

Tree Improvement 101: Module 1.



Introduction to tree improvement and forest genetics

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Tree improvement has been used for decades to grow more wood, and better wood, in less time.

The technology and science have benefits for non-industrial uses as well.

Forest Genetics

Studies of genetic variation – without imposing selection.



Tree Improvement

The science and art of using selection and breeding to develop seed or clones with specific traits

- Growing trees with high volume in less time
- Growing straighter trees
- Developing resistance or tolerance to invasive pests



Yarrow plant

Plants are a diverse life form! Trees are also diverse but share many life history traits

For the next few slides we'll focus on life history traits of trees vs other taxa.



Atlantic white cedar

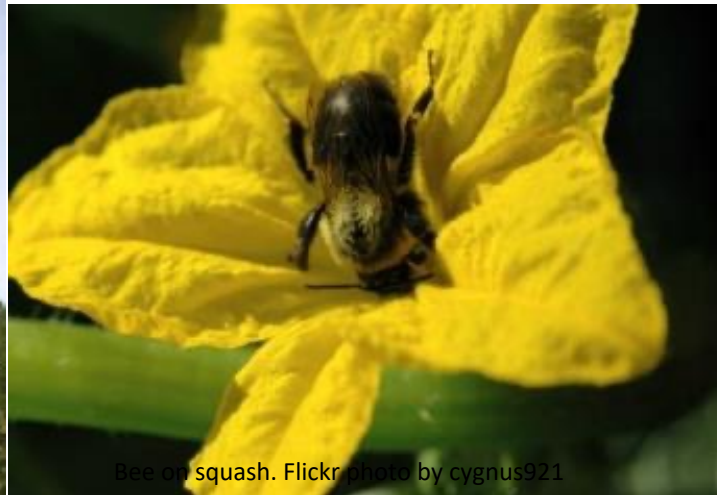


What is a life history trait?
Characteristics of an organism that affect reproduction

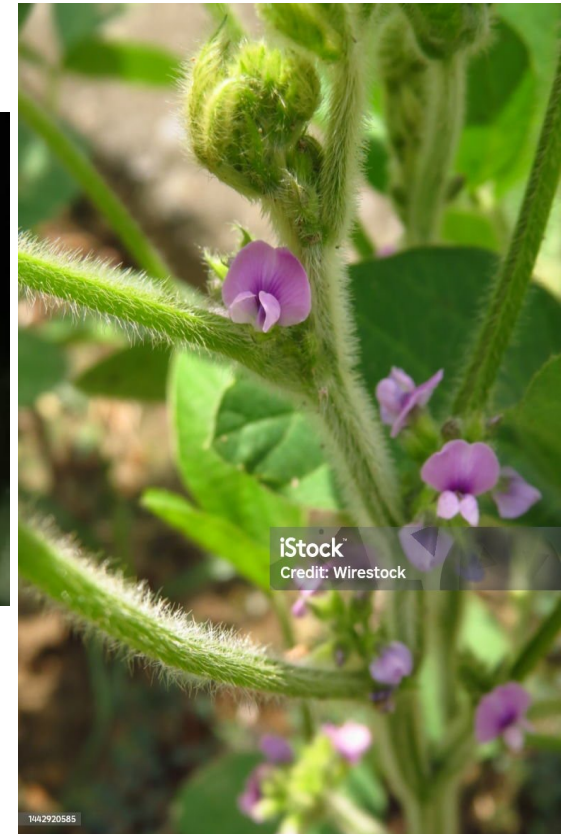
- Longevity: annual or perennial?
- Normal life expectancy?
- Modes of reproduction? (asexual vs sexual)
- How is pollen dispersed?
- How is seed dispersed?

Know your mating system!

Is pollen dispersed by wind, animal, or can it self-pollinate? How is seed dispersed?



Bee on squash. Flickr photo by cygnus921



iStock
Credit: Wirestock



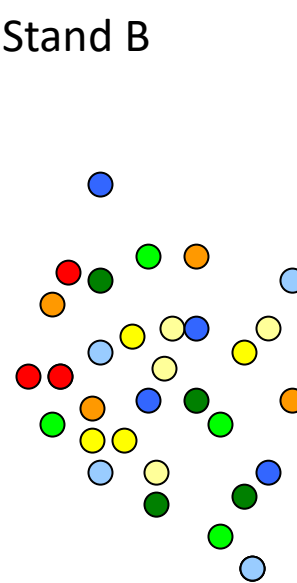
Knowing your mating system can give clues about how the genetic diversity is structured among individuals within a population and among populations.



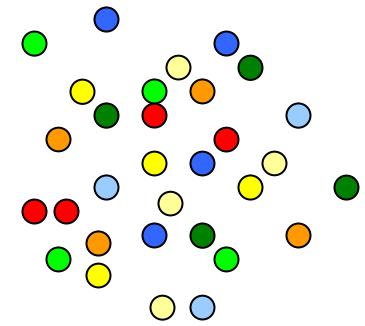
Most tree species have “low” population structure because of excessive gene flow



Stand B



Stand A

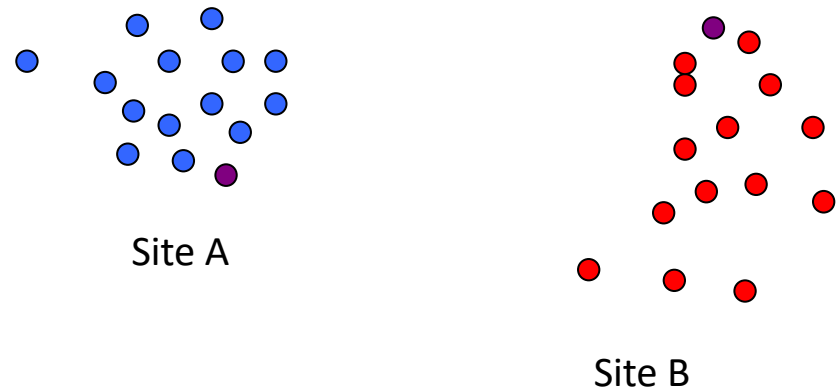


Each dot represents a different phenotype. Same-colored dots have similar phenotypes.

- * Large differences within a population or stand. (high within-stand variation)
- * Few differences among populations, or stands (low among-stand variation)

“High” population structure

Self-crossers, or plants with limited pollen or seed dispersal



Species that are highly structured may be prone to **outcrossing depression**: connecting the populations or moving pollen/seed may be detrimental to fitness!!

These two populations are “highly differentiated”

- * Large differences between populations.
- * Small differences within populations.

These might be classified as different ecotypes which is uncommon in forest trees

Many of our native trees have huge continental-wide ranges!

Natural
range of
black
spruce



Some have a limited range

Natural
range of
slash pine



And some are endangered!

Quercus acerifolia:
highly endangered and
only occurs in a few
locations in Arkansas!

Beckman et al. Conservation Gap Analysis of Native U.S. Oaks: *Quercus acerifolia*. The Morton Arboretum.

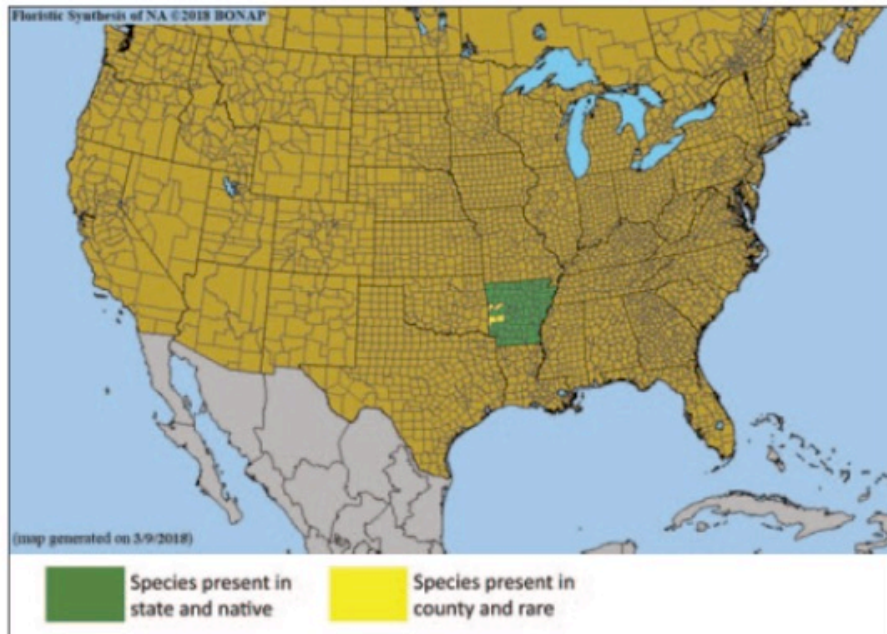


Figure 1. County-level distribution map for *Quercus acerifolia*. Source: Biota of North America Program (BONAP).³

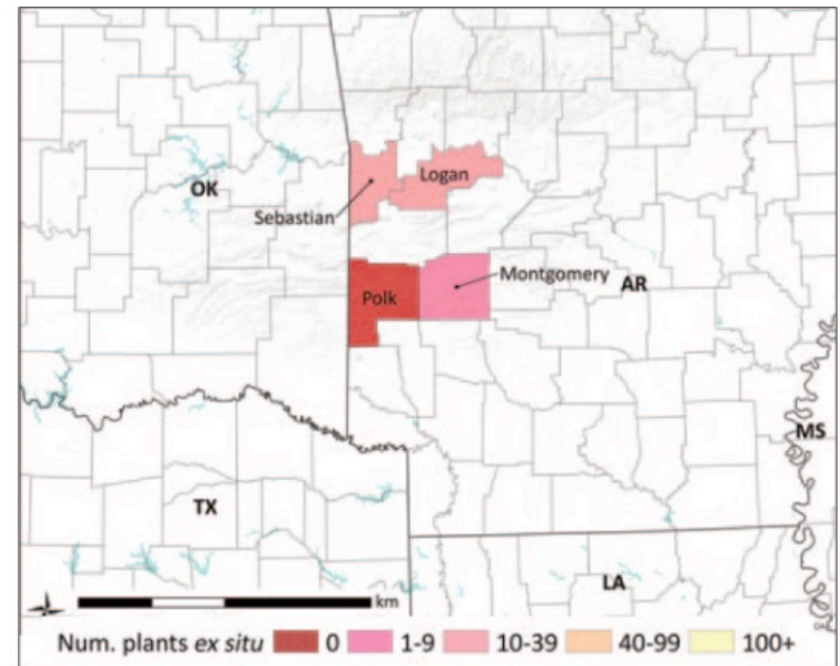


Figure 4. *Quercus acerifolia* counties of *in situ* occurrence, reflecting the number of plants from each county in *ex situ* collections.

Population genetics: the study of how genetic variation is structured across the landscape

Genetic diversity: the total number of genes or gene variants associated with a sample.

A few quick definitions

Gene or gene locus = location on a chromosome

Allele = variants of the gene that occupy that gene locus

Haplotype = a group of alleles, that tend to be inherited together, associated with a specific group of individuals.

Diploid = organism with 2 sets of chromosomes

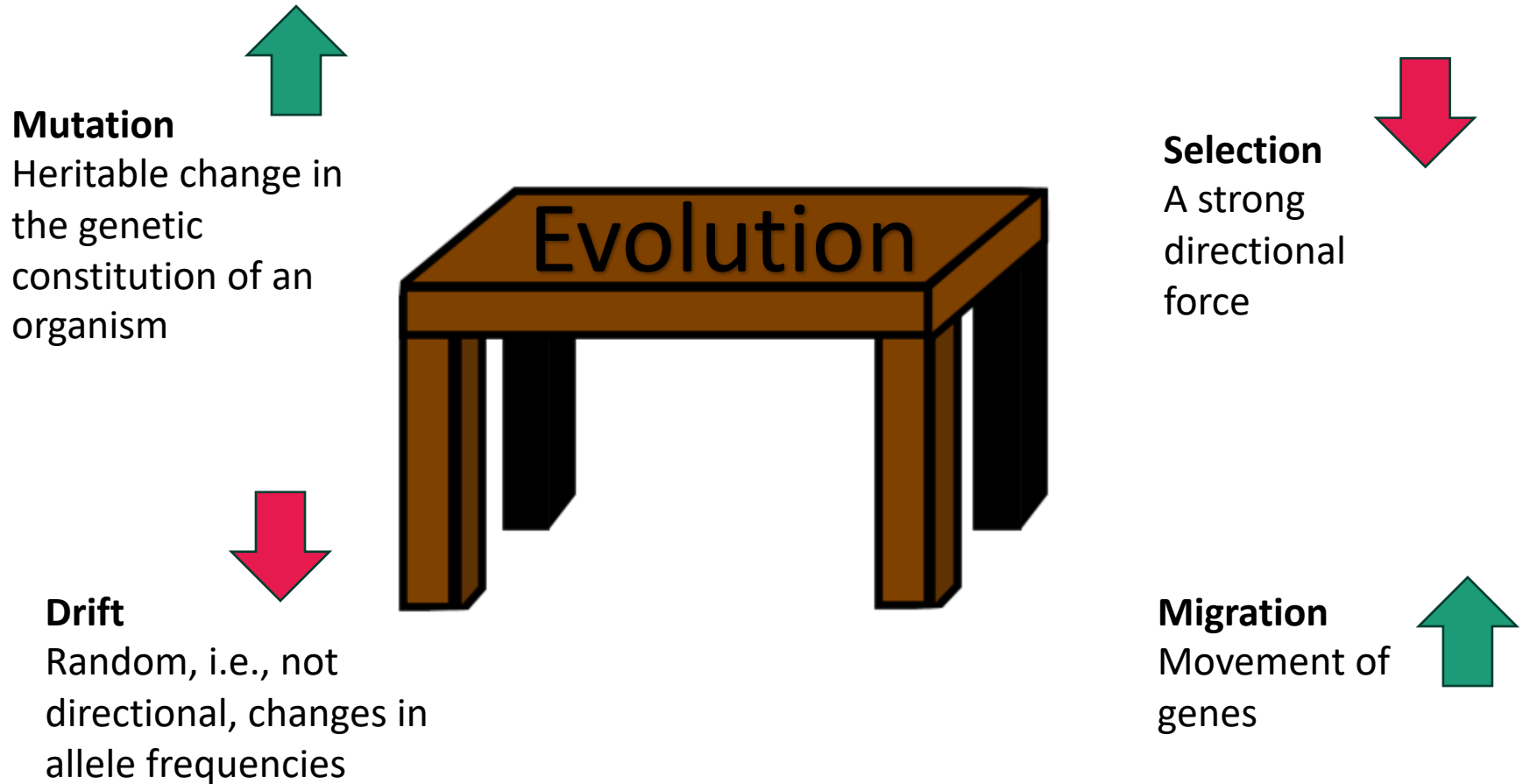
Polyploidy = condition when organism has >2 sets of chromosomes

Heterozygosity = the alleles at a given locus (2 if diploid) are different.

Different types of DNA used in population genetics = mitochondria, chloroplast, nuclear

Neutral DNA = genes that we can study but don't necessarily code for traits of interest.

Four sources of genetic variation





How population genetics studies are executed

Collect leaves, seeds, or other tissue. Origin of each sample is retained.

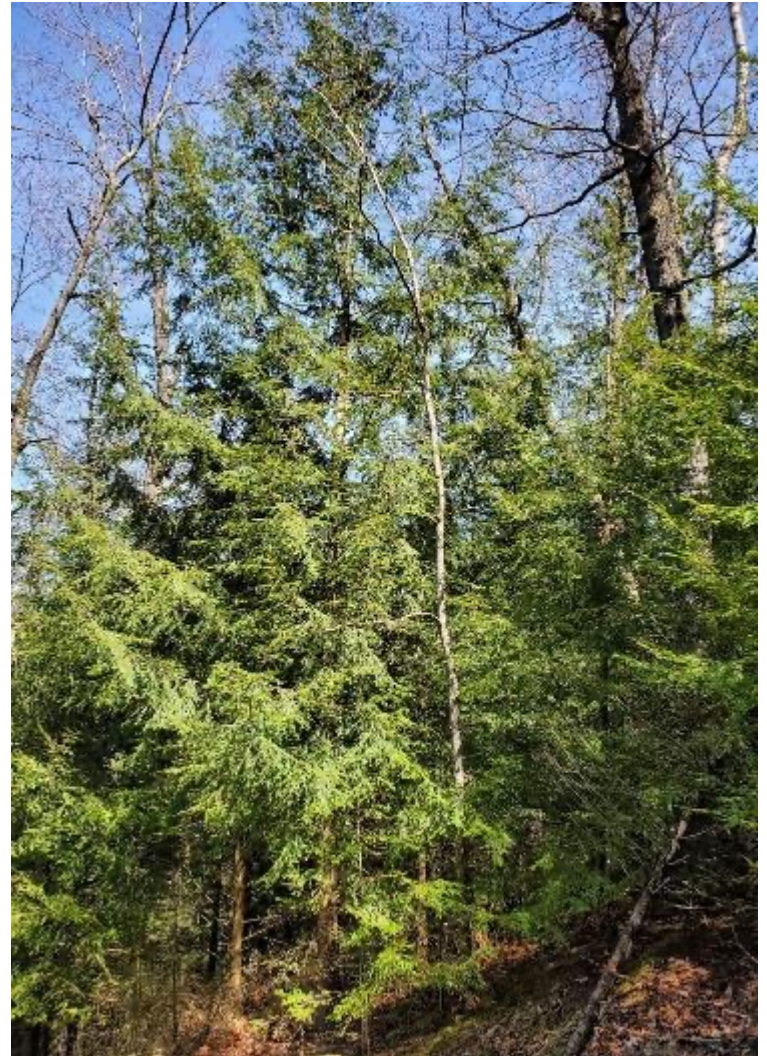
DNA is extracted and neutral (presumably) molecular markers (microsatellites [nuclear, chloroplast, mitochondrial] or Single Nucleotide Polymorphisms) are used to study genes.

These studies do not match genotype to phenotype.

These studies often guide gene conservation efforts and may be useful for tree improvement.

Population genetics of eastern hemlock

- Mesophytic, shade-tolerant, late successional species
- Threatened by invasive pests: hemlock woolly adelgid and elongate hemlock scale
- Eastern hemlock, like other conifers, has a very large genome
- Monoecious (produces male and female flowers), wind pollinated
- Large geographic range (eastern US)
- Unlike most other conifers, genetic variation is relatively low!



Widespread inbreeding and unexpected geographic patterns of genetic variation in eastern hemlock (*Tsuga canadensis*), an imperiled North American conifer

Kevin M. Potter · Robert M. Jetton ·
William S. Dvorak · Valerie D. Hipkins ·
Rusty Rhea · W. Andrew Whittier

- Conducted range-wide genetic variation study for eastern hemlock
- Amplified 13 highly polymorphic nuclear microsatellite loci in 1,180 trees across 60 populations.

Different metrics that describe genetic variation

$A = m$

$P_p = \%$
polymorphic
loci

expected
heterozygosity

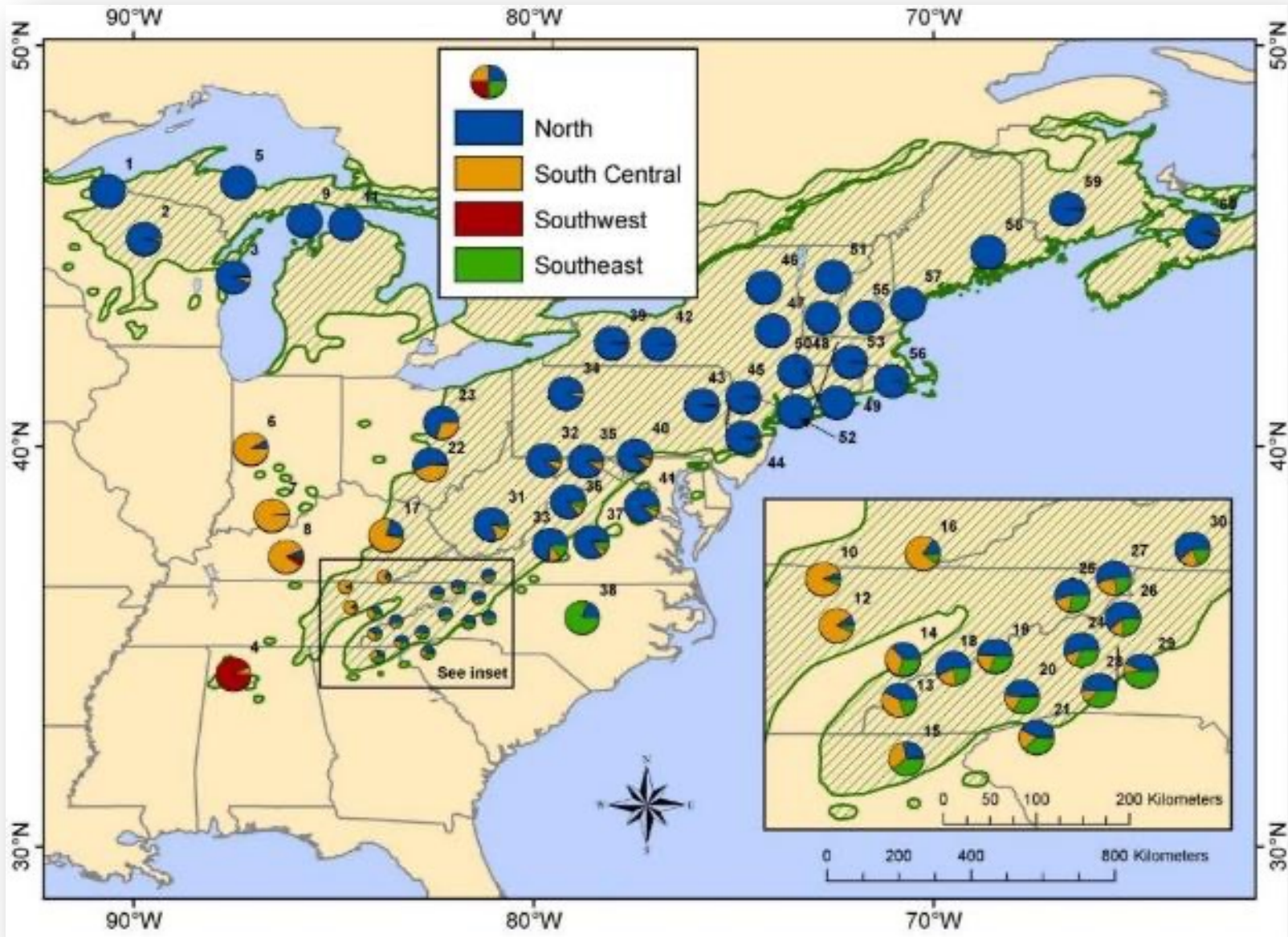
F_{IS}

HWE = heterozygote
deficiency

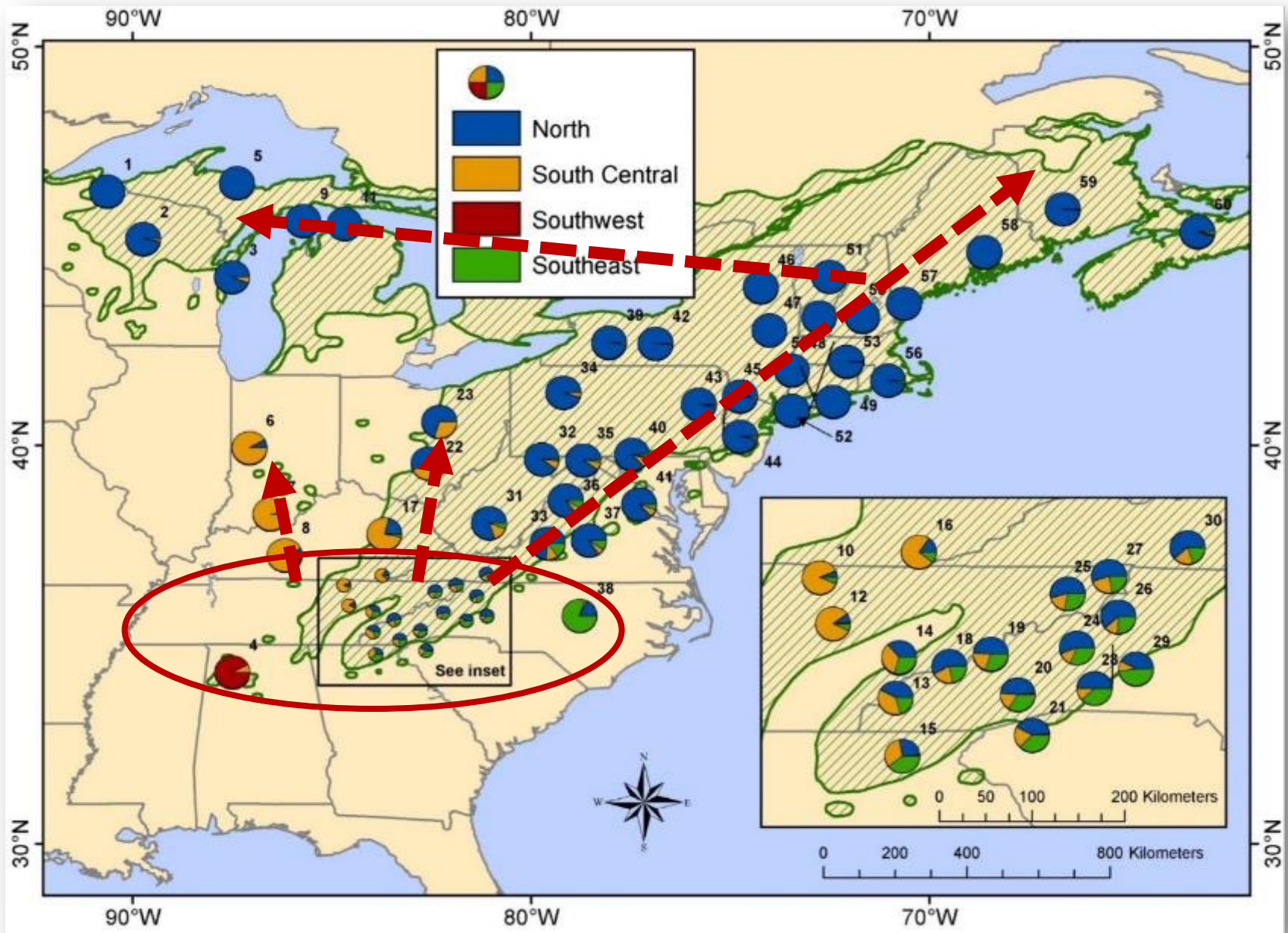
Table 3 Measures of genetic variation

ID	Population	A	A_U	P_P	H_O	H_E	A_E	F_{IS}	HWE	Mean D_C	H_{def}
1	Copper Falls State Park	4.92	1	92.3	0.463	0.535	2.15	0.137	*	0.041	0.055
2	Council Grounds State Park	4.62	0	92.3	0.52	0.53	2.13	0.019	NS	0.041	0.170
3	Point Beach State Forest	5.00	0	92.3	0.638	0.573	2.34	-0.117	NS	0.040	0.212
4	Bankhead National Forest*	5.08	1	92.3	0.469	0.566	2.31	0.176	*	0.135	0.170
5	Presque Isle Park	4.54	0	92.3	0.508	0.568	2.32	0.109	NS	0.045	0.715
6	Shades State Park*	3.69	3	100.0	0.475	0.476	1.91	0.003	NS	0.078	0.108
7	Hemlock Cliffs*	2.62	1	84.6	0.312	0.329	1.49	0.055	*	0.095	0.289
8	Mammoth Cave National Park*	4.62	0	100.0	0.523	0.604	2.53	0.137	*	0.058	0.916
9	Cross Village	5.00	3	100.0	0.519	0.555	2.25	0.066	NS	0.045	0.047
10	Scott State Forest	4.92	0	100.0	0.484	0.552	2.23	0.126	*	0.054	0.040
11	Douglas Lake	4.69	1	92.3	0.558	0.577	2.37	0.035	NS	0.043	0.545

Potter et al. 2012. Widespread inbreeding and unexpected geographic patterns of genetic variation in eastern hemlock (*Tsuga canadensis*), and imperiled North American conifer. Conservation Genetics. 13: 475-498,



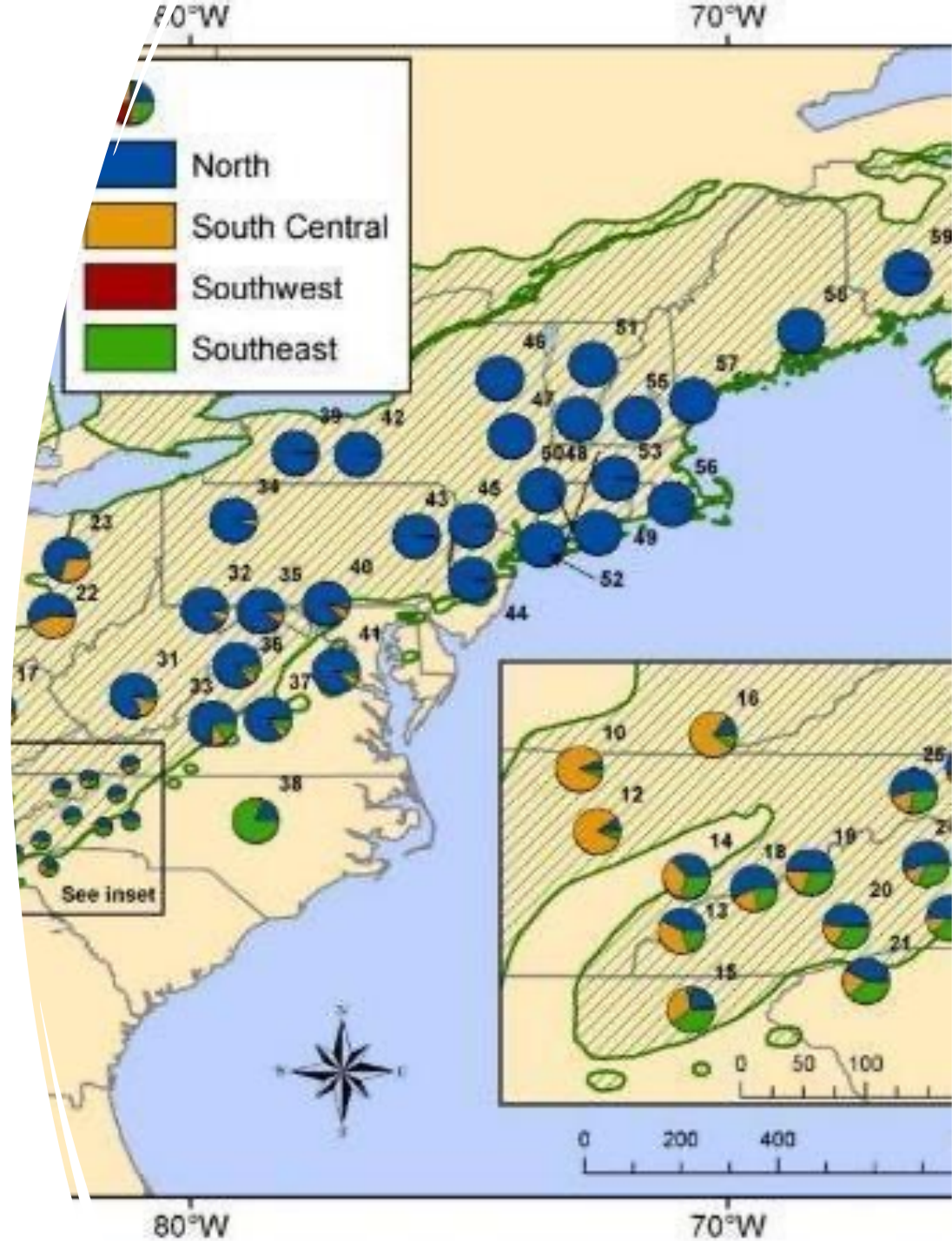
The proportion, within each eastern hemlock population, of inferred ancestry from the four genetic clusters defined using the Bayesian clustering program TESS (Potter *et al.* 2012).



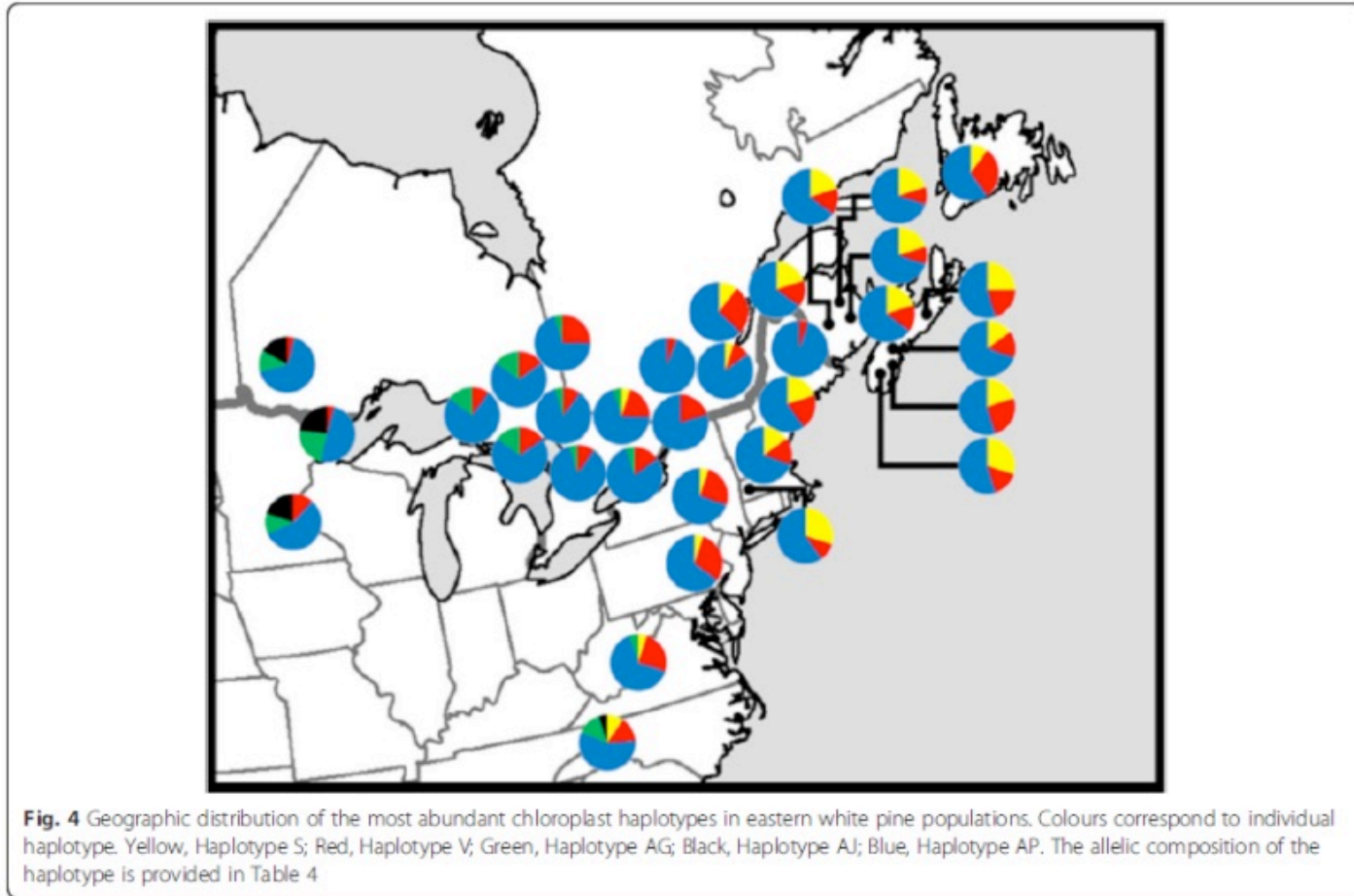
This information was used to track variation over space and time.

How is this useful for tree improvement or for restoration?

- Useful for gene conservation purposes.
- This may help you decide where to look for mother trees.
- You may decide to over collect from areas where the genetic variation is highest and focus less on areas with low genetic variation or inbreeding.

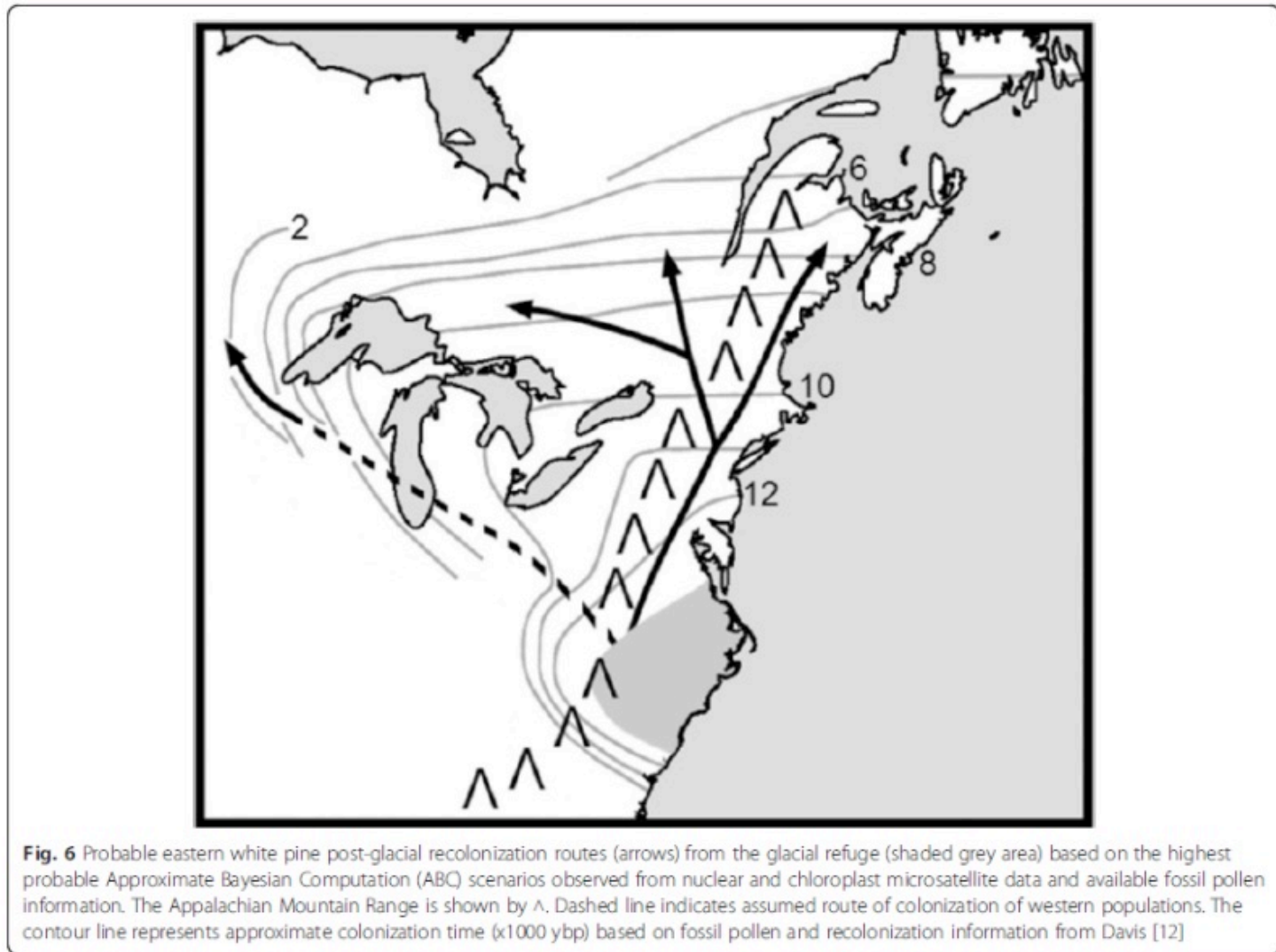


Another conifer example: eastern white pine has high genetic variation that is well distributed across the landscape of North America but some genetic structure is present



Zinck and Rajora BMC Evolutionary Biology (2016) 16:56

We can infer prior post-glacial expansion from this information.



This type of study can be done with phenotypes but these types of studies are far less common (but still awesome)

Jack pine example

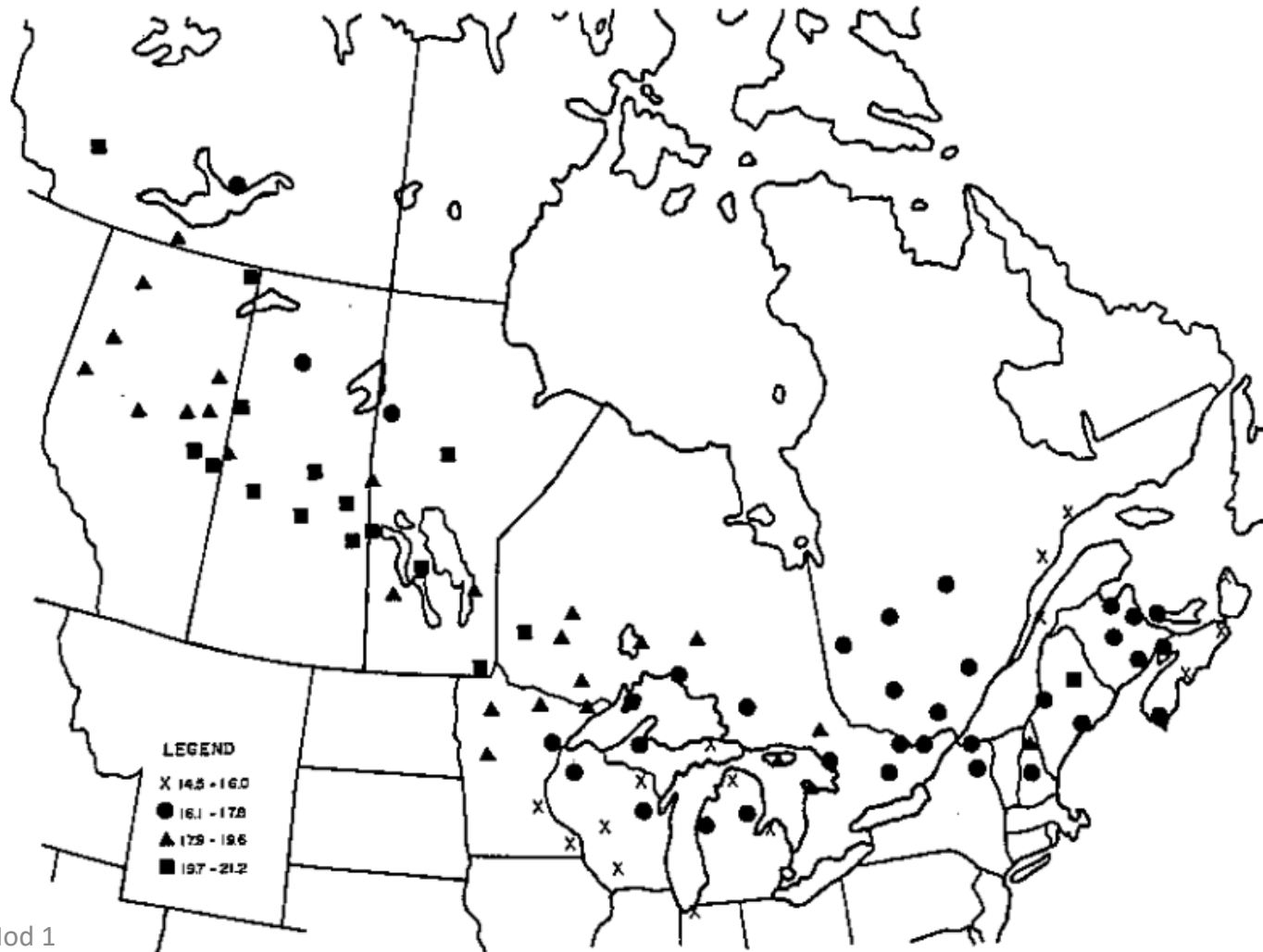


Schoenike 1976: Sampled 37 traits from across the range of jack pine

- Tree size, age, diameter
- Bark thickness, earlywood, latewood
- Branch angle, branches/whorl
- Needle length, width, curvature, resin canals, etc.
- Cone serotiny, abundance, specific gravity, knobbiness, volume, weight, etc.

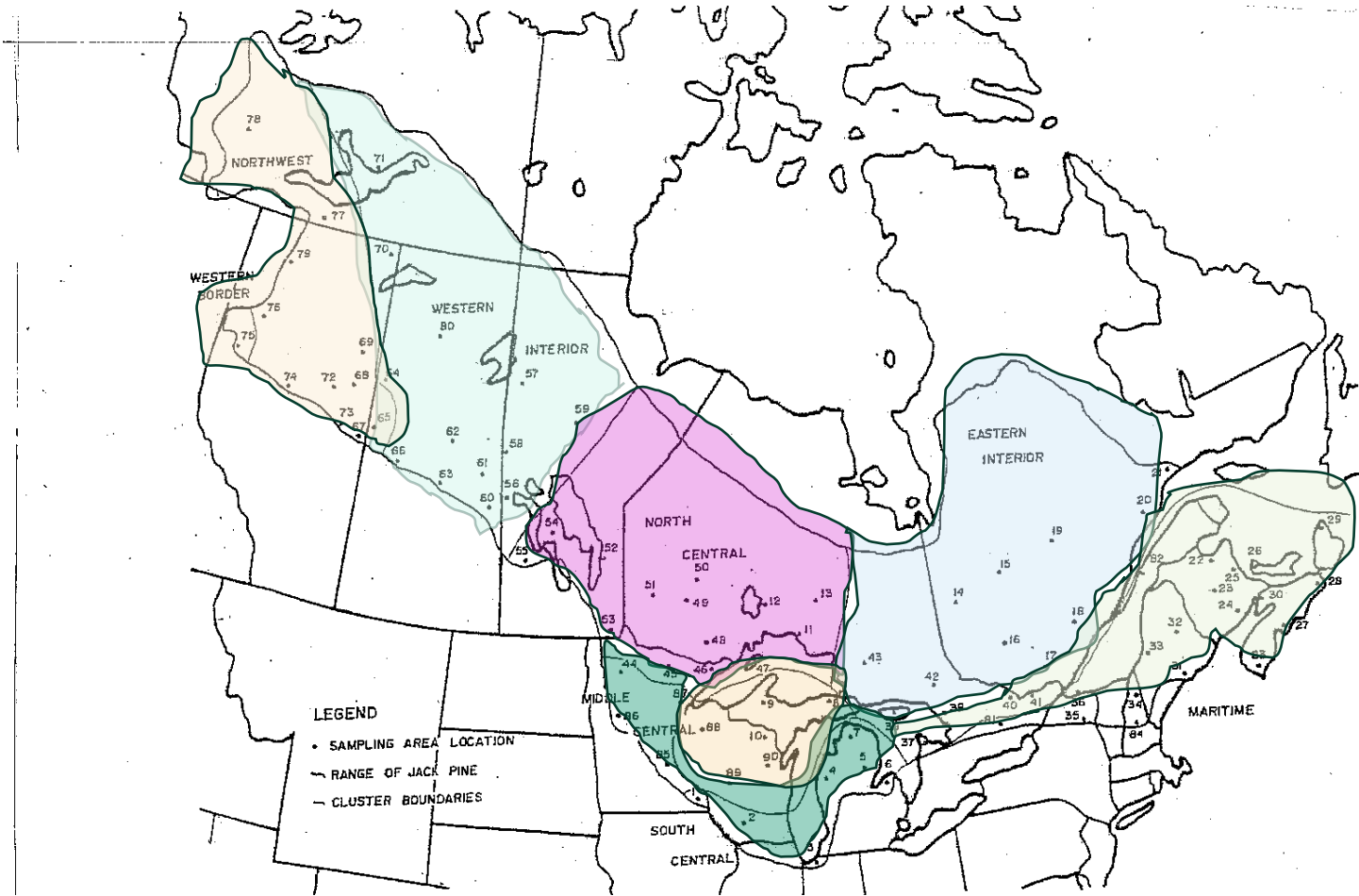


Figure 30. The pattern of geographic variation in jack pine for cone scale apophysis length (millimeters)



Jack pine has a lot of population “structure” compared to other conifers.

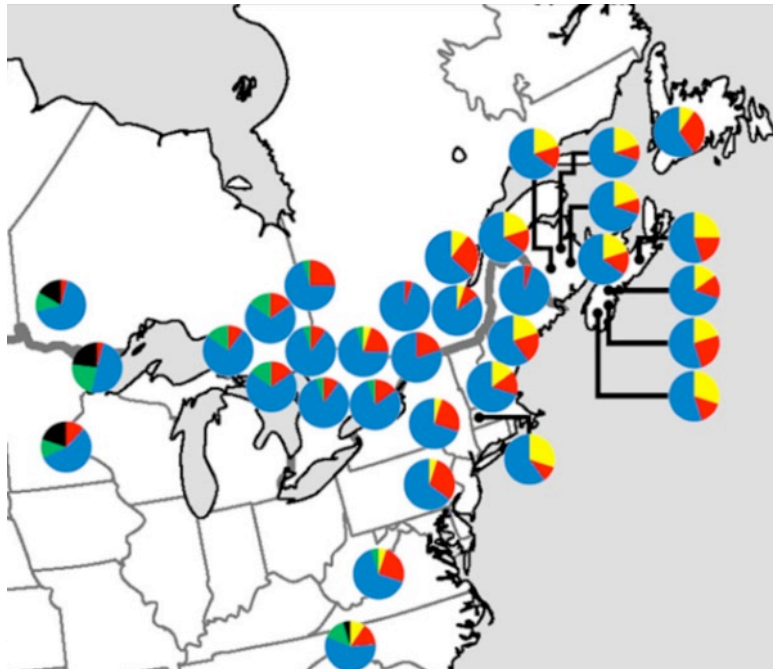
From R.A.Schoenike 1976 Geographical variations in jack pine (*Pinus banksiana*)



Trees tend to have clinal variation, not so much ecotypic variation

Why?

- Because they are prolific at dispersing pollen/seed across the landscape.
- Unique ecotypes rarely form – they get swamped out by pollen or seed from other populations.





Summary: population genetics

Tree species possess more genetic variation than most other life forms.

Gene flow in trees is high so genes get well-dispersed across the landscape. This may not be the case for tropical trees!!

Some species may have low underlying genetic variation from a prior bottleneck (glaciation).

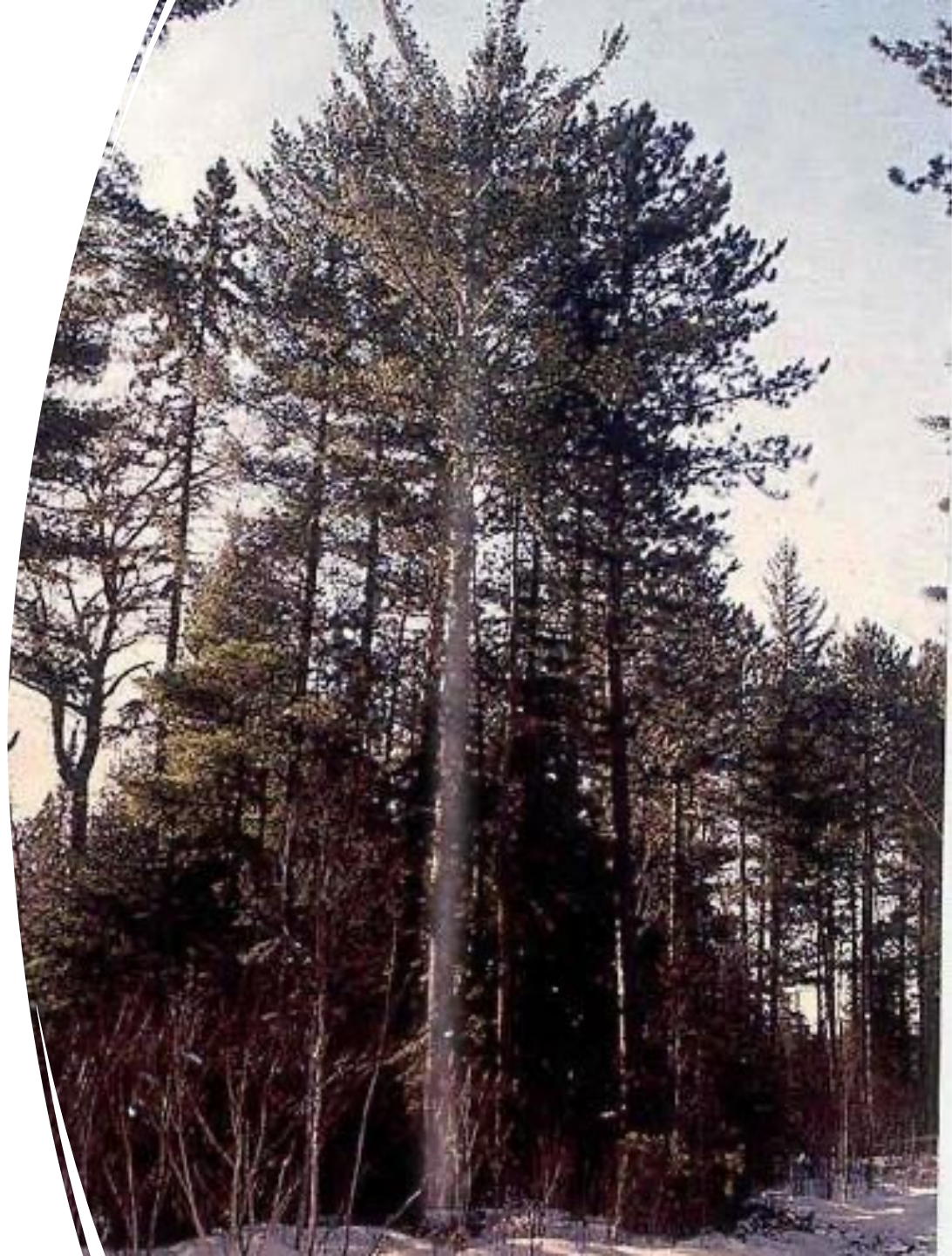
Neutral DNA can highlight historical mutation, migration, and drift events on a species.

Common gardens are needed to study effects of **natural selection**.

Tree improvement
starts with natural
populations in the
woods!



Next we'll focus first on
phenotypes of interest.



Phenotypes used for tree improvement programs depends on these two questions:

What trait are you trying to improve?

How is it measured?

What types of field measurements best represent the desired phenotype over space and time?

Benefits of tree improvement will depend on the trait(s) you are selecting upon!

1. Bigger trees in same time (shorter rotation cycle)
2. Straighter trees
3. Smaller knot sizes
4. Improved resistance to insect or disease
5. Increase wood density/specific gravity
6. Many more!

Improvement is incremental from one generation to the next. Some traits can be improved quickly, within a generation, while others might require a few generations to reach the desirable phenotype.

Most traits we rely upon in improvement programs are “quantitative traits”



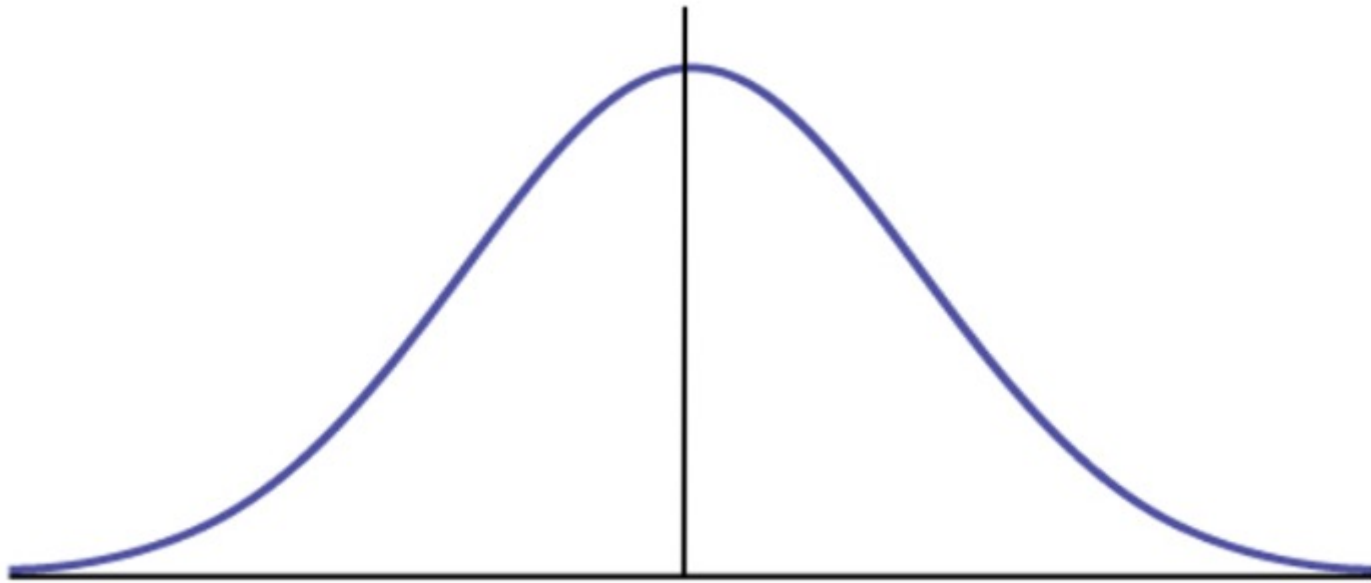
These are traits that you measure on a continuous scale.
Example: height, diameter

These traits tend to be controlled by many genes and different combinations of alleles.

Some traits also closely interact with the environment.

Quantitative traits vary on a continuum : histogram example

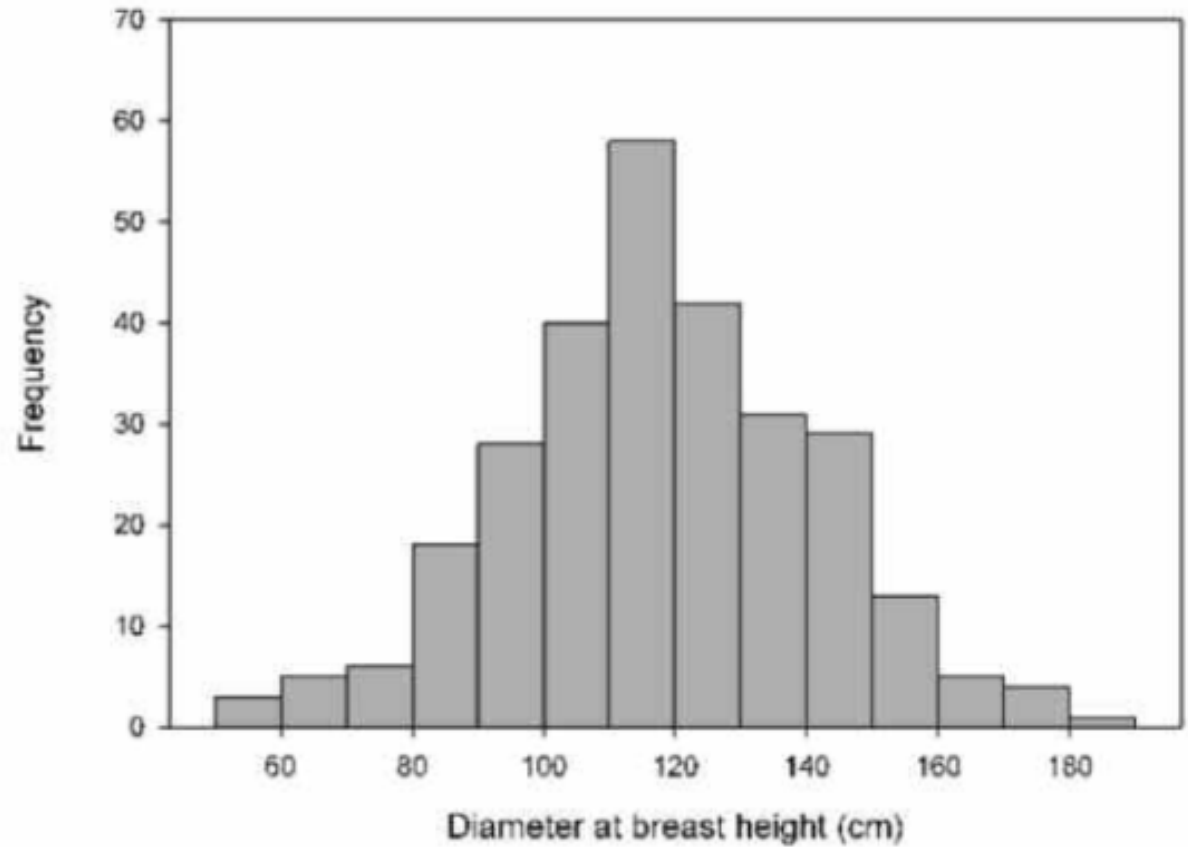
Y axis: number of individuals in that size class



X-axis: height, for example.

Quantitative traits are often normally distributed if we have a large enough sample size.

In reality,
the
histograms
look like
this →





Qualitative traits, in contrast, are measured with scores or classification

- Humans: blood types (A, B, A/B, O; HR factor positive vs negative)
- Mendel's peas: wrinkled, smooth
- Dog coat colors: black, white, yellow
- Serotiny in cones: open, closed, mixed

Categorical traits can be analyzed in a tree improvement program but they don't meet assumptions of normality.



Qualitative traits

Sometimes we convert a quantitative trait into a qualitative trait to help with our assessments.



6-point scale of infection for eastern white pine to white pine blister rust disease

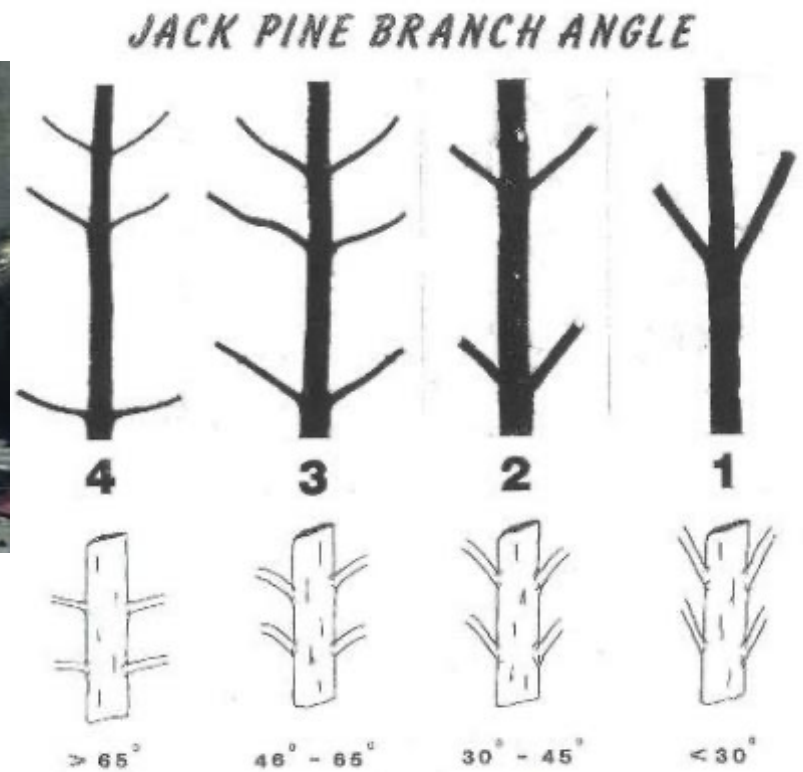


Image from New Brunswick Tree Improvement Council handbook

Binary traits are relatively easy to analyze but may have limited inference.



Northern red oak:

- Branch angle greater than or less than 45 degrees (yes, no)
- Stem sweep (yes, no)
- Survival

Disease resistance (more in module 4)

Traits: survival (binary), percent infected, days to mortality, infection (categorical), percent crown dieback, etc.



Assumptions for different data types

- Quantitative: should resemble a normal distribution or transform into something that approximates a normal distribution.
- Categorical: Use enough categories to be approximately normal. Or convert to a binary variable.
- Binary: overall survival for a trait, for example, should be more than 20% and less than 80%.
- How many genotypes should you include in your population? How many replications per family/genotype?

AS MANY AS POSSIBLE

At a basic level, inheritance of all traits follow Mendelian rules – it just gets more complicated with many loci associated with quantitative traits

Punnett square: Gene locus “A”
2 alleles: A, a. Diploid organism

Mom

		A	a
Dad	A	AA	Aa
	a	Aa	aa

Ratio of 1:2:1 of homozygotes and heterozygotes
(Basic Mendelian genetics)

In tree improvement, many traits interact closely with the environment: soils, silviculture, spacing, climate.

We need to unpack the effects of the environment to better model genetic effects.

Phenotype (expression of the trait)
= Genotype (genetics of the trait) +
Environment (confounding noise)

We sort out the genetic and environmental effects in a common garden (one site or many) grown with seedlings or clones.

Typical characteristics of common gardens

- A common garden consists of various sources of ONE SPECIES.
- We generally do not MIX species together – the goal is uniformity of soil, light, water, land features.
- We look for sites that have uniform soils, landscape features.
- Old agricultural fields can work well – but beware of compacted soils/hardpans



We'll explore 2 main types of common gardens used in tree improvement programs:
provenance trials and progeny tests



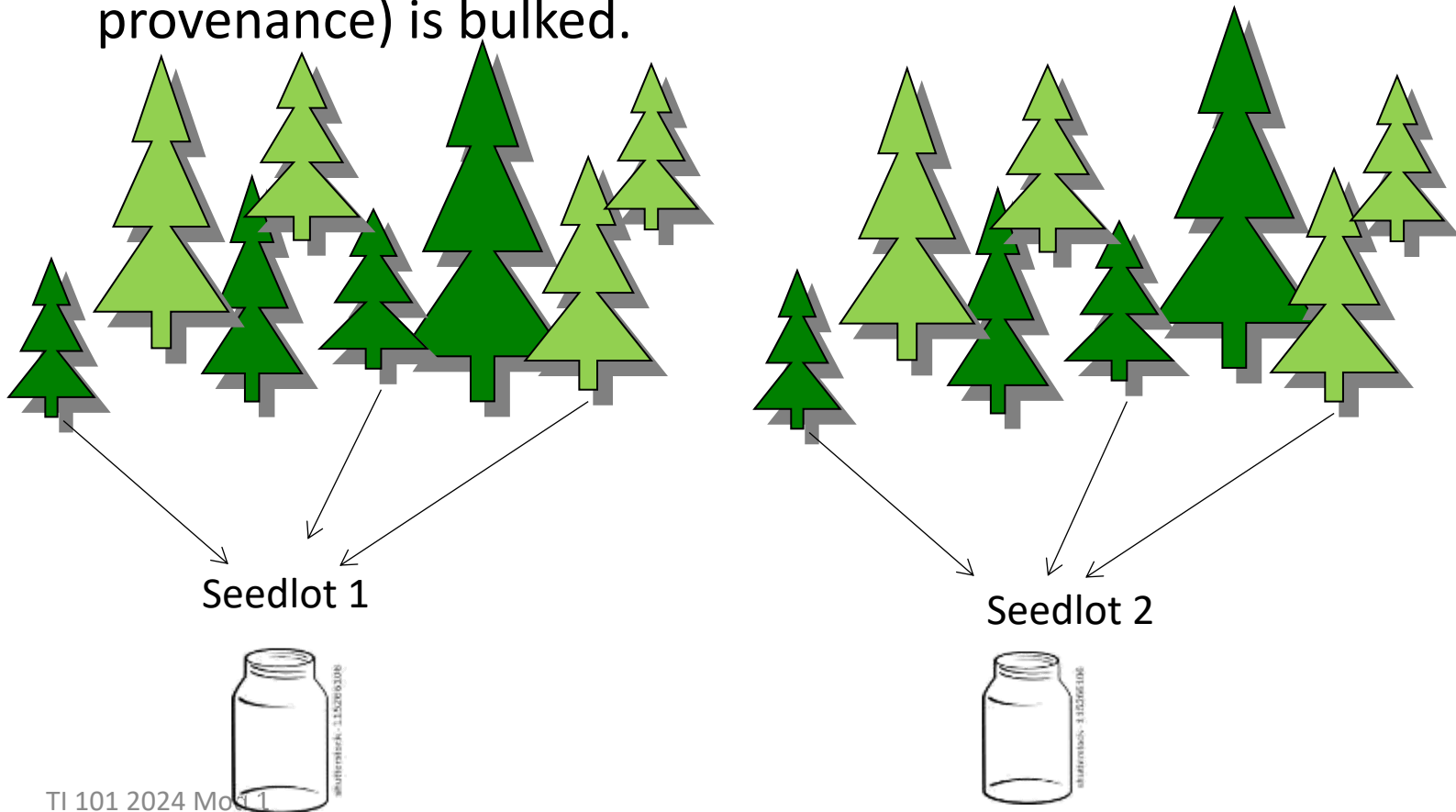
Study population variation across a species range



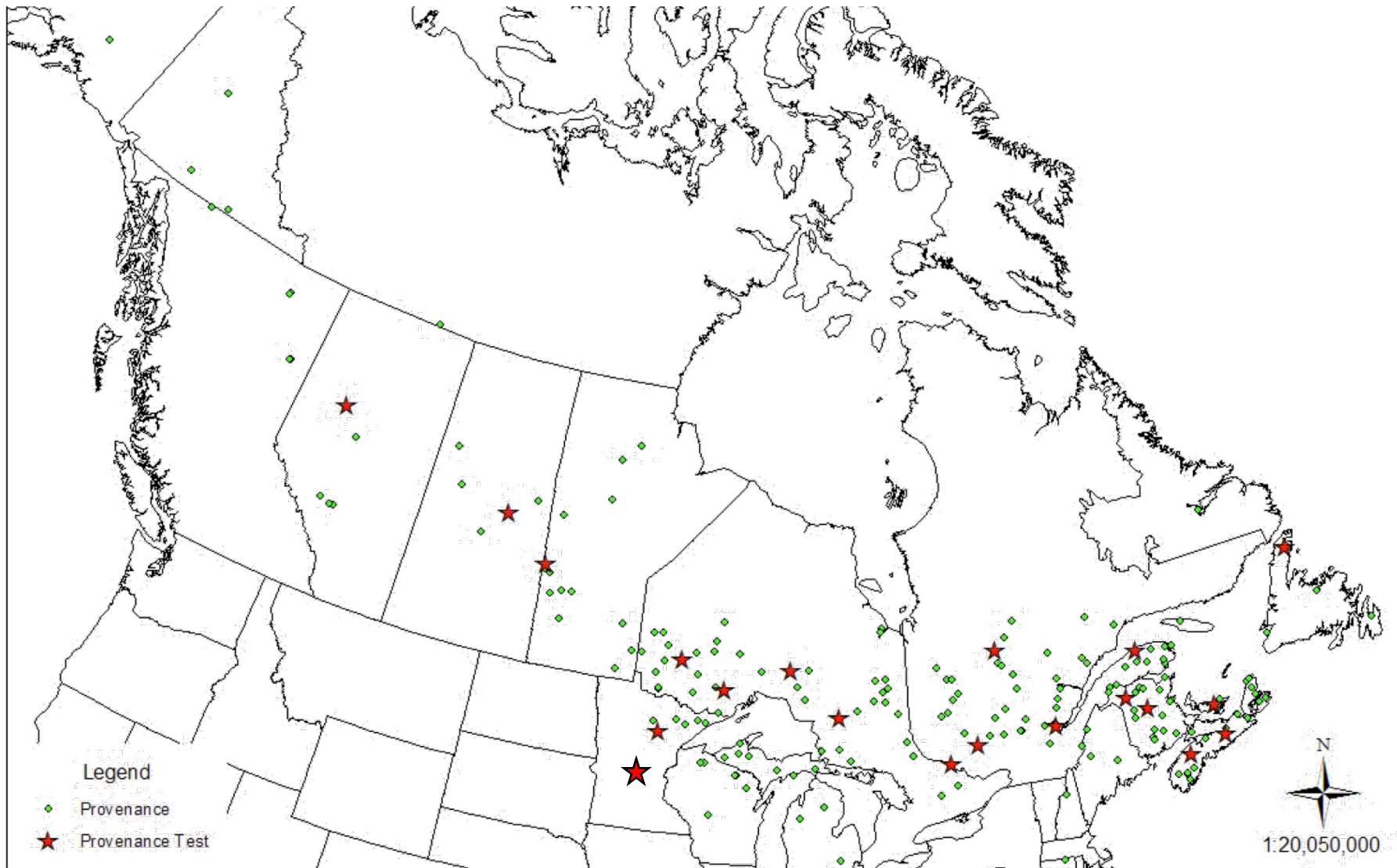
Study family variation – may be sampled across the range or a region.

Provenance trial: common gardens that study adaptive variation

- Seed is collected across a broad geographic area (can be range-wide or region-wide).
- Seed from a bunch of trees from a particular area (or provenance) is bulked.



Provenance trial of black spruce



William H. Parker, Claire L. Riddell and Mark R. Lesser. 2004. Identification of Black Spruce Seed Sources to Compensate for Loss of Growth Resulting from Climate Change. Final Report – Living Legacy Trust Project 04-059/478-02

These are the types of questions that provenance trials can help answer

- How does a seed source from Alaska perform when planted in Minnesota (for example)?
- How far can you move seed before growth is compromised?
- How does a seed source perform in a different climate?
- What climatic factors influence growth and survival?



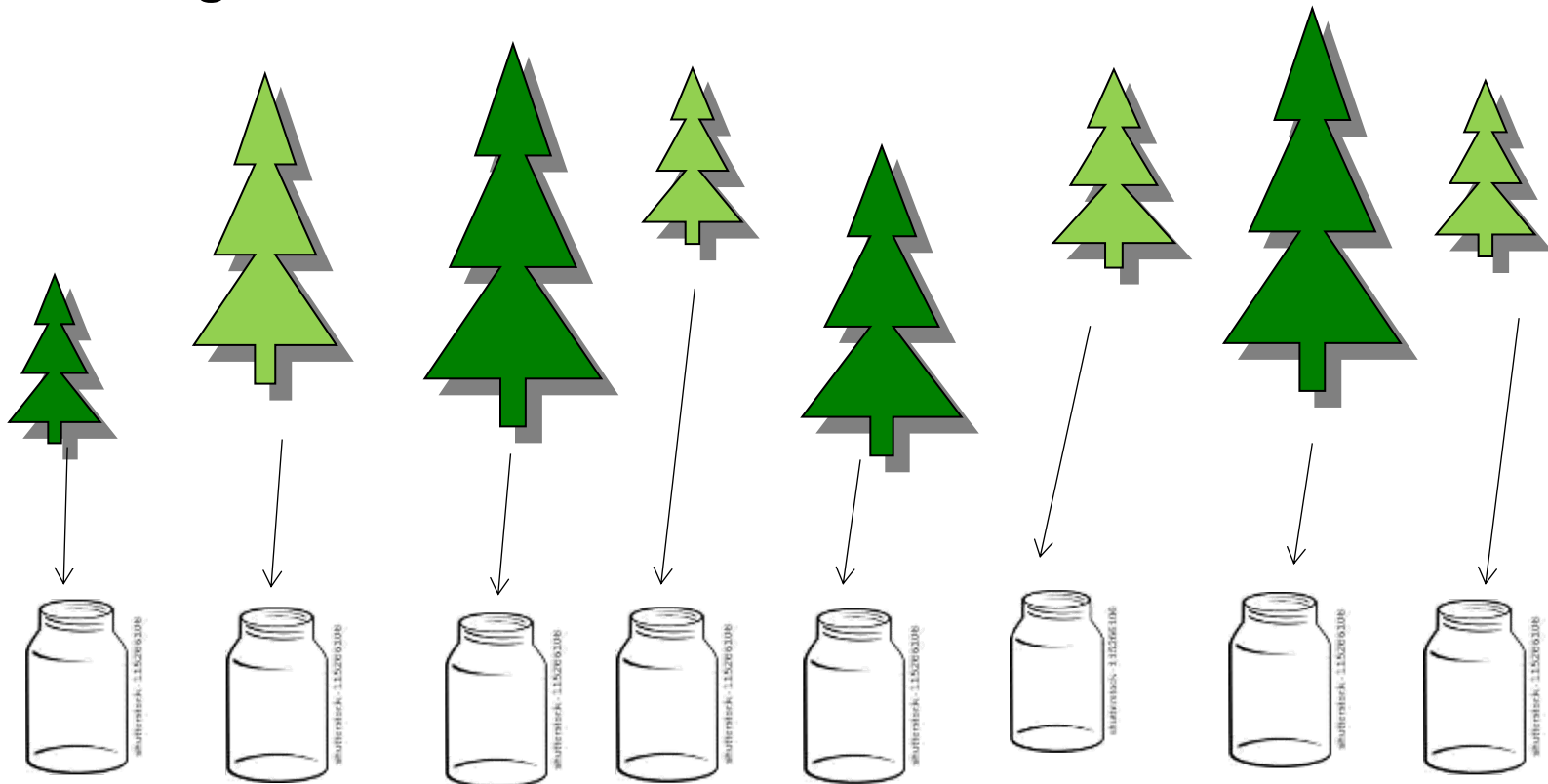
These are the types of questions that provenance trials can help answer

- You may find provenances where the seed has with broad adaptability (such as southeastern Ontario white spruce)
- Allows you to study plasticity of a seed source



The progeny test: common gardens that study adaptive variation for selection

- Seed is collected across a broad geographic area (can be range-wide or region-wide).
- Seed origin is tracked to the mother tree



Progeny tests are typically used in tree improvement

We track performance of maternal sources to guide selection and breeding decisions



Progeny tests: plant offspring (open- or control-pollinated) families to compare performance of siblings

- Scope of inference is limited to the geographic area tested.
- Replicated in space, sometimes in time.
- Often tested to at least half-rotation age.
- Thinning is done systematically depending on the goals.



Review

- Trees have high genetic diversity, big genomes, and are super dispersers of pollen/seed.
- Population genetics studies use neutral DNA to show patterns of historical migration and bottlenecks.
- Common garden studies have shown that phenotypic variation is generally clinal, not ecotypic.
- Most traits used in forest genetics vary on a continuum (quantitative traits).
- Phenotype = Genotype + Environment + GxE
- We take great measures to control environmental variables so that we can study the expression of G using common gardens such as provenance trials and progeny tests.

Please join us for module 2

Modes of selection in tree improvement programs.

Falconer, D.S. and Mackay, T.F.C. 1996.

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Thank you!!

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