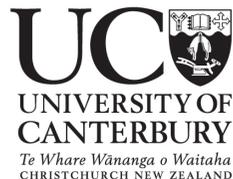


Small (and quick) is beautiful: understanding and exploiting genetic variation of wood quality in corewood

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Understatement: we have a wood quality problem in New Zealand.

Almost 90% of the planted area is *Pinus radiata*, with ~50% of the volume with low stiffness and poor dimensional stability.

Moving poor quality to decent quality is more valuable than decent quality to good quality.

We can use genetics/breeding to improve wood quality, but there are a few requirements...

To use genetics/breeding to improve wood quality, we need a few things:

1. Economic importance

Number of
samples

2. Variability

10s

3. Genetic control

100s

4. Relationship with other traits

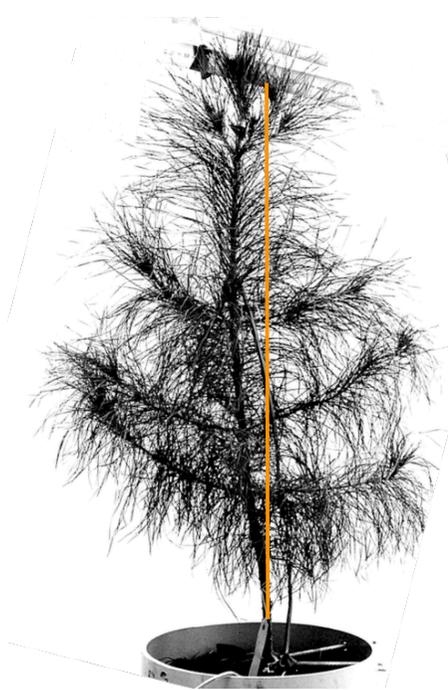
1000s

In summary, we need the ability to assess wood traits as **cheaply** and **quickly** as possible

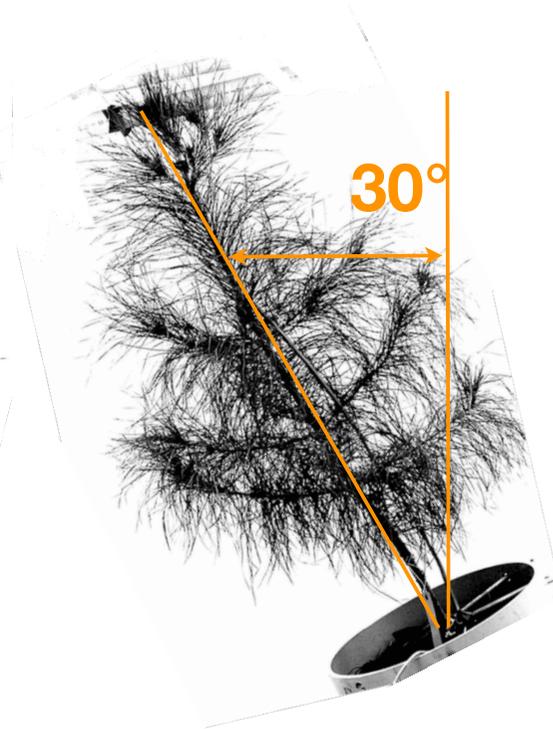
Once upon a time (2007)

4 clones:
A, F, K & W

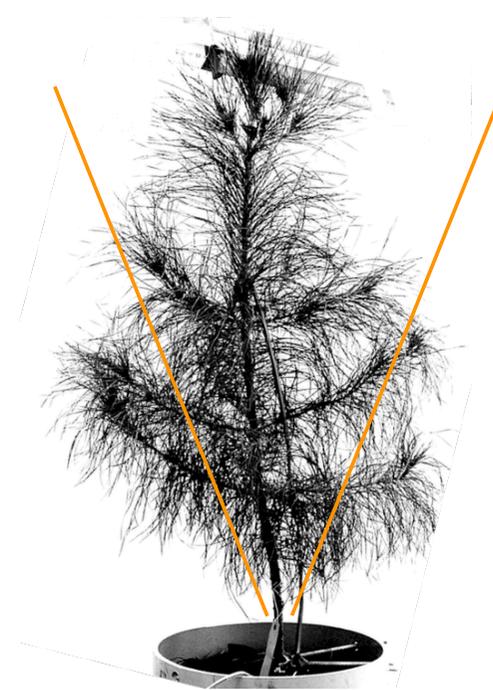
3 positions



Standing

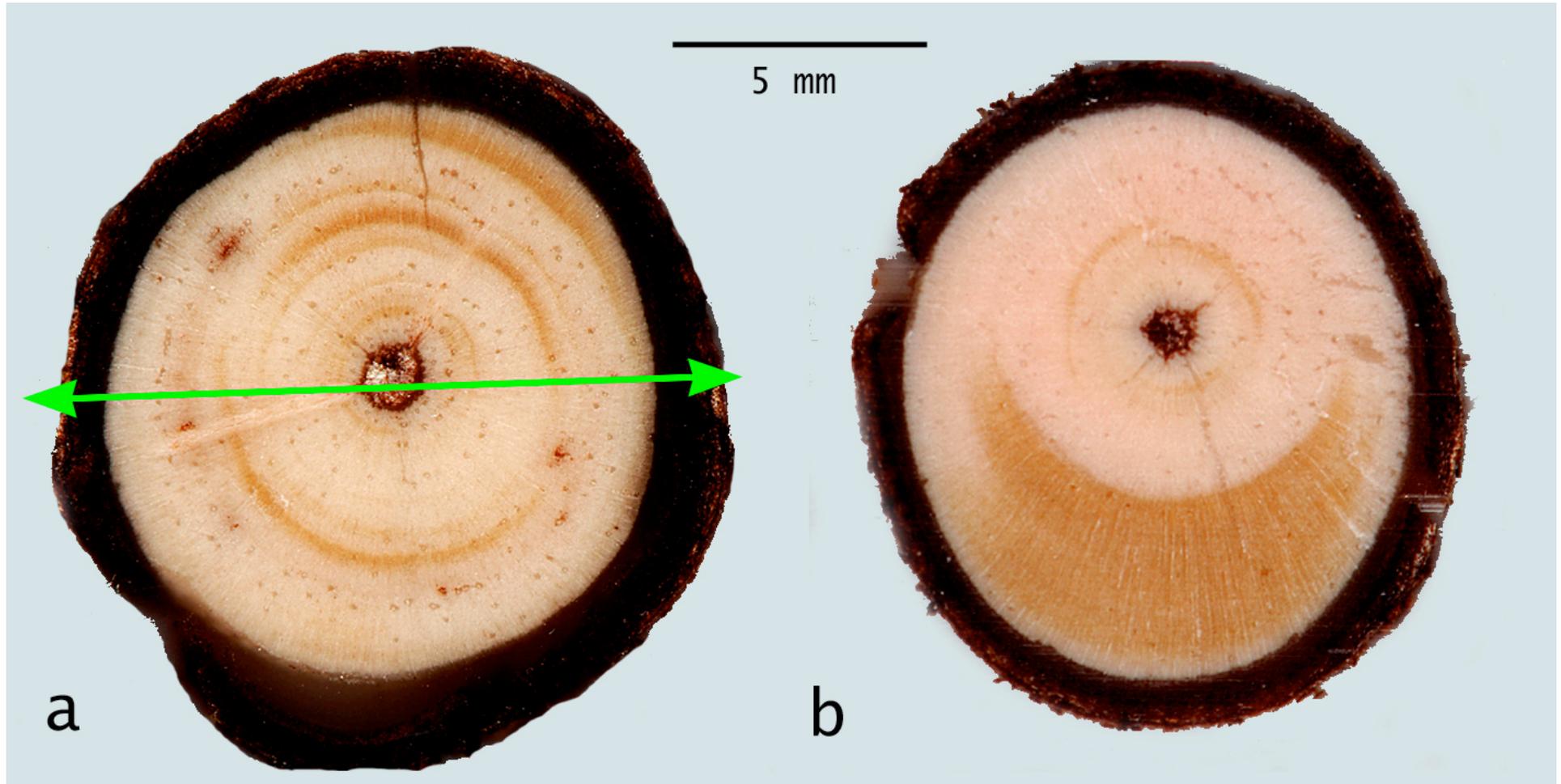


Leaning



Rocking

Leaning to avoid intermixing of reaction and normal wood



a

b

Rocking/standing

Leaning

Amberley trial (2007-2010)

49 families, 48 trees each

- 
- Trees were variable, both in size and in the severity of the lean.
 - Winter water-logging resulted in mortality and variable growth.
 - Between-tree variability was greater than we would have liked.

Harewood trial (2009-2011)

20 clones, 35 trees each

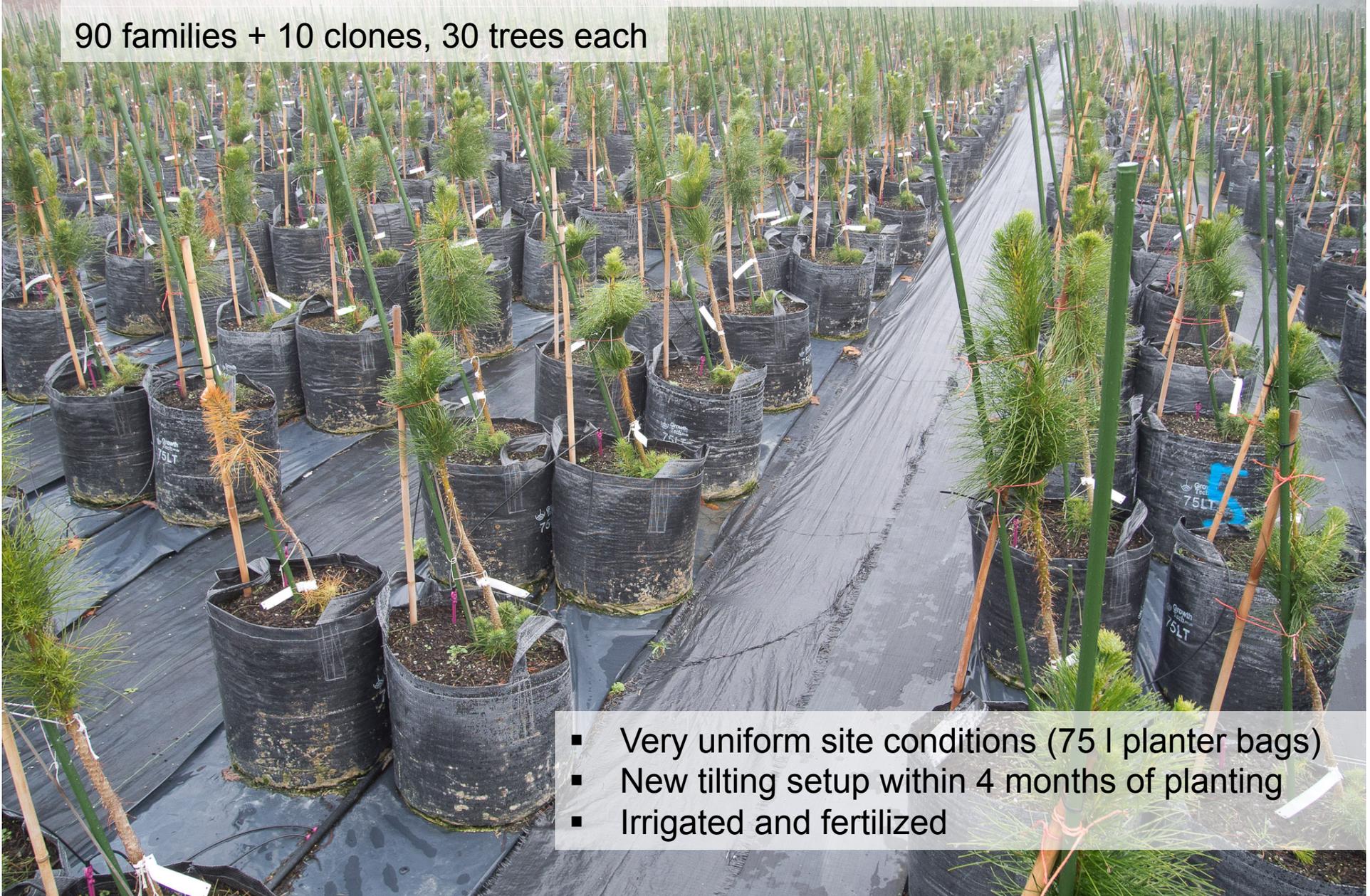
- Very uniform site conditions (100 l planter bags)
- Tilted the trees within 4 months of planting
- Irrigated and fertilized



Harewood trial II (2011-2013)

90 families + 10 clones, 30 trees each

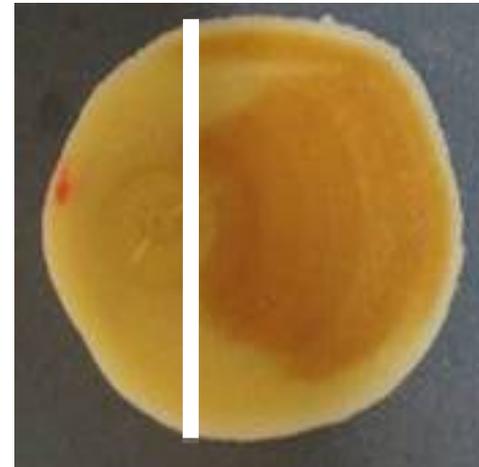
- Very uniform site conditions (75 l planter bags)
- New tilting setup within 4 months of planting
- Irrigated and fertilized



How can we process thousands
of samples?
(can't afford > 5 minutes per sample)

Miniature sawmill with linear bearings to cut 50-100 mm diameter logs

Separating normal / compression wood



WoodSpec: fast, reliable, repeatable measurements of acoustic velocity

Using a piezo-source there is no significant mass loading, thus no effect on resonance frequency.



Resonance occurs at higher frequencies in small samples, output is captured by microphone and processed.



Longitudinal shrinkage

A simple jig measures the longitudinal dimension.



Two map pins inserted in line on the opposite ends of each specimen. The pin heads provide reference points for length measurement.



We measure the **change** in length

Very fast and highly repeatable



Let's use this in a couple of examples

Amberley Seed Orchard

Screening for wood quality the parents of the largest orchard in the Southern Hemisphere



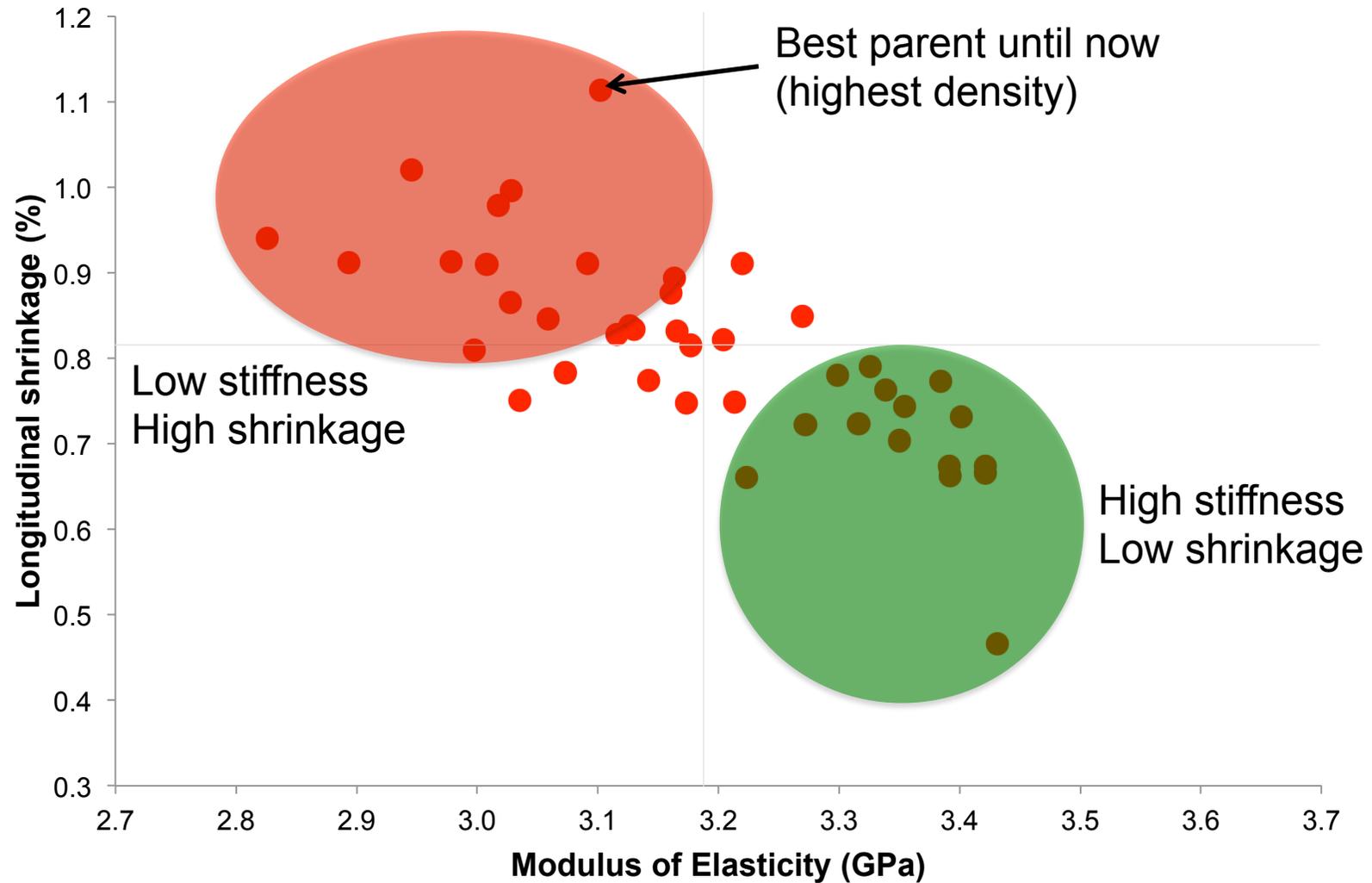
Amberley trial (2007-2010)

49 families, 48 trees each

- Variability (CV%):
 - MoE = 11.96
 - SHR = 37.24%
 - DEN = 6.19 %
- Degree of genetic control:
 - $h^2_{\text{MoE}} = 0.26$
 - $h^2_{\text{SHR}} = 0.24$
 - $h^2_{\text{DEN}} = 0.40$
- Correlations:

	MoE	SHR
DEN	0.69	-0.18
MoE		-0.72

How do we implement this?

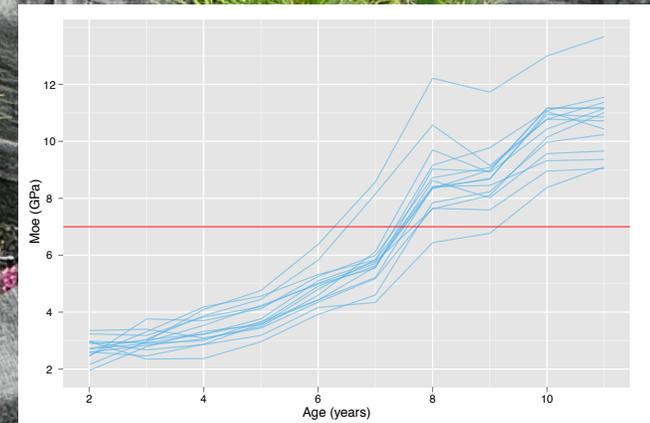


Genetic analysis of Amberley trial, to be published (Sharma & Apiolaza)

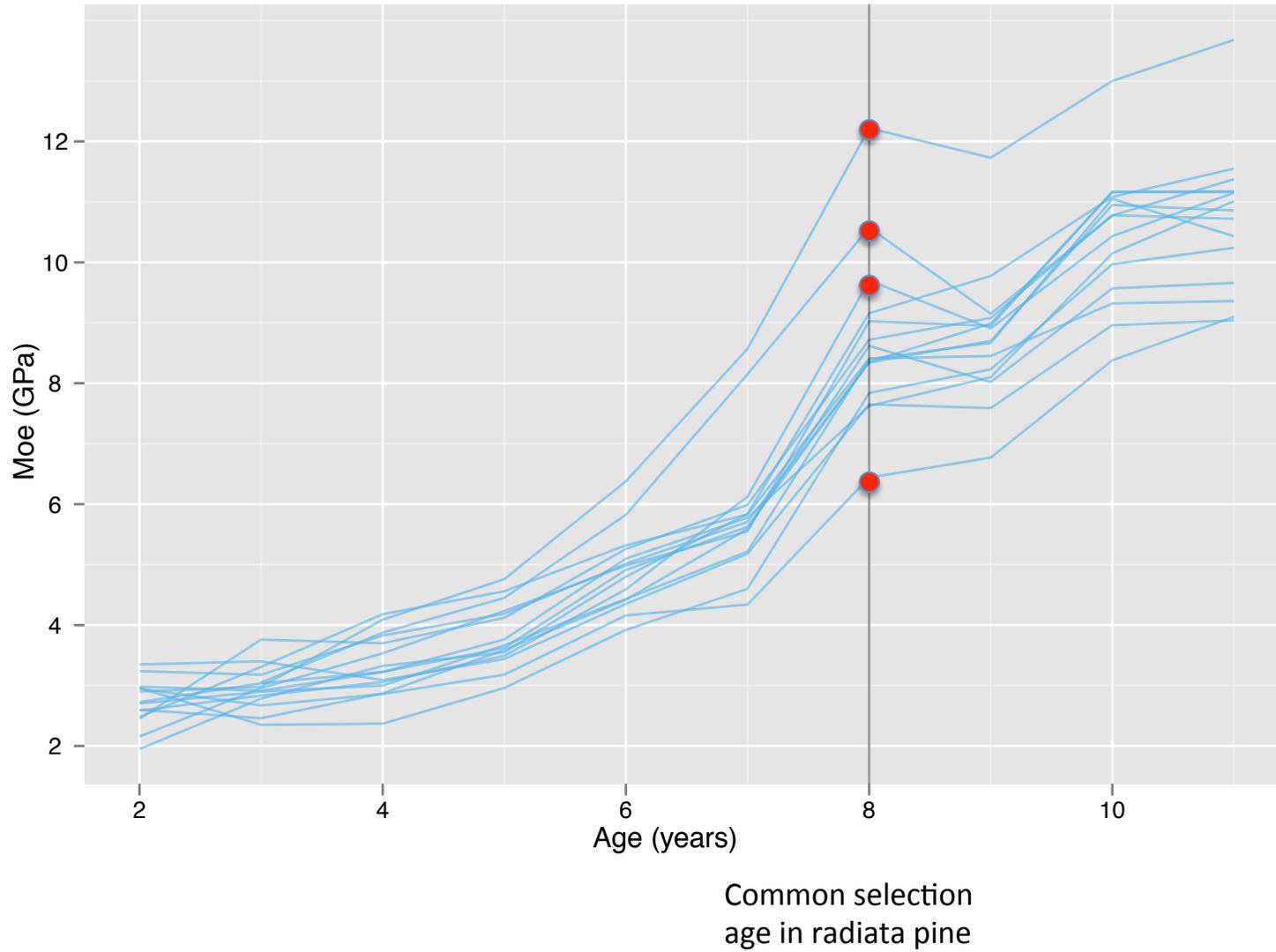
Eventually we want to see how
early screening matches older
trees

Harewood trial (2009-2011)

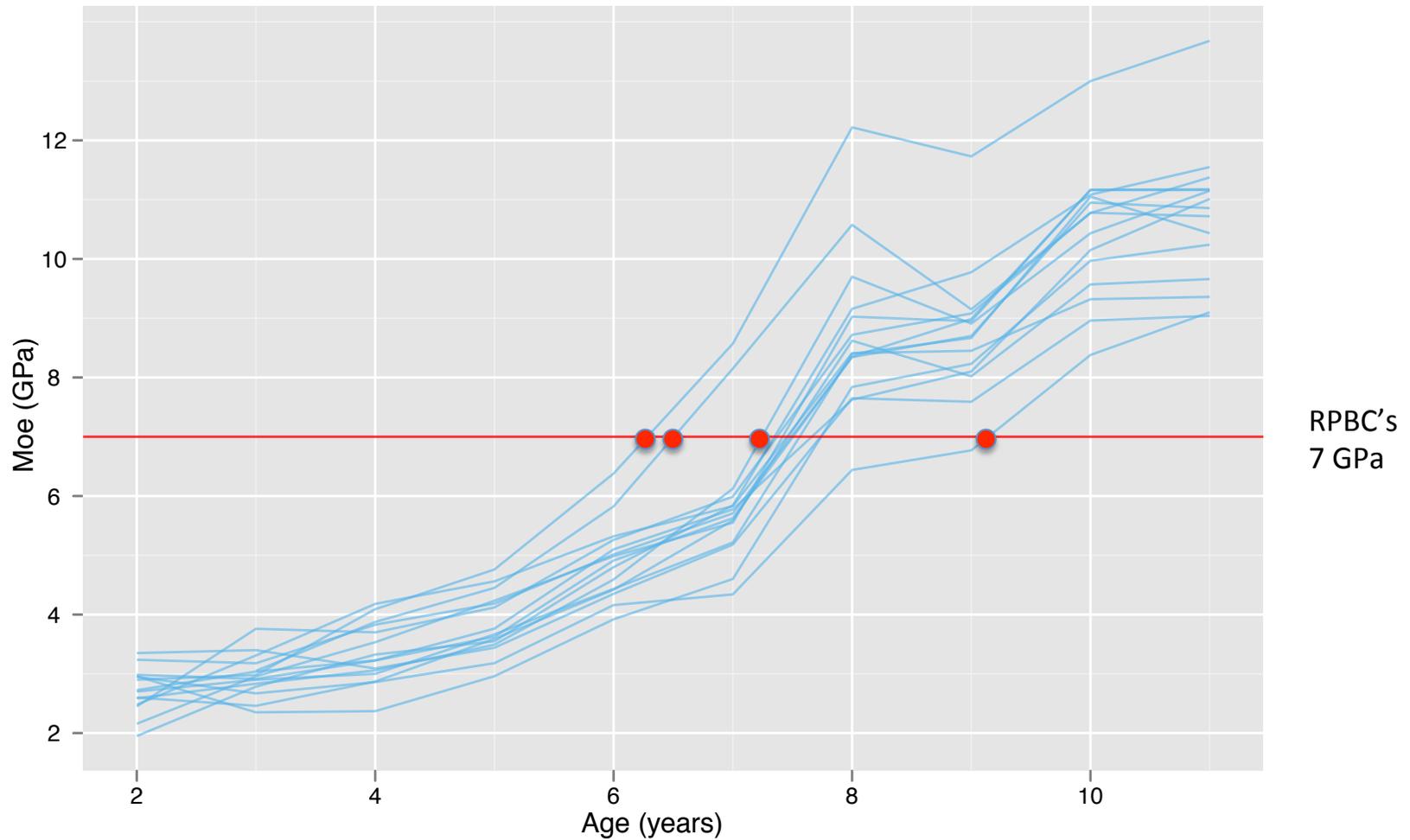
20 clones, 35 trees each



Reframing the selection process: from maximum stiffness to meeting early thresholds



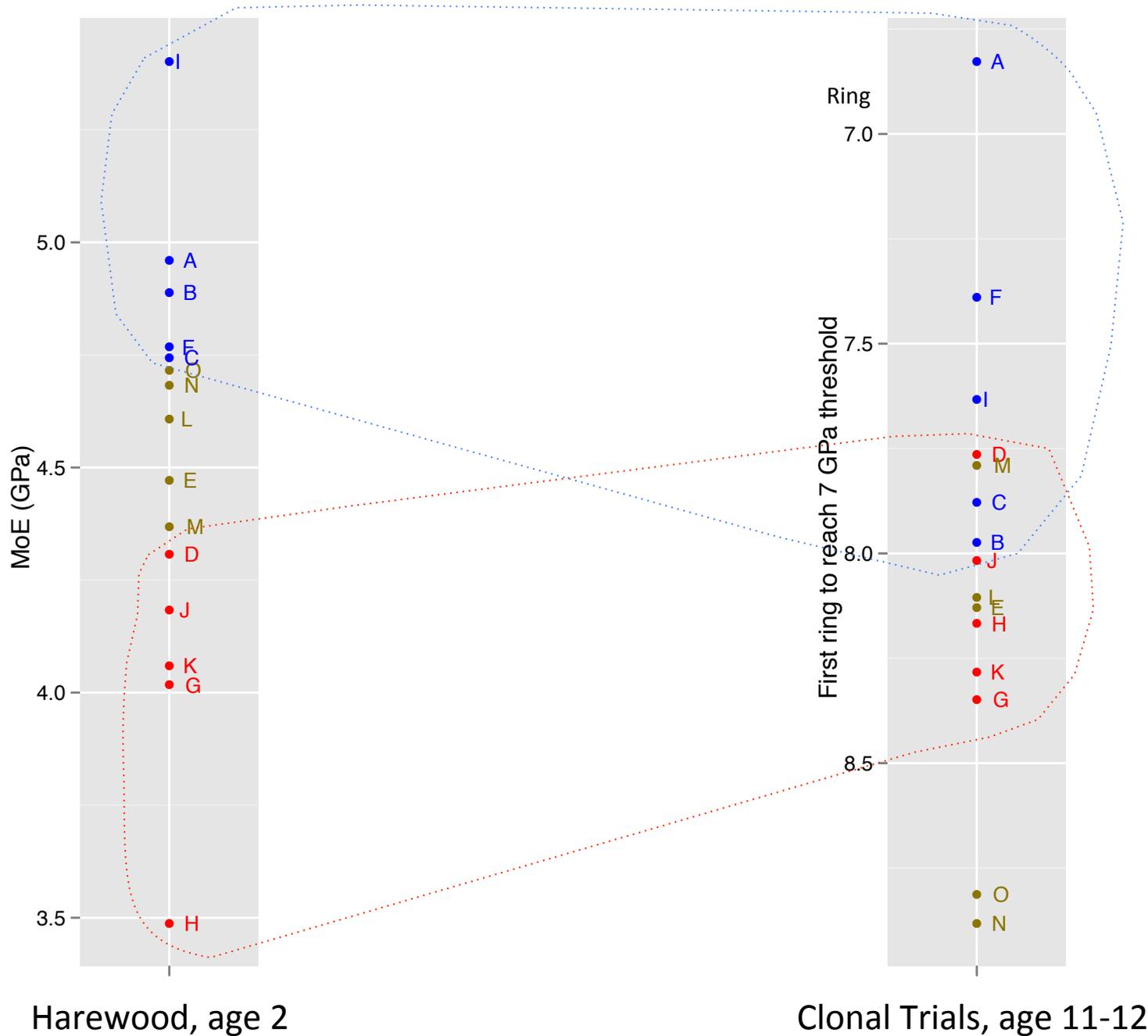
Reframing the selection process: from maximum stiffness to meeting early thresholds

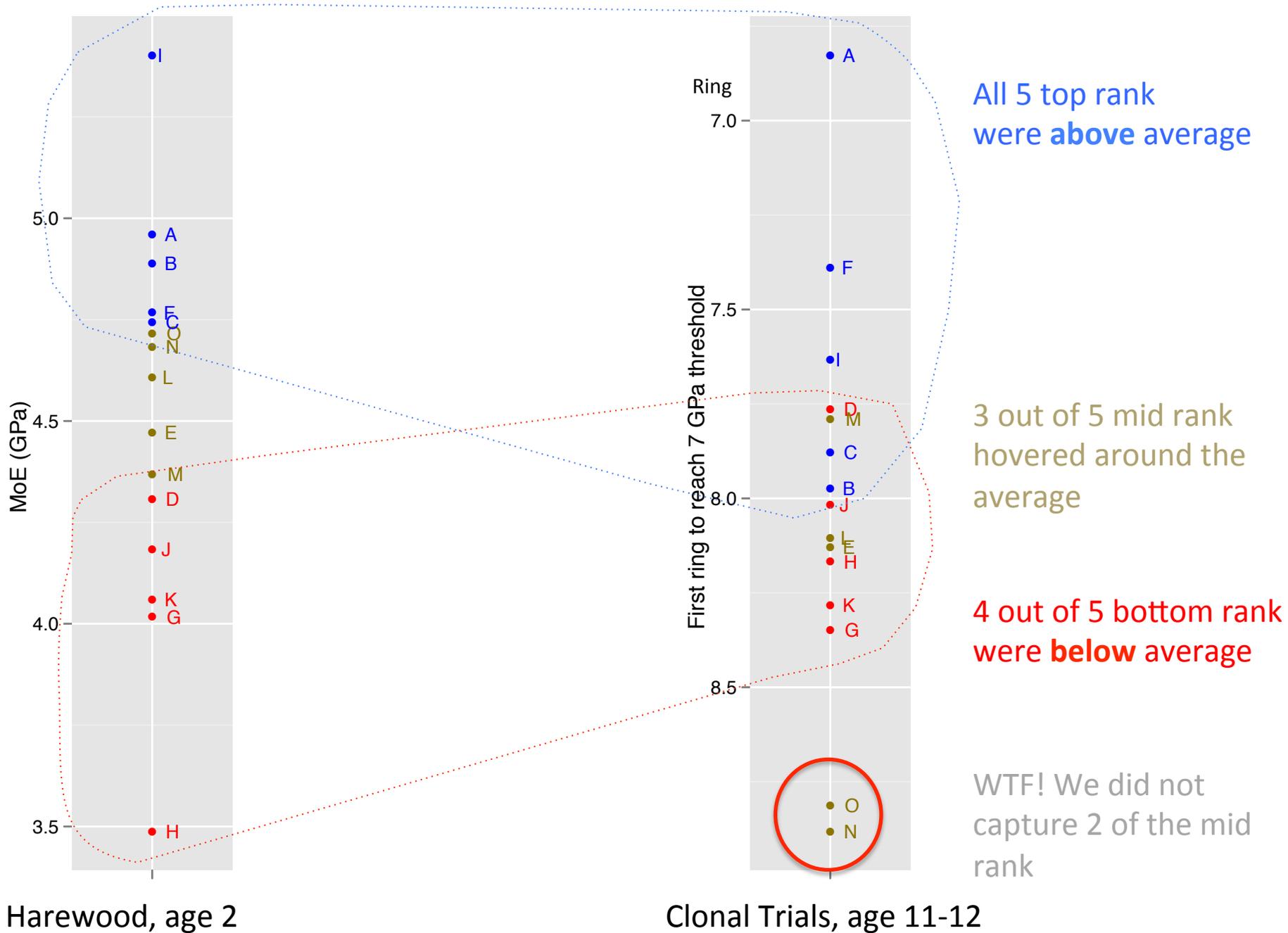


5 top rank

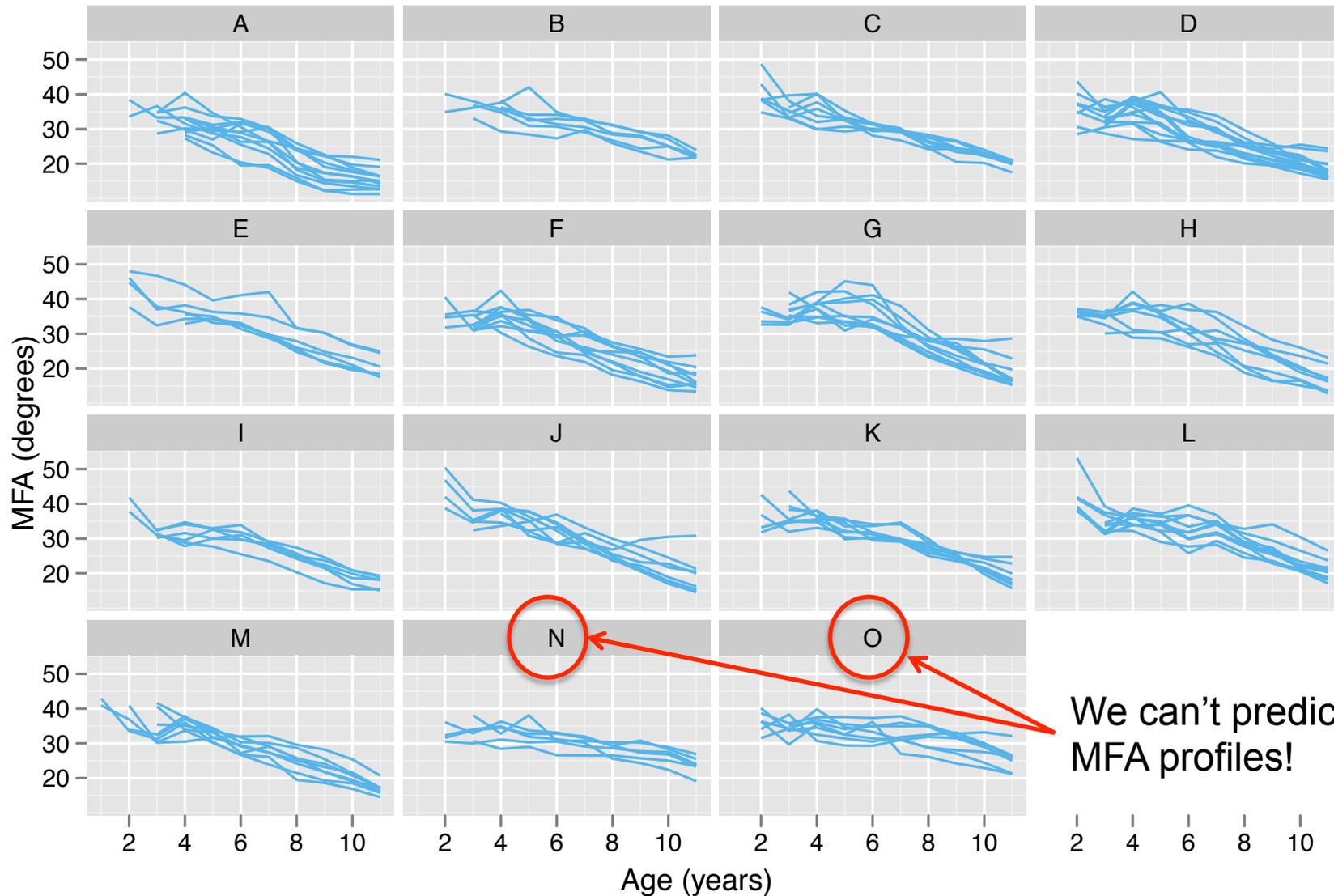
5 mid rank

5 bottom rank





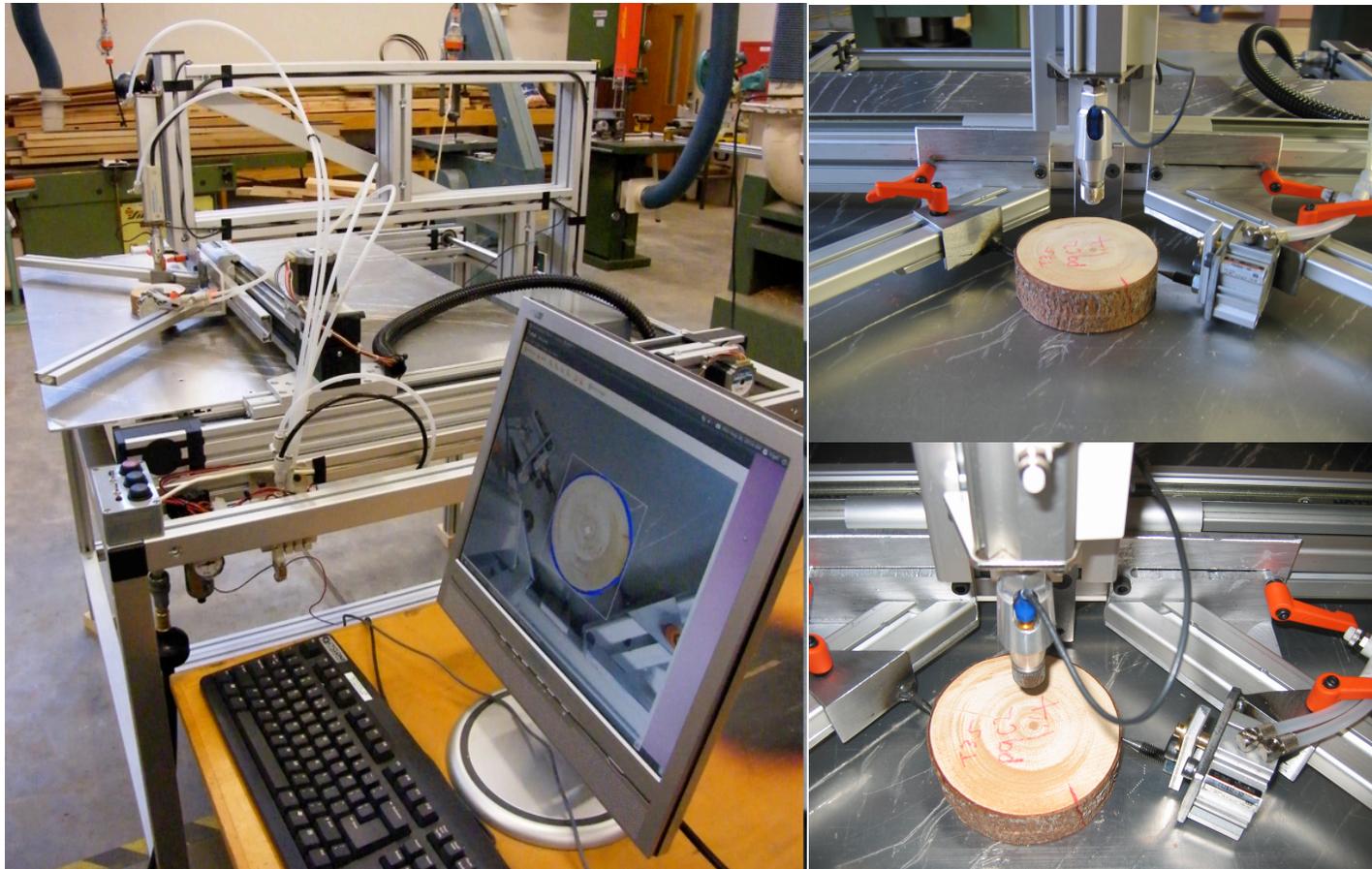
So what is the problem?



More details on this validation exercise in Paul McLean's talk!

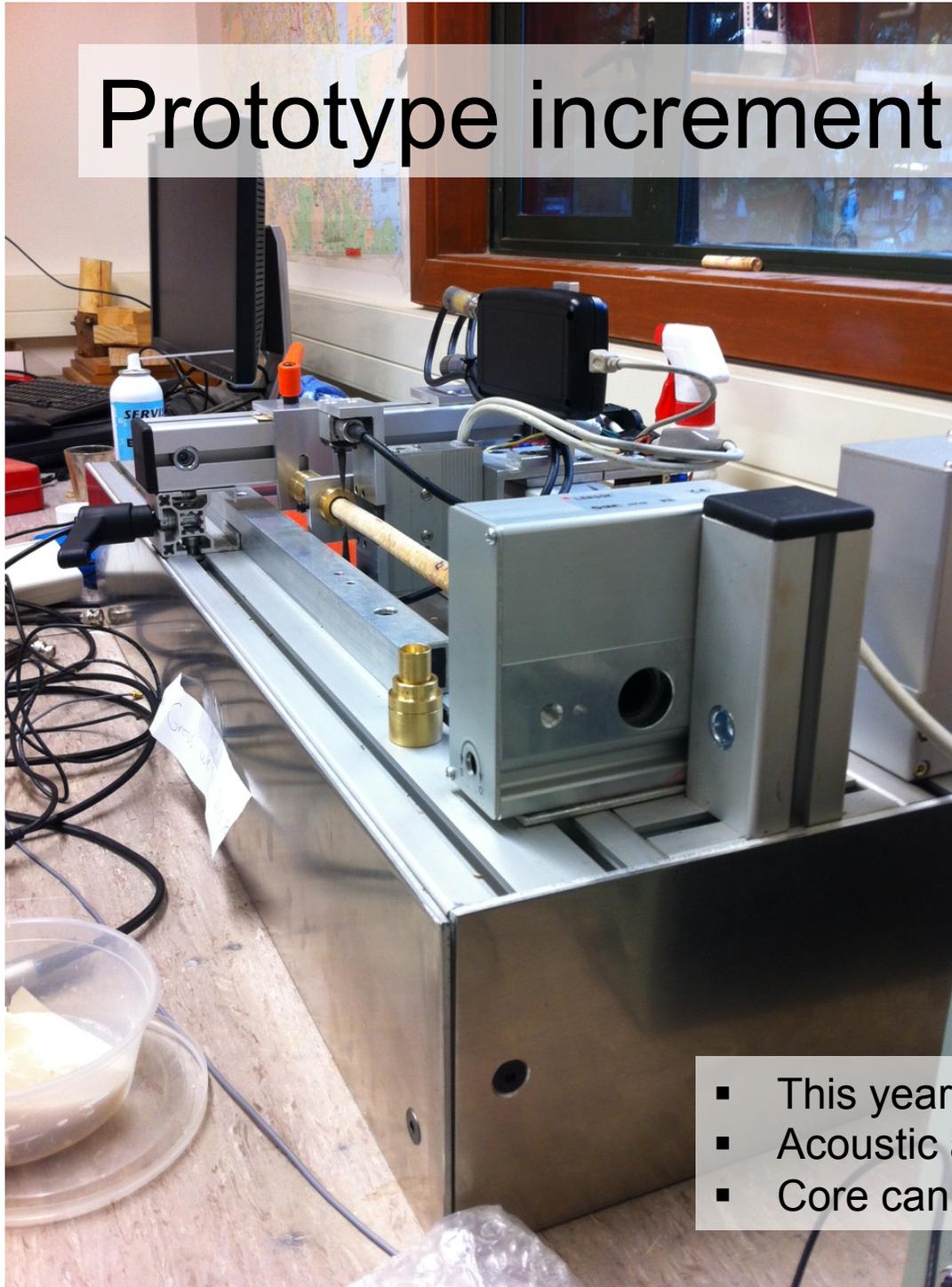
Eventually we also want to describe **many** older/bigger trees (new tool development)

Ultrasonic automated x-y disc scanner



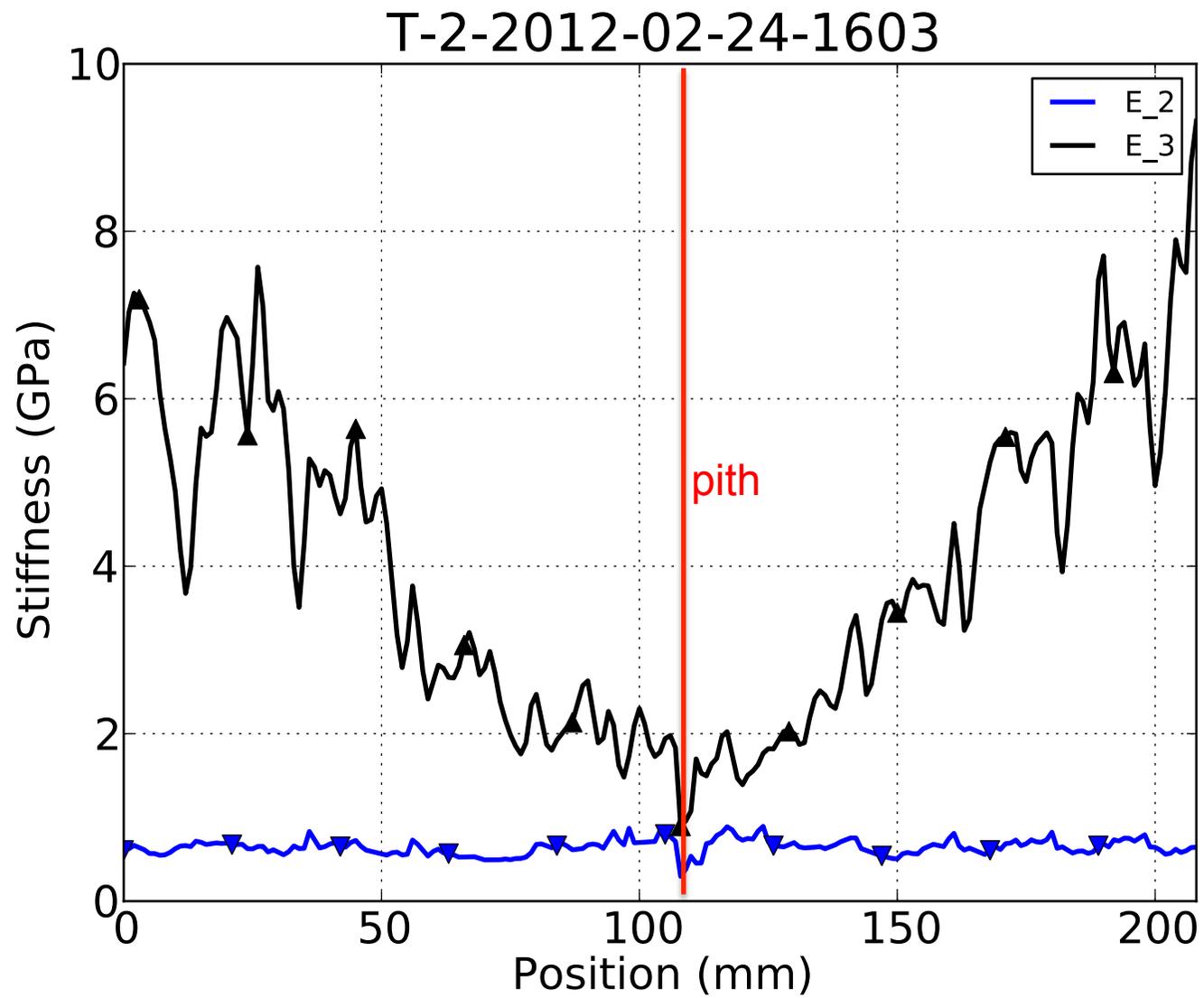
As soon as we showed our new machine to foresters and breeders they said 'but we don't want to use disks, **we want to use cores!**'

Prototype increment core scanner

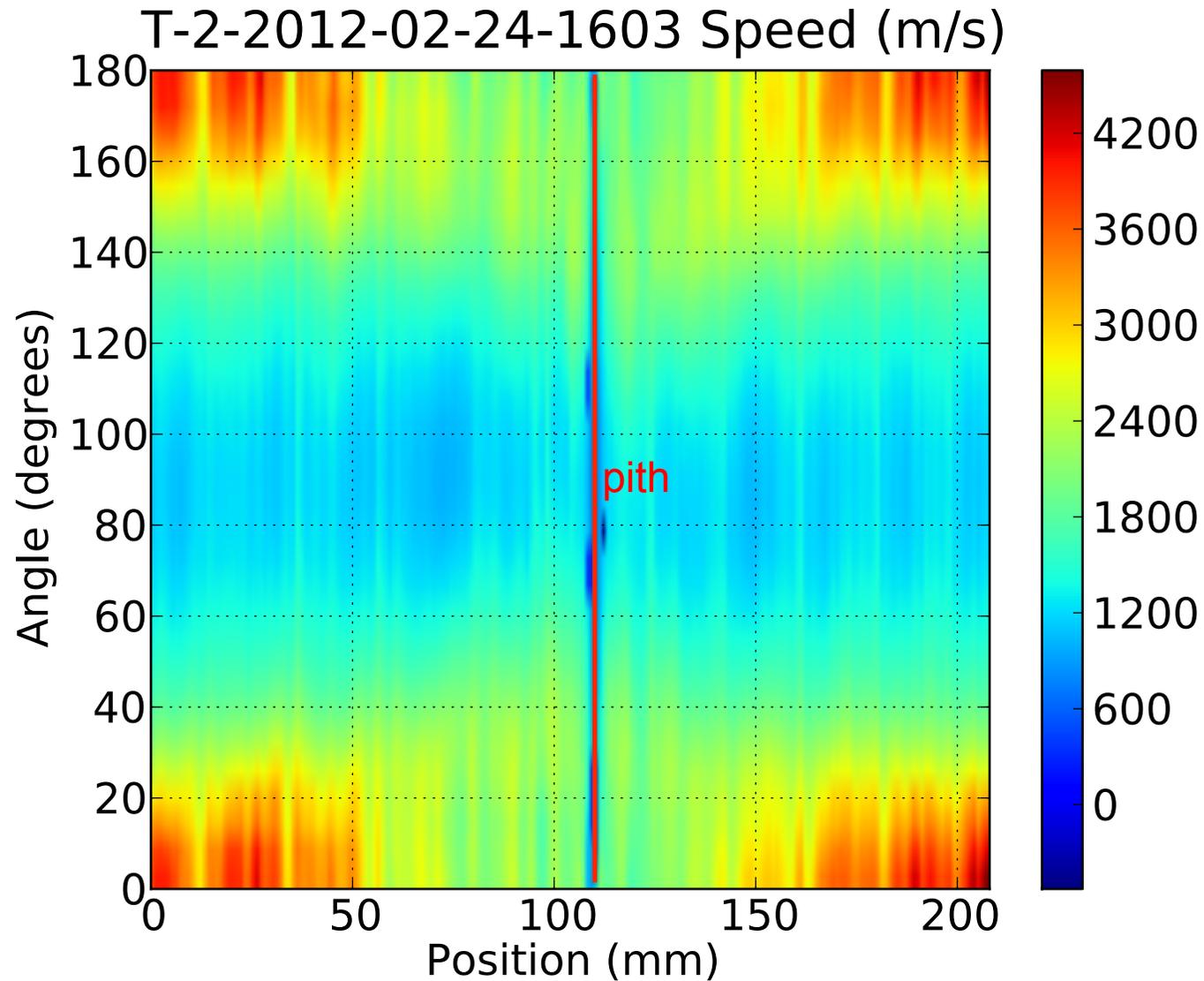


- This year's table-top prototype.
- Acoustic assessments along the core.
- Core can be rotated every 6 degrees.

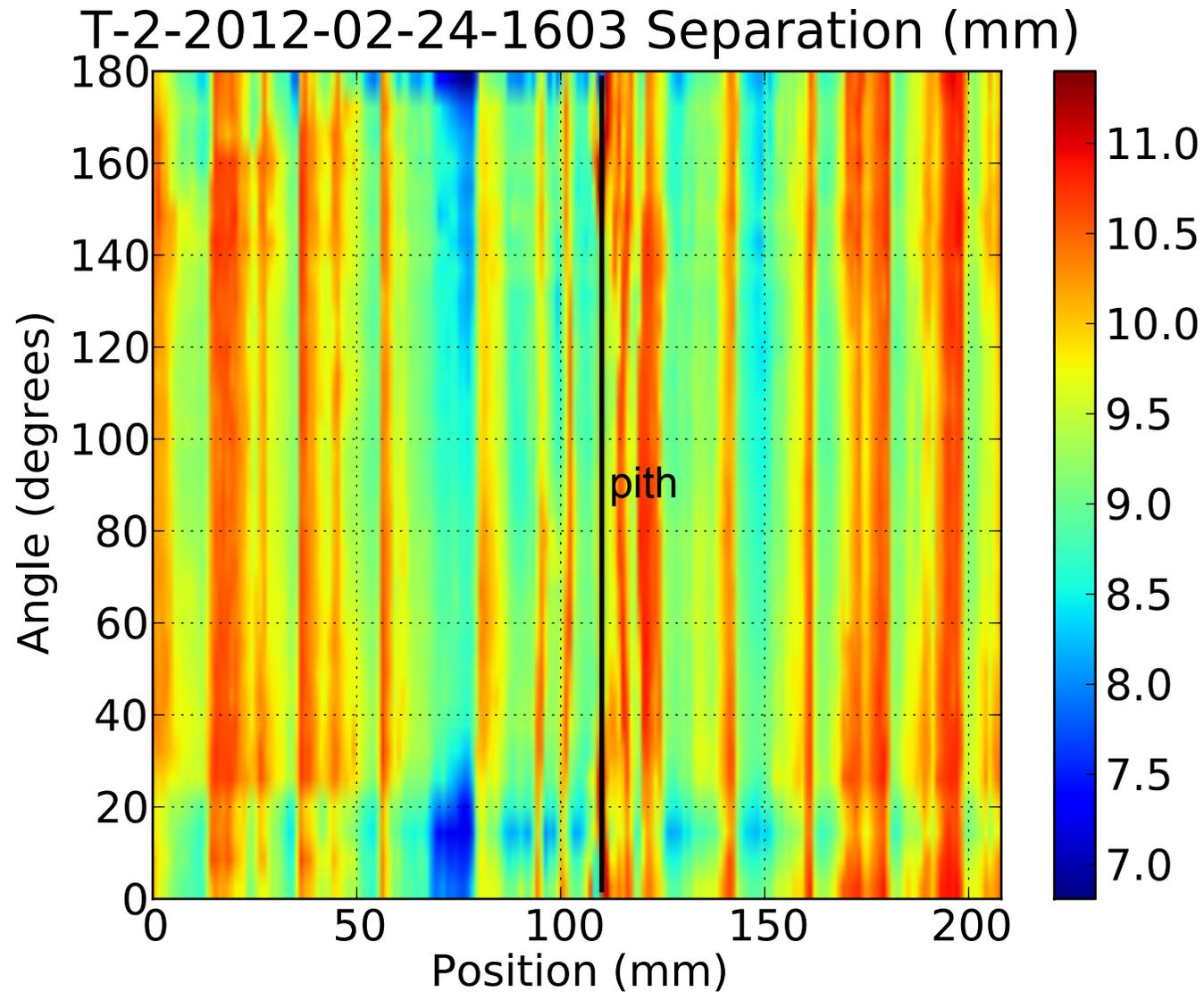
Acoustic velocity along the core



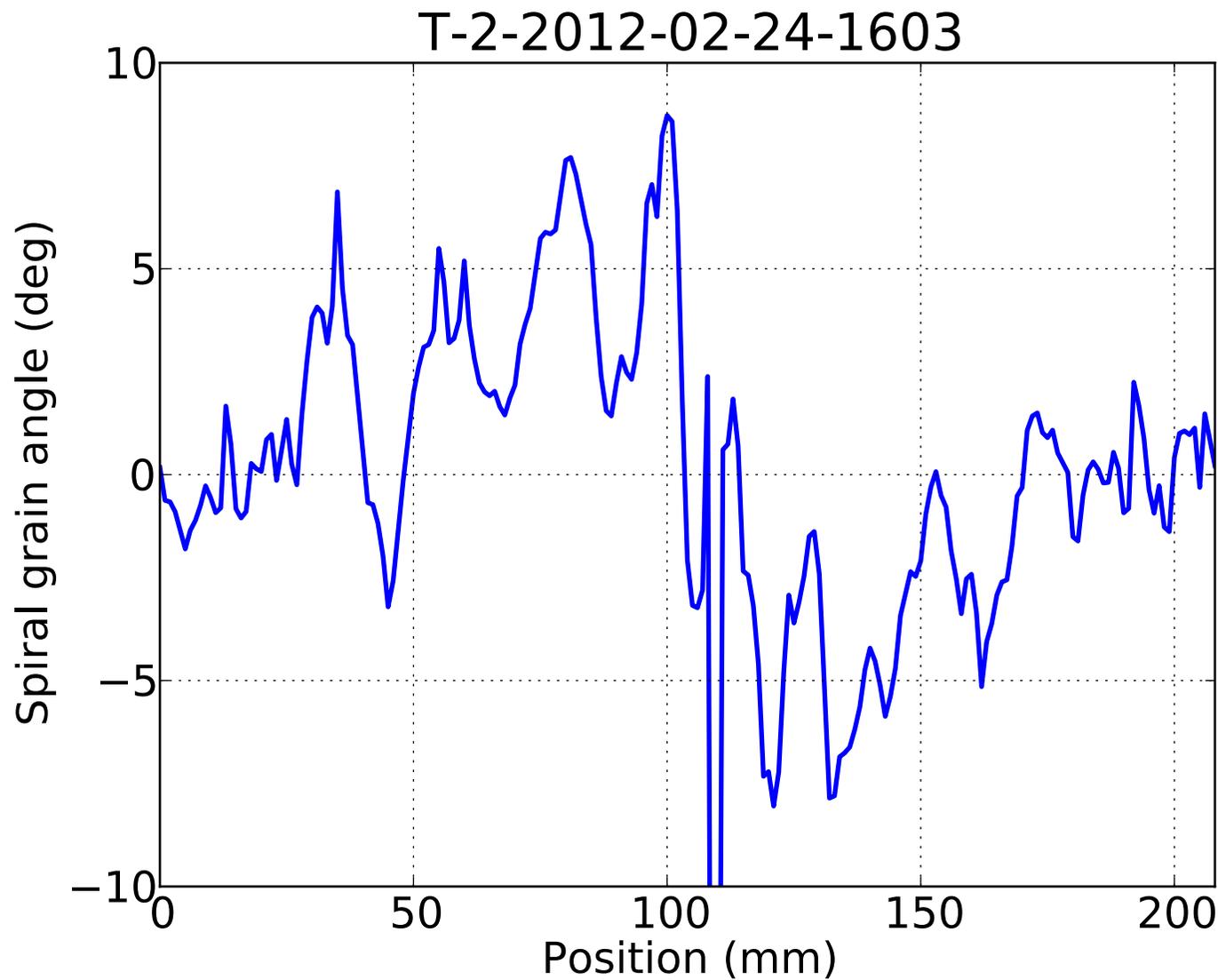
Acoustic velocity along & around core



Penetration along & around the core



Spiral grain along the core



Processing the signal differences when rotating the core we can estimate spiral grain.

In summary I

There is variability for 2 yo wood quality traits (from 6% for basic density to 37% for longitudinal shrinkage).

This variability is under genetic control (heritabilities between 0.25 & 0.40).

Acoustics velocity is a better predictor of quality than density at this early age (gen. correlation -0.7).

Early predictions are **useful enough** for screening purposes (correlation 0.6).

In summary II

Intervention points: **best bet** is deployment populations (seed orchards, clonal programs).

New Harewood trial will expand the verification process to 2 sister trials that will run for at least ten years.

Tool development has expanded to include characterization of older trees.

There is another half of the project (not covered in this presentation) looking at the role of wood chemistry.

Acknowledgements: Shakti **Chauhan** (screening techniques), Clemens **Altaner** (validation samples for core scanner), Paul **McLean** (validation with older clones), Nigel **Pink** (disc and core scanner), Ryogo **Nakada** and Monika **Sharma** (assessments).