

FRST302: Forest Genetics

Lecture 4.1 - Accelerating Tree Improvement I

Welcome to Module 4!

- Module test will be a mix of multiple choice and short answer questions
- The test questions will test your understanding of concepts and ask you to apply it
- **Terminology** will be covered on lecture slides
- **Concepts** will be covered in lectures
- If you are lost with the concepts or terminology make use of office hours, the Canvas Discussion board and ask questions in class!

Module 1 Genes, Genomes and Sequencing

Module 2 Population Genetics and Local Adaptation

Module 3 Quantitative Genetics and 20th Century Breeding

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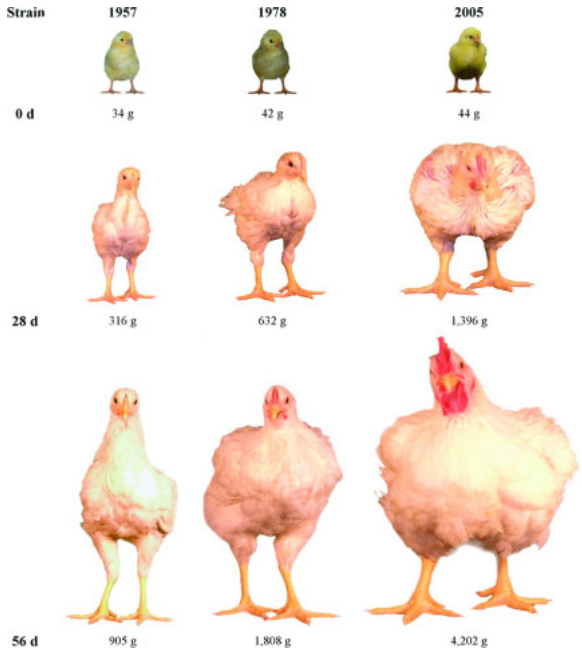
Module 4 Advancing Forest Genetics with Recent Technology

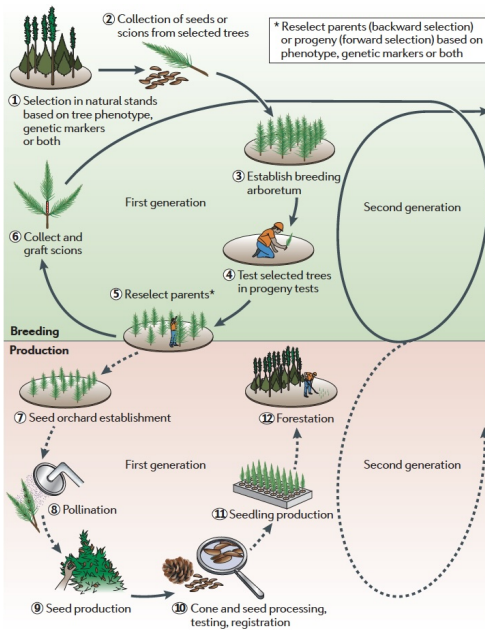
Selective breeding has been extraordinarily successful in human history



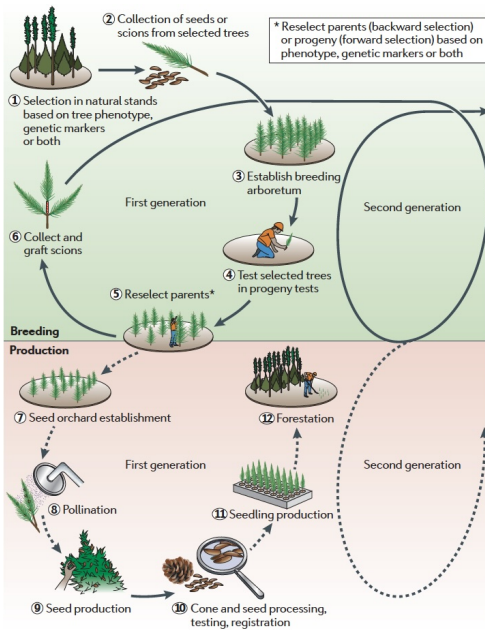
a) *Brassica rapa* morphotypes; b) *Brassica oleracea* morphotypes - from Cheng *et al* 2016

Quantitative
genetic models
work and have been
very effective in the
last 100 years!





Conventional Tree Breeding

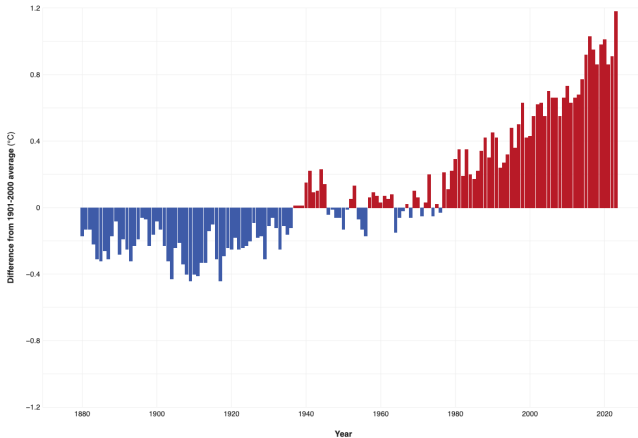


Conventional Tree Breeding

Each cycle takes from 20-30 years!

Can We Afford to Take That Long?

GLOBAL AVERAGE SURFACE TEMPERATURE

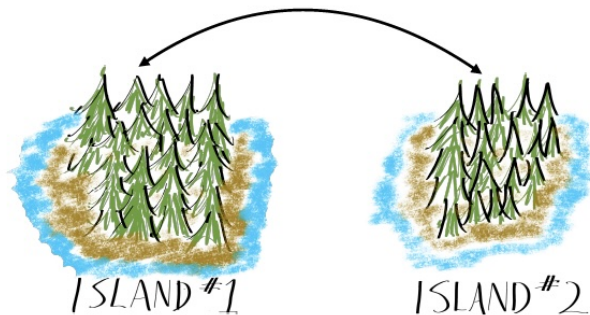


<https://www.climate.gov/news-features/understanding-climate/climate-change-global-temperature> - *Hopefully the webpage still exists...*

How could you advance tree breeding with what you learned in the last three modules?

Many of the interventions we may want to take would involve knowing the genes that underly important traits For species that are intractable to cultivate in a lab, how can we identify important genetic variation?

Let's Build a Model!



- Imagine a tree species inhabiting two islands
- Pollen flows between them
- A height of 10m is selectively favoured on both islands
- 95% of the time trees pollinate individuals from their own island

There are no environmental differences between the islands!

This gives an expected F_{ST} of 0.05

The Genetics of our Model



The Genetics of our Model

- Diploid individuals



The details on this slide are just for understanding the model. You *will not* be tested on memorizing these numbers and/or parameters

The Genetics of our Model



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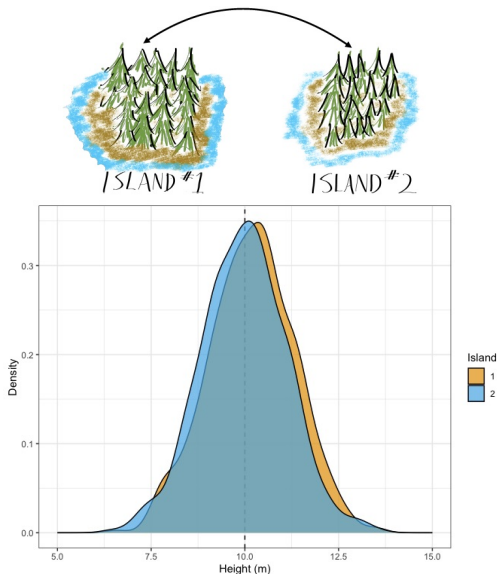
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- Heritability of height $h^2 = 0.4$

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Phenotypic Variation on the Islands



- Mean height is on 10.18 on Island 1 and 9.98 on Island 2
- This slight difference was statistically significant ($p < 0.001$)
- **Not** driven by differences in selection

I'll add a picture here of the chromosome with a marker...

Testing for Genetic Associations With Tree Height

To test for an association of a trait (in this case height) with SNP, we can do a statistical regression:

$$\hat{Y}_i \sim \alpha + \beta_j X_i + \epsilon$$

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\hat{Y}_i : The phenotype of individual i

α : The population mean

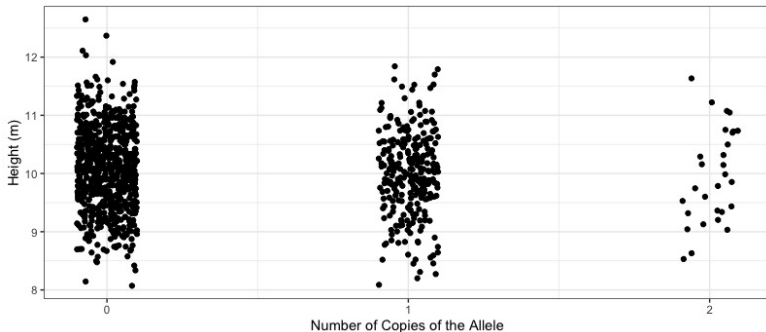
β : The effect of marker j on the trait

i : The number of copies of marker j that individual i possesses

ϵ : The effect of the environment on the trait

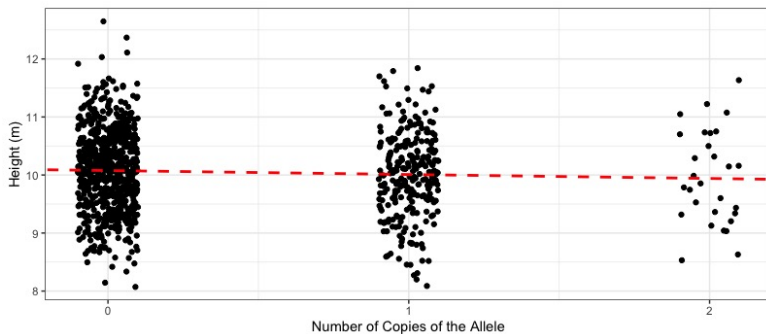
By fitting a regression to the data we can estimate the effect size of a particular marker on a trait and test for statistical significance...

Testing Association at a Single Marker



The allele is at a frequency of 0.16 across both islands

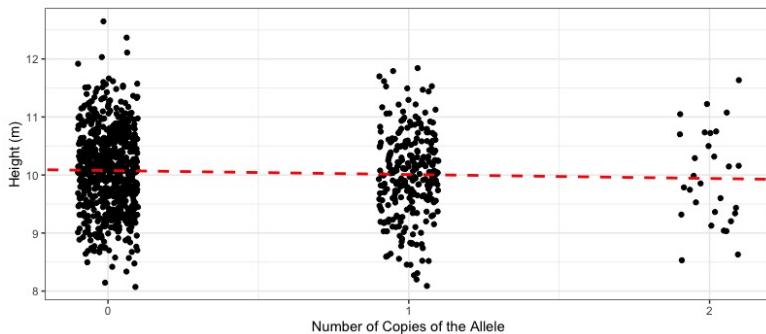
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The p - value for this regression was $p = 0.108$

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What can we say about this marker?

Genome-Wide Association Study

Now, what if we look at the whole genome, and at each marker in it

There's nothing special about $-\log_{10}(p\text{-value})$, it's just the $p\text{-value}$ of an association expressed in an easy to visualise way

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Can anyone think of any problems with the approach we have taken so far?

Association Genetics Caveat: Population Structure/Relatedness

Population structure and/or relatedness can lead to genetic associations when traits vary

Association Genetics Caveat: Multiple Testing

Let's now correct for the issues we have identified so far...