The future is genomic: rapid clone selection for teak productivity and value

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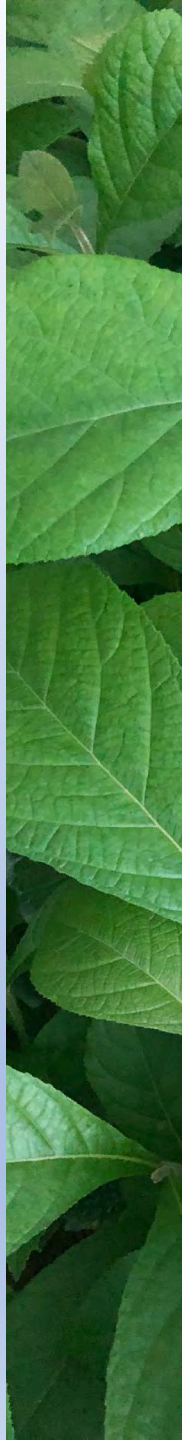
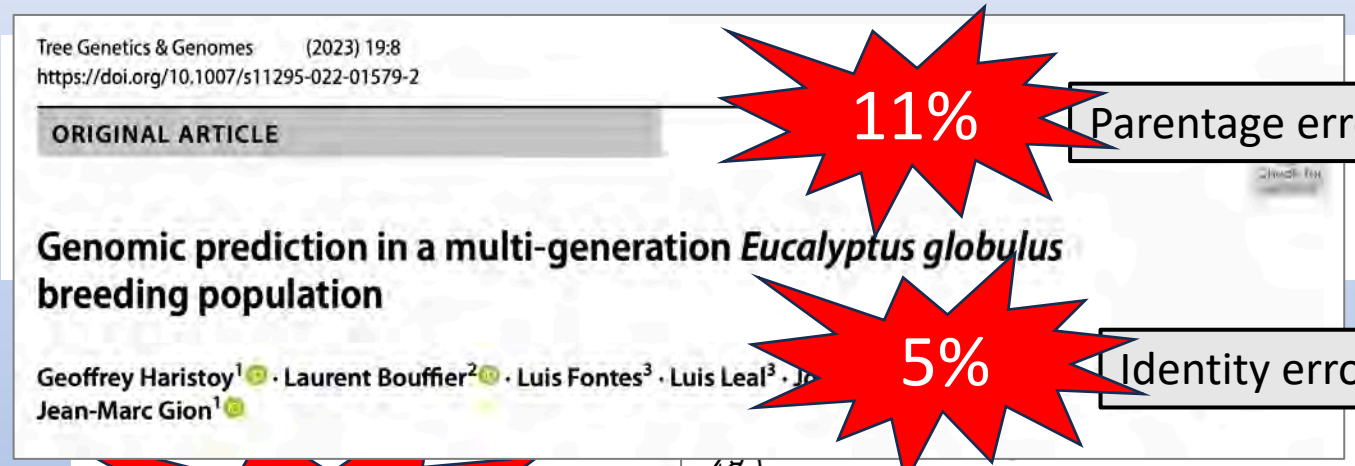
MAIN MESSAGES

1. Genomic tools have improved tree improvement outcomes across species
2. Teak improvement programs could benefit enormously:
   - Correcting pedigree and identity errors
   - Pedigree reconstruction and population merging
   - Improved genetic value accuracy
   - Faster clone selection
3. Our case study demonstrates pedigree reconstruction and genomic prediction for teak clone selection
4. Starting from scratch: what is required to ‘get in the game’?
5. The best way forward is *collaborative*



Benefits of error detection

"To make no mistakes is not in the power of man"
(Plutarch, Greek philosopher)


Tree Genetics & Genomes (2023) 19:8
https://doi.org/10.1007/s11295-022-01579-2

ORIGINAL ARTICLE

Genomic prediction in a multi-generation *Eucalyptus globulus* breeding population

Geoffrey Haristoy[1] · Laurent Bouffier[2] · Luis Fontes[3] · Luis Leal[3] · J
Jean-Marc Gion[1]

11%

Parentage errors

5%

Identity errors

30%

Douglas-fir

147

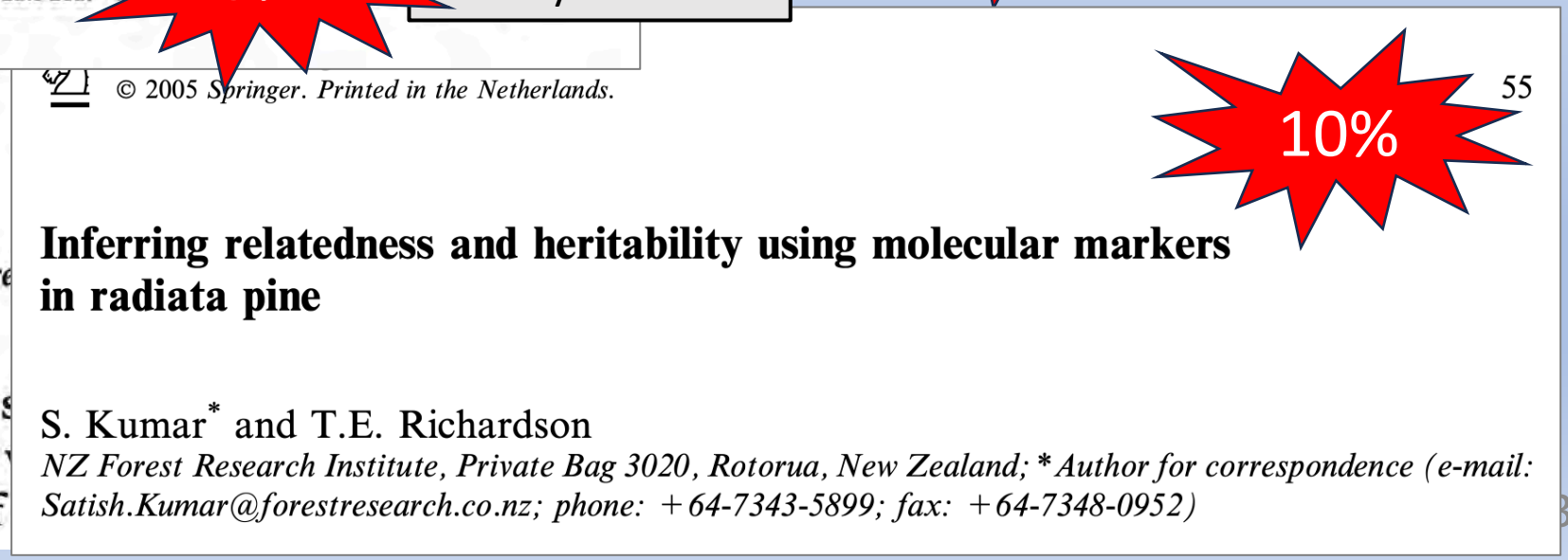
33%

Loblolly pine

6% - 38%

Paweł Przybylski, Jan Kowalczyk, Ire

Identyfing alien genotypes
consequences for genetic
in clonal seed orchards of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55

10%

Inferring relatedness and heritability using molecular markers in radiata pine

S. Kumar* and T.E. Richardson
*NZ Forest Research Institute, Private Bag 3020, Rotorua, New Zealand; *Author for correspondence (e-mail: Satish.Kumar@forestresearch.co.nz; phone: +64-7343-5899; fax: +64-7348-0952)*

Benefits of pedigree reconstruction

RESEARCH ARTICLE

Exploration of genetic architecture through sib-ship reconstruction in advanced breeding population of *Eucalyptus nitens*

Jaroslav Klápště*, Mari Suontama, Emily Telfer, Natalie Graham, Charlie Low, Toby Stovold, Russel McKinley, Heidi Dungey

Scion (New Zealand Forest Research Institute Ltd.), 49 Sala Street, 3046 Rotorua, New Zealand

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PLOS ONE | https://doi.org/10.1371/journal.pone.0185137 September 22, 2017

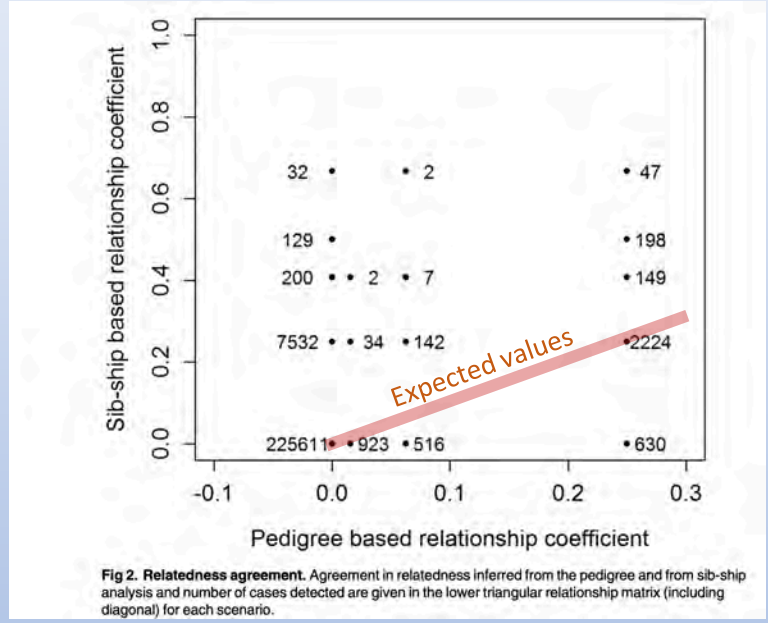


Fig 2. **Relatedness agreement.** Agreement in relatedness inferred from the pedigree and from sib-ship analysis and number of cases detected are given in the lower triangular relationship matrix (including diagonal) for each scenario.

Table 2. Accuracy of breeding values estimated in single trait model, multi-trait model based on documented pedigree and multi-trait model based on information from sib-ship reconstruction.

	Single trait analyses						
Model	**WD**	**GS1**	**GS2**	**ST1**	**ST2**	**DBH**	**TS**
Pedigree	0.67	0.53	0.44	0.55	0.39	0.33	0.65
Sibship—A	0.70	0.61	0.59	0.60	0.48	0.44	0.66
Sibship—AD	0.70	0.61	0.59	0.59	0.46	0.44	0.64

Benefits of faster clone selection

For example, Lebedev et al. 2020 review:

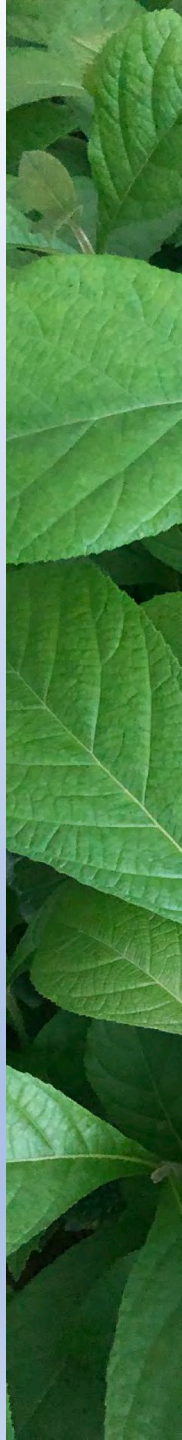
- More than 60 genomic prediction studies with forest trees
- 25 species and 4 hybrid complexes

Review

Genomic Selection for Forest Tree Improvement: Methods, Achievements and Perspectives

Vadim G. Lebedev [1,*], Tatyana N. Lebedeva [2], Aleksey I. Chernodubov [3] and Konstantin A. Shestibratov [1,3]

Forests **2020**, *11*, 1190; doi:10.3390/f11111190



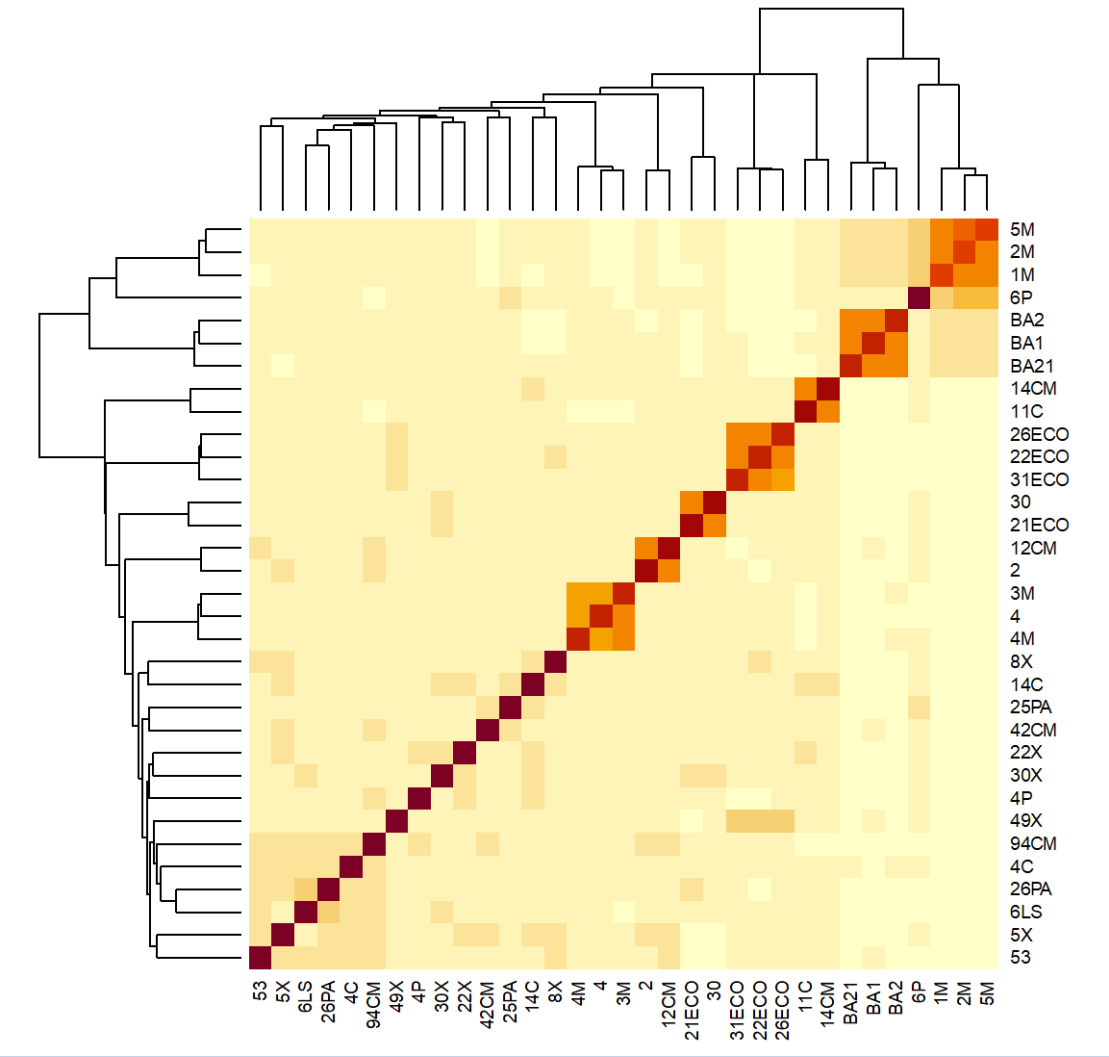
Demonstration study:
genomic prediction for teak clone selection

GENFORES: Company cooperative across 6 Latin American countries

Data and samples were generated from a single-site clone trial in Central Costa Rica:

- Genotypes for 33 clones
  - 10,816 SNP markers
- Genetic clone values from analysis in SELEGEN for 8 traits in 36 clones
- 26 clones were common to genotyped and phenotyped sets

Relationships discovered!



Seven small full-sib families,

Each containing 2 to 3 clones.

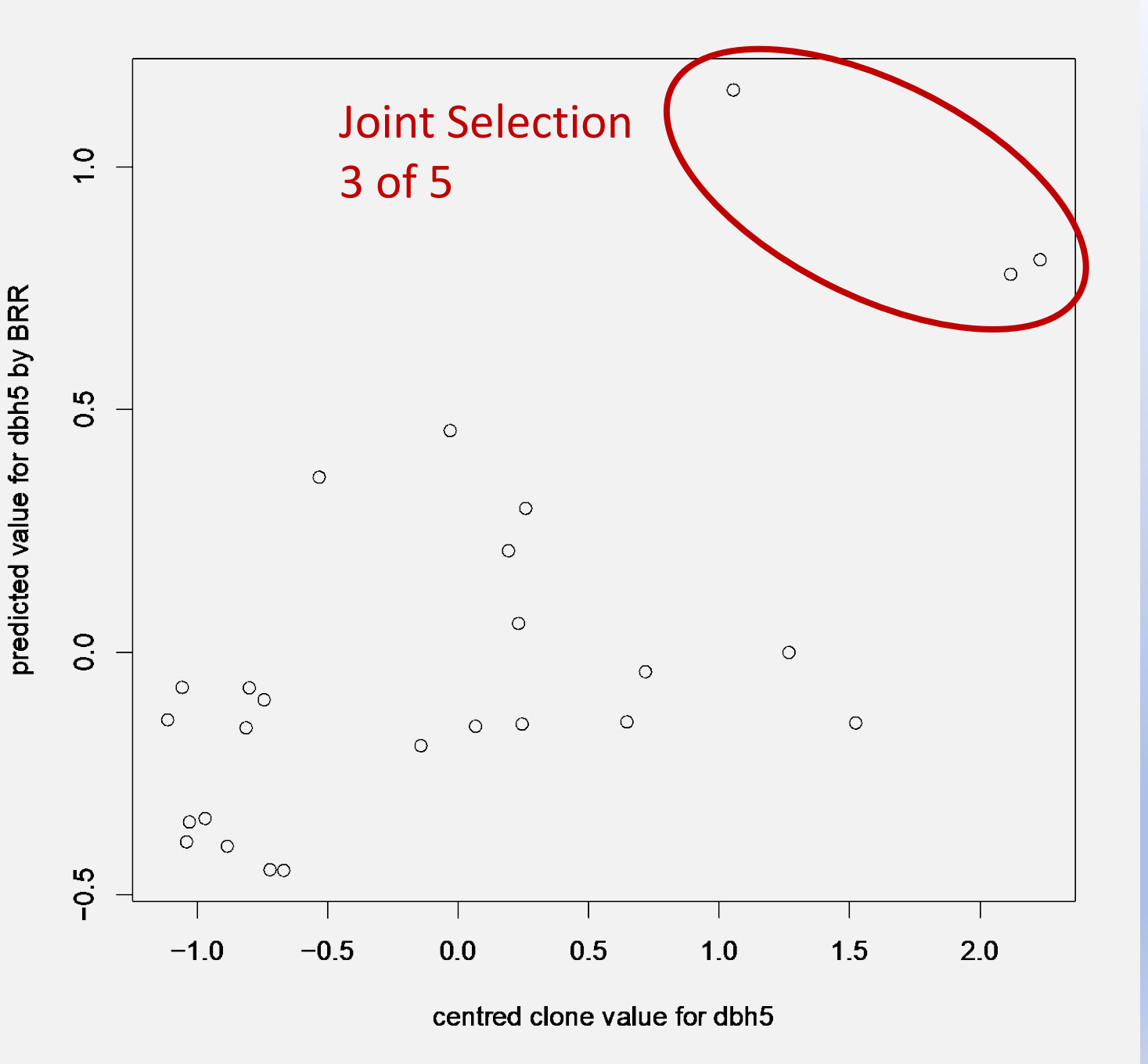
- Clone 6P is half-sib to the full-sib family [5M, 2M, 1M]

Genomic Prediction results

	Predictive Ability					Top 5 of 26
Trait	BayesA	BayesB	BayesC	BayesLasso	**BRR**	Joint Selection
Form	0.40	0.40	0.39	0.37	**0.40**	3
Volume	0.60	0.59	0.57	0.58	**0.60**	3
DBH	0.65	0.64	0.66	0.56	**0.66**	3
Specific Gravity	0.58	0.57	0.58	0.51	**0.59**	2
Heartwood%	0.38	0.40	0.39	0.38	**0.40**	2
colorA	-0.46	-0.51	-0.51	-0.49	-0.51	0
colorB	-0.03	-0.03	-0.12	-0.22	-0.08	0
colorC	-0.13	-0.09	-0.14	-0.16	-0.11	4

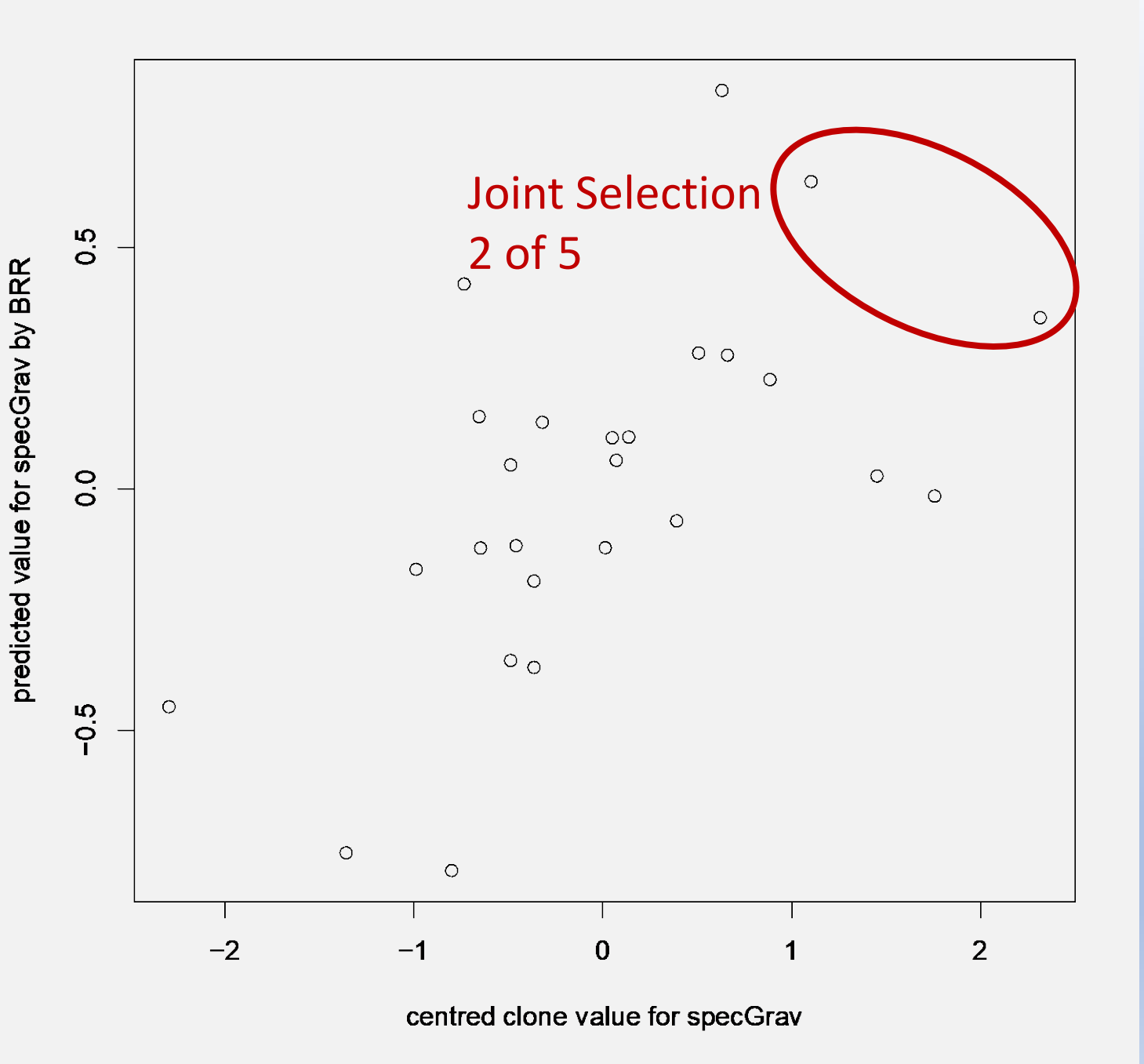
Predicted-Observed clone values for **DBH** (*r*=0.66):

- Correlation is strongly dependent on three data points.
- Skewed distribution of predicted values



Predicted-Observed clone values for **Specific Gravity** (*r*=0.59):

- Data are reasonably well distributed.

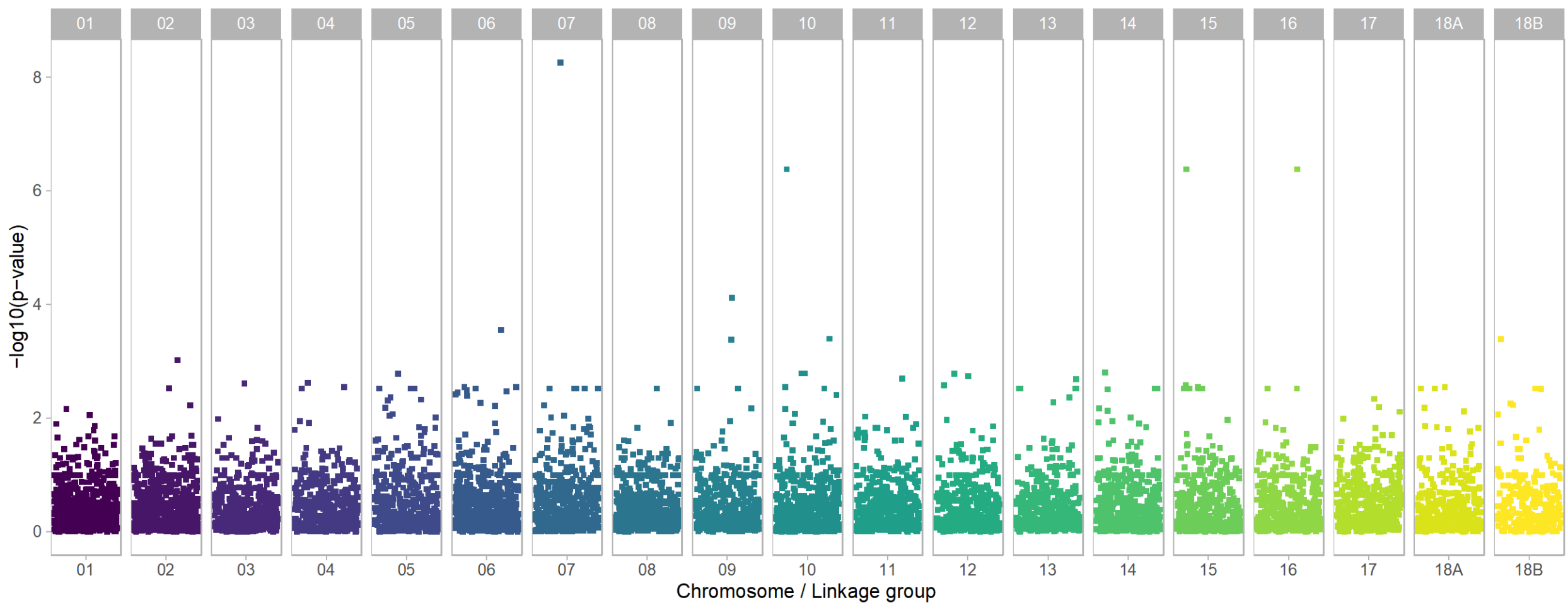


Marker Associations: all traits

Trait	Significant Markers
Stem Form	4 (4)
Volume	11 (8)
DBH	8 (7)
Specific Gravity	9 (8)
Heartwood %	0
Color A (lightness)	11 (5)
Color B (redness)	0
Color C (yellowness)	1 (1)

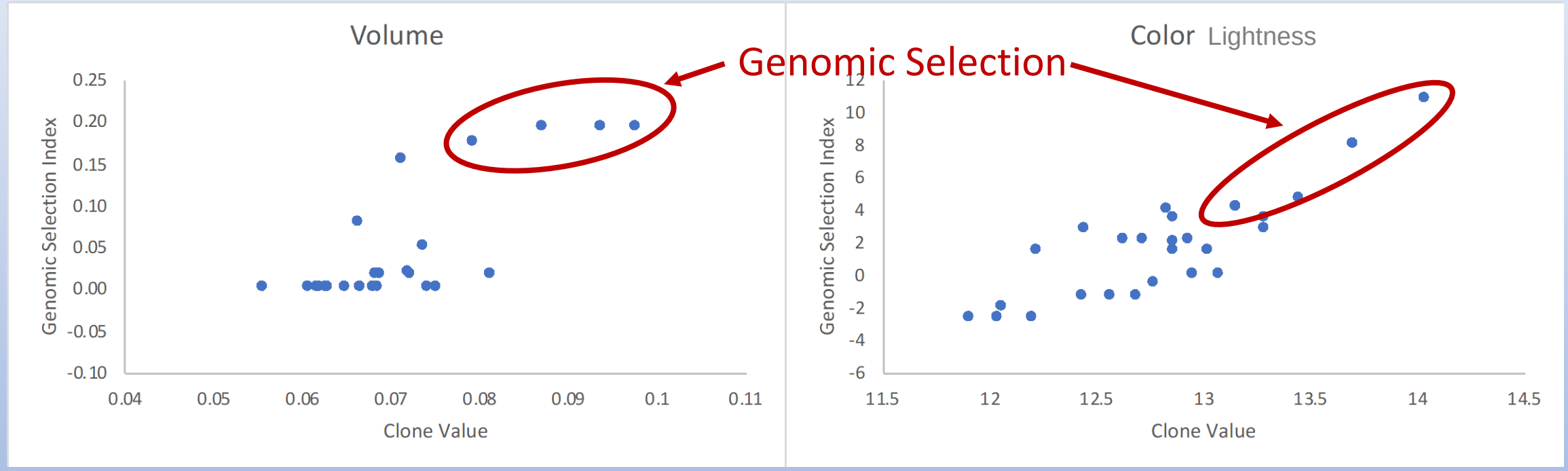
11 significant markers but
3 were completely collinear.
8 Markers contributing information

Marker Associations for volume



The ‘Manhattan Plot’ shows **statistical significance** of each marker’s trait association

Marker Associations: Clone Selection



Plots of **genomic index** *VS* **clone value** for two promising traits –
Color A has a better distribution of genomic index amongst its 5 informative markers than Volume does amongst its 8 informative markers (less collinearity for Color Lightness)

Is genomic selection profitable for teak?

Commercial situations are unique, however in general:

- **State enterprises:**
  - ☒ Longer rotations/lower MAI
  - ☑ Higher value product
  - ☑ Very large estates
  - ☑ Large and diverse breeding populations

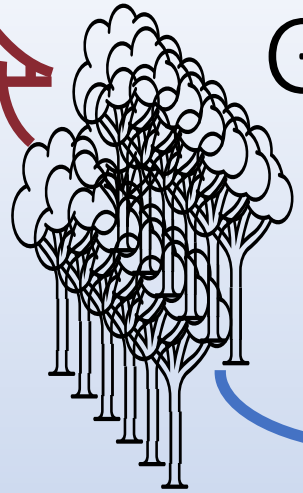
- **Investment fund-driven enterprises:**
  - ☑ Shorter rotations/higher MAI
  - ☒ Smaller estates
  - ? Wide variation in access to breeding material

LET'S HAVE A CLOSER LOOK:

Assuming:

- 4000 ha estate
- 20-year rotation with thinning at 12 years
- 10 commercial clones already in deployment
- Mean MAI 7.0 m^3/ha/year
- Stumpage 80 USD/m^3

Genomic Selection at scale: an example



Breeding population
(including commercial clones)

Progeny-testing
(including progeny
of clones)

~ 5 years

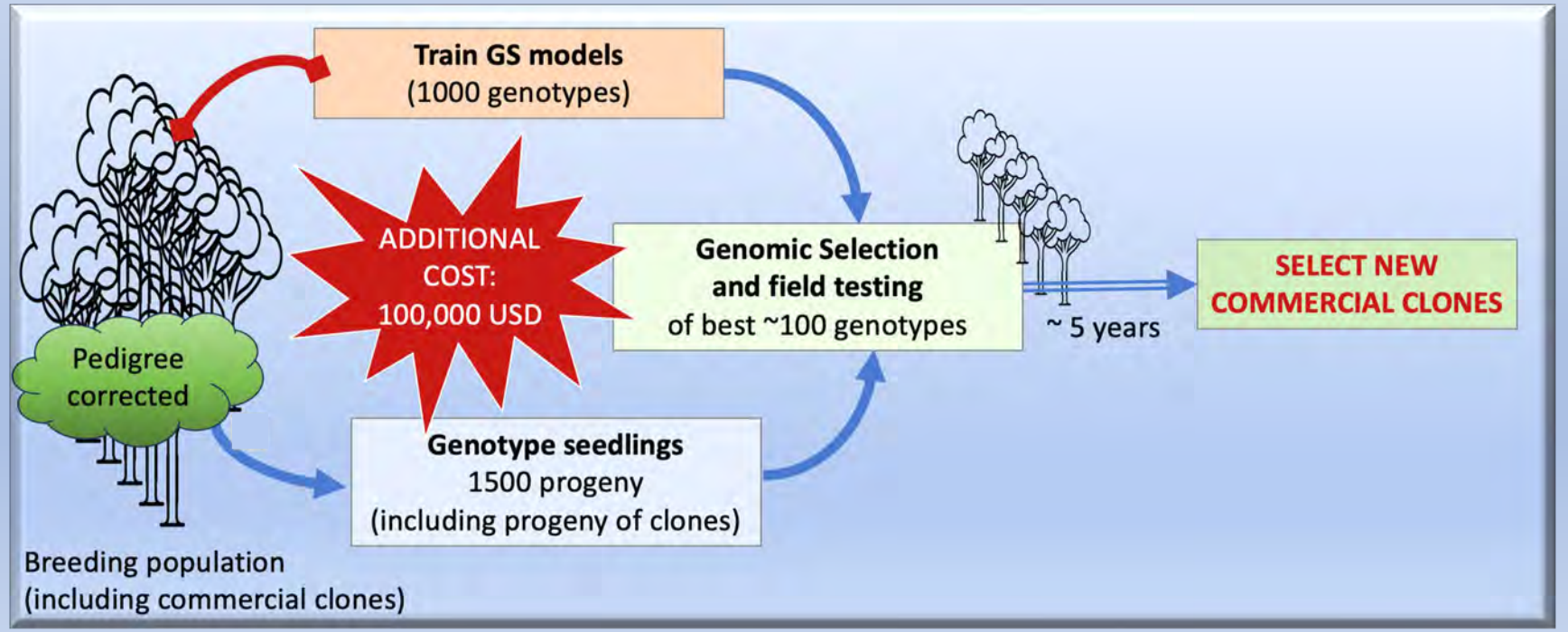
Clone testing
of best ~100
genotypes

~ 5 years

SELECT NEW COMMERCIAL CLONES

Breeding As Usual

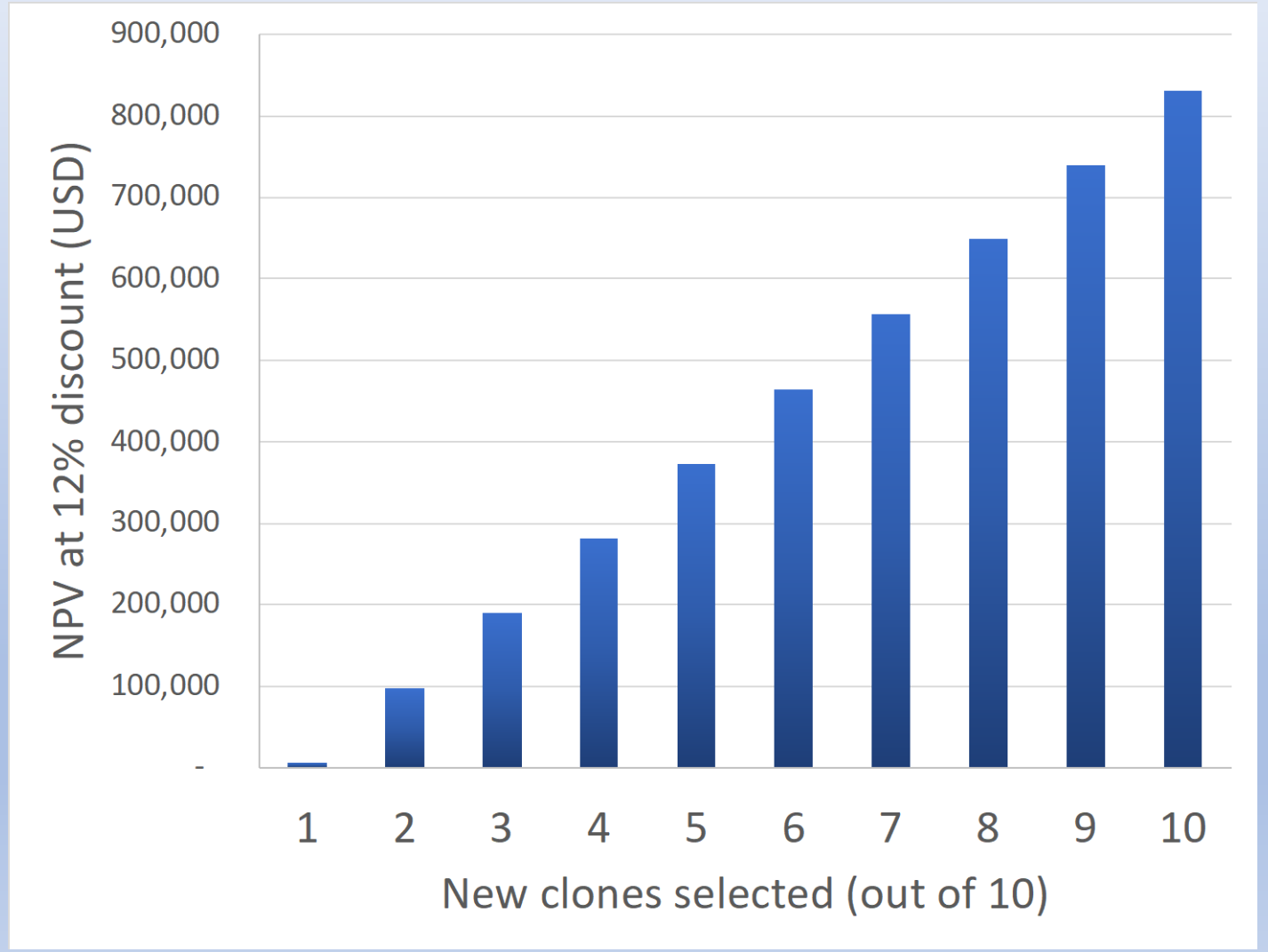
Genomic Selection



NPV for GS in short-rotation teak

NET PRESENT VALUE

- Compared with ‘Breeding As Usual’
- Initial spend **100,000 USD** on genomics (e.g. 2500 genotypes @ 40USD each)
- **5 years** shorter selection cycle
- **12%** discount rate
- 10 commercial clones already in deployment
- Variable 1 to 10 new clones with 10% greater productivity
- Mean MAI 7.0 m^3/ha/year
- Stumpage 80 USD/m^3



Yeah, but…

We can't afford it

Collaborate!

A consortium of companies could reduce the development cost to ~ $10K each

We don't have a breeding population

Collaborate!

Genomics can be used to discover relationships amongst different material sets

What if it doesn't work?

Collaborate!

Spread the risk

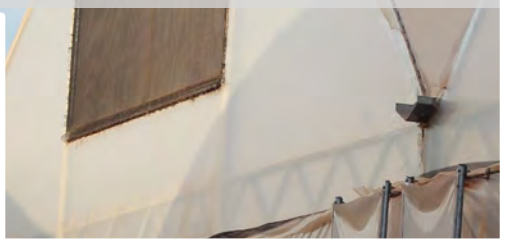
Share in the know-how

That technology isn't in our country

Collaborate!

Share in the skills

Our scientists don't have these skills

COLLABORATE!

Thank You!