Molecular methods in forestry: From seeds to trees

Connections Through Seed Surrey, BC 17 October, 2018

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Outline

- The state of molecular tools
- An example from:
  - Seeds: pedigree reconstruction
  - Seedlings: genomic selection
  - Trees: understanding natural adaptation
- The challenge of conifer genomics

The state of molecular tools

- All biological systems are machines
- Molecular tools let us see “under the hood”

Phenotype
- Looks like a baby tree

Genotype
- Doesn’t like the cold
- Will grow tall
- Likes jazz music

Phenotype
- Looks like a baby tree

Genotype
- Disease-resistant
- Sets bud early
- Enjoys long walks on the beach

Phenotype
- Looks like a baby tree

Genotype
- Very cold-hearty
- Prone to lammas
- Hates broccoli

Phenotype
- Looks like a baby tree

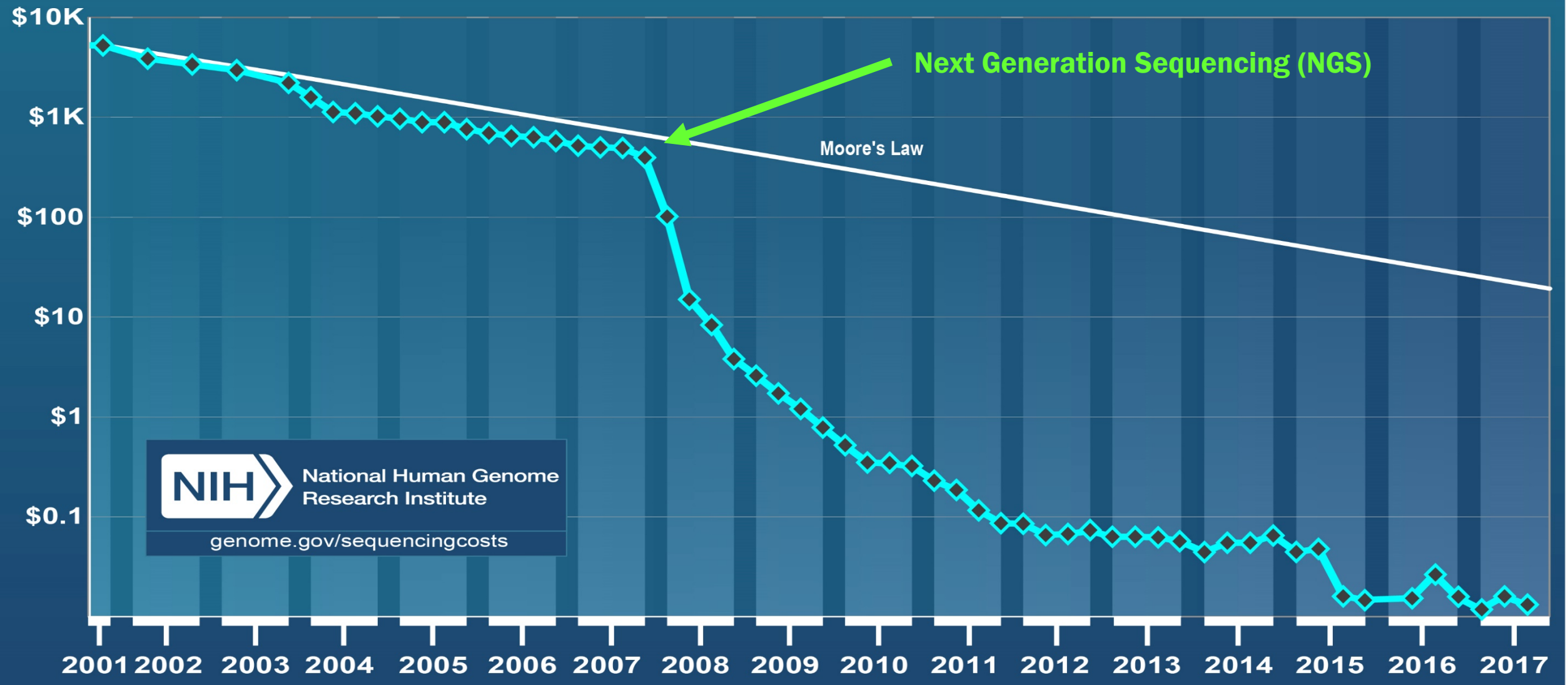
Genotype
- Will grow short and fat
- flushes late
- Doesn’t play well with others

The state of molecular tools

- 1970s – 2000s: Genetics
  - Neutral markers
  - 1 – few
  - Time consuming

- 2010s – present: Genomics
  - Markers neutral or under natural selection
  - Causal markers, or nearby
  - 1,000s – 1,000,000s
  - Fast!

Cost per Raw Megabase of DNA Sequence



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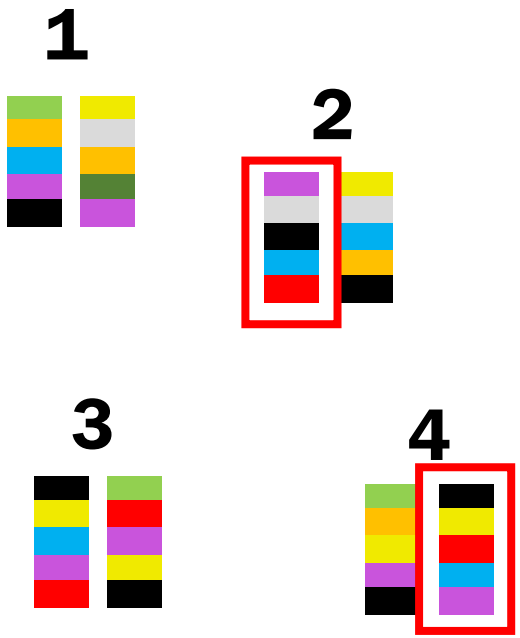
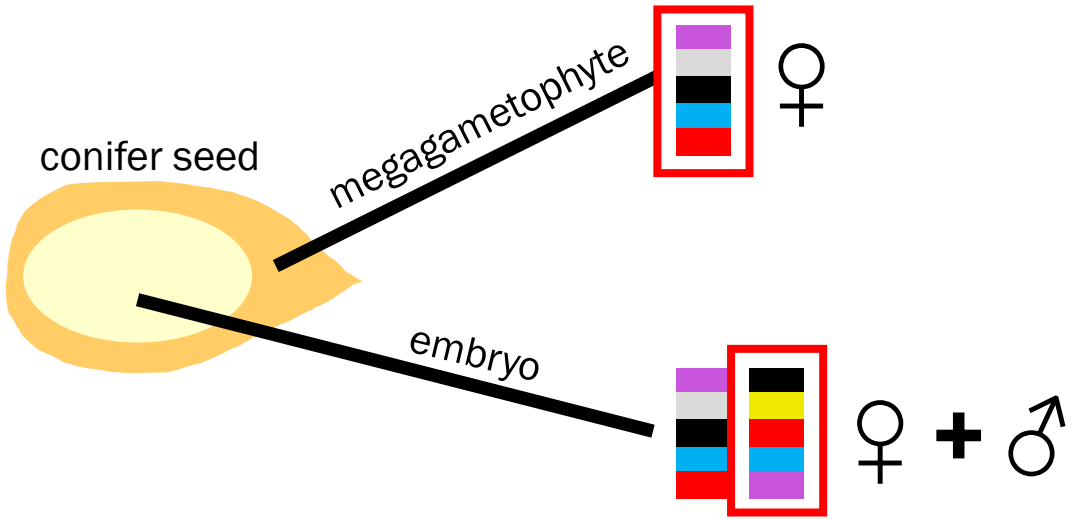
Molecular tools: Seeds

Pedigree reconstruction

- Using genetic markers to reconstruct parentage from bulk seed





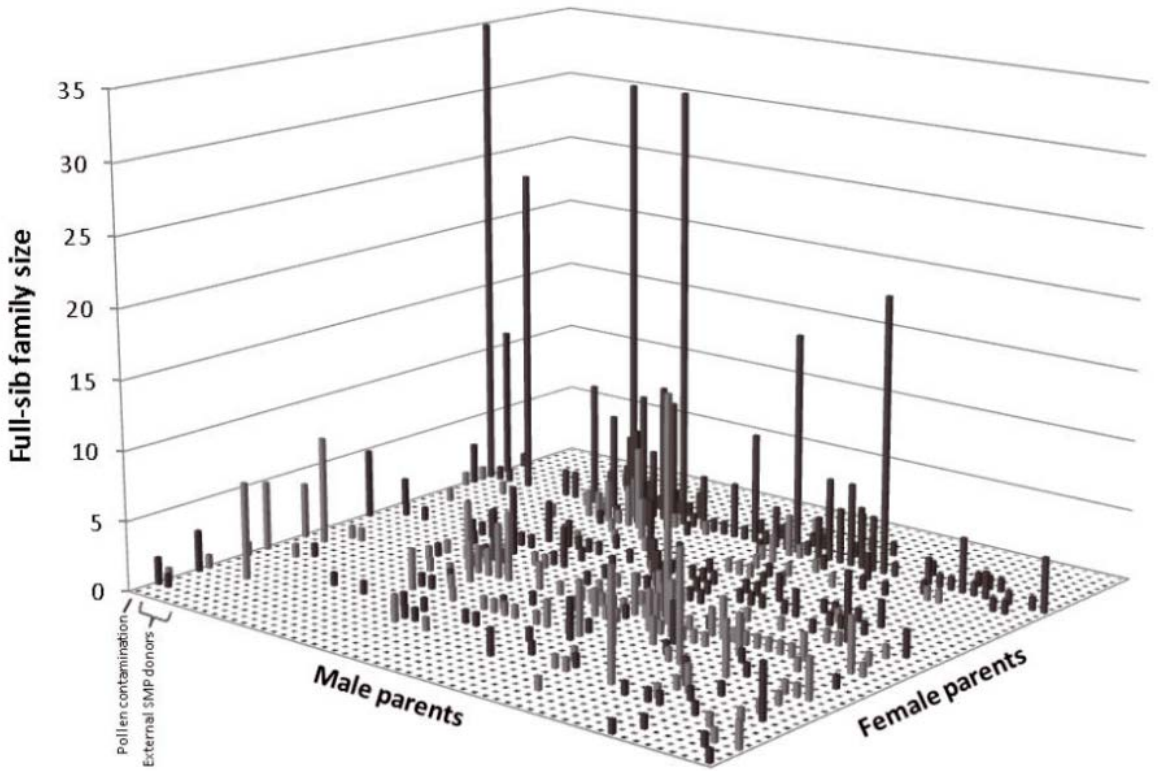
♀ parent: 2

♂ parent: 4

Molecular tools: Seeds

Pedigree reconstruction

- Using genetic markers to reconstruct parentage from bulk seed



Year	80% Gametic Contribution			Gene Flow (%)	Overall Selfing (%)
	♀ (%)	♂ (%)	♀ + ♂ (%)		
2005[c]	23	45	37	10	15
2007[d]	39	55	52	13	12
2008[e]	57	59	64	28	16
2009[f]	39	45	49	18	17

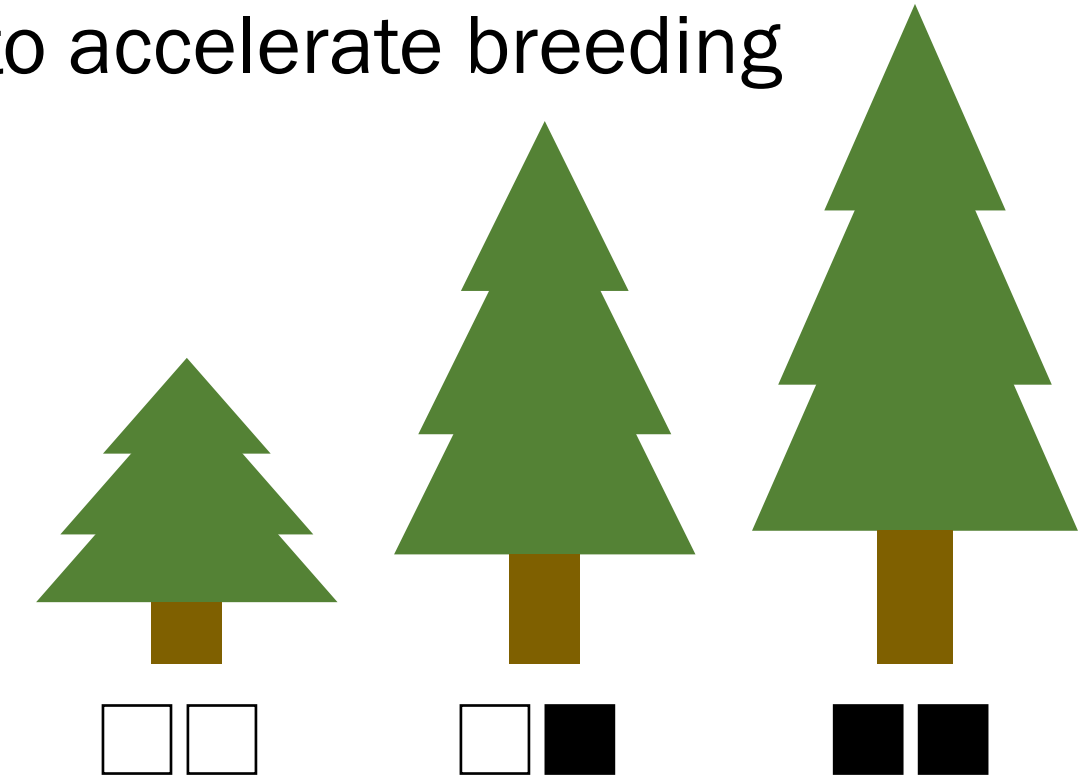
Modified from Song *et al.* (2018) Sci. Rep. 8:11593

Lai *et al.* (2010) Ann. For. Sci. 67: 808

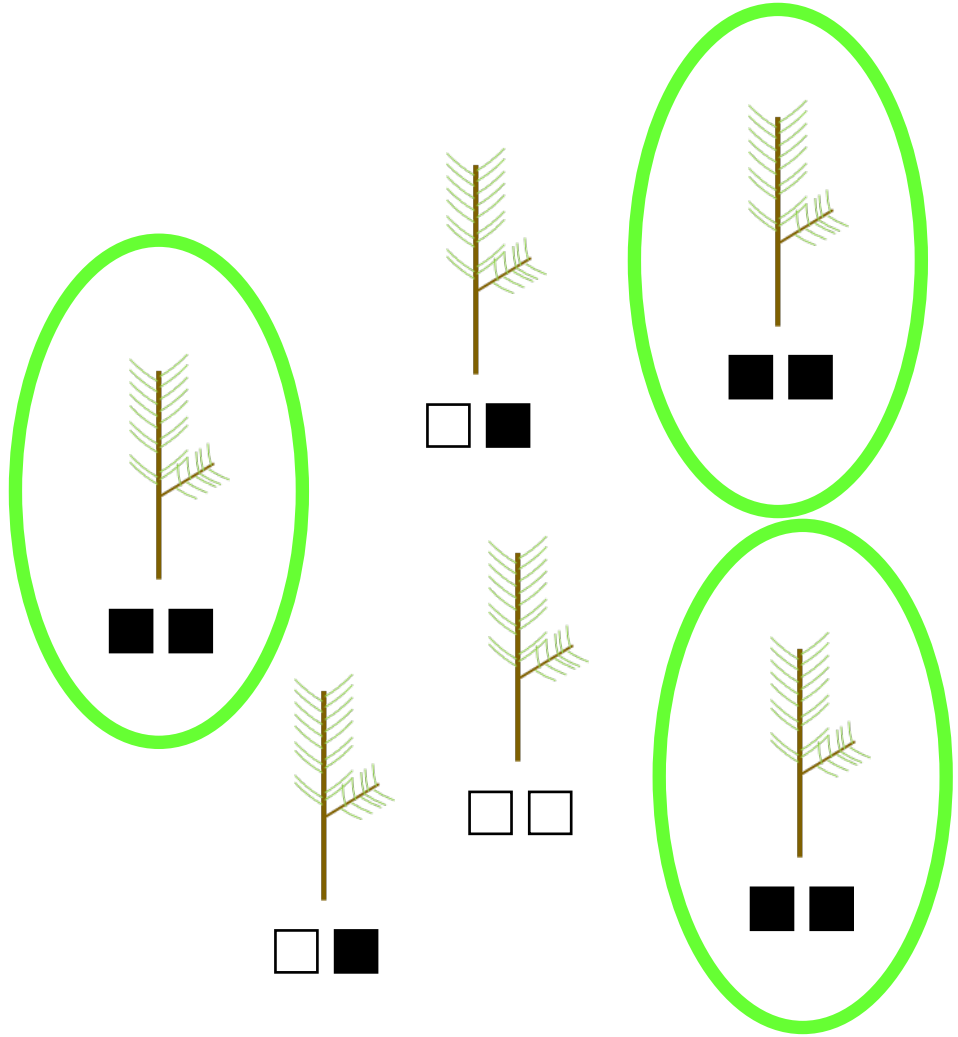
Molecular tools: Seedlings

Genomic selection

- Using marker-trait associations to accelerate breeding



field trial

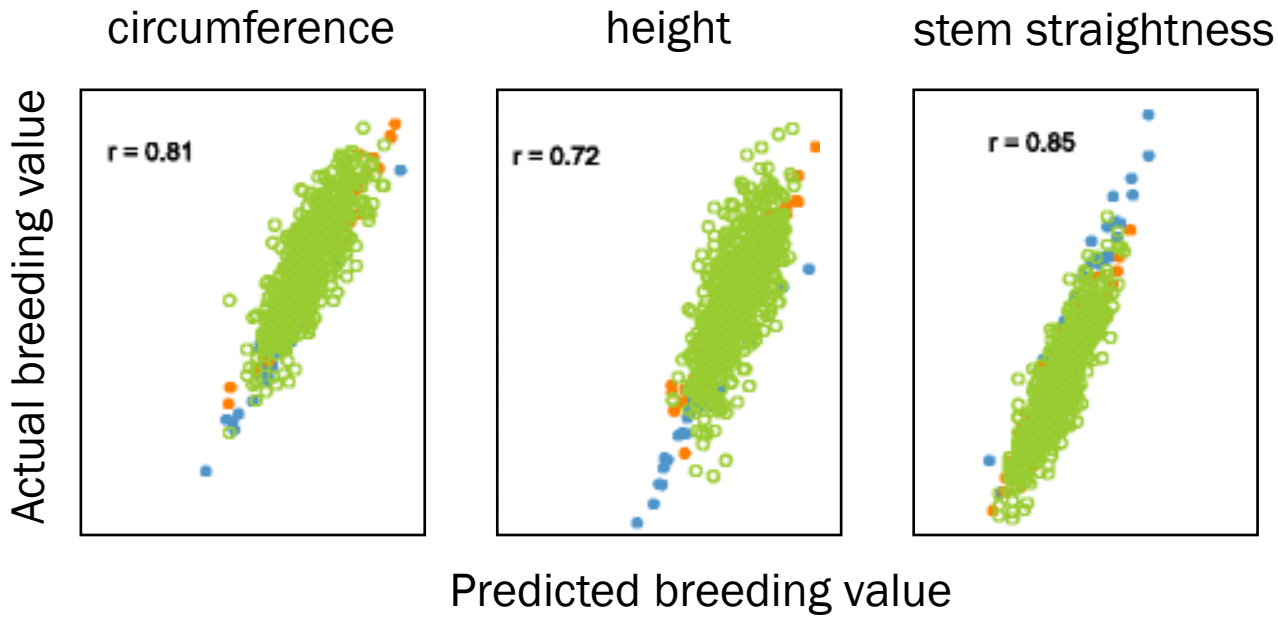


progeny screening

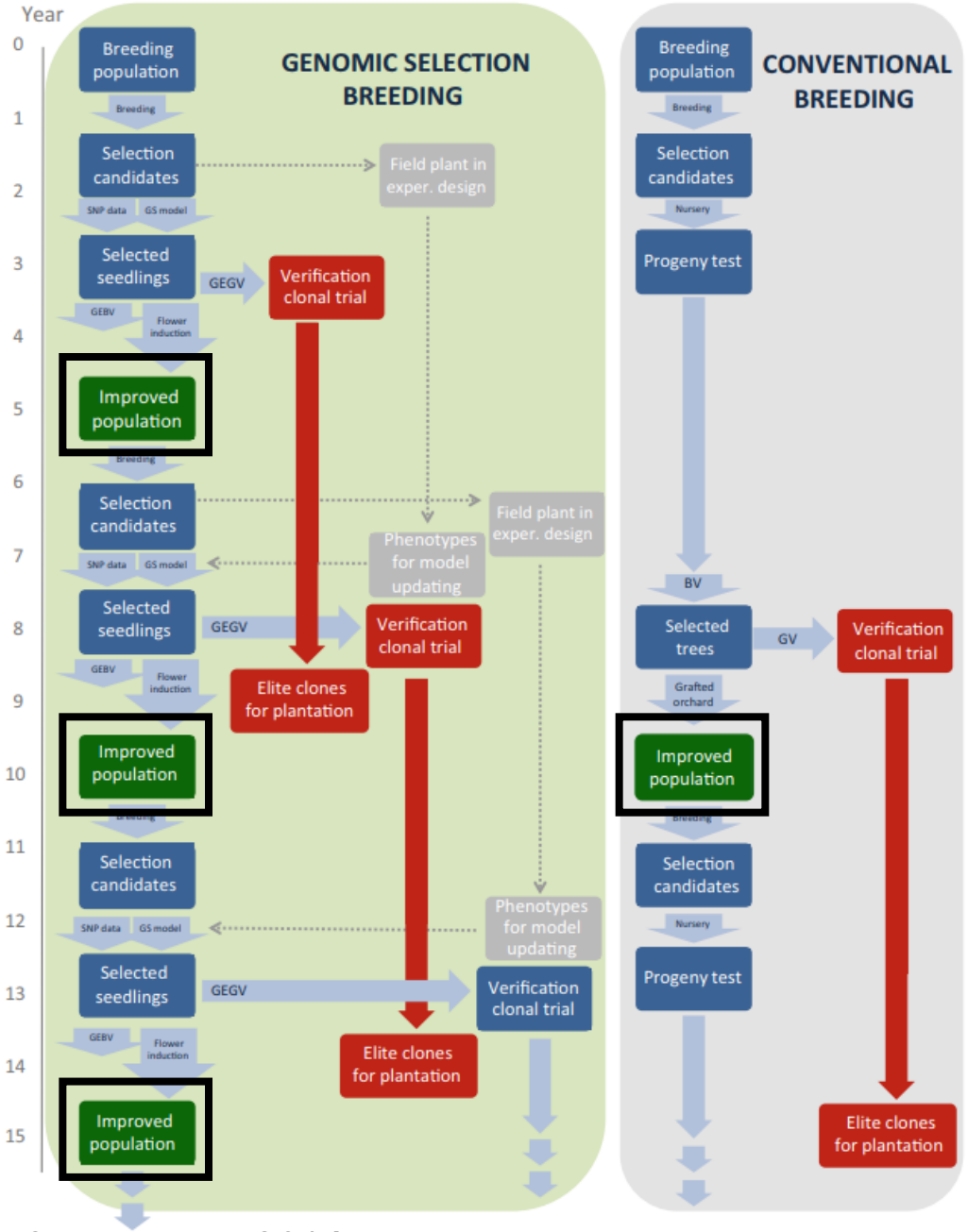
Molecular tools: Seedlings

Genomic selection

- Using marker-trait associations to accelerate breeding



Modified from Bartholomé *et al.* (2016) BMC Genomics 17: 604

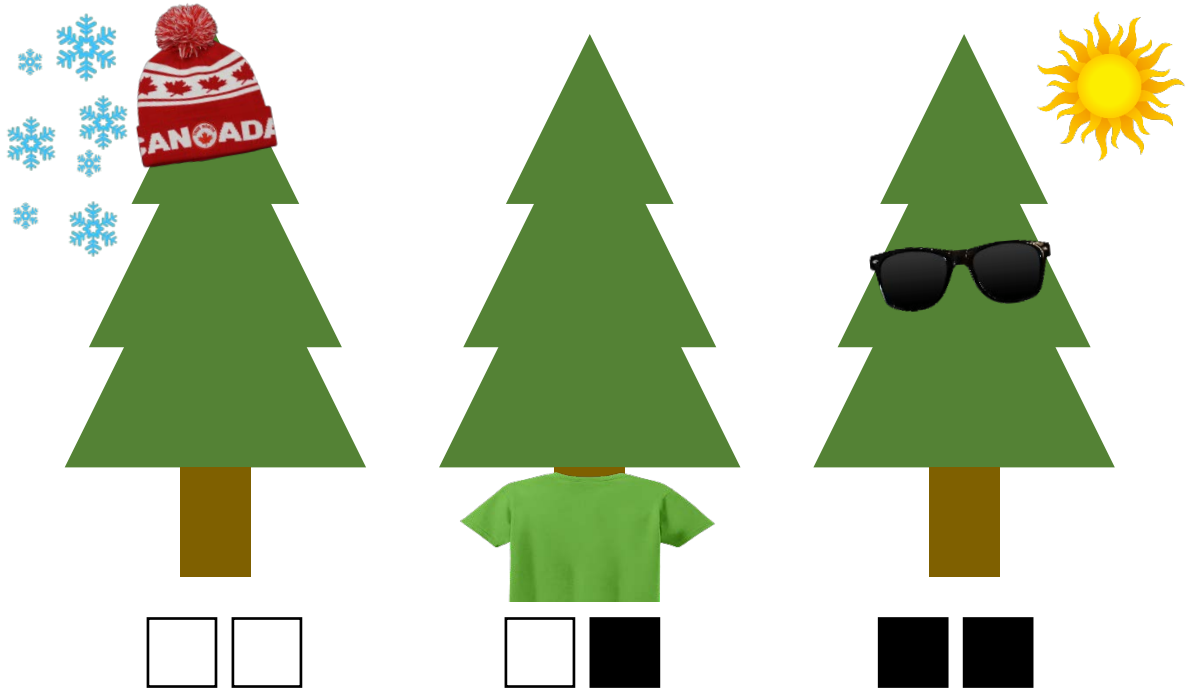


Grattapaglia (2014)
Advances in genomics of plant genetic resources

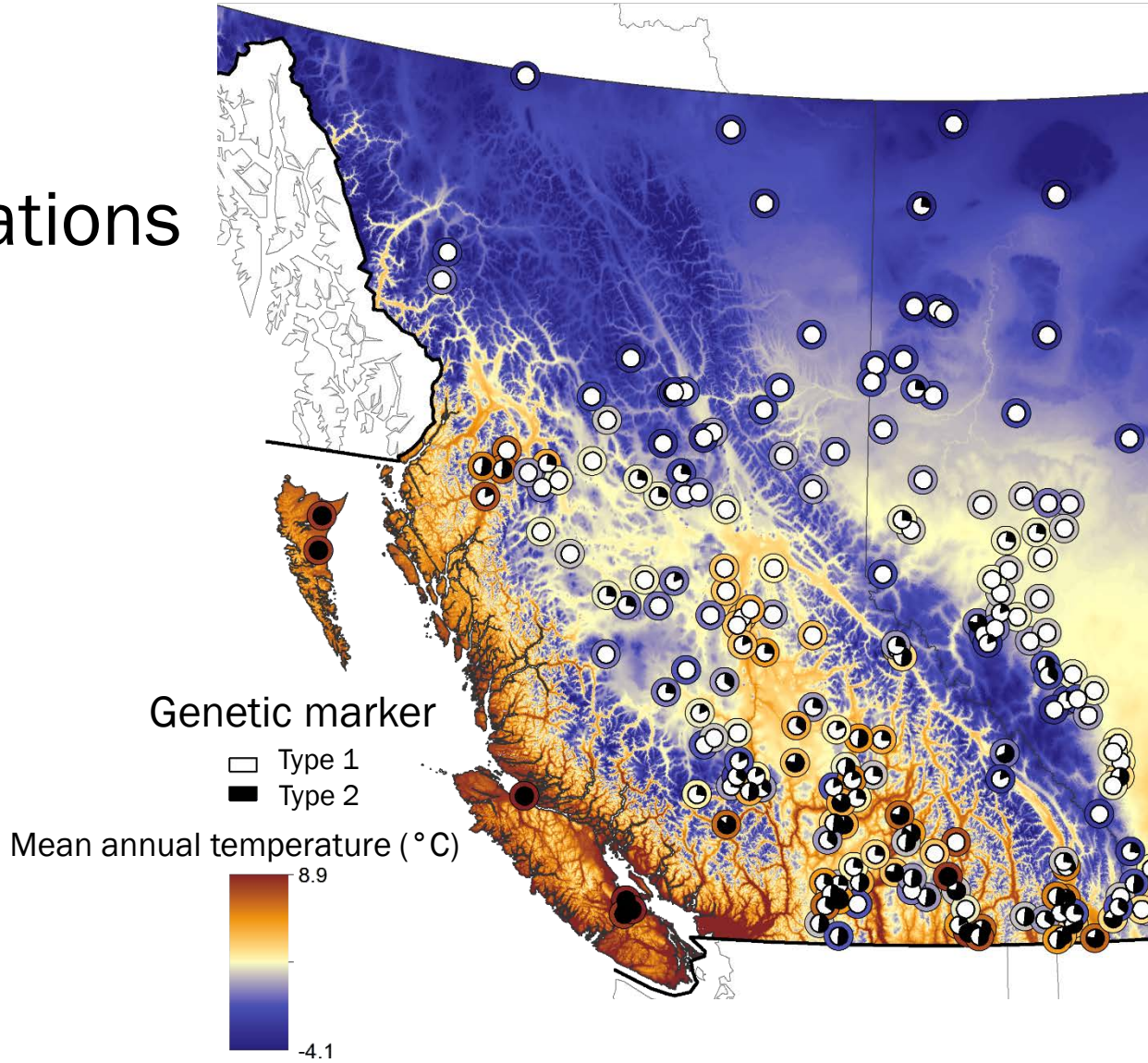
Molecular tools: Trees

Understanding natural adaptation

- Using marker-environment associations to infer natural selection



Natural populations



Molecular tools: Trees

Understanding natural adaptation

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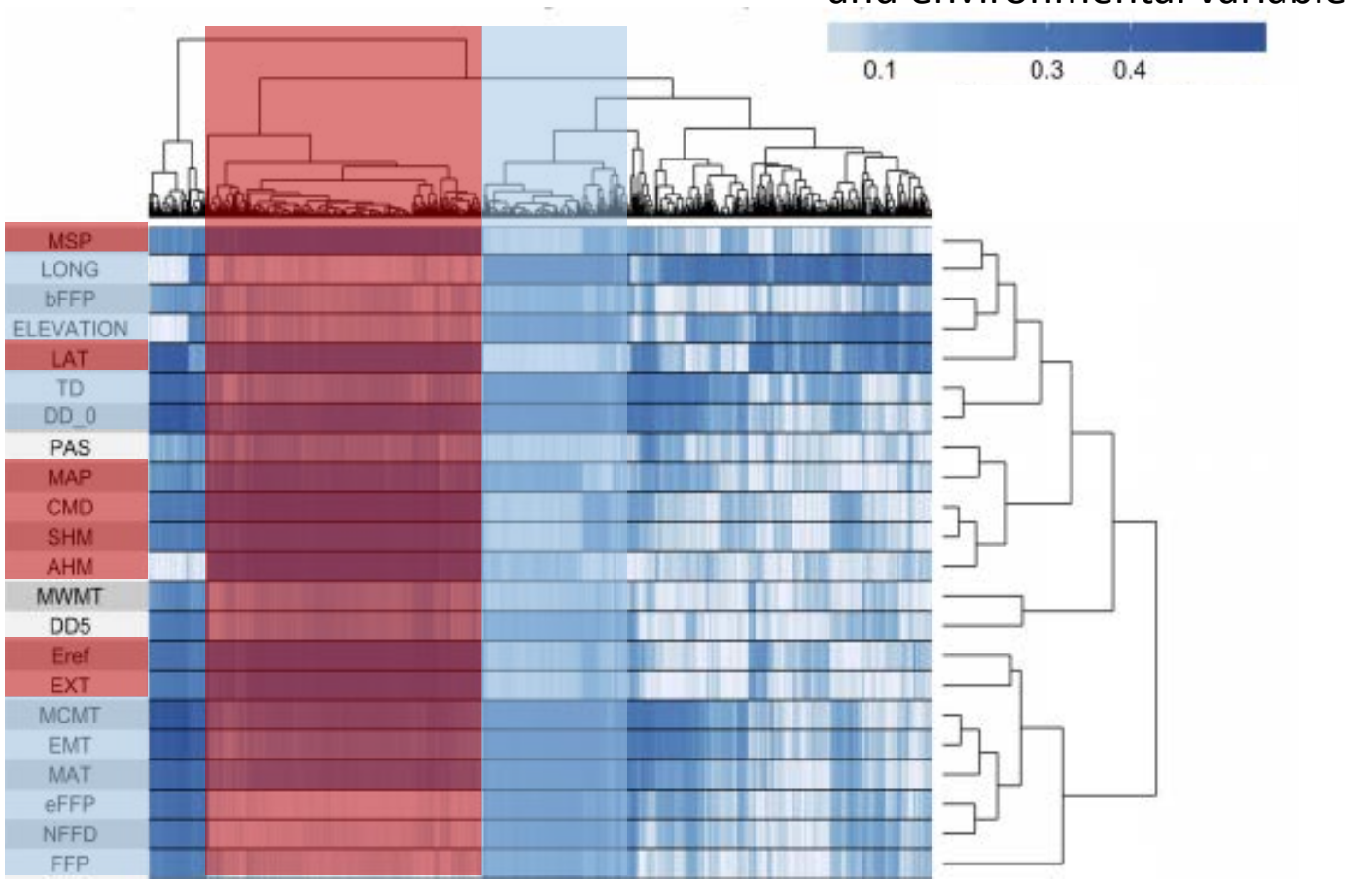

Aridity-related climate variables

Frost-related climate variables

Modified from Lotterhos *et al.* (In Press) Gen. Biol.

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- The challenge of conifer genomics

The challenge of conifer genomics

- Genomic methods are “simple” if your organism has:
  - ☒ **A small genome**
  - ☒ A complete reference genome
  - ☒ Standardized lab methods
  - ☑ No sex chromosomes

- Conifer genomics is… complicated.


trees

Interior spruce

2000 pages

Summary

- Molecular methods are developing rapidly
- There is potential at every stage of reforestation
- Molecular methods for conifers are difficult, but improving.

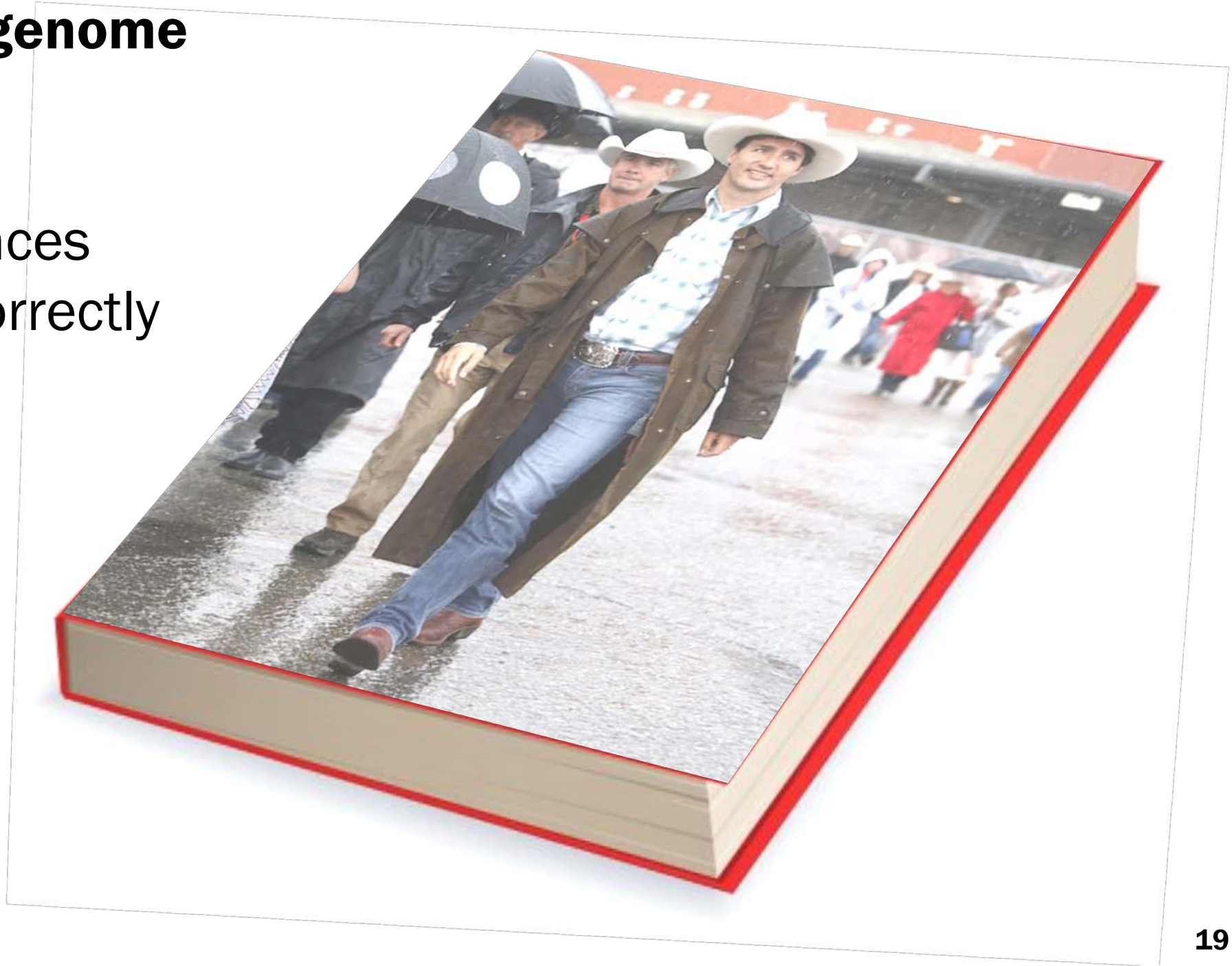
The challenge of conifer genomics

- Conifer genomics is… complicated.

- Genomic methods are easy if your organism has:
  - ☒ A small genome
  - ☒ **A complete reference genome**
  - ☒ Standardized lab methods
  - ☑ No sex chromosomes

Human reference genome

- 300 pages
- 23 chapters
- Complete sentences
- Words spelled correctly



Spruce reference genome

- 5 million scraps of paper
- 0-50 words per scrap

Summary

- Molecular methods are developing rapidly, both in scale and accessibility
- There is potential at every stage of reforestation
- Molecular methods for conifers are difficult, but improving