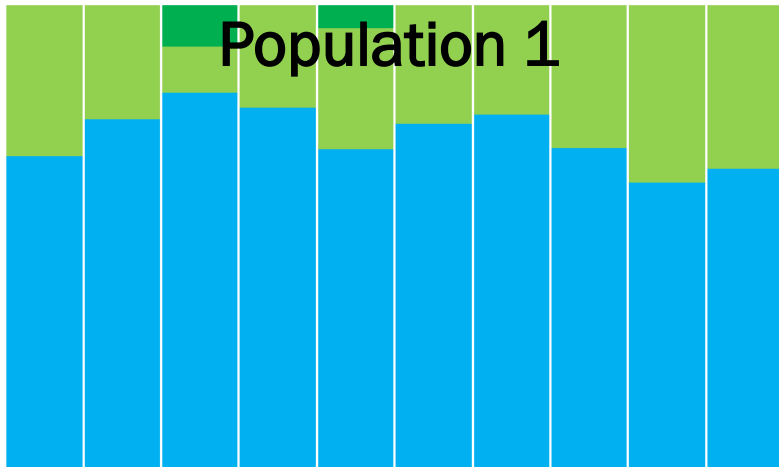
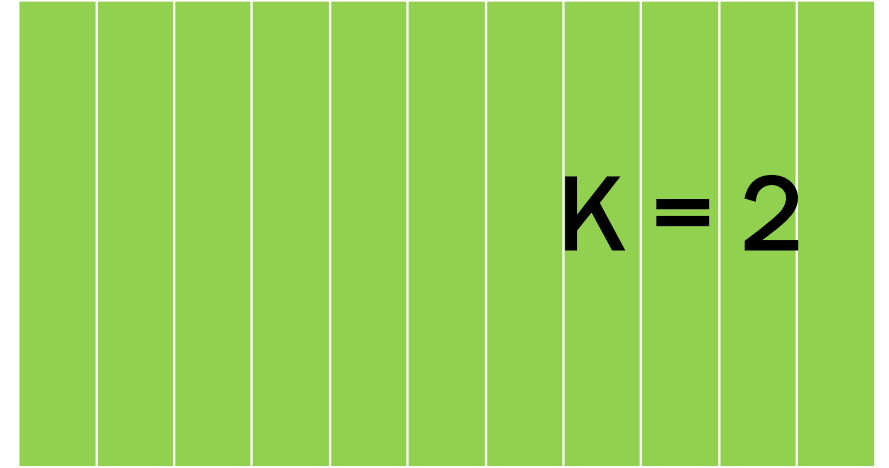
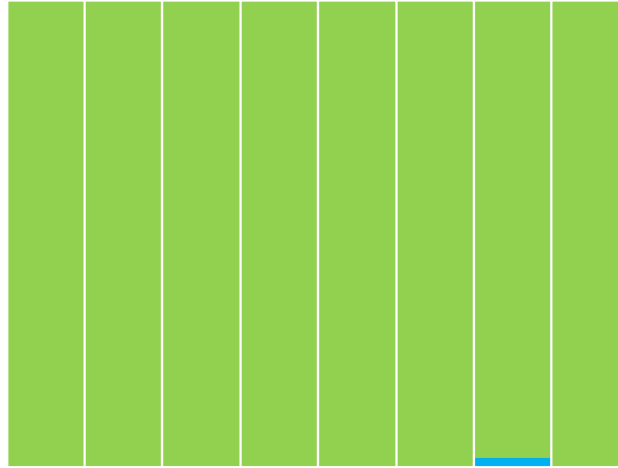
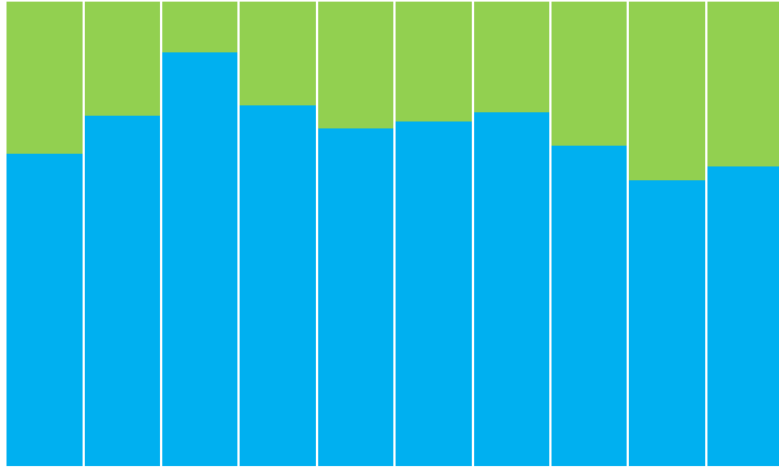
Genetic clustering

ADMIXTURE (Alexander *et al.* 2009)

- Maximum likelihood estimates of shared ancestry
- 2 - 5 genetic clusters supported
 - CVE_{\min} at $K=5$



Ancestry plots



Background



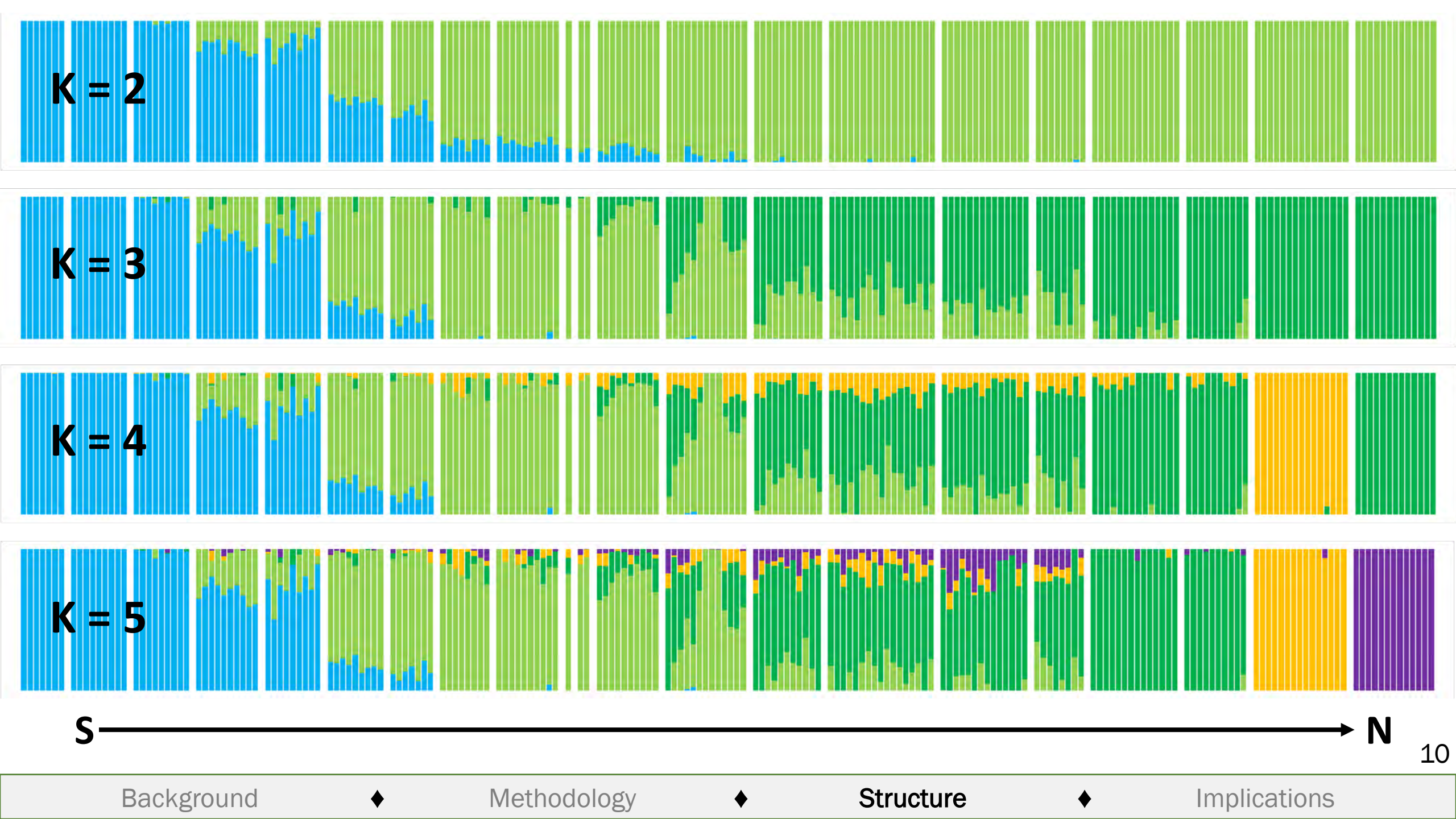
Methodology



Structure

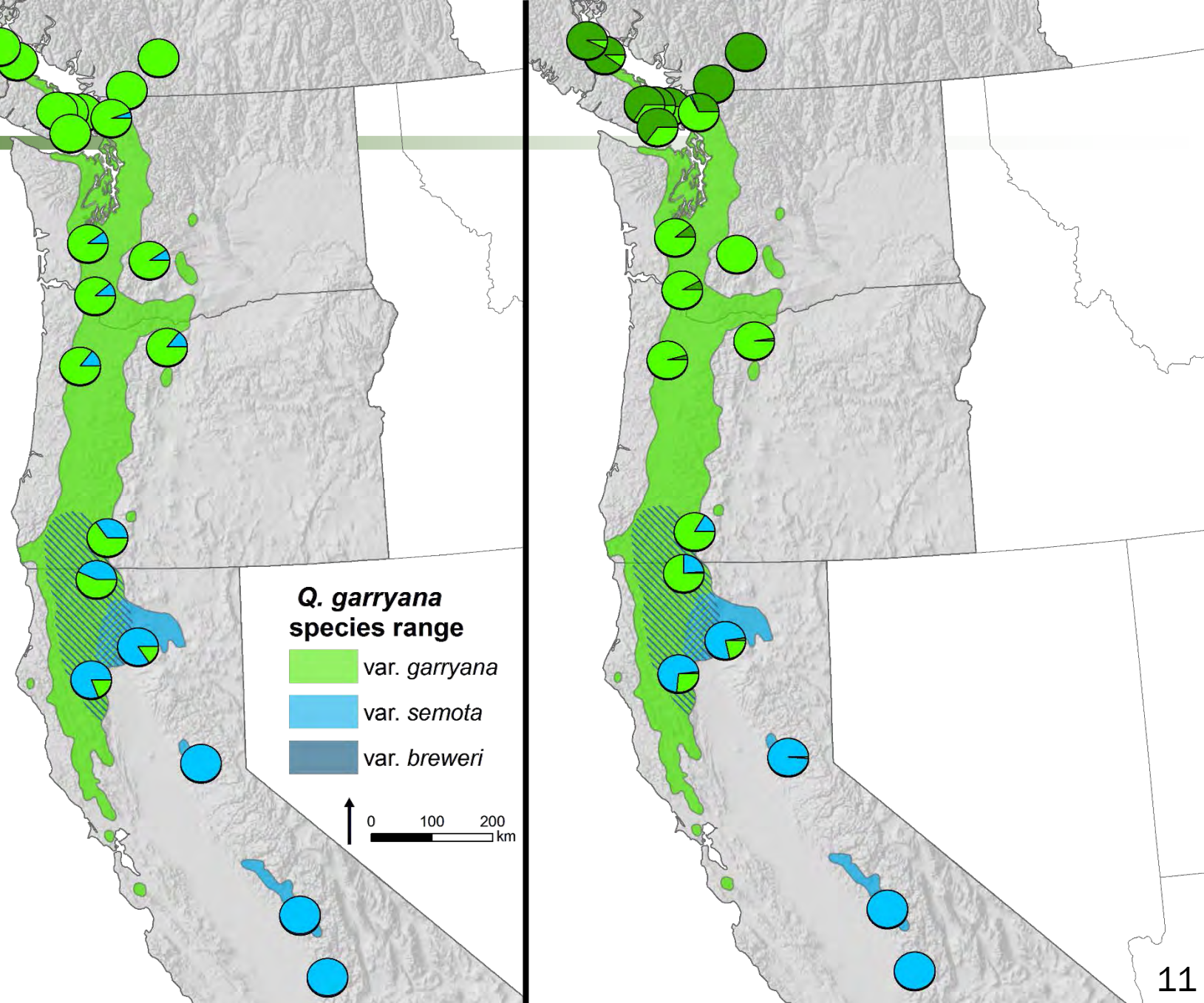


Implications



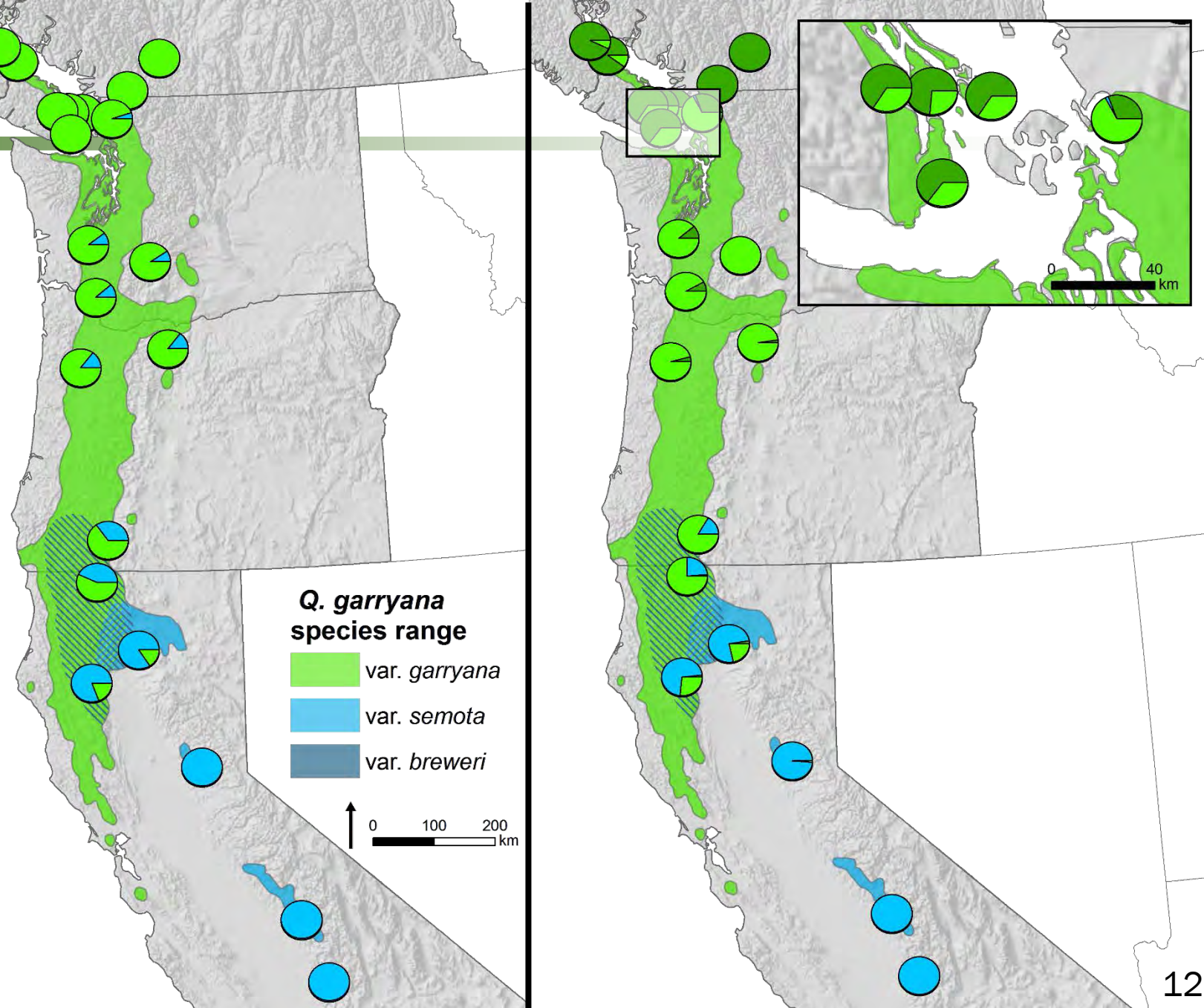
Genetic clustering

- K = 2 (left) captures division between var. *garryana* and shrub varieties
- K = 3 (right) additionally captures a northern cluster



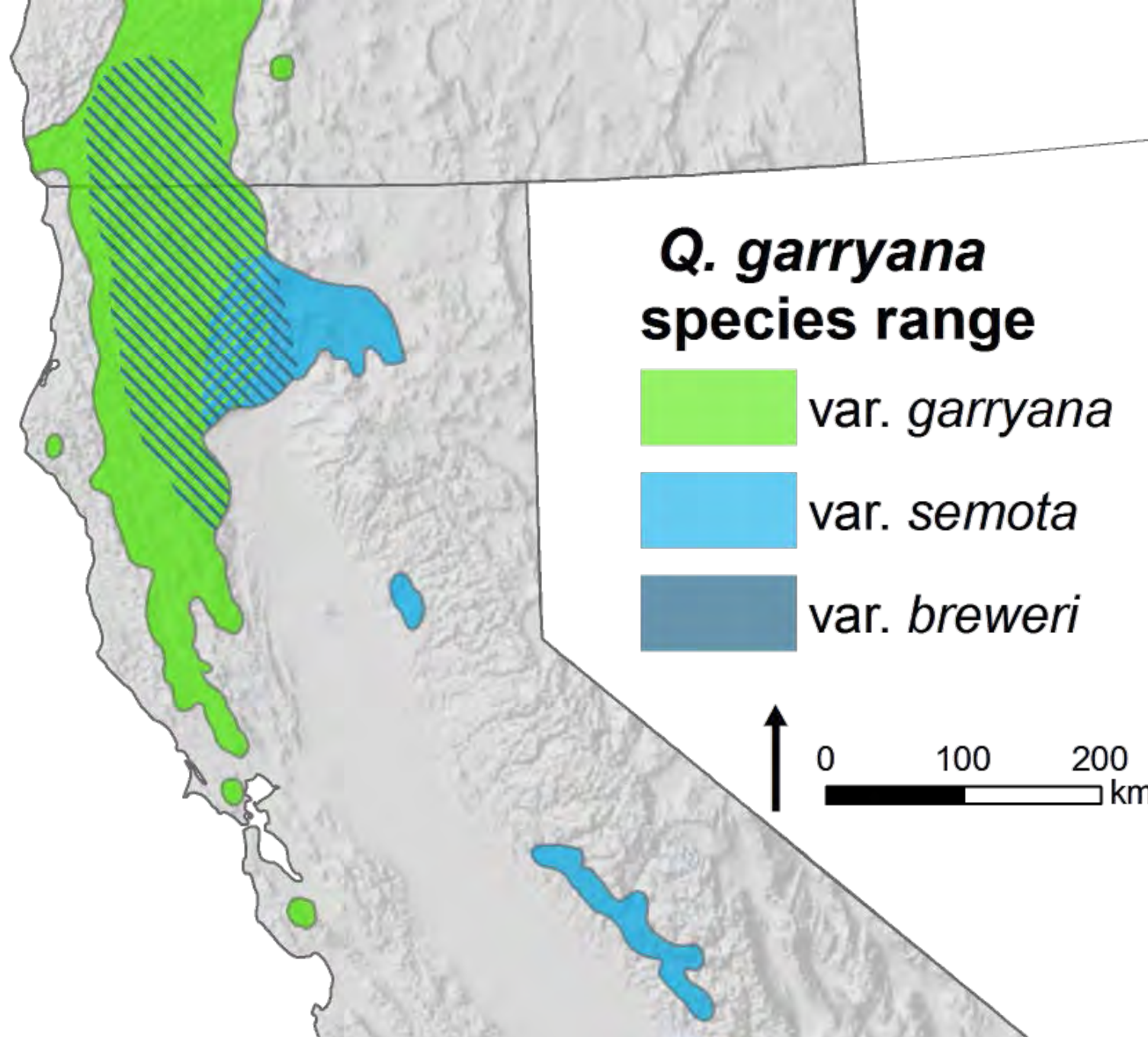
Genetic clustering

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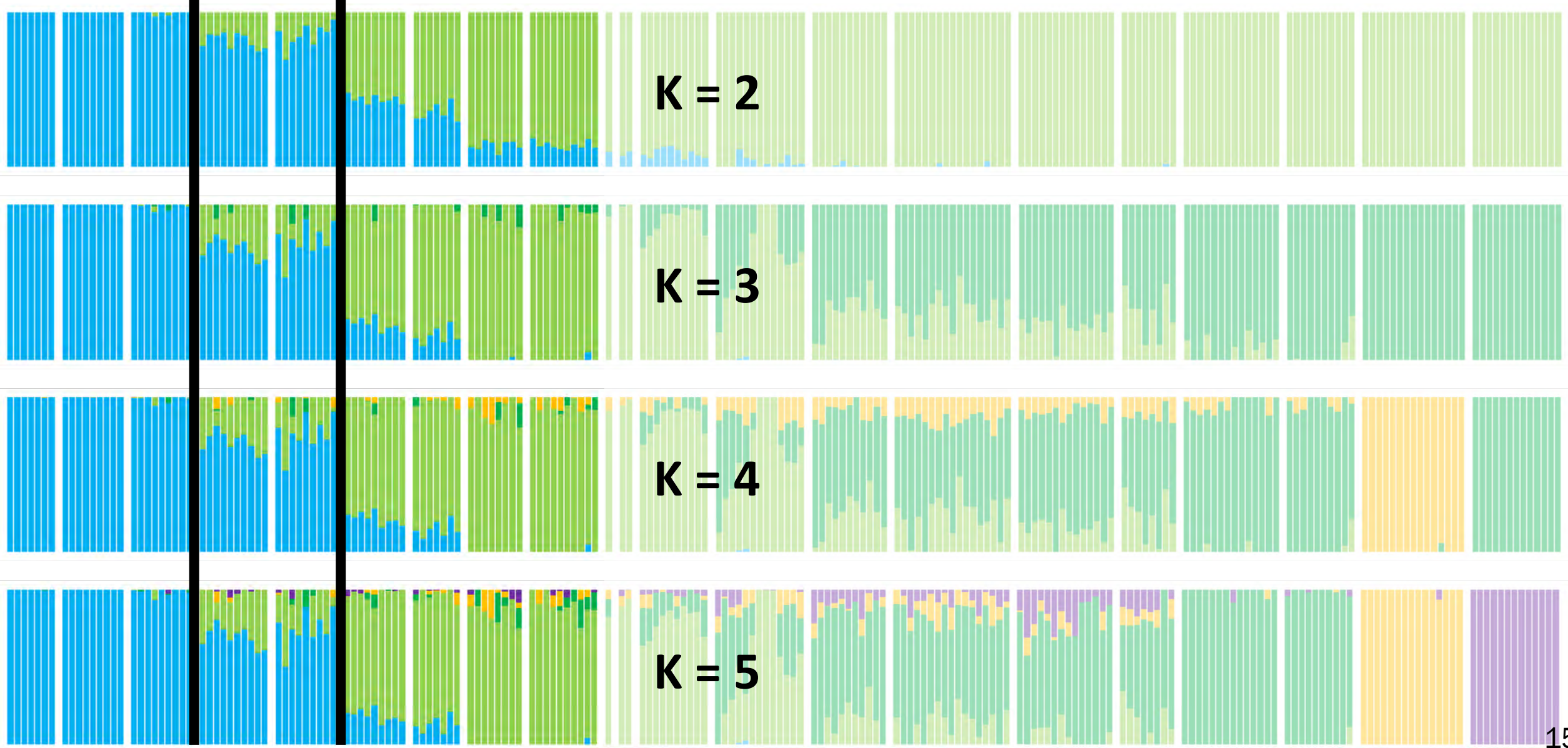


Research questions

- How distinct are populations of *Quercus garryana*?
- **Does genetic data support the current taxonomy?**
- Can we identify the origin of isolated inland populations in BC?

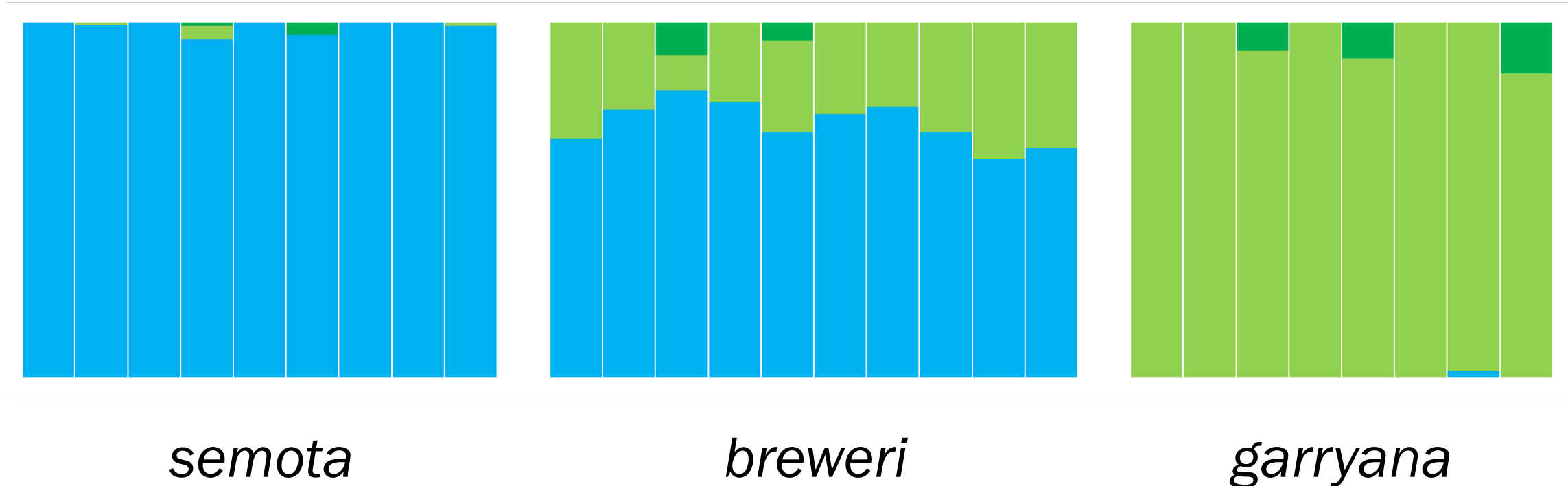


semota *breweri* *garryana*



Taxonomy

- No analyses supported division between vars. *breweri* and *semota*
- “Var. *breweri*” likely *Q. garryana* var. *garryana* x *semota*
- Low sample size of pure “var. *breweri*”



Research questions

- How distinct are populations of *Quercus garryana*?
- Does genetic data support the current taxonomy?
- **Can we identify the origin of isolated inland populations in BC?**

United States

BC

Sumas Yale

K = 2

K = 3

K = 4

K = 5

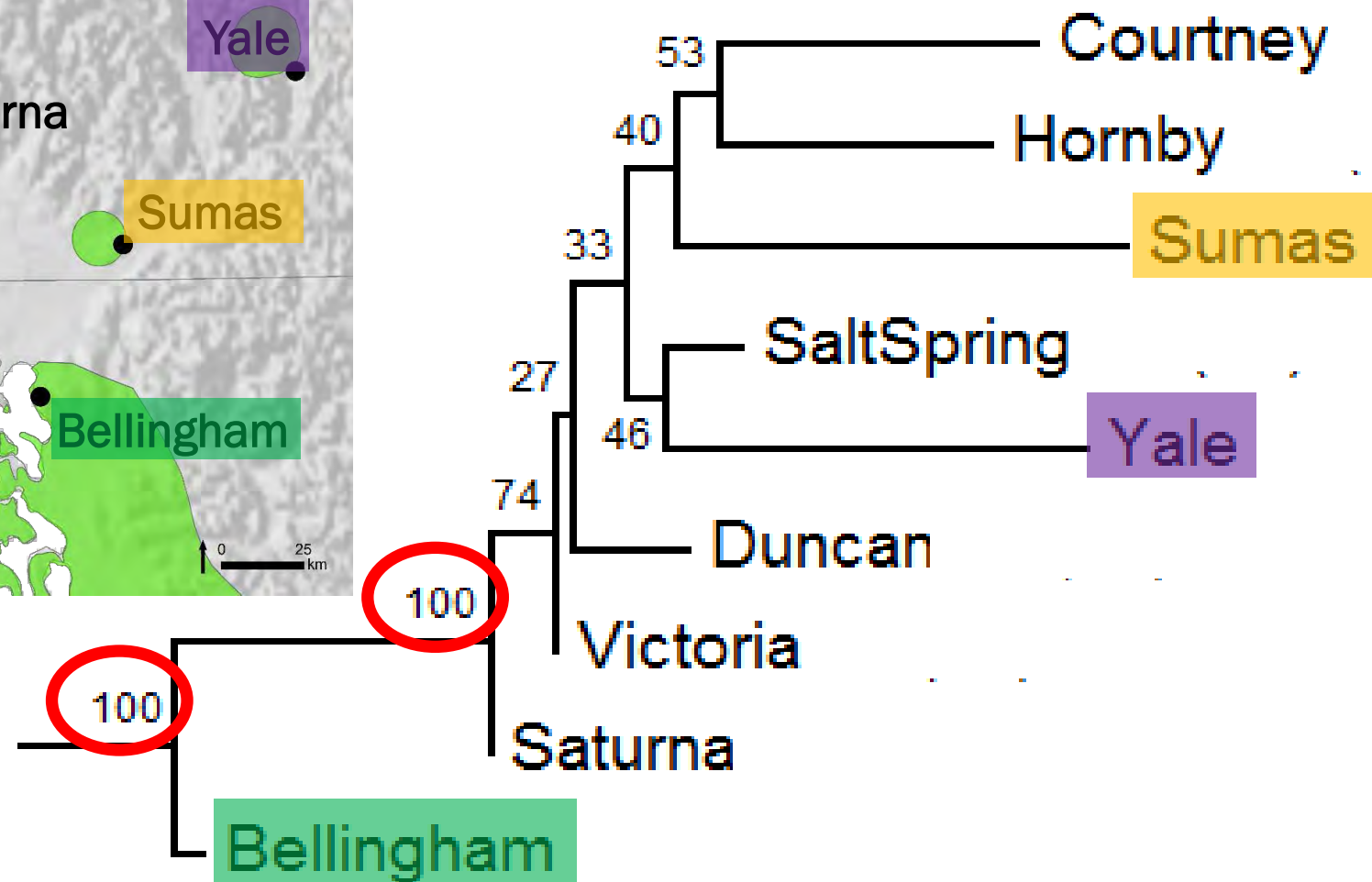
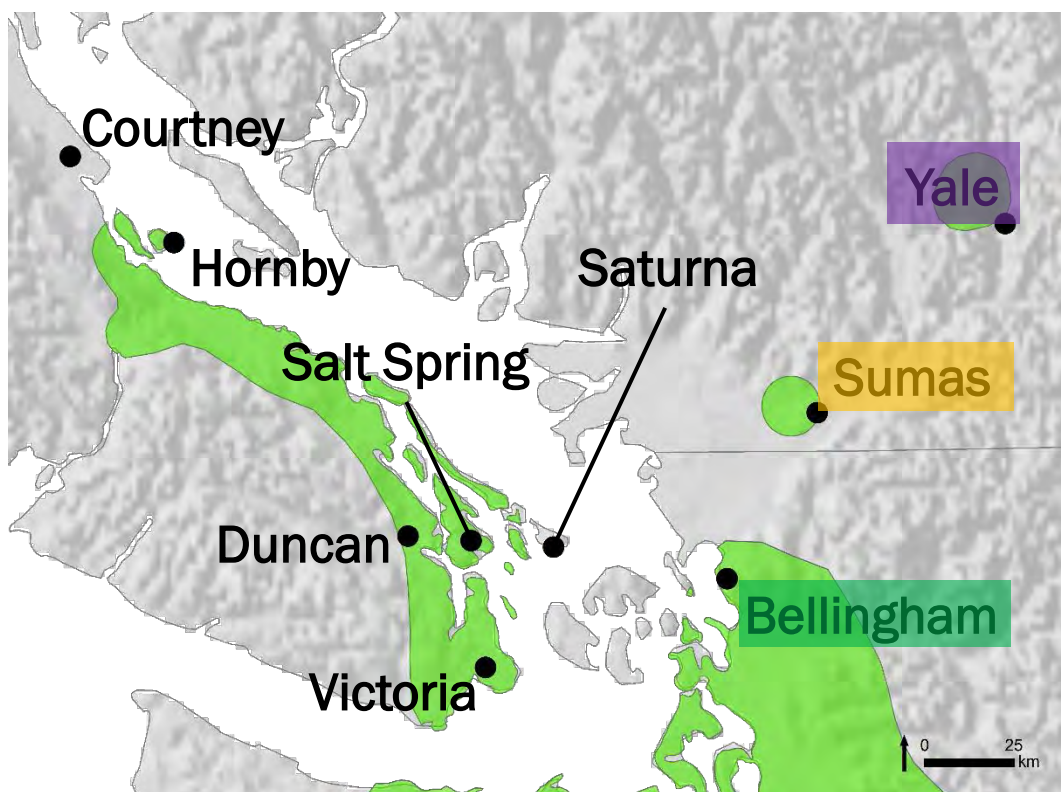
Background

Methodology

Structure

Implications

Isolated inland BC populations



Acknowledgements

Sally Aitken - Funding, ideas, time

Kristin Nurkowski - Support and wetlab troubleshooting

Sean King - Assistance in grueling treks through flowering Garry oak meadows

Sam Yeaman - Advice on bioinformatics/server assistance

Thanks for listening!

Summary

- Gene flow occurring between all major genetic populations
- Populations in BC genetically distinct from US
- Two taxonomic varieties genetically supported
- Inland BC populations apparently of Gulf Island origin



Jonathan Degner

Centre for Forest Conservation Genetics
University of British Columbia; Vancouver, BC

jcdegner@alumni.ubc.ca

References and credits

- References

Alexander, D., Novembre, J., and Lange, K. 2009. Fast model-based estimation of ancestry in unrelated individuals. *Genome Research* **19**: 1655-1664.

Elshire, R., Glaubitz, J., Sun, Q. et al. 2011. A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PLoS* **6**(5): e19379.

Huebert, C. 2009. The ecological and conservation genetics of Garry oak (*Quercus garryana* Dougl. Ex Hook). M.Sc. thesis, Department of Forestry, University of British Columbia.

Jombart, T., Devillard, S., and Balloux, F. 2010 Discriminant analysis of principal components: A new method for the analysis of genetically structured populations. *BMC Genetics* **11**.

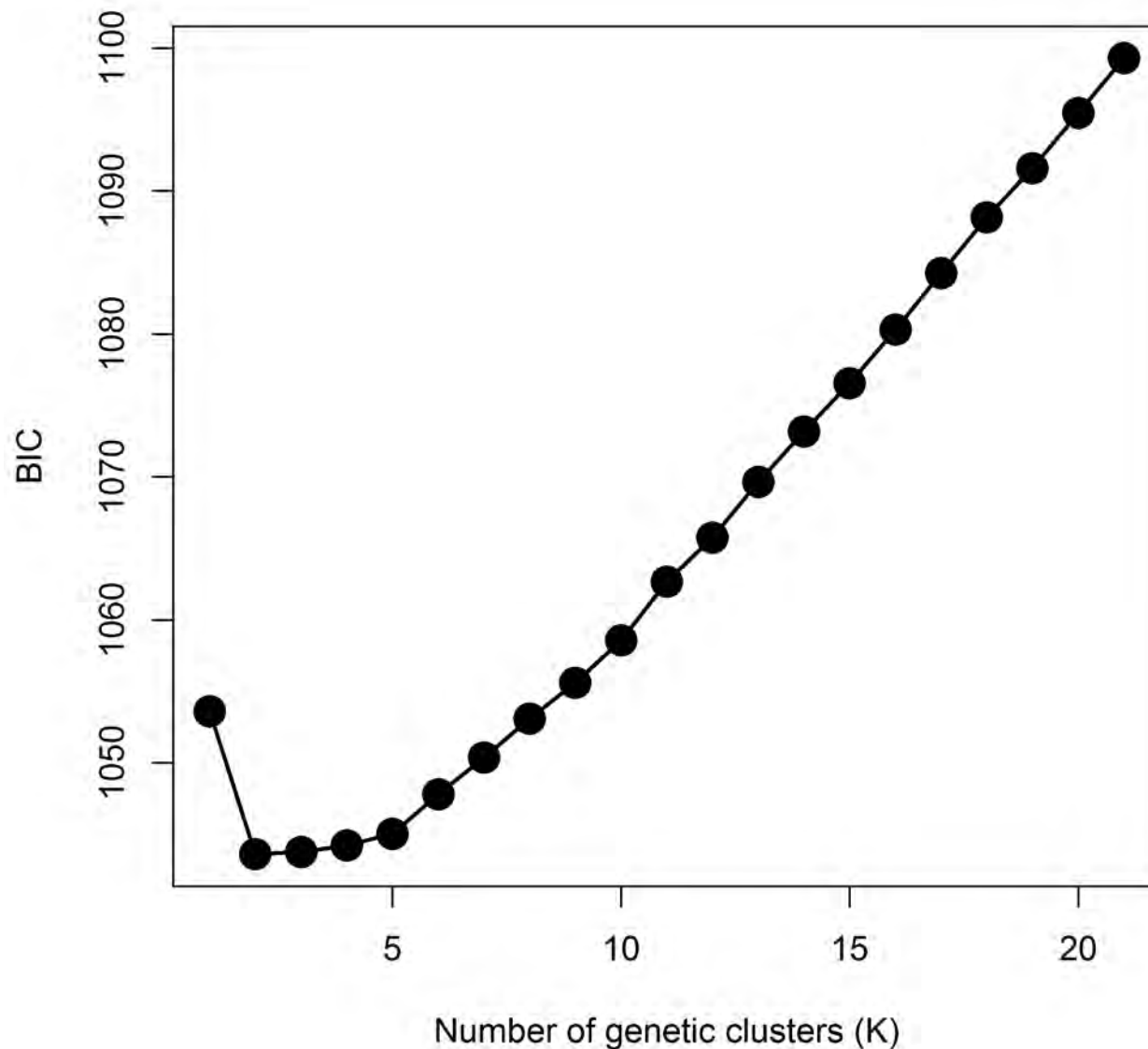
Jost, L. 2008. GST and its relatives do not measure differentiation. *Molecular Ecology* **17**(18): 4015-4026.

Little, E. 1971. Atlas of United States trees, volume 1: conifers and important hardwoods. USDA misc. publ. 1146

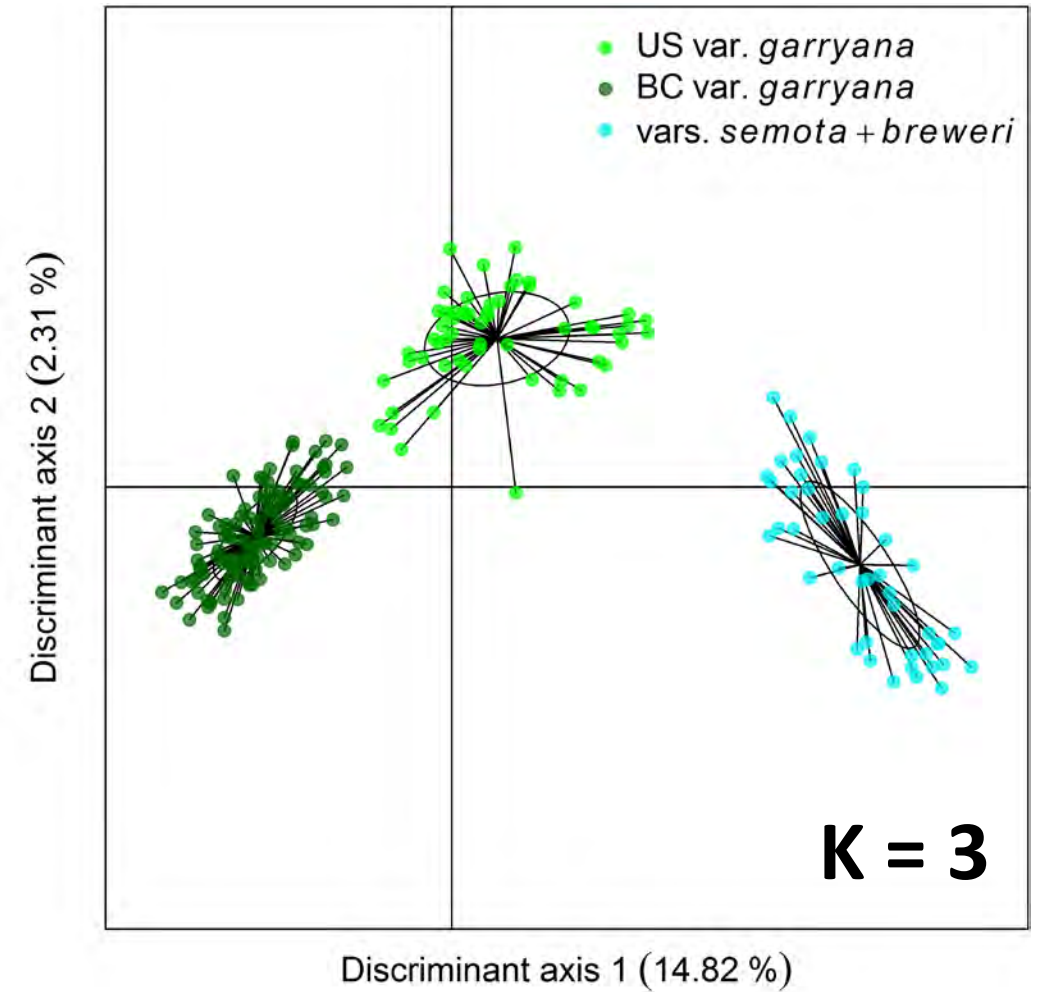
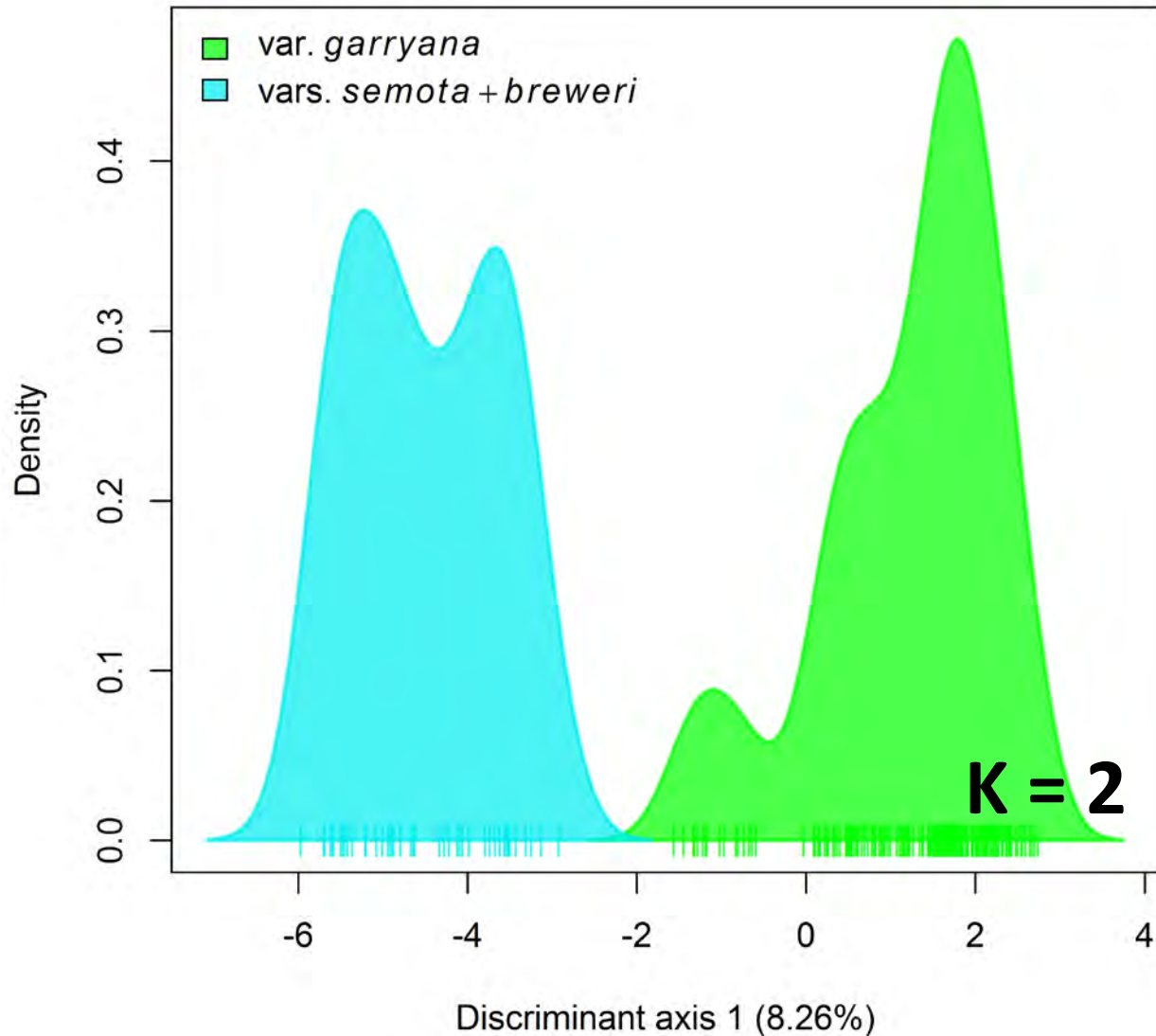
Population structure

DAPC (Jombart *et al.* 2008)

- Model-free estimates of genetic similarity
- 2 - 5 genetic clusters supported
 - BIC_{\min} at $K = 2$



Population structure



Isolated inland BC populations

Shrub varieties

Mainland US

Vancouver Island and Gulf Islands

Sumas

Yale

- 212 highly informative SNPs from DAPC
- Neighbor-joining tree using Nei's genetic distance corrected for sample size bias
- 5000-replicate bootstrap

