

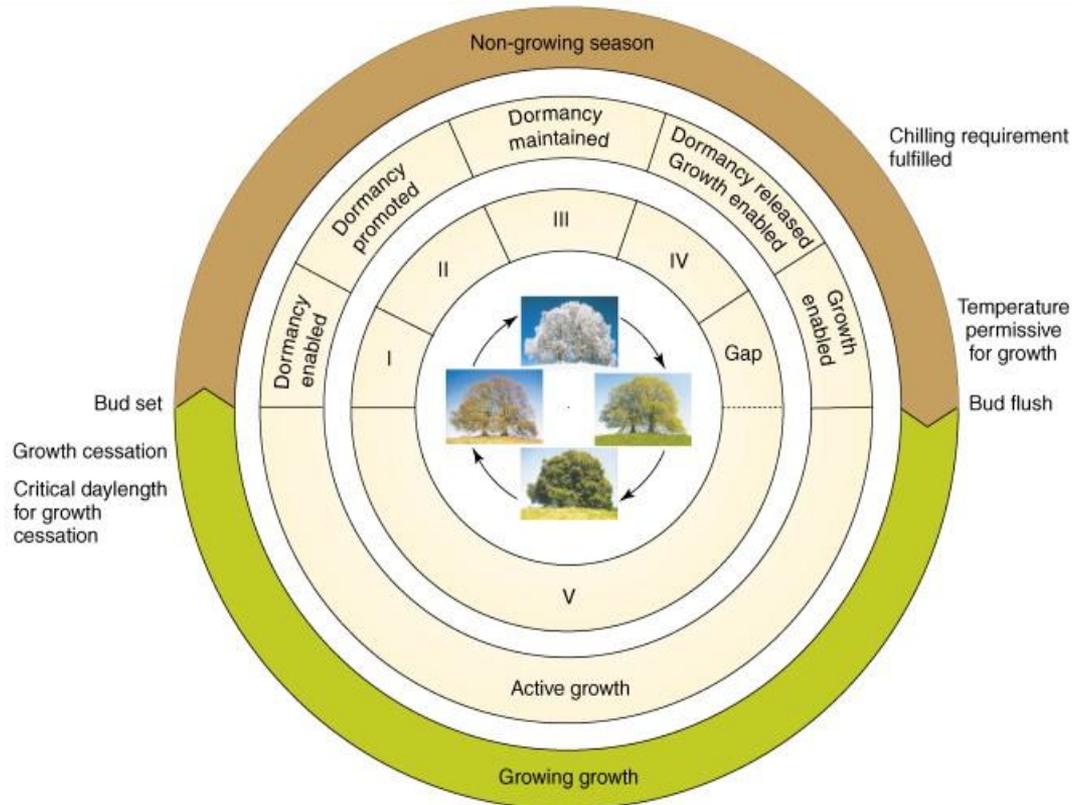
Genomics of Local Adaptation in Trees

Jason Holliday, Virginia Tech



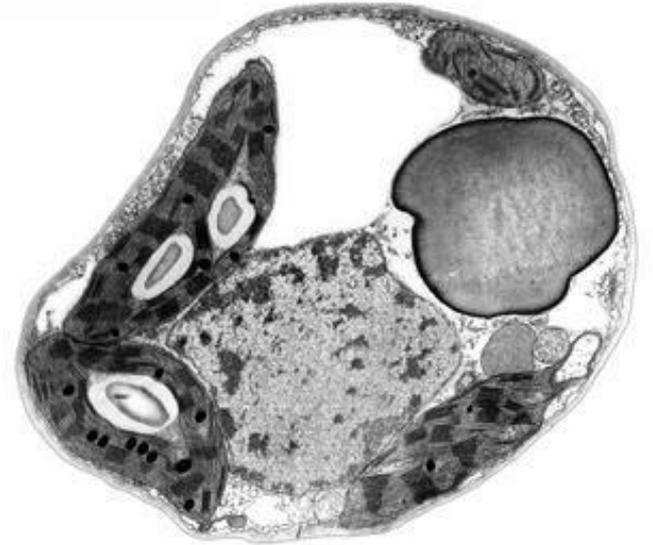


Local climatic adaptation in temperate and boreal tree species



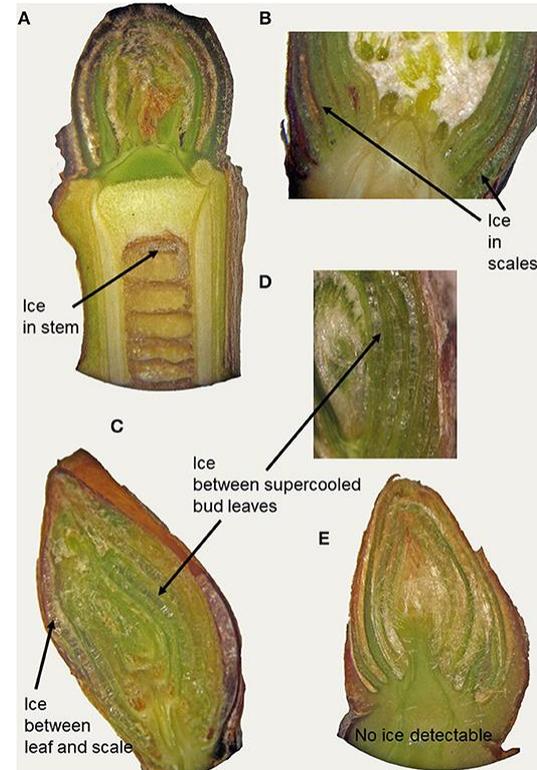
Seasonal dormancy: a response to the cellular stresses imposed by freezing

- Direct thermal effects on macromolecules
- Chemical stress imposed by dehydration of macromolecules
- Mechanical stress on membranes due to dehydration
- Oxidative stress
- Electrical potential at ice-H₂O interface



Mechanisms of freezing tolerance in trees

- Supercooling
 - Antifreeze proteins/metabolites
 - Prevent ice from freezing and/or propagating
 - Good to -30C or -40C, at which point ice spontaneously nucleates
- Dehydration
 - No water left to freeze
 - Can survive submersion in liquid nitrogen (-196°C)
- Chestnut probably supercools, which explains its northern range limit



Clinal variation for dormancy and cold hardiness is pervasive among widespread tree species

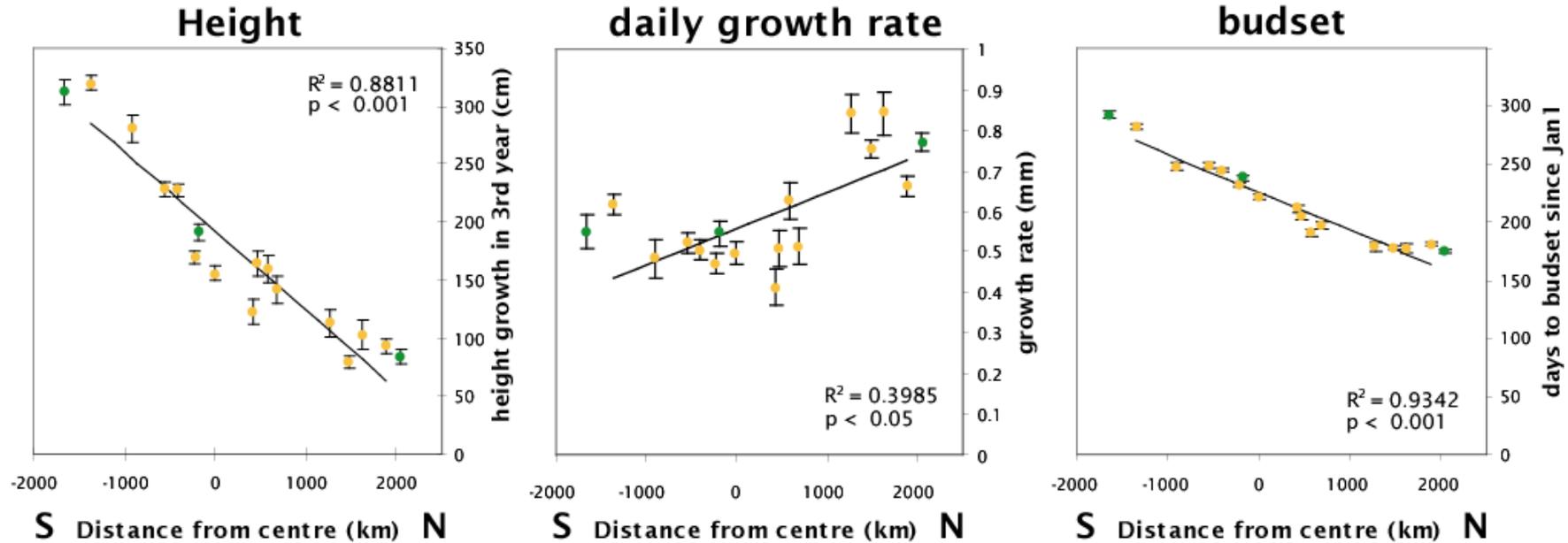


Center

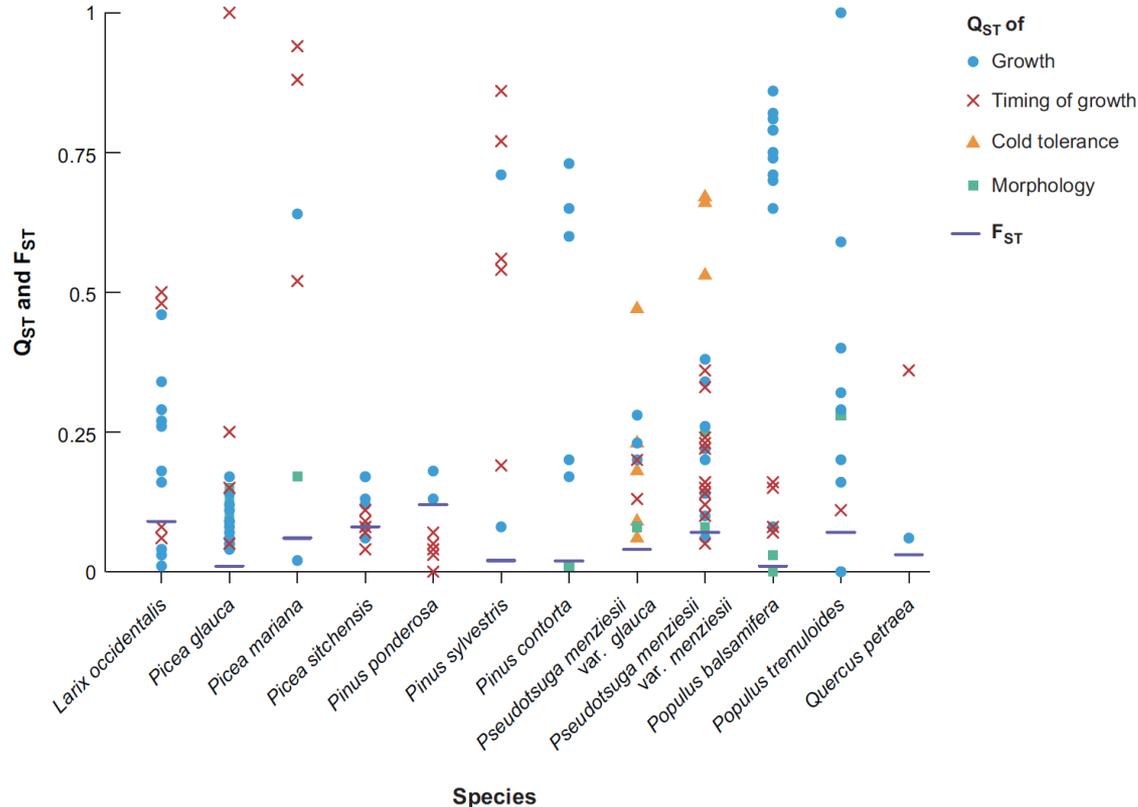
North

South

Clinal variation: evidence of adaptation



Local adaptation is common in northern tree species in spite of strong population connectivity via pollen flow



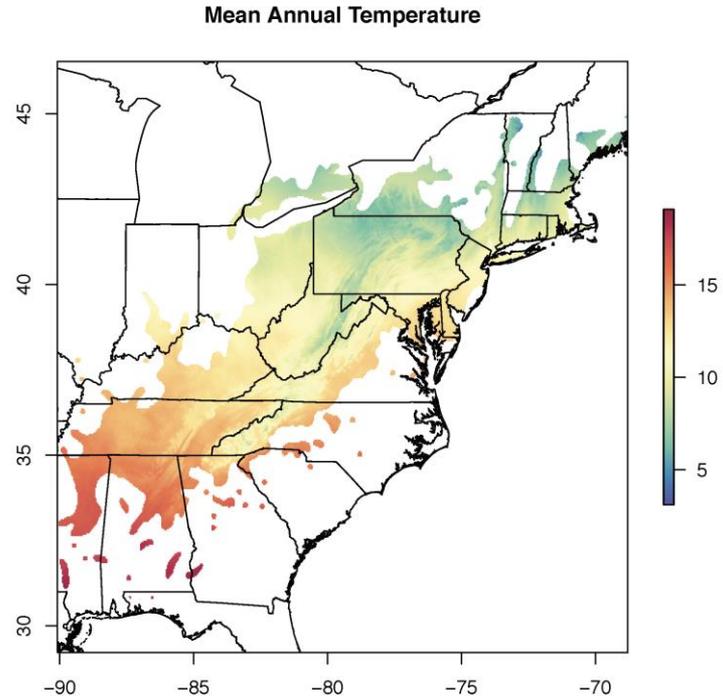
- Q_{ST} : population differentiation for traits
- F_{ST} : population differentiation across the genome

Local adaptation to additional environmental factors

- Bud phenology and cold hardiness usually show the strongest signature of local adaptation, but additional selective pressures may be important:
 - Water availability and seasonality
 - Pest/pathogen/mutualist interactions
 - Herbivory
 -

Successful chestnut restoration must deploy locally adaptive genetic variation

- Blight resistance is necessary but not sufficient to recover the species
- Particularly an issue for the OxO transgenics, which began with a single genetic background
- Provide for adaptation to both current and future planting environments

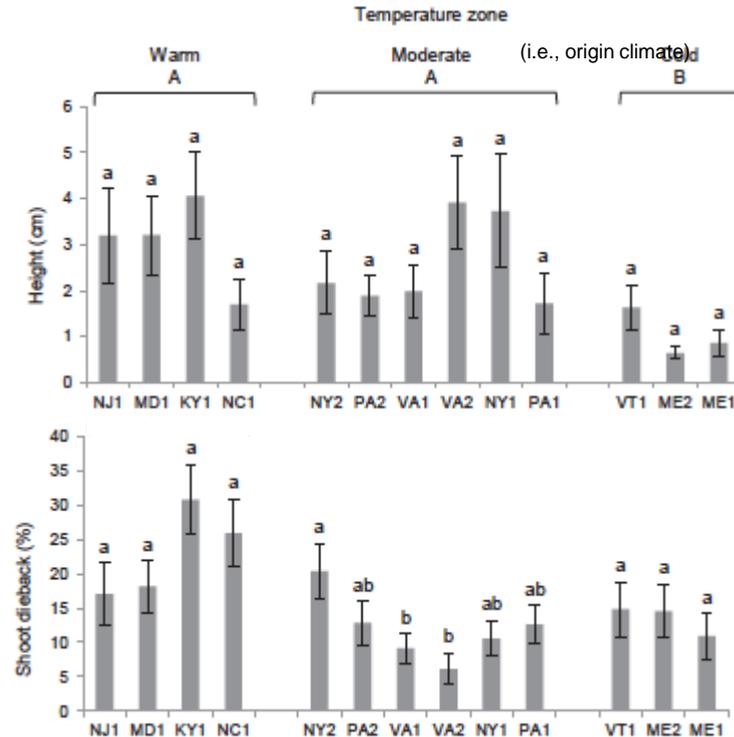


How do we characterize adaptive variation so we can capture it in the breeding programs?

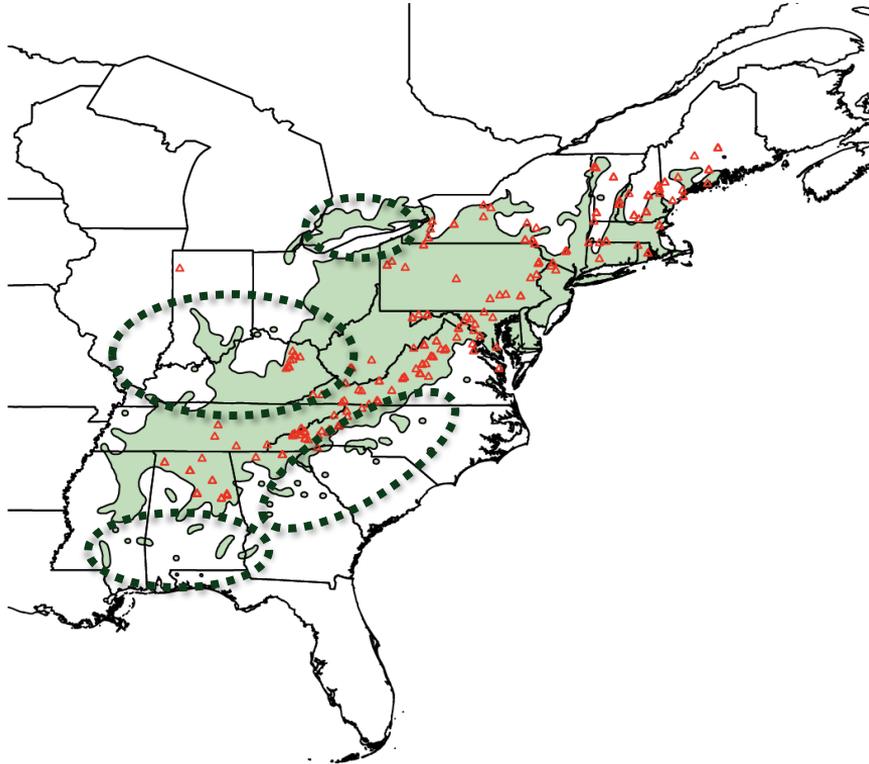
- Two general approaches
 - Indirect: provenance trials in common gardens to understand patterns of phenotypic variation across the species range (e.g., spruce example)
 - Direct: genome sequencing coupled with environmental data to detect genotype-environment correlations

Provenance tests in American chestnut

- Difficult to study as wild trees usually don't produce viable seed
- Among 13 provenances, significant differences in growth and frost damage in a Vermont common garden



Landscape genomics of American chestnut



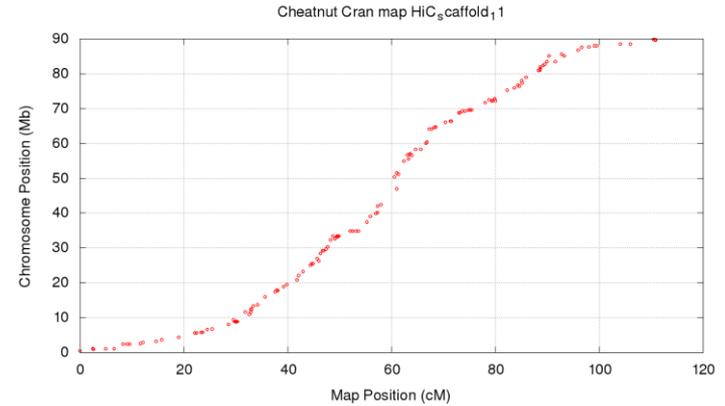
- Leaves from ~500 stump sprouts representing the full historical climatic envelope of chestnut



Alex Sandercock,
PhD student

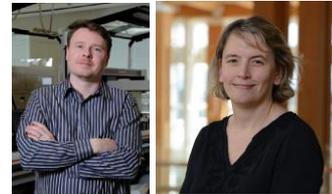
Genomic Data

- Sequence the full genome of all 500 samples
- Align to the (beautiful) Ellis1 genome sequence
 - “The best heterozygous genome we’ve assembled” – Jeremy Schmutz



Jeremy Schmutz

Jane Grimwood



Detecting the footprint of natural selection: genotype-environment relationships

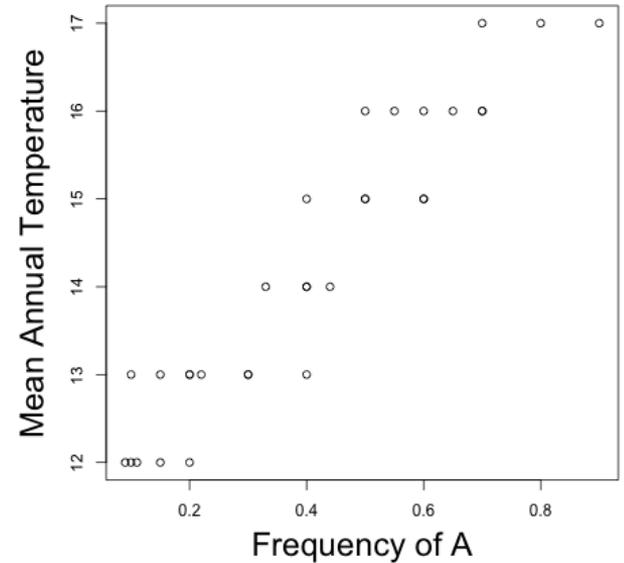
- Genotypes

- Ind1
ATC**G**TCA
- Ind2
ATC**A**TCA
- Ind3
ATC**A**TCA
- Ind4
ATC**G**TCA
- Ind5
ATC**A**TCA
- Ind6
ATC**G**TCA

+

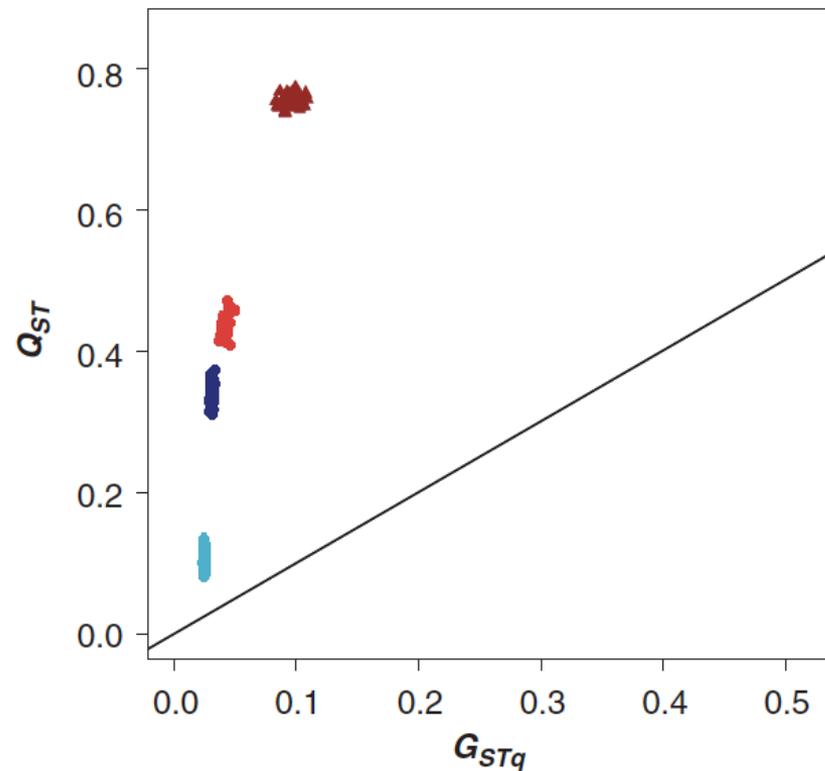
- Environment
(MAT)

- Ind1 13°C
- Ind2 17°C
- Ind3 18°C
- Ind4 12°C
- Ind5 16°C
- Ind6 13°C
- ...
- IndN 15°C



How successful are these genome-scans for local adaptation likely to be?

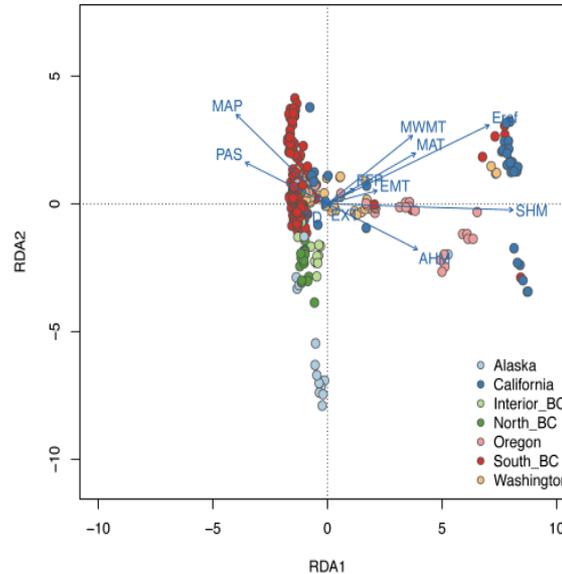
- In spite of great effort, population geneticists have not been able to comprehensively connect trait variation with its underlying genetics
- Likely because many, many genetic variants involved, most with vanishingly small effects
 - i.e., we can't differentiate them from background



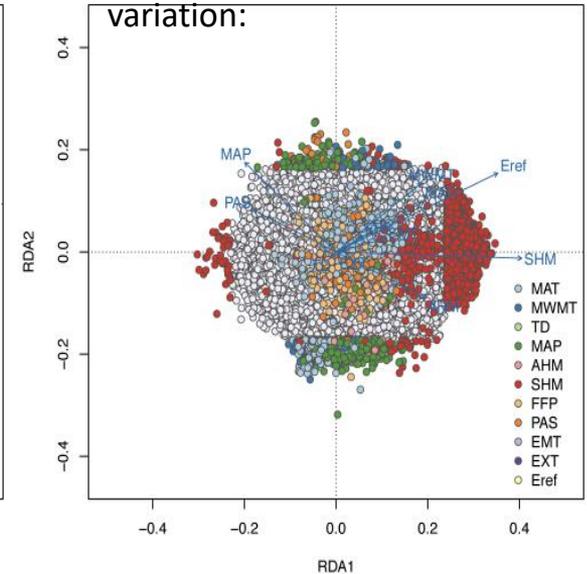
Multivariate approaches may be more useful

- Redundancy analysis allows many genetic variants to be analyzed simultaneously
- Identifies groups of loci that covary with the environment
- May lead to more false positives, but in this case I don't especially care

Variation in climate across sampling locations:

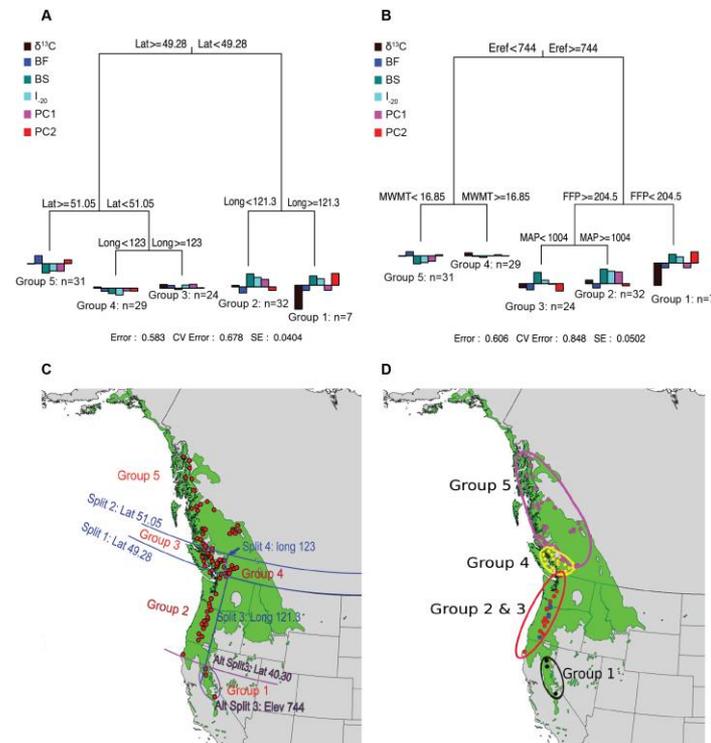


Relationship between genetic variation and climate variation:

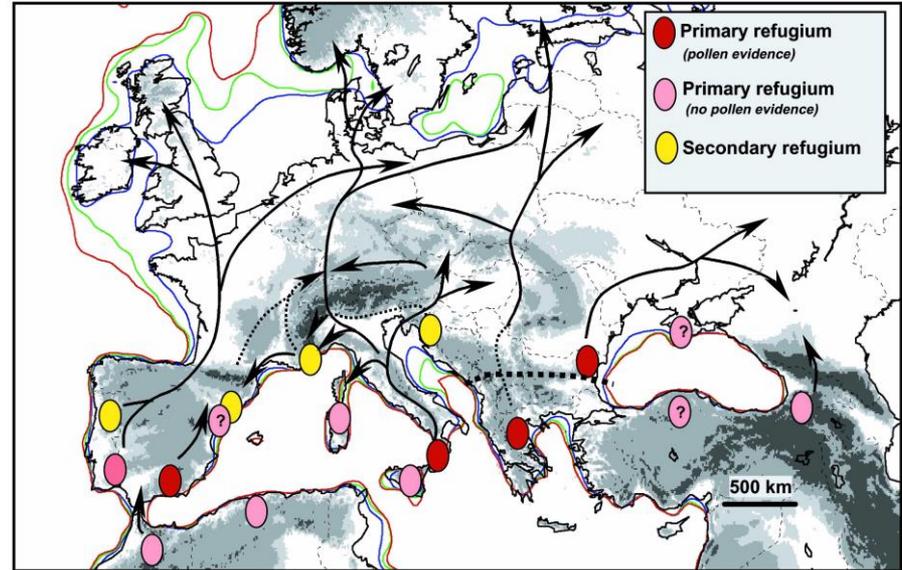


How do we synthesize all of this information into a germplasm conservation strategy?

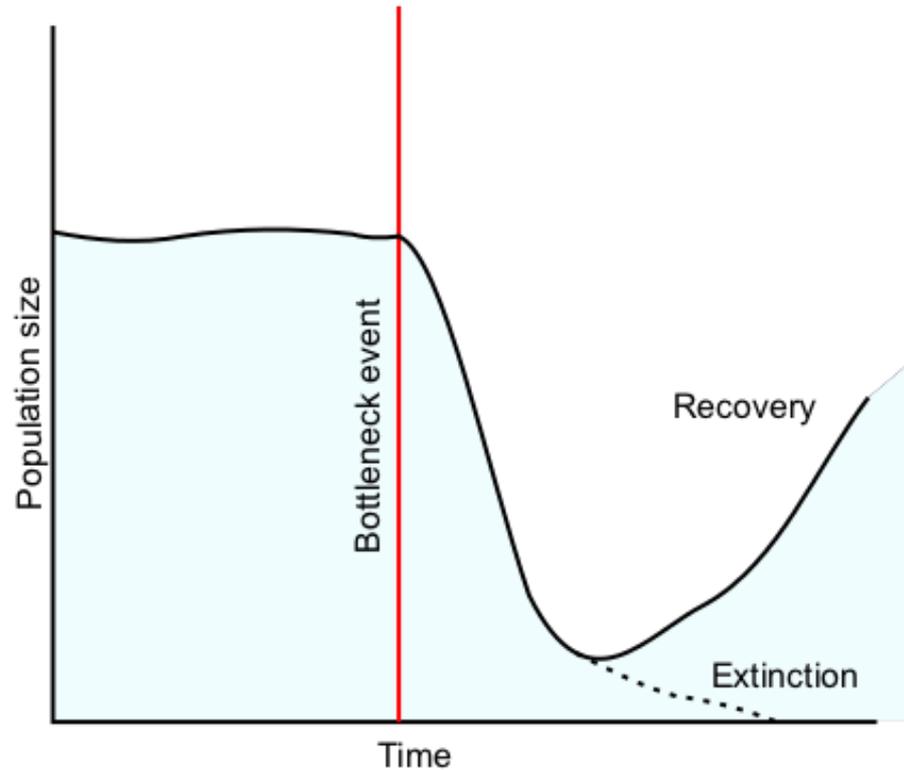
- Classification trees may be useful
- Goal is to split observations according to predictor variables that yield relatively homogeneous groups



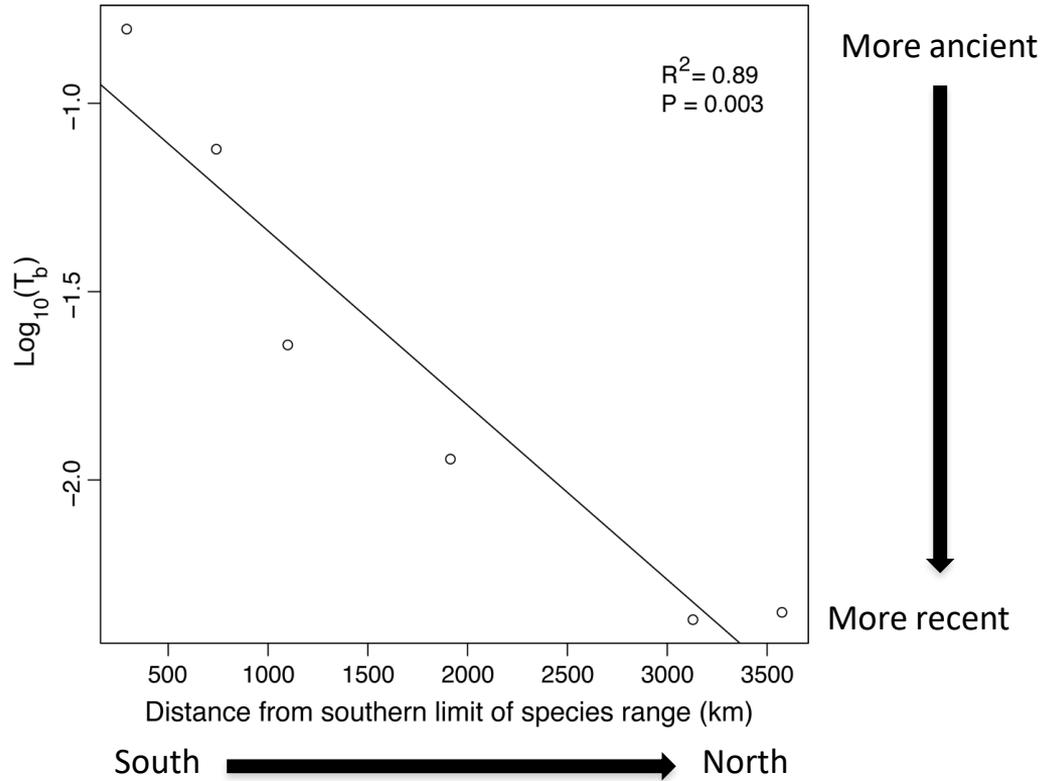
Local adaptation is only one strong evolutionary force governing genetic variation in temperate and boreal trees



Postglacial migration likely involves population bottlenecks

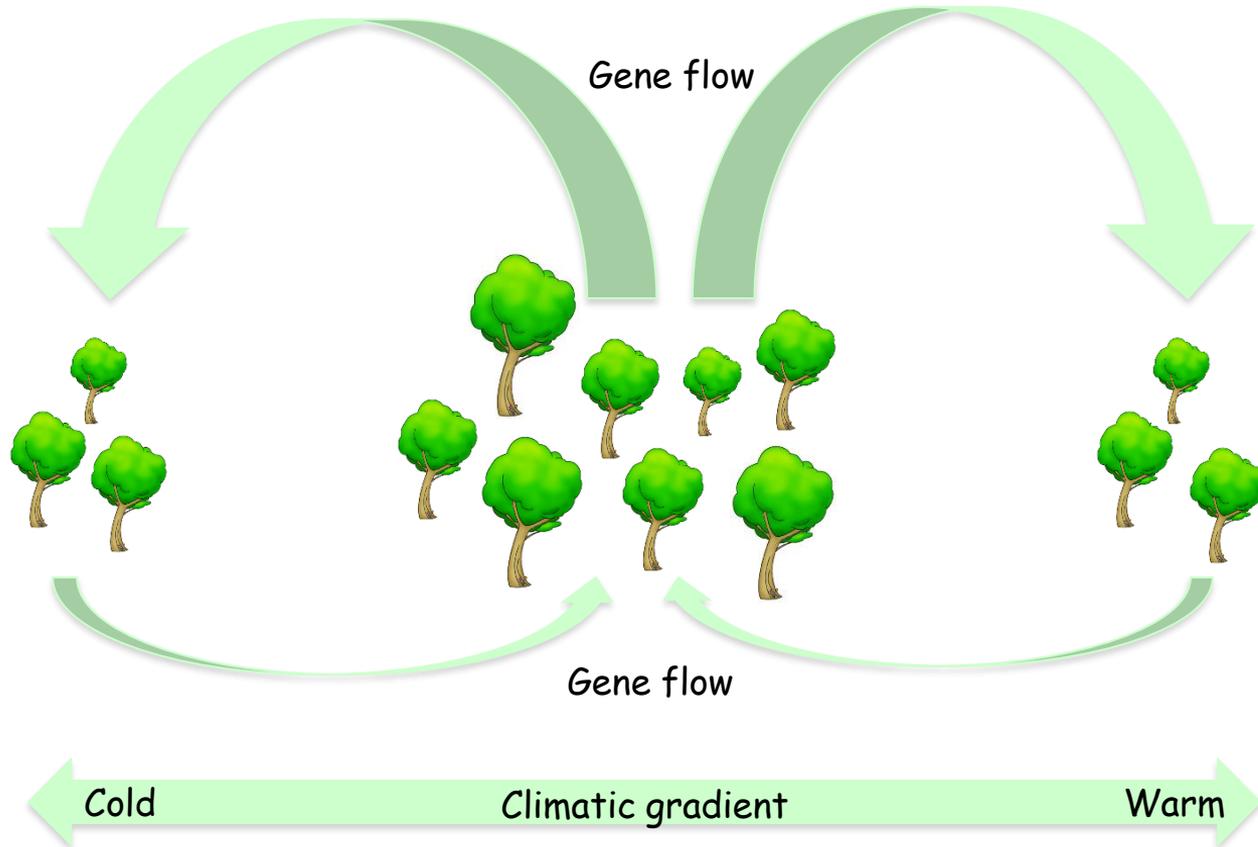


Bottlenecks associated with postglacial migration in Sitka spruce

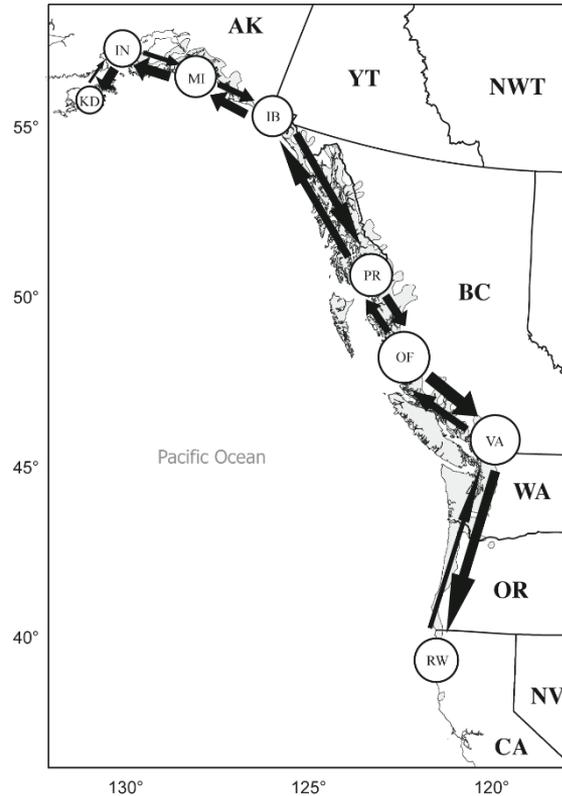


Didn't chestnut also go through a rather extreme bottleneck very recently (i.e., due to the blight)?

Central-peripheral structure

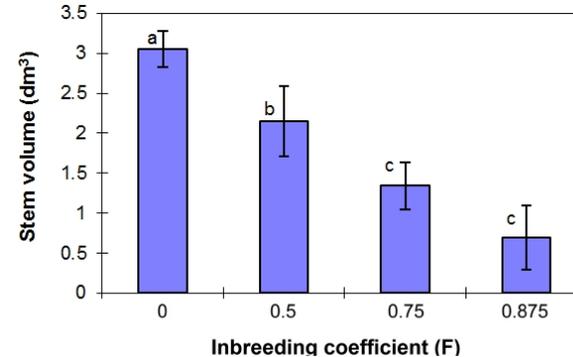
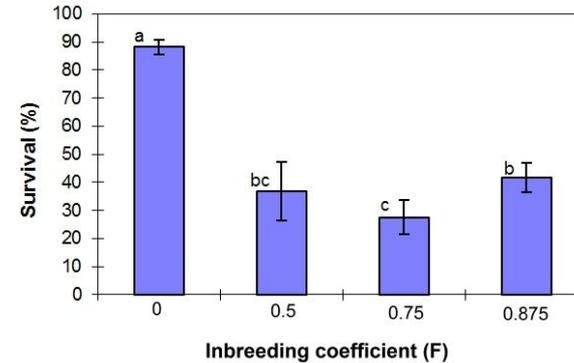


Evidence for an abundant range center in spruce

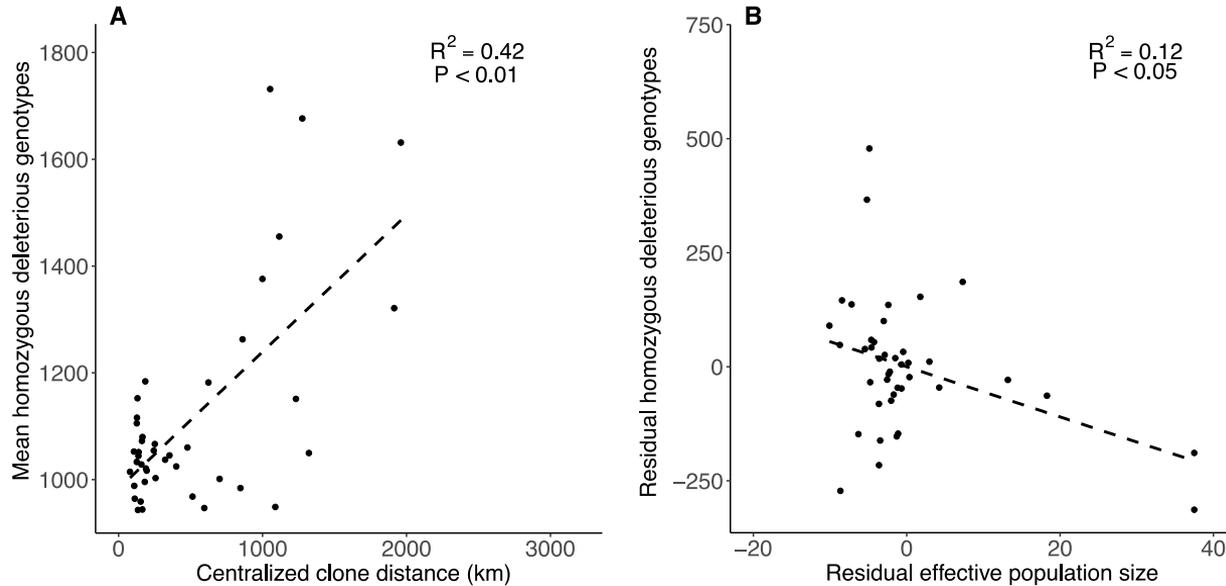


Deleterious alleles

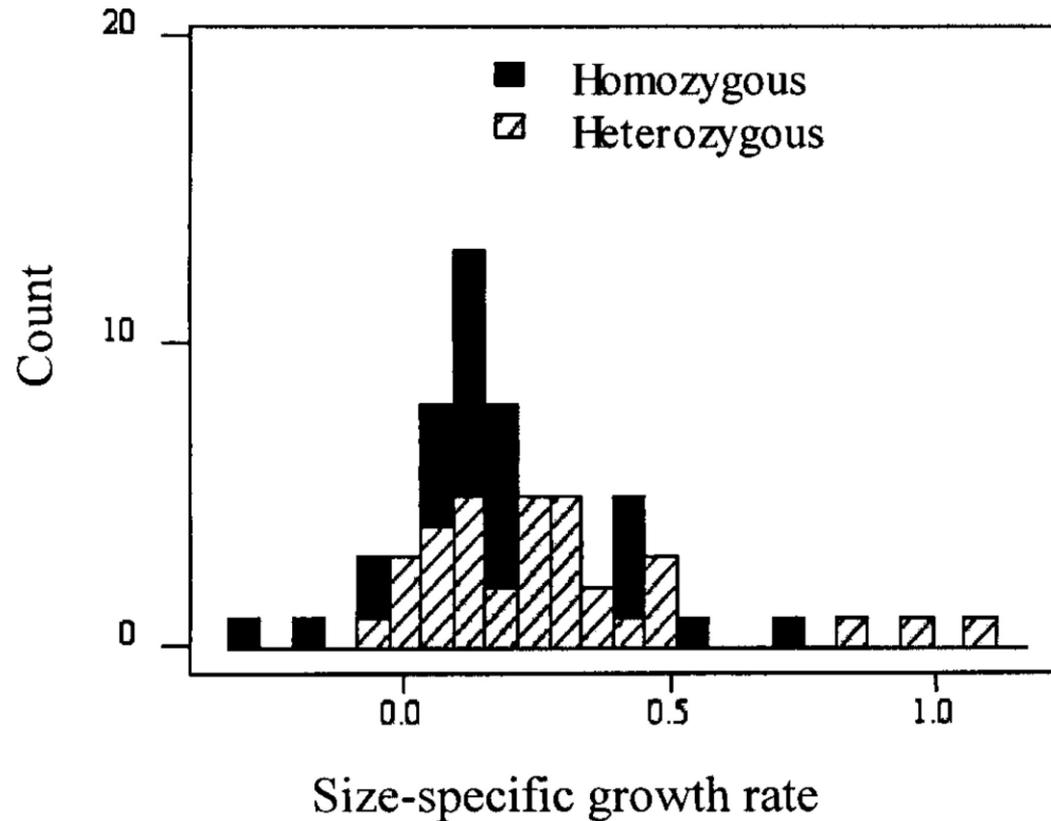
- Many tree species suffer substantial inbreeding depression, while hybrid vigor is common
- Likely in part due to accumulation of deleterious alleles



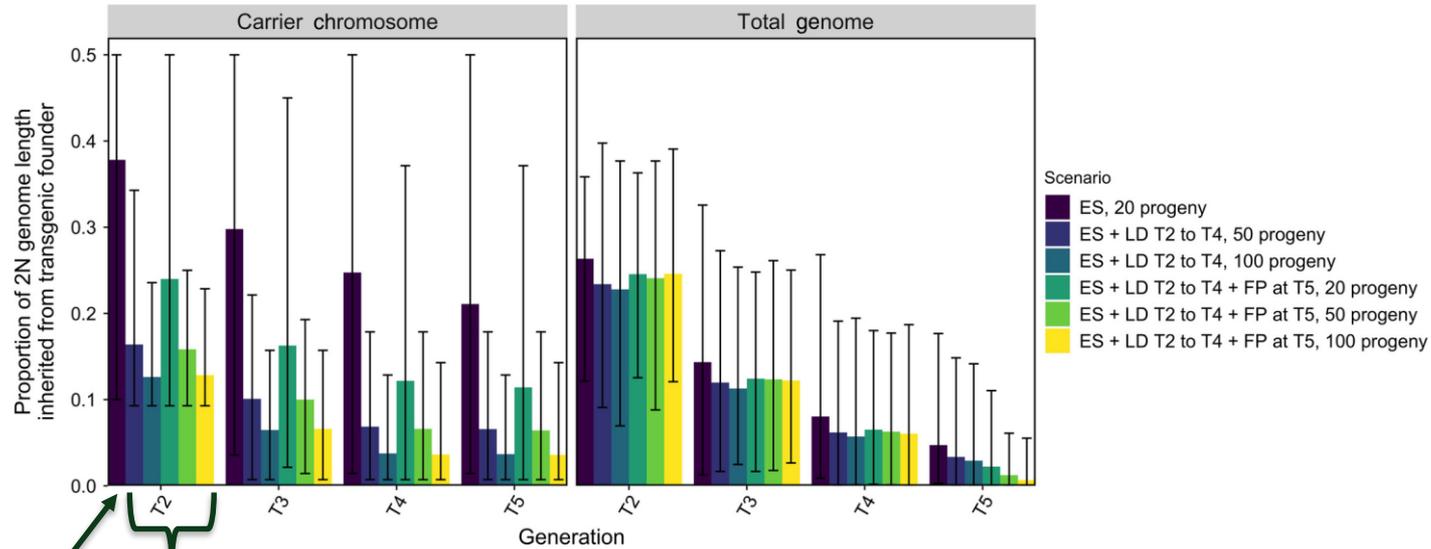
Impact of demographic history on rangewide distribution of deleterious alleles



Impact of deleterious alleles on chestnut growth



Selection for OxO during outcrossing may bring deleterious baggage

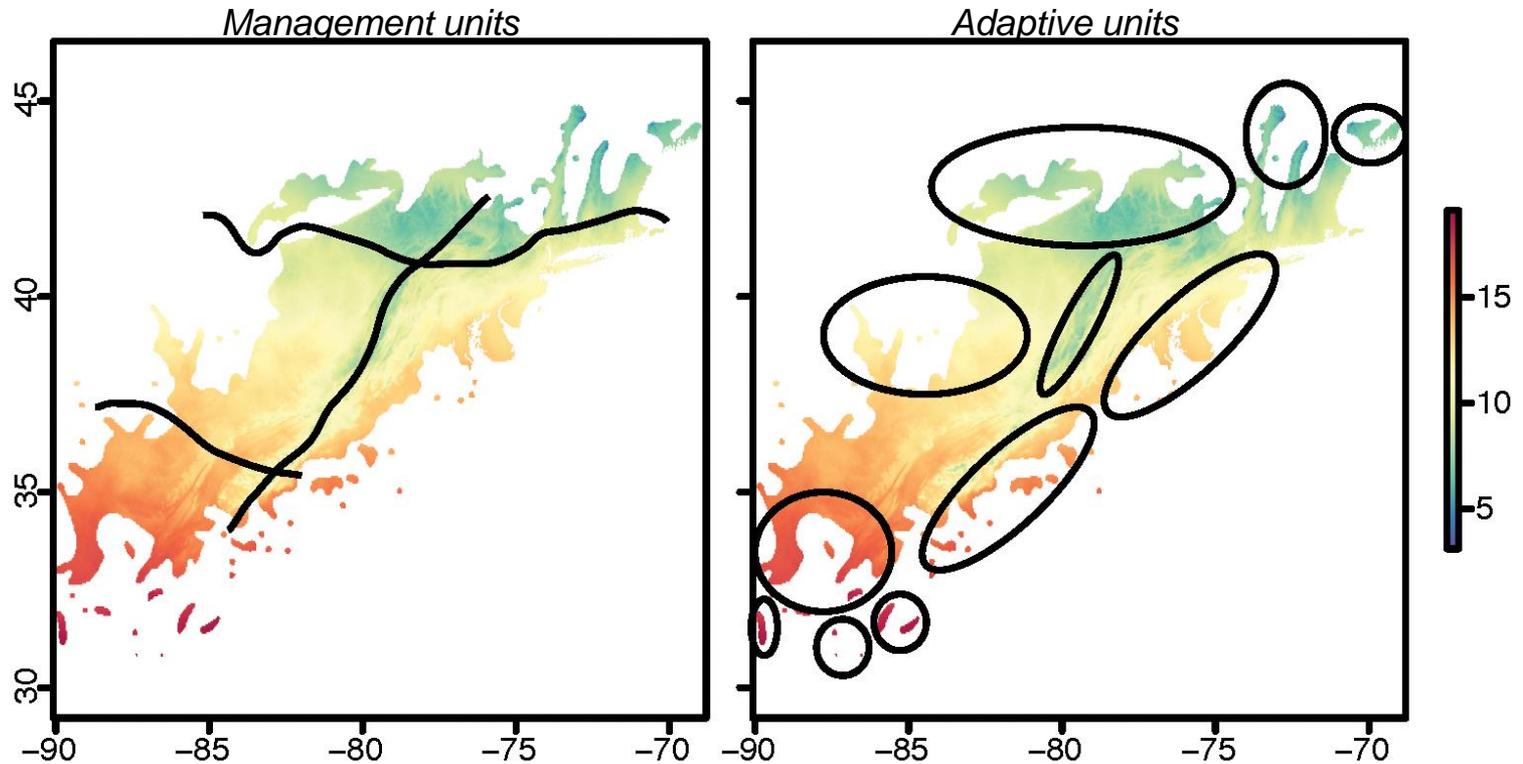


Selection for OxO only

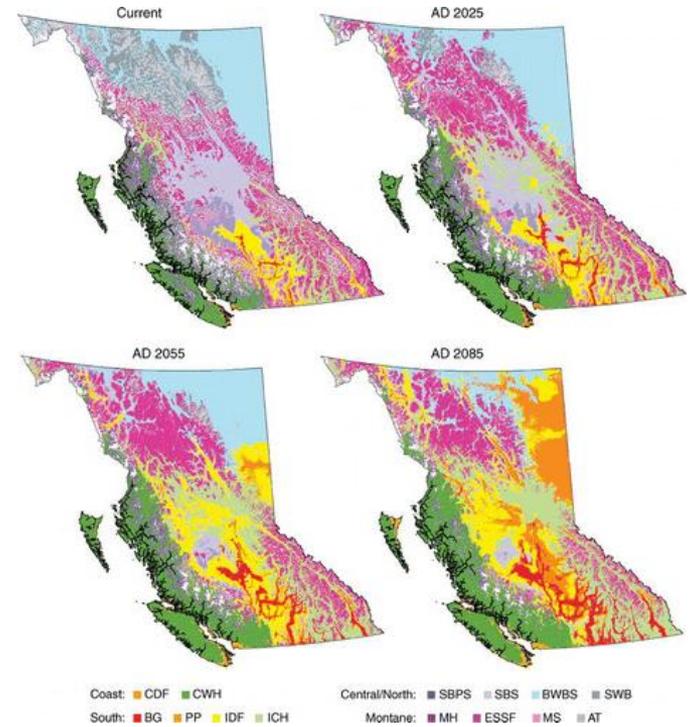
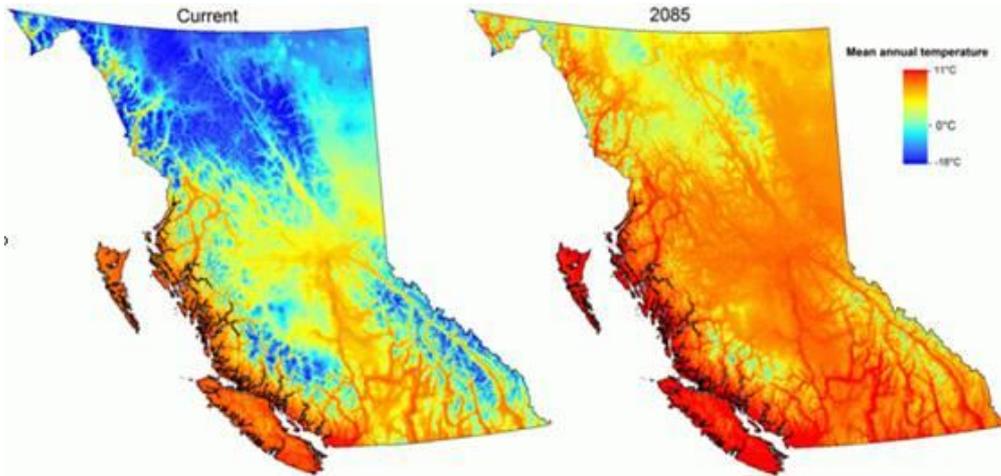
Why these demographic processes matter from a practical perspective

- Extant peripheral populations may be depauperate of variation due to recent bottlenecks, and harbor an excess of deleterious alleles
 - Deploy putatively adaptive genetic variation to enhance evolutionary potential
- Historical migration routes and barriers to migration may mean contemporary populations are distinct
 - Consider them as separate ‘management units’
- Populations in the south that persisted through glacial periods may represent reservoirs of adaptive variation
 - May not survive climate change, but may be valuable as a genetic resource

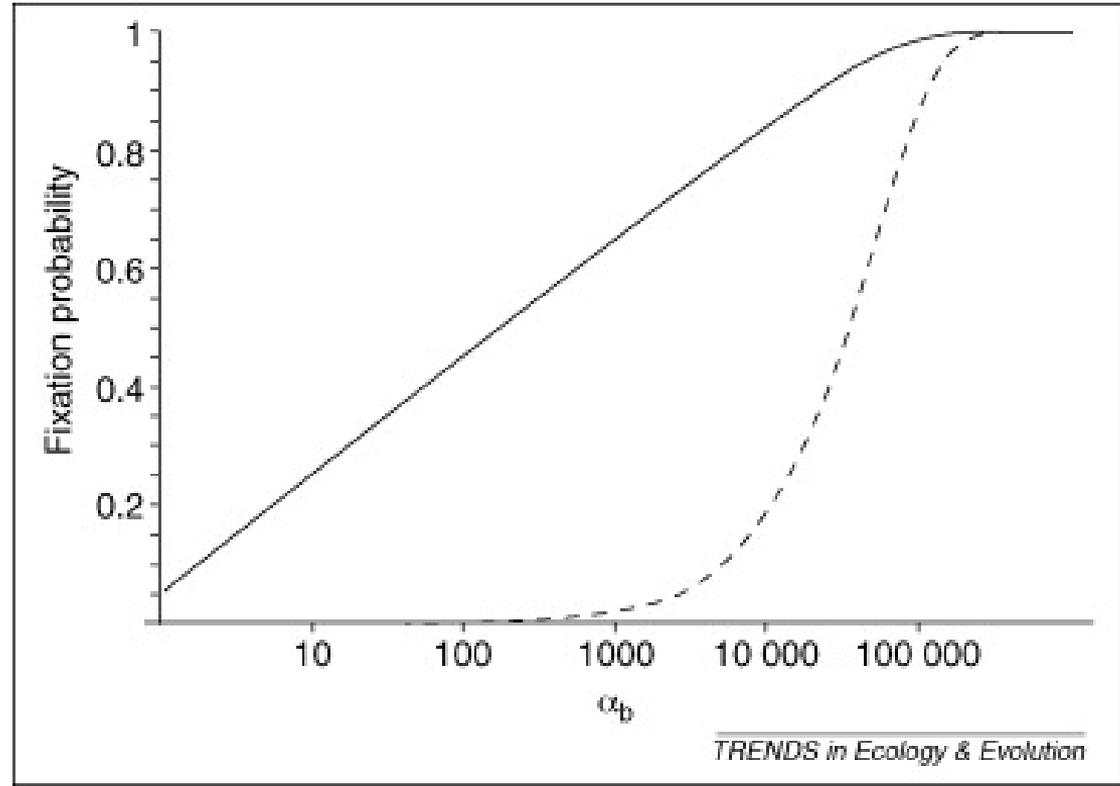
Incorporating neutral and adaptive processes into a germplasm conservation and breeding strategy



Deployment needs to consider future climates



Adaptation from standing variation vs new mutation



Summary

- Local adaptation is pervasive among widespread temperate/boreal tree species
 - Main driver is temperature but other factors important
- Genotype-environment tests can uncover the genetic underpinnings of adaptation
 - Combine this information with historical/contemporary demography to devise an *ex situ* conservation and breeding strategy



Acknowledgements

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