

Tree Improvement: An International Perspective and Opportunities for the U.K.

John MacKay

ICF Annual Conference - 27 April 2016

Productivity

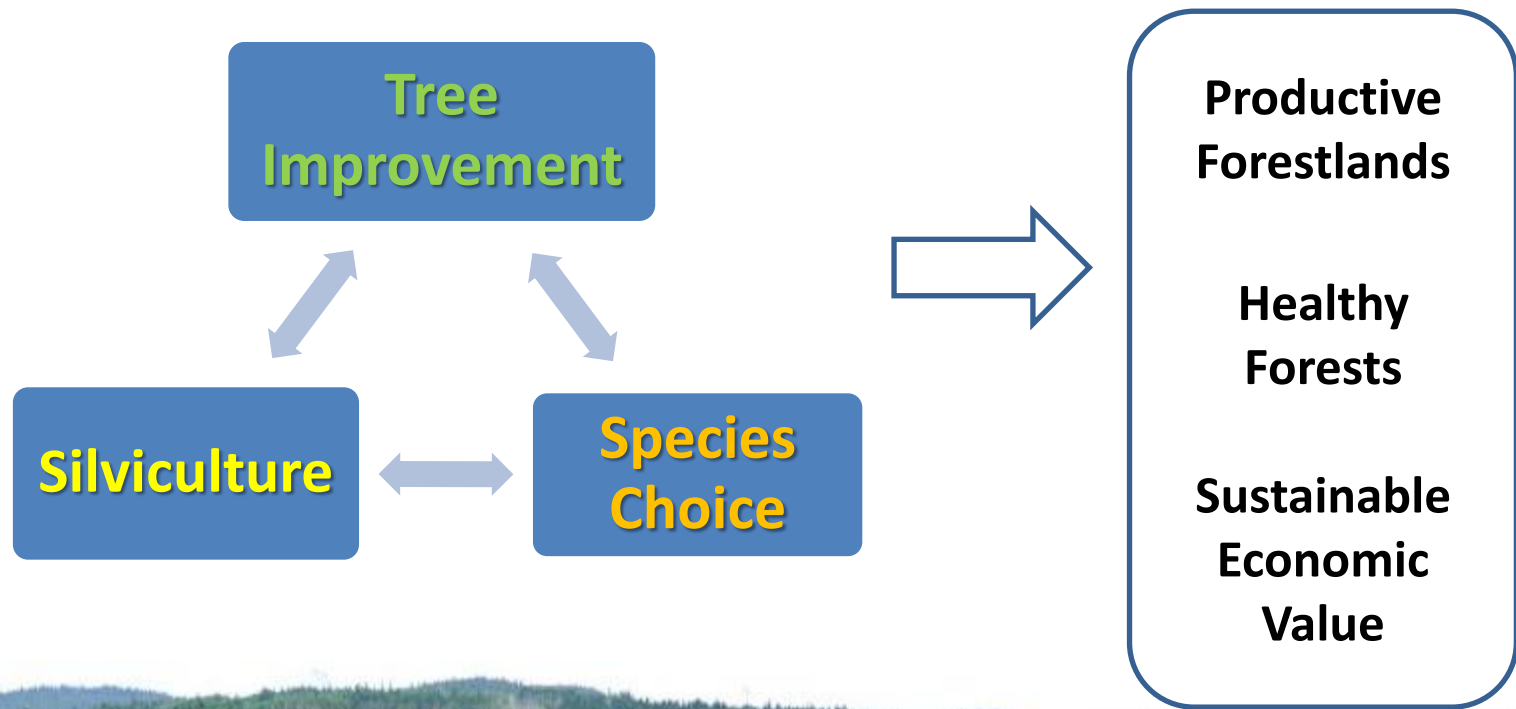


Diversity



Sustainability





Outline

Tree Improvement (TI)

- Productivity
- Forest health

Genomics

- The Power
- And The Promise

Opportunities for the UK

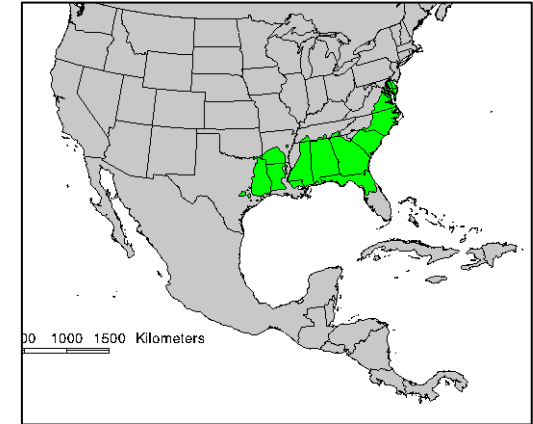
Productivity

Large Impacts Delivered

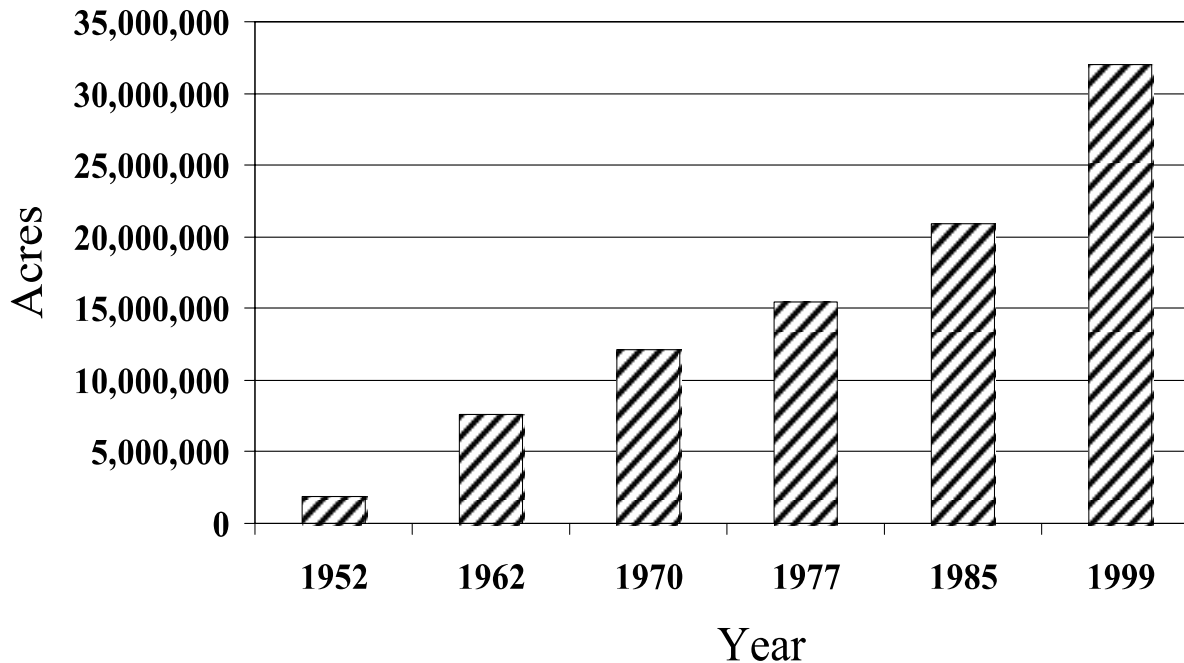
Loblolly pine (*Pinus taeda*)

S-E USA

- Produces 18% of the world's industrial round wood
- Pine planted area: 2% of world's forests



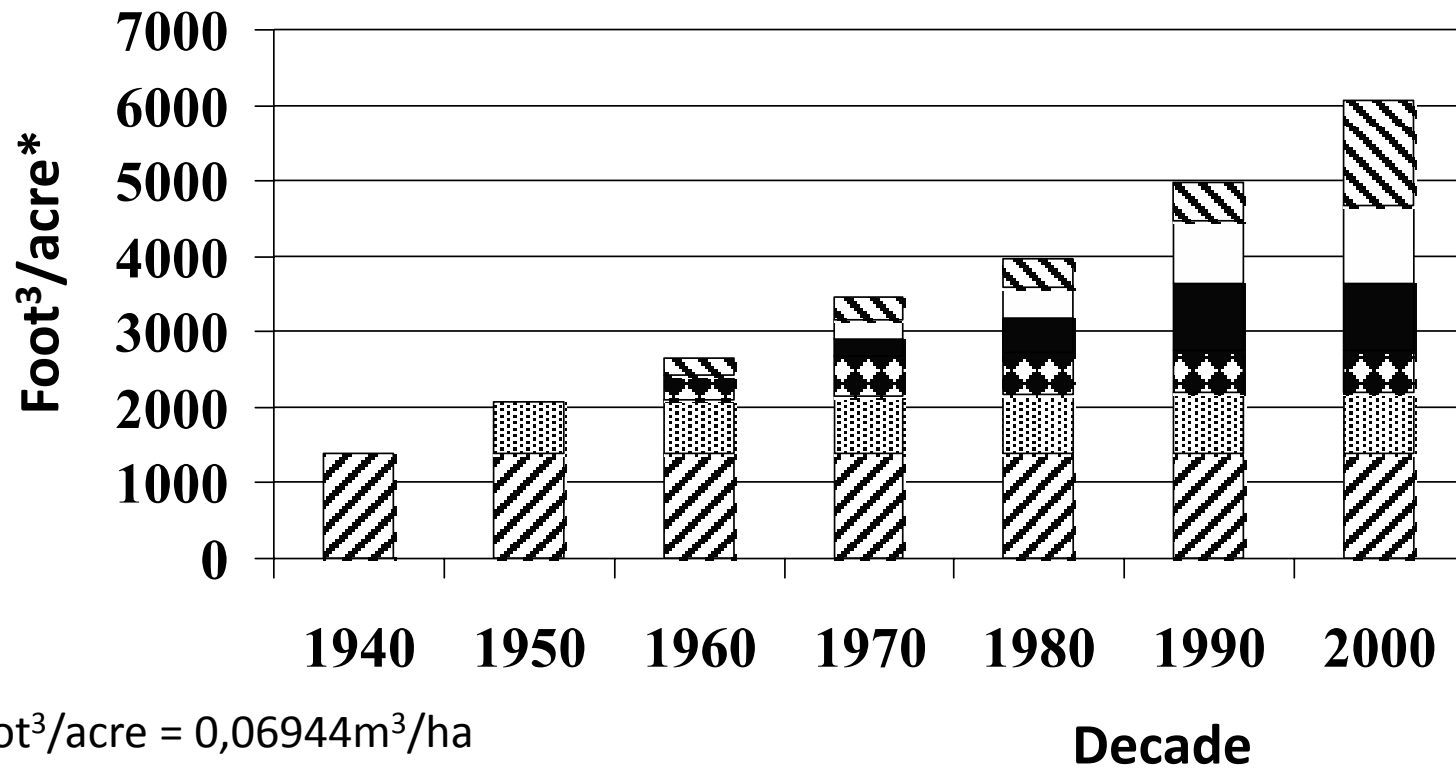
Area of pine plantation in the S-E USA



Sources: www.fs.fed.us/database/

Fox T.R., Jokela J. and H.L. Allen 2007; Zhang and Stanturf 2008

Impacts of silviculture and Tree Improvement



*1 foot³/acre = 0,06944m³/ha

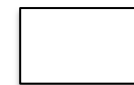
1 hectare (ha) = 10,000 m²



Natural stand



Site preparation before planting



Fertilization



Plantation



Competition control after planting

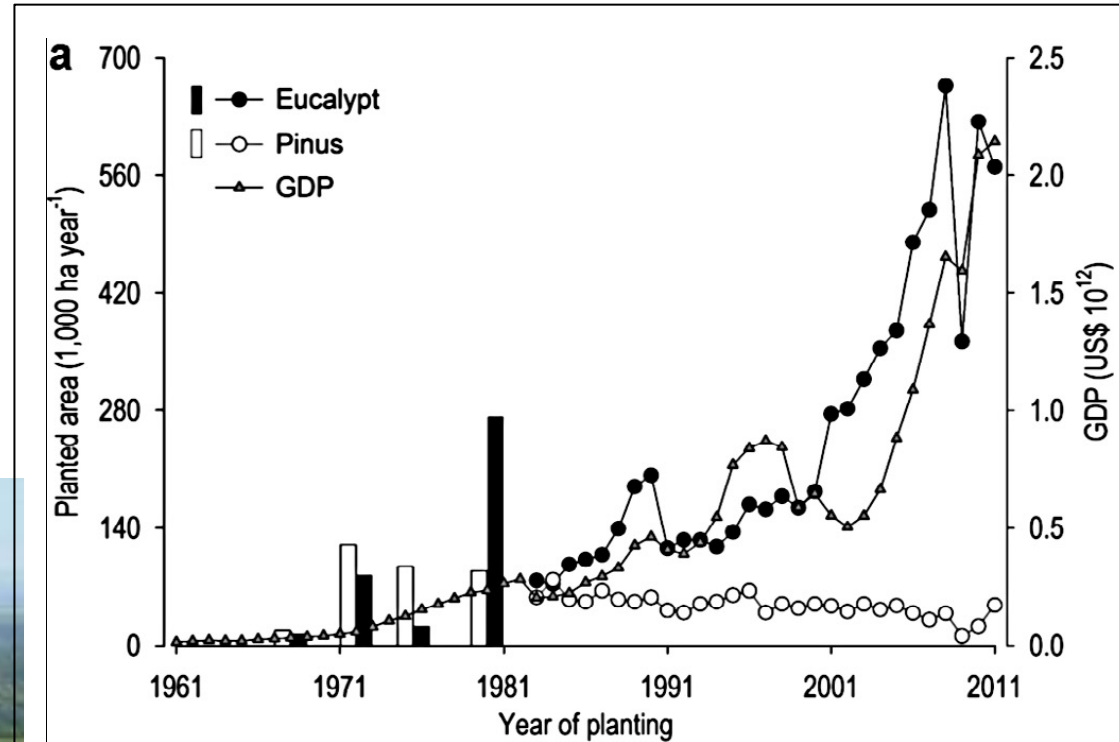


Tree improvement (genetics)

Eucalyptus Plantation : Brazil

Eucalyptus

- Native of Australia
- 734 known species
- From tropical and sub-tropical areas



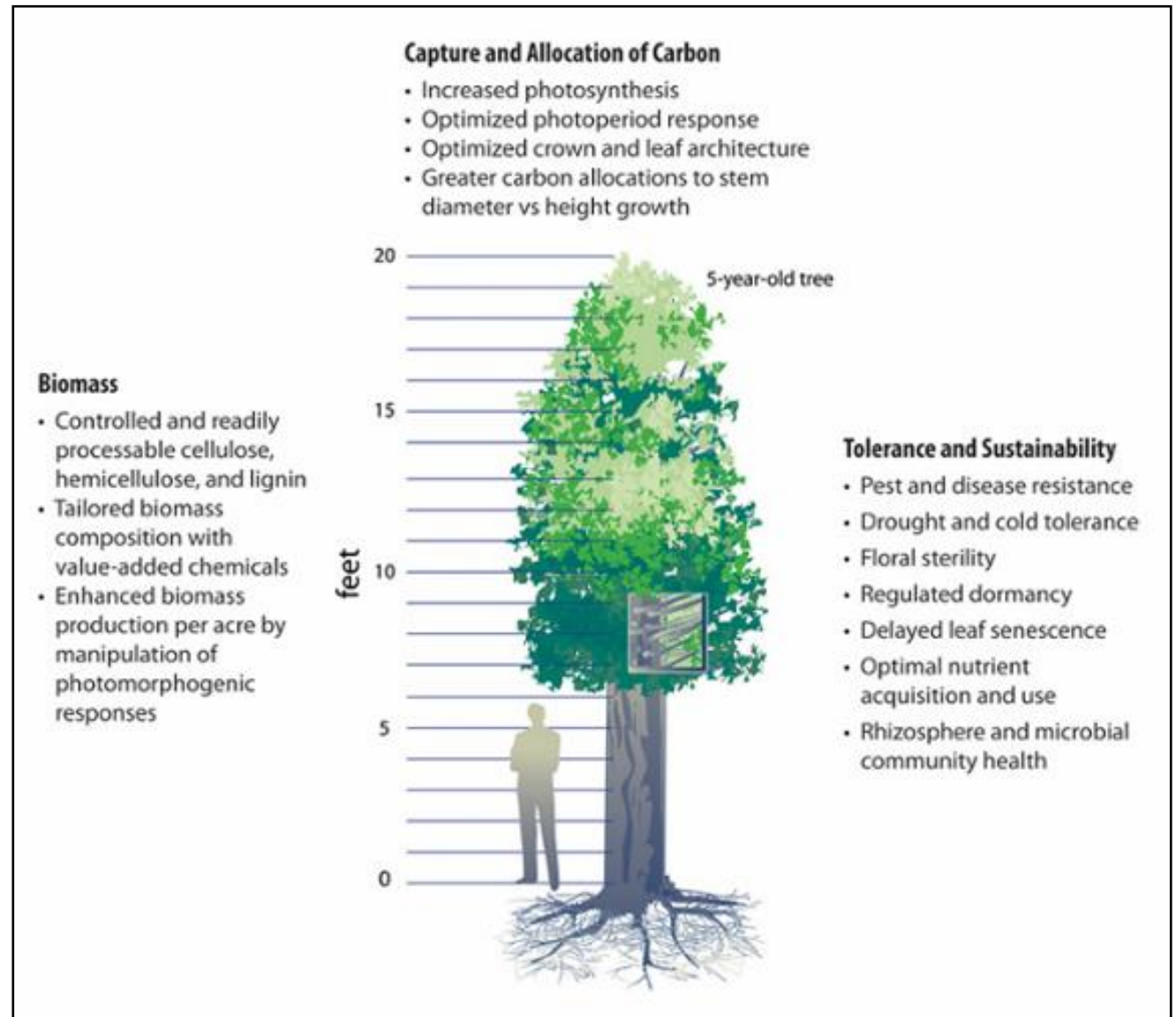
Eucalyptus yields from intensive Tree Improvement and silviculture

Decade	1970	1980	1990	2000
Wood volume (m ³ /ha / year)	30	35	45	50+
Wood fibre yield (dry tons /ha /year)	6.4	8.1	10.2	11.3



Wood for Biomass and Bio-Energy

Aggressive DOE (USA) tree domestication targets



<http://genomics.energy.gov/gallery/biomass/detail.np/detail-01.html>

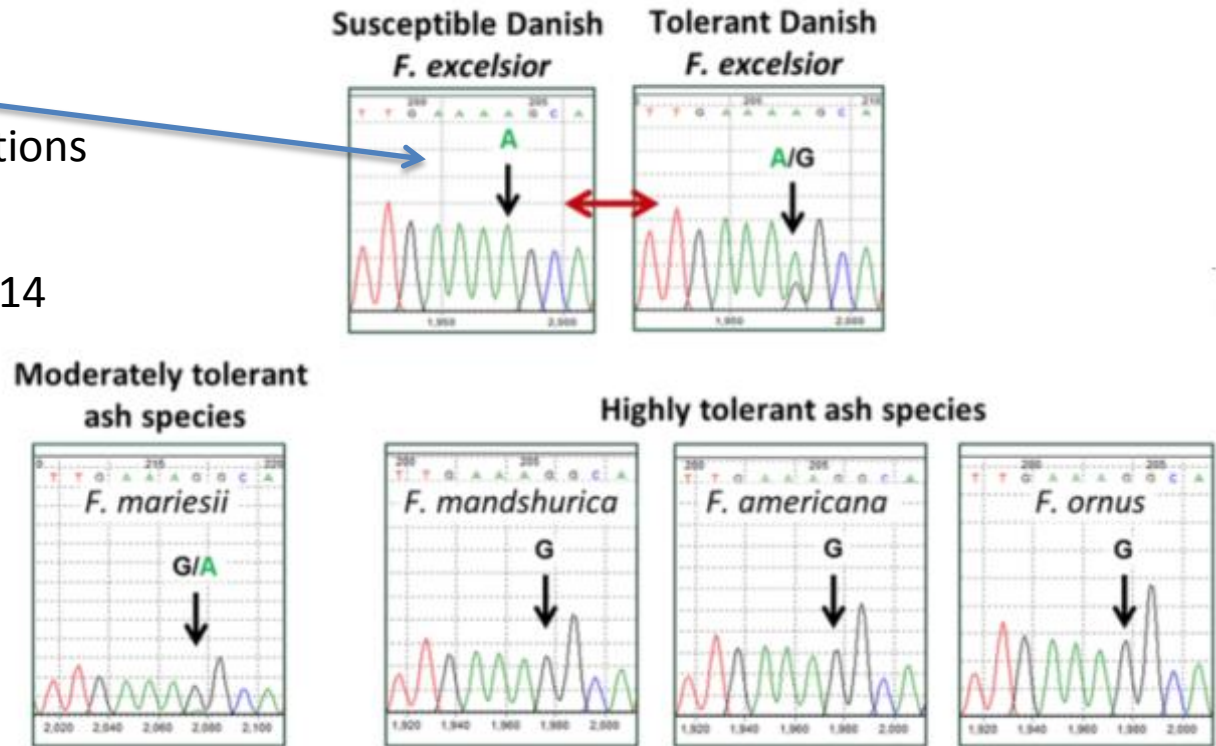
Forest Health

Developing the Science

Ash Dieback Tolerance

Association study in population that included resistant trees from Denmark

- Identified:
 - DNA variations
 - Gene expression variations
- Predictive value:
 - Combined index of all 14 markers combined gave a correlation of $R^2 = 0.24$



Harper et al. 2015 Molecular markers for tolerance of European ash..., Scientific Reports,6: 19335

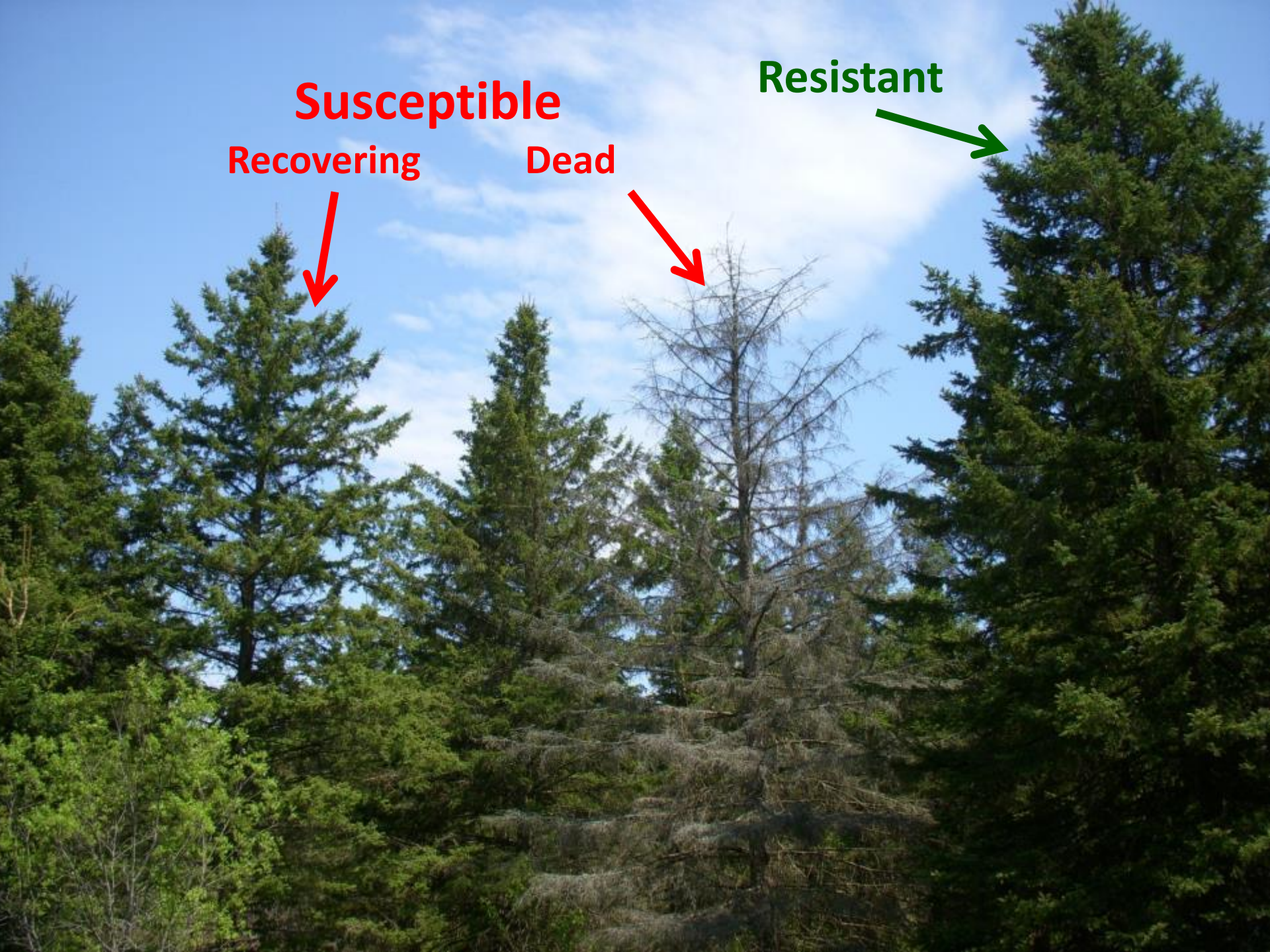
Figure 1. Sequence chromatograms showing the cSNP position in a number of Fraxinus species. Gene_22343_Predicted_mRNA_scaffold3139:2378 was assayed by PCR and Sanger sequencing directly from the cDNA of both susceptible and tolerant Danish *F. excelsior* accessions, as well as the moderately tolerant species *F. mariesii*, and the extremely tolerant species *F. mandshurica*, *F. americana* and *F. ornus*. The "G" base is either not present at all in *F. excelsior*, or at a low level compared to the "A" base. In contrast, the "G" base is prevalent in the more resistant species, with only a low level of the "A" base being detected in the moderately tolerant *F. mariesii*.

Susceptible

Resistant

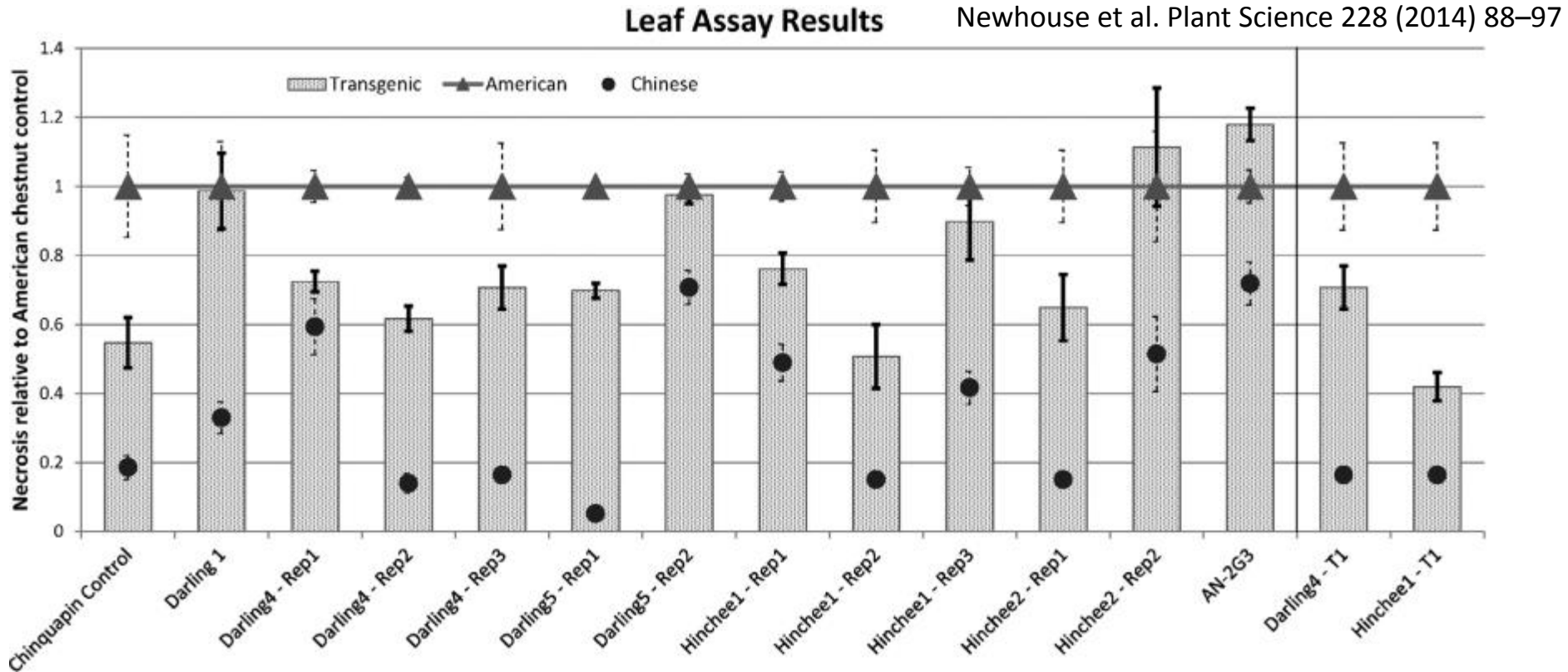
Recovering

Dead



GM of American chestnut for blight resistance

- Resistance breeding: hybridizing with Chinese chestnut (co-evolved with pest)
- Developing side-by-side with GM work



Transgene: wheat oxalate oxidase gene driven by the VspB vascular promoter.
Breaks down oxalic acid produced by the fungal pathogen

Commercial deployment : Insect tolerant poplars in China

Insect tolerance for defoliators and borers

- “Tree North” forest belt
- Bt toxin gene



Research plantation



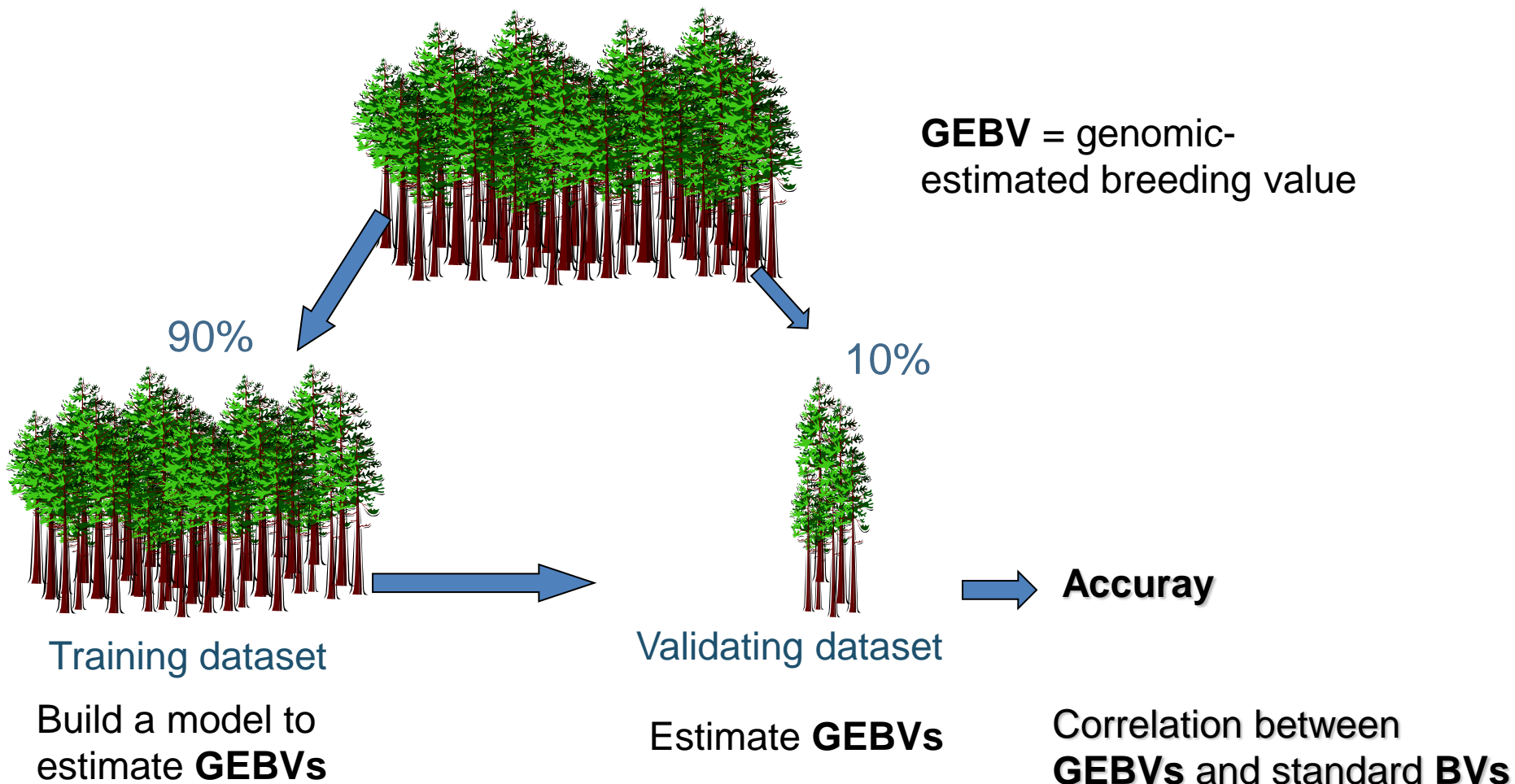
- Only known commercial-scale cultivation of insect tolerant GM forest trees
- Two varieties planted since 2002, in seven provinces: 490 ha (= 4.9 km²) by 2011

The Power of Genomics

Predicting Outcomes

Genomic Selection: Predicting Breeding Value (BV)

Breeding populations



Publication

Beaulieu *et al.* *BMC Genomics* 2014, **15**:1048
<http://www.biomedcentral.com/1471-2164/15/1048>



RESEARCH ARTICLE

Open Access

Genomic selection accuracies within and between environments and small breeding groups in white spruce

Jean Beaulieu^{1,2*}, Trevor K Doerksen^{1,2}, John MacKay², André Rainville³ and Jean Bousquet²

Abstract

Background: Genomic selection (GS) may improve selection response over conventional pedigree-based selection if markers capture more detailed information than pedigrees in recently domesticated tree species and/or make it more cost effective. Genomic prediction accuracies using 1748 trees and 6932 SNPs representative of as many distinct gene loci were determined for growth and wood traits in white spruce, within and between environments and breeding groups (BG), each with an effective size of $N_e \approx 20$. Marker subsets were also tested.

A Case Study: Genomic Selection in White Spruce

Advanced-Breeding Population

Trait	Accuracy	
	Conventional	GS
Height (cm)	0.80	0.71
Diameter (DBH) (cm)	0.84	0.73
Wood density (Kg/m ³)	0.88	0.80
Cellulose microfibril angle (degrees)	0.86	0.77

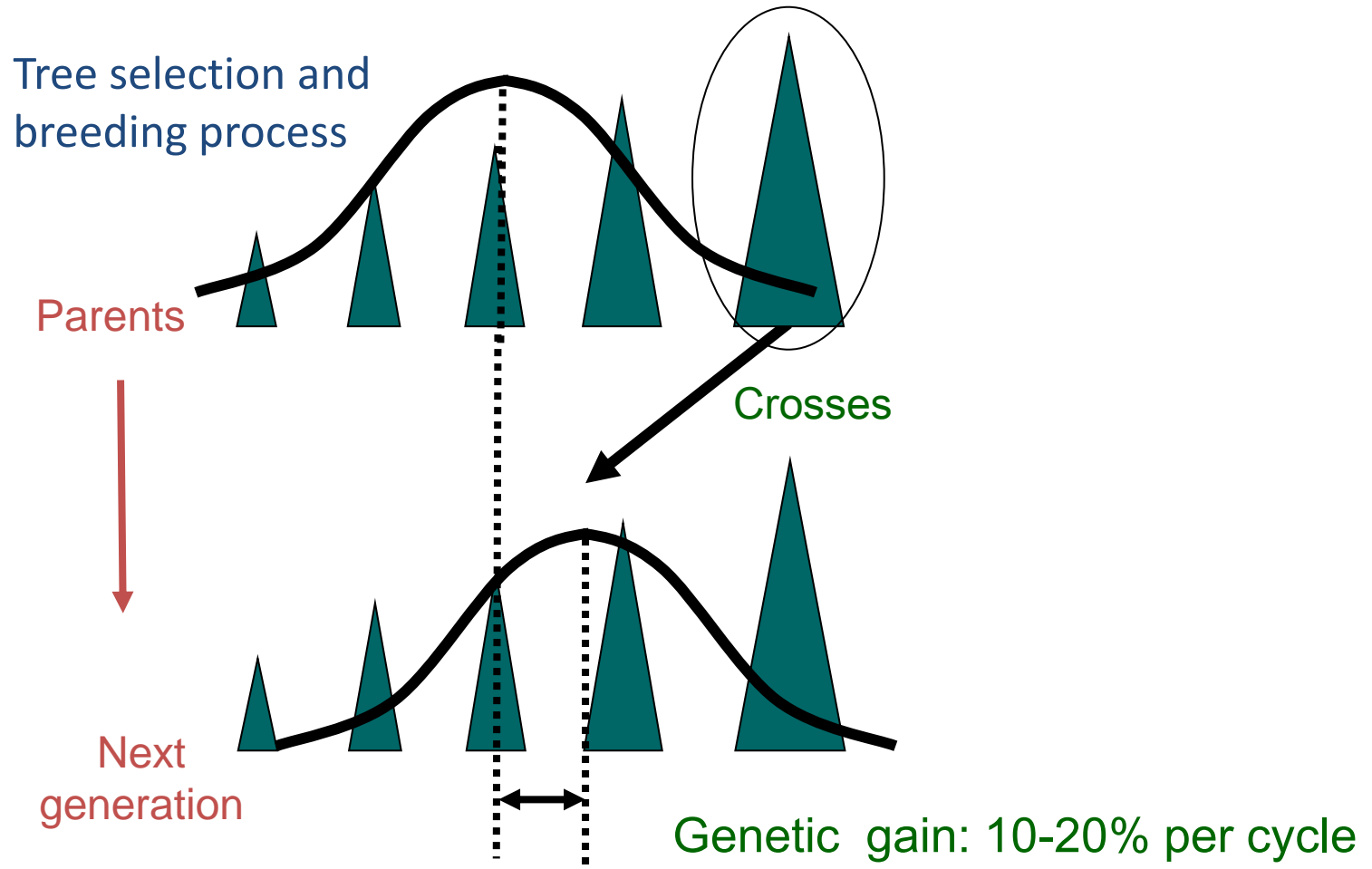
- **Validates in black spruce**
- **We have learned how GS works and what causes it not to work**

Genomics – The Promise

- Accelerate the Outputs of Breeding
- Sitka spruce in the U.K.

Forest Genetics: Tree Improvement

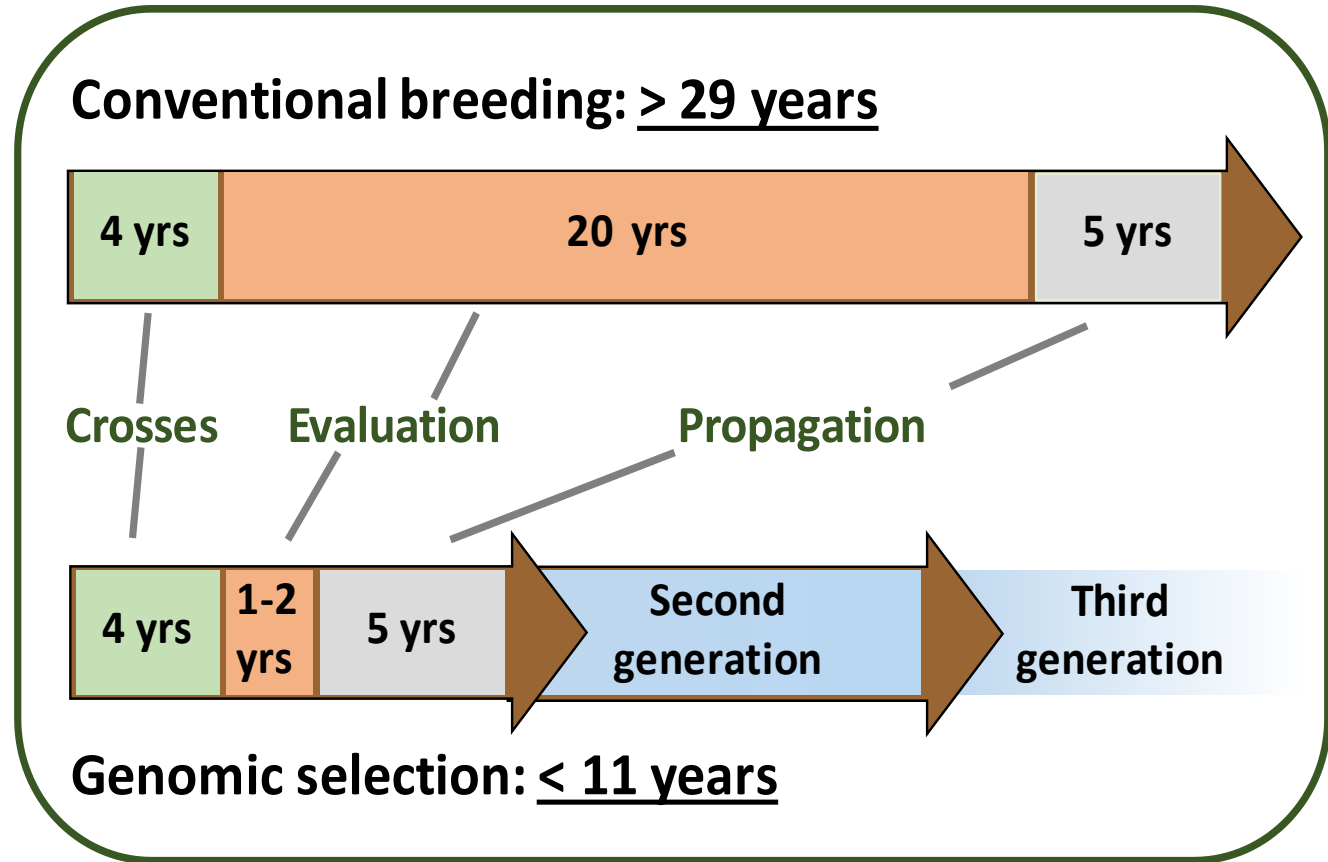
Goal of Tree Improvement (TI): Select, breed and propagate trees that produce higher yield or quality outputs in plantations

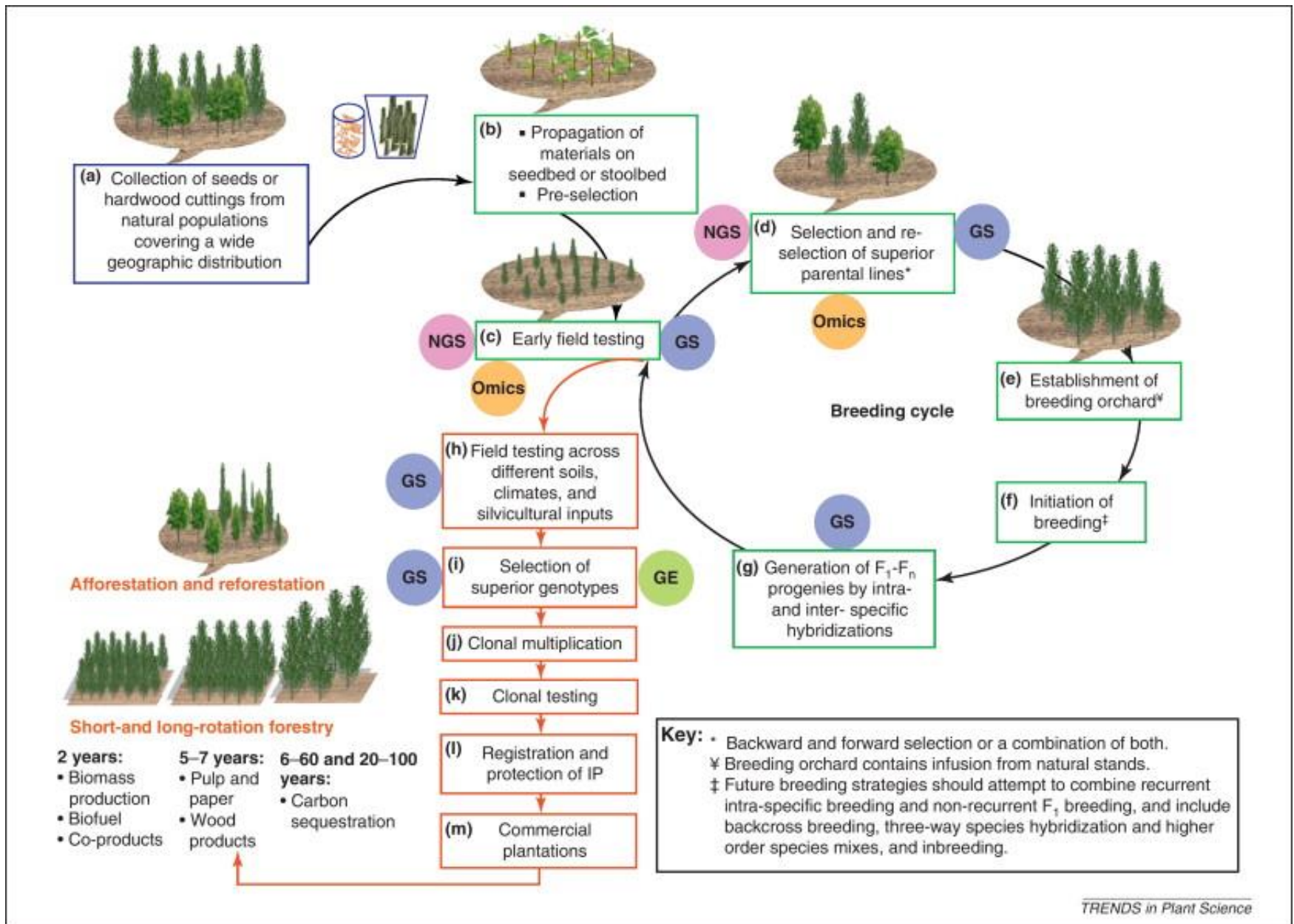


Goal of Genomic Selection: Shortening the Tree Breeding Cycles by Reducing Testing Time

Expected impact of genomics on the duration of conifer breeding cycles.

Genetic gain:
2.5 – 3 times more gain per unit of time expected in white spruce study





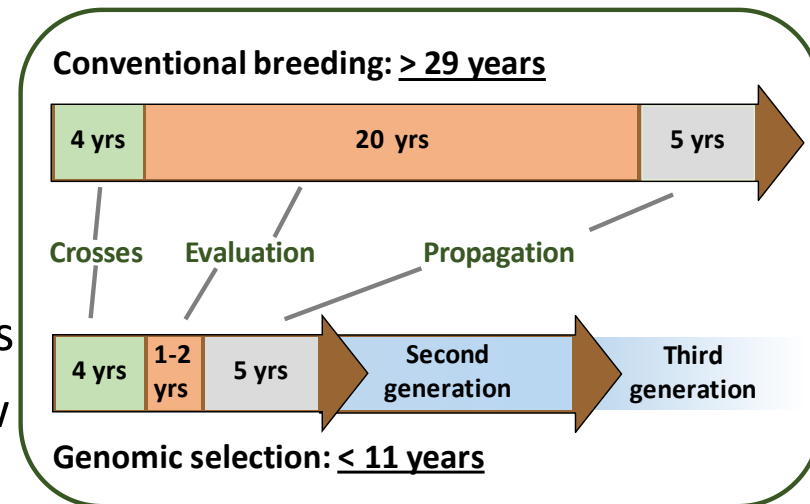
How could predictive genomics benefit species like Sitka Spruce in the U.K.?

Productivity, sustainability and adaptation impacts:

1. Accelerate breeding – short term
2. Intensification of production – short rotations while maintaining quality
3. Sustainability from improved genetic diversity management
4. Adaptation of the forest estate to changing conditions – long term

Novel tools and capacity impacts:

1. Next generation breeding tools
2. Novel capacity from genomic resource
3. Leverage global conifer genome resources
4. Update technical and scientific know-how

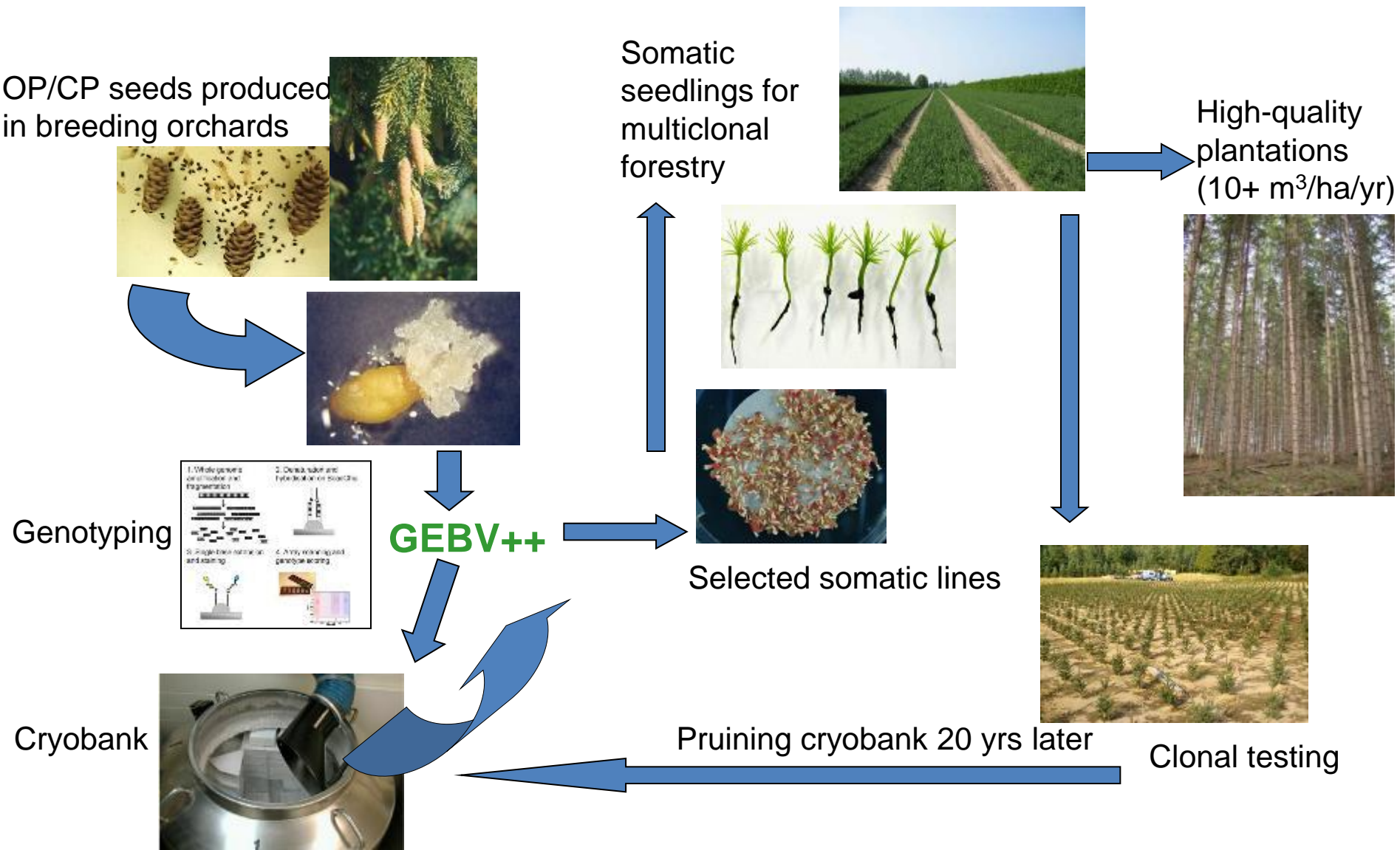


Summary and Conclusions

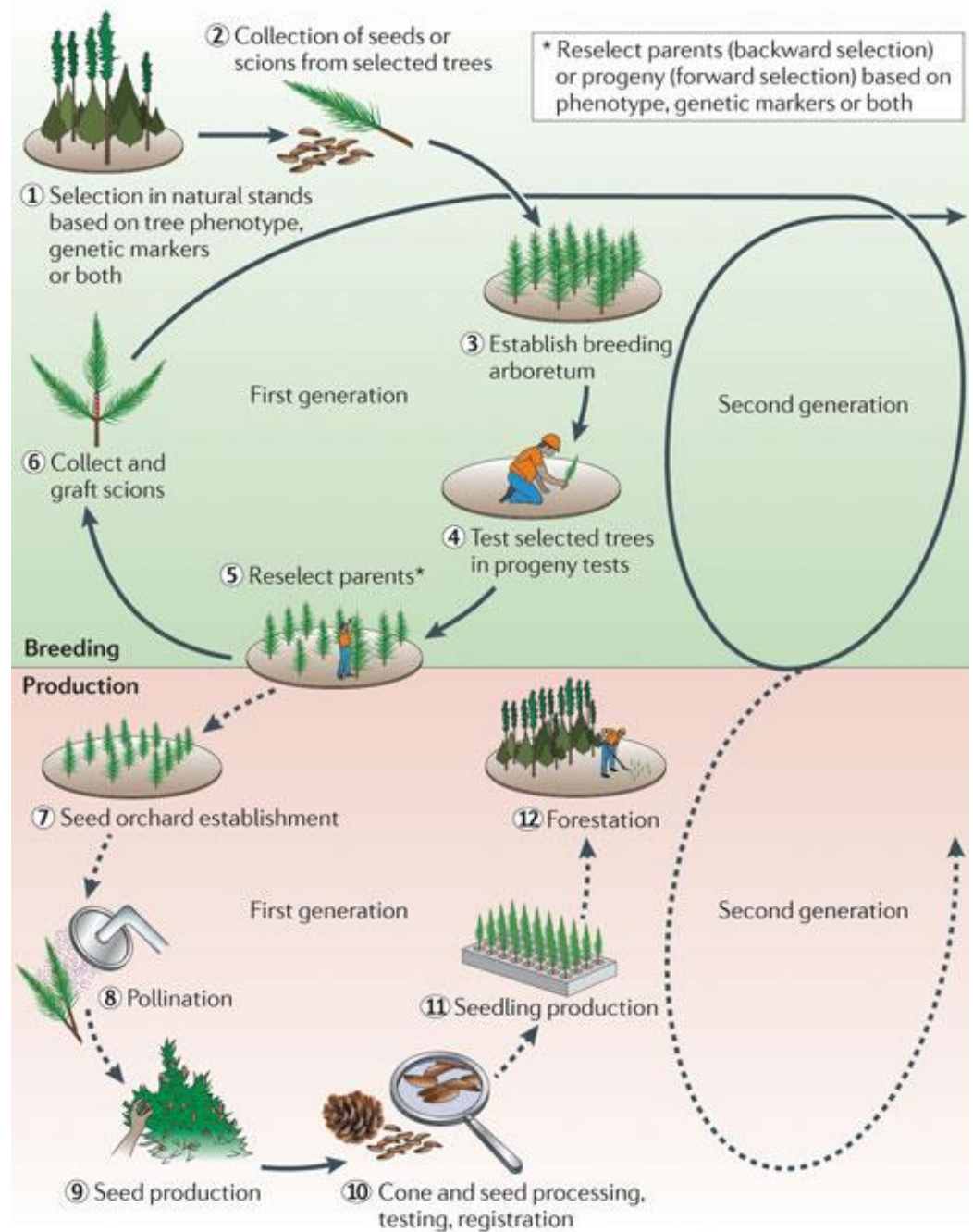
1. TI has increased productivity very substantially
2. Breeding for forest health is challenging but knowledge in this area is progressing rapidly
3. Genomics offers powerful tools to predict the outcomes of tree breeding
4. The tools of genomics hold much promise to accelerate outputs and address sustainability challenges
5. Next generation breeding is just around the corner for conifers like Sitka spruce

Questions?

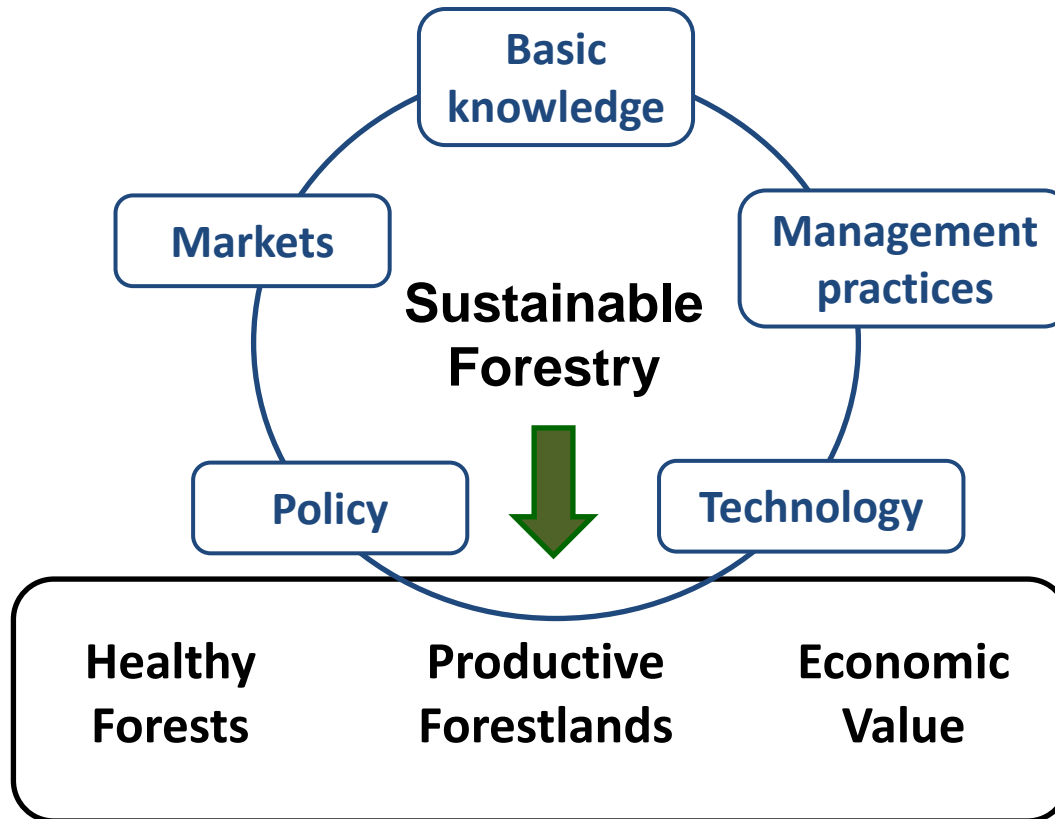
Deploying Forward Genomic Selection with Somatic Embryogenesis



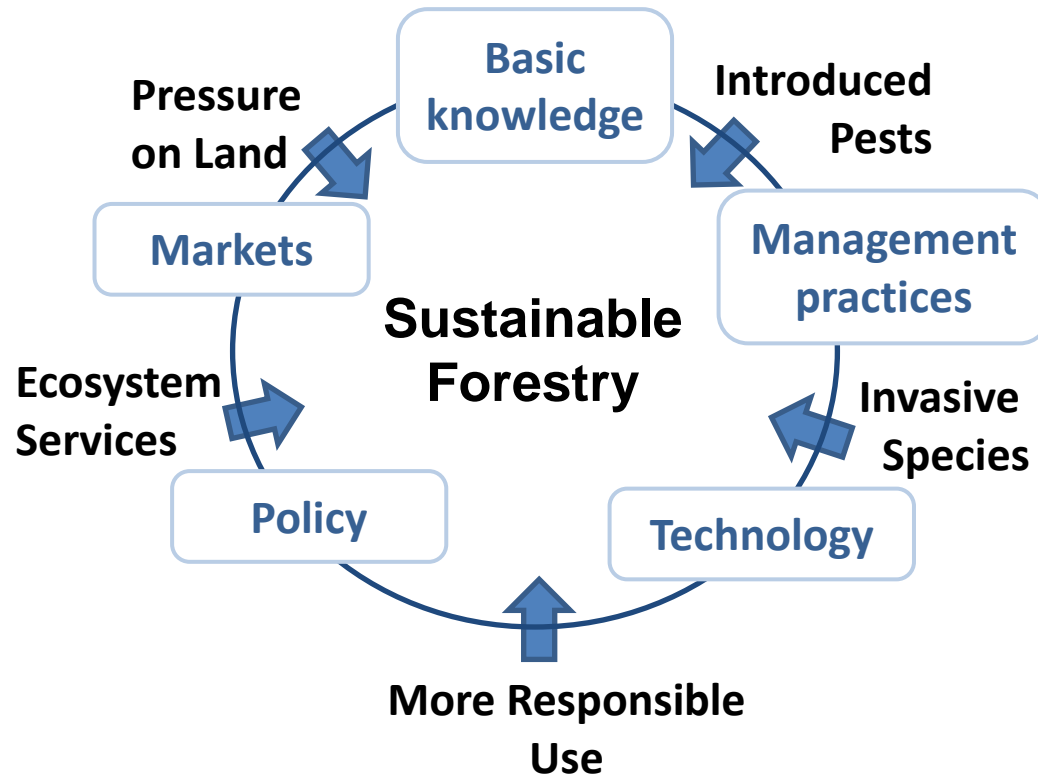
General scheme of tree improvement activities leading to forestation

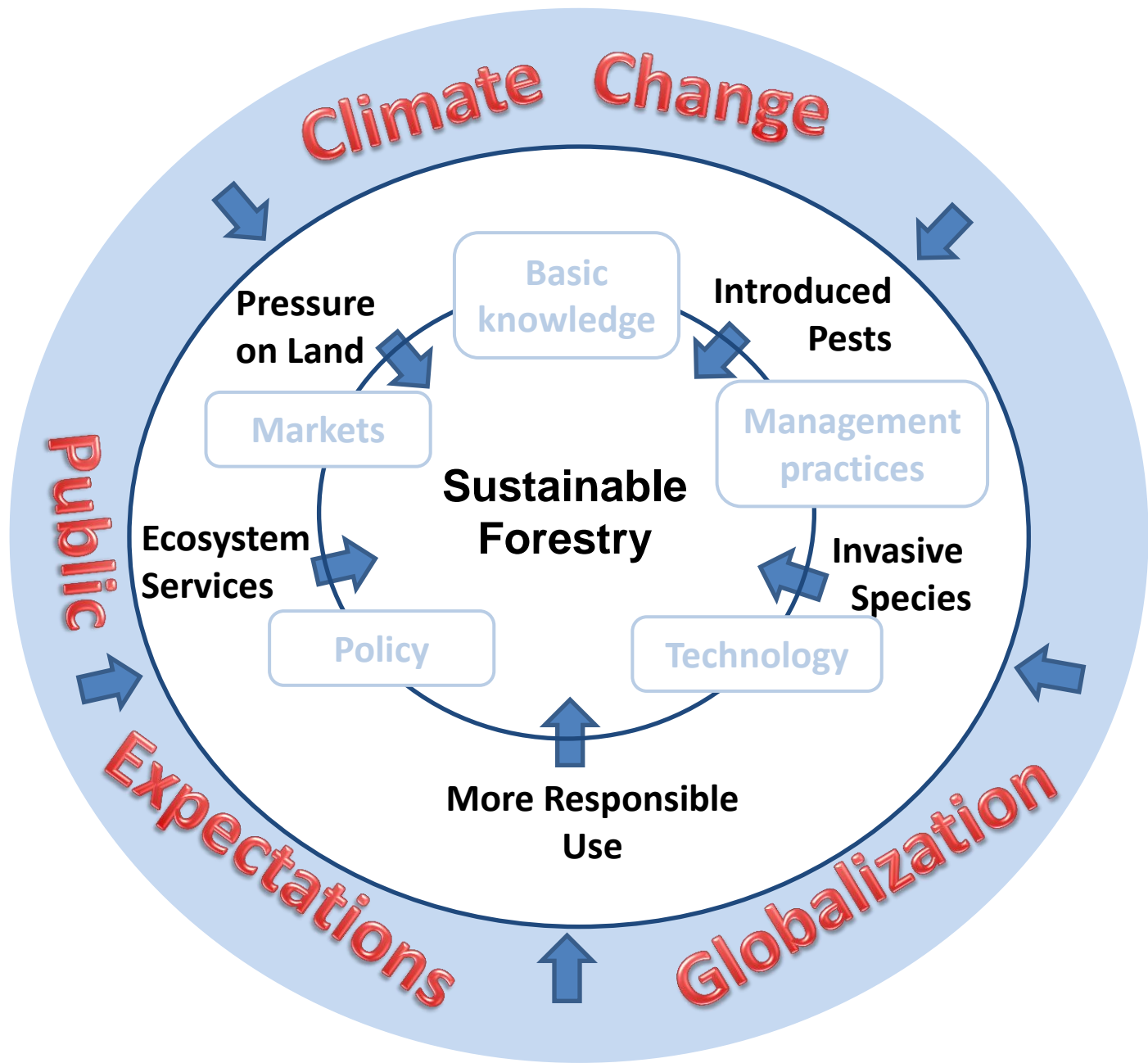


Sustainable Forestry: Goals and Means



21st Century Forestry: New Challenges





Pine



Oak



Arabidopsis



Life Habits:	Long-lived Large	Short-lived Small
Mating System:	Outbred	Inbred
Genetics:	Heterozygous*	Homozygous
Genome:	Large size Slow evolving	Small size Fast evolving
Ecological role:	Keystone or Founder species	???

* Nearly all trees are diploid. Heterozygous: two different variants (alleles) of a given gene.