

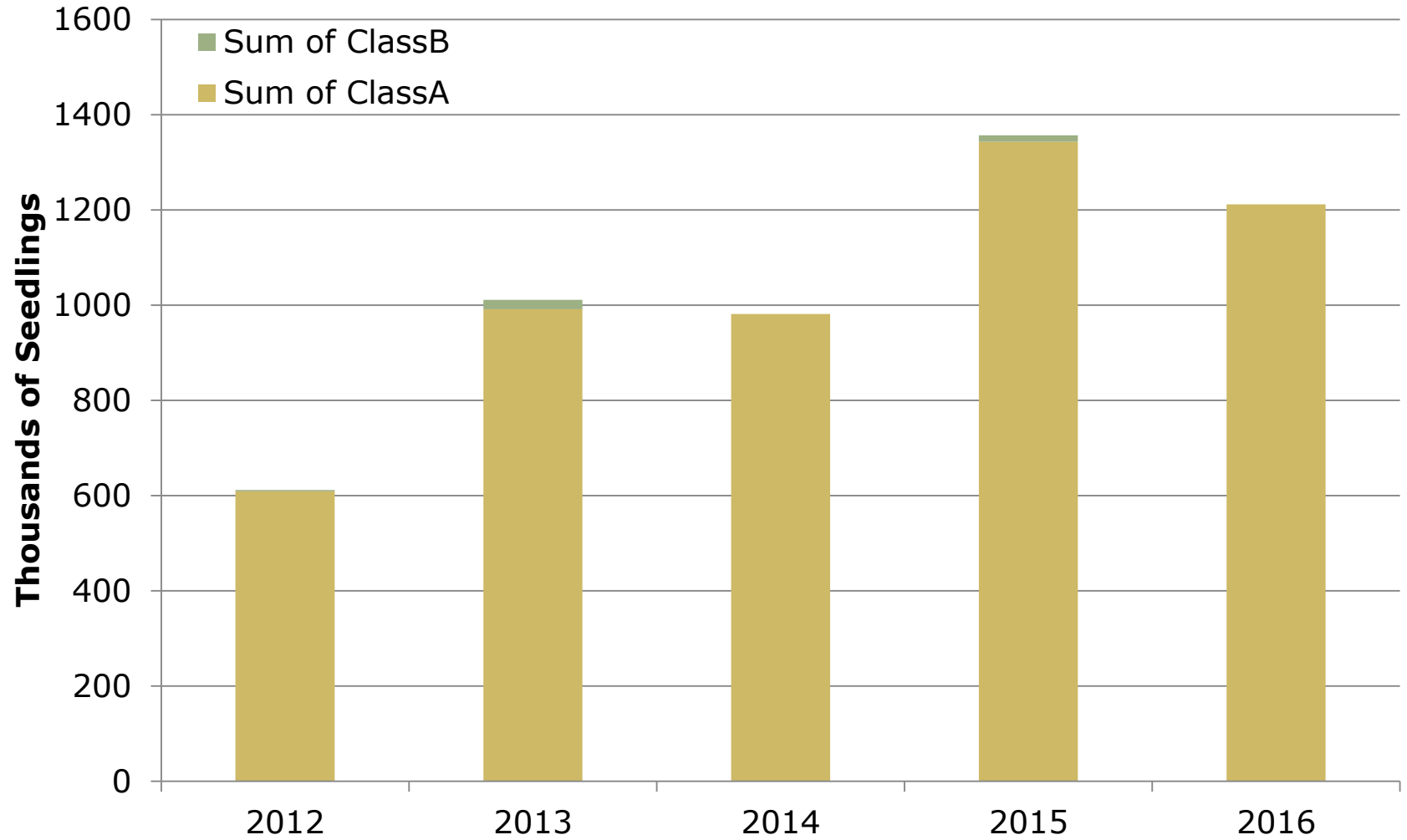
Western White Pine (Pw) & Lodgepole Pine (Pli) Breeding Programs

Nick Ukrainetz

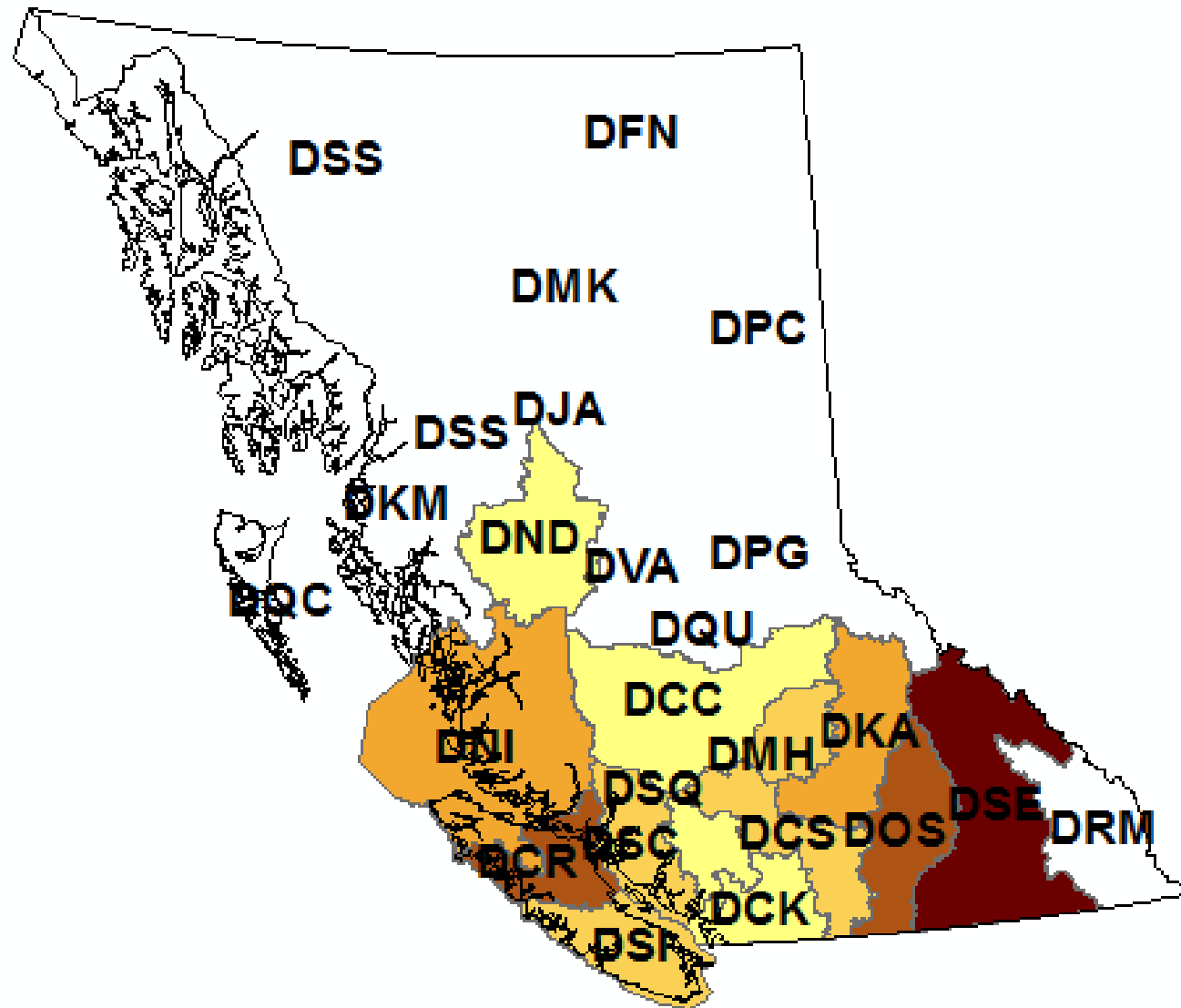


Ministry of
Forests, Lands and
Natural Resource Operations

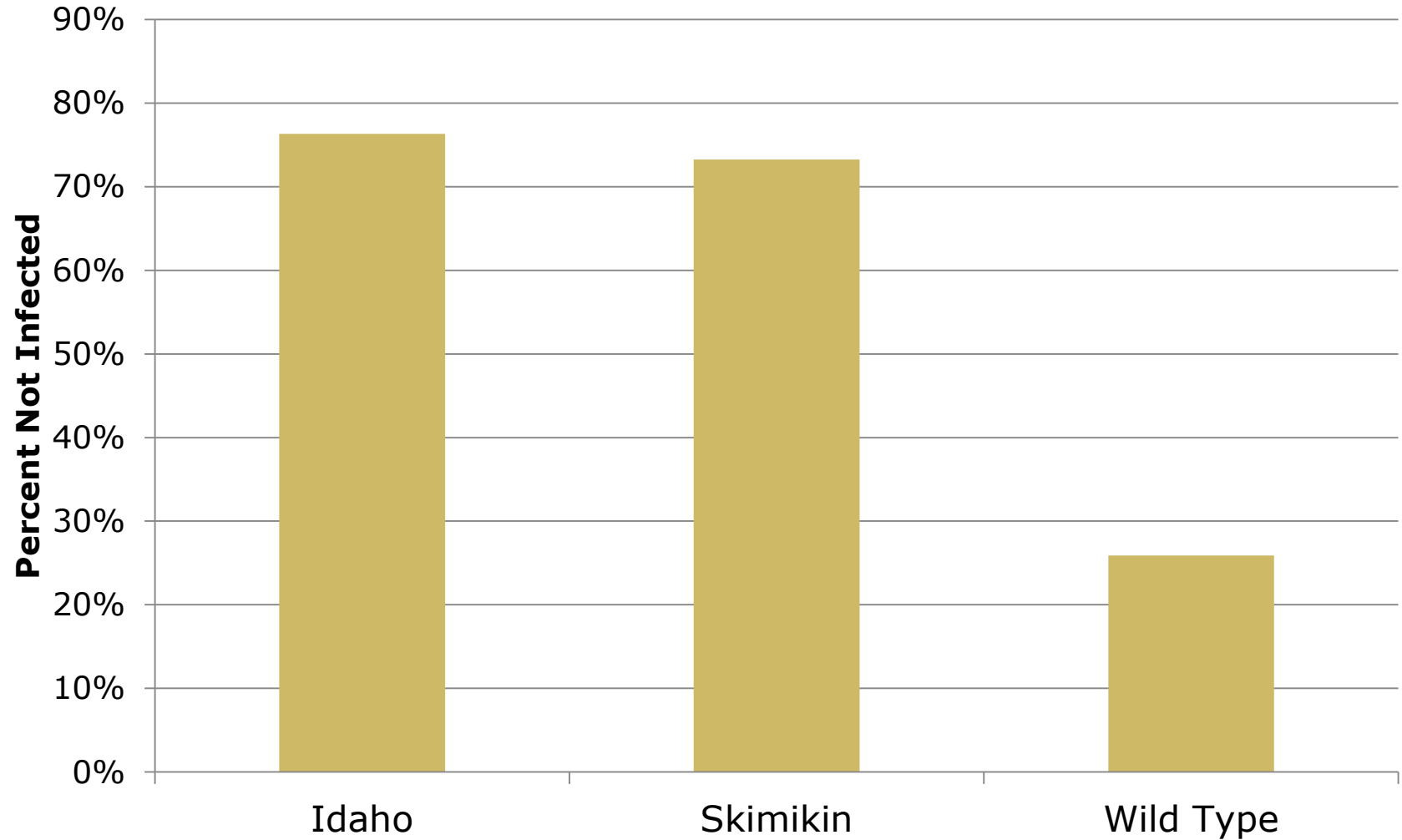
Pw Planting Stats



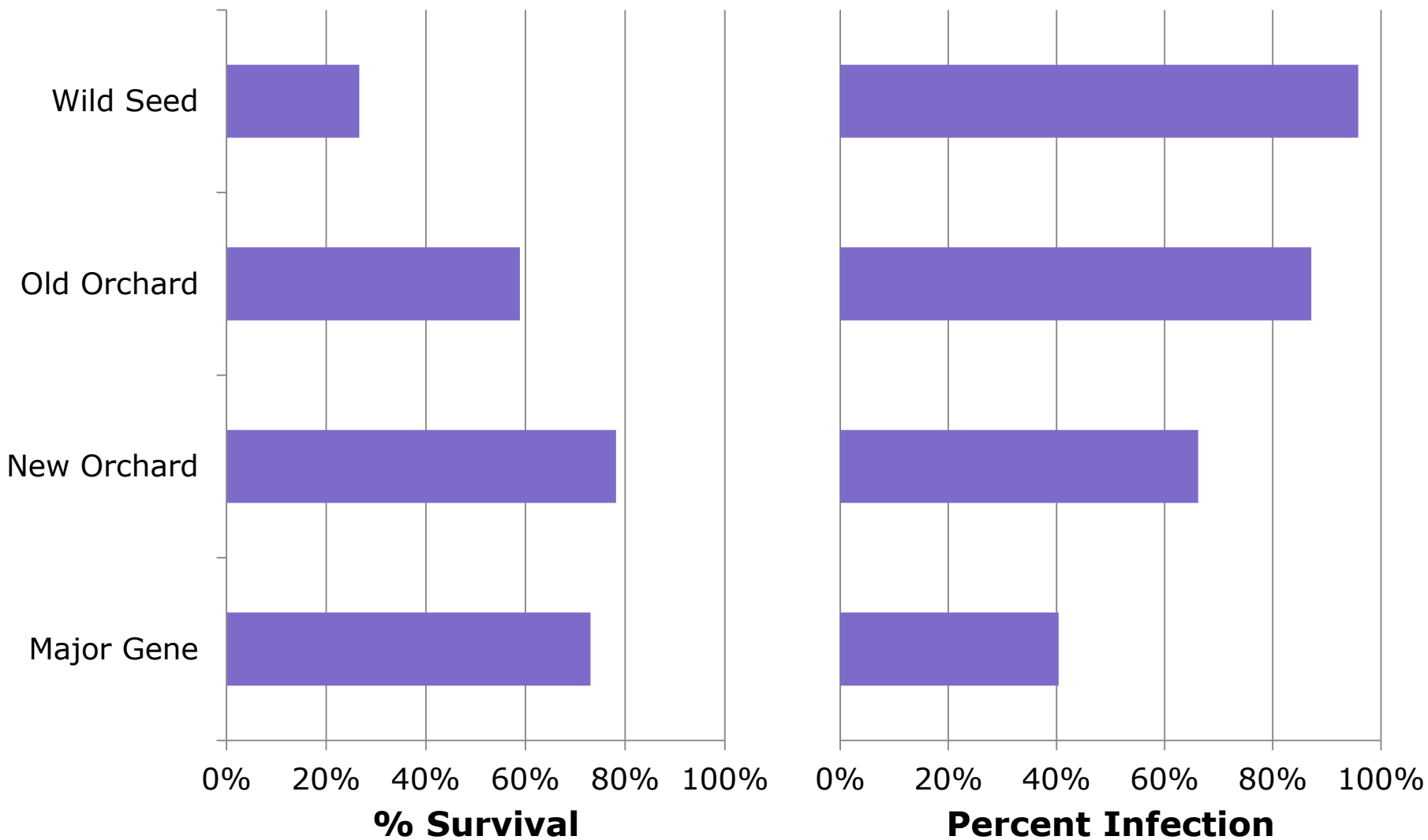
Pw Planting Stats



Pwi Realized Gain – Age 15



Pwc Realized Gain

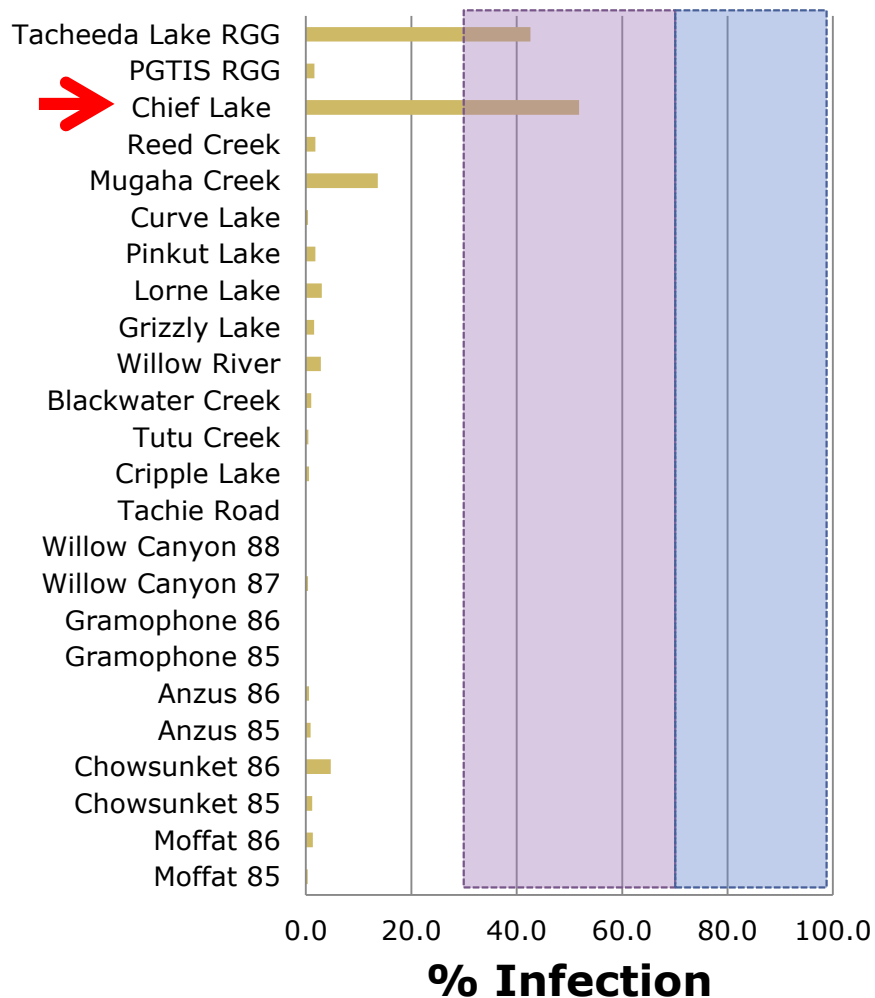


Lodgepole Pine Disease Resistance Update

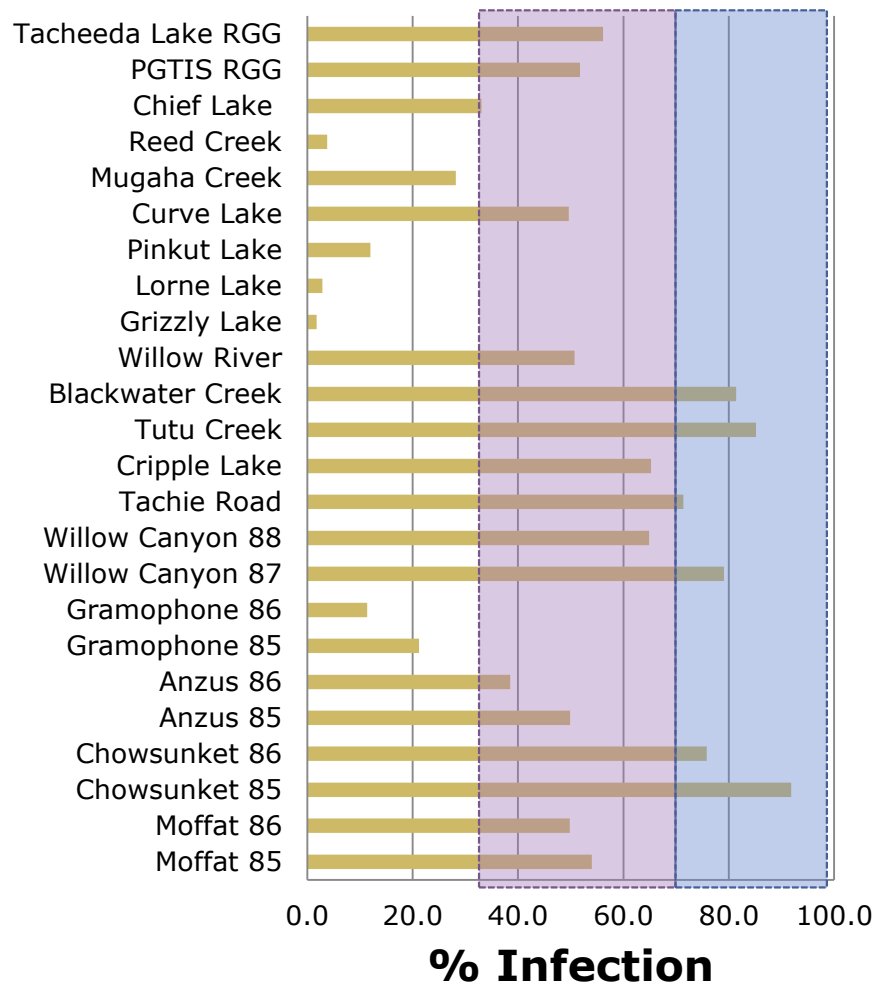


Forest Health Surveys by Richard Reich

Comandra



Gall Rust

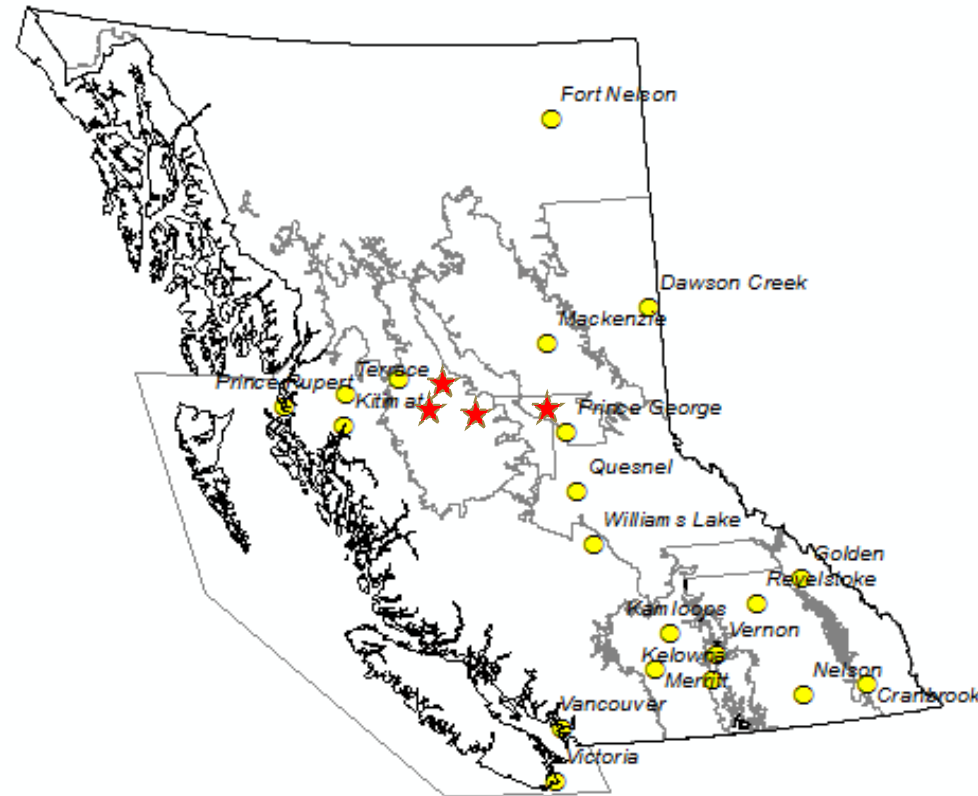


Comandra Resistance

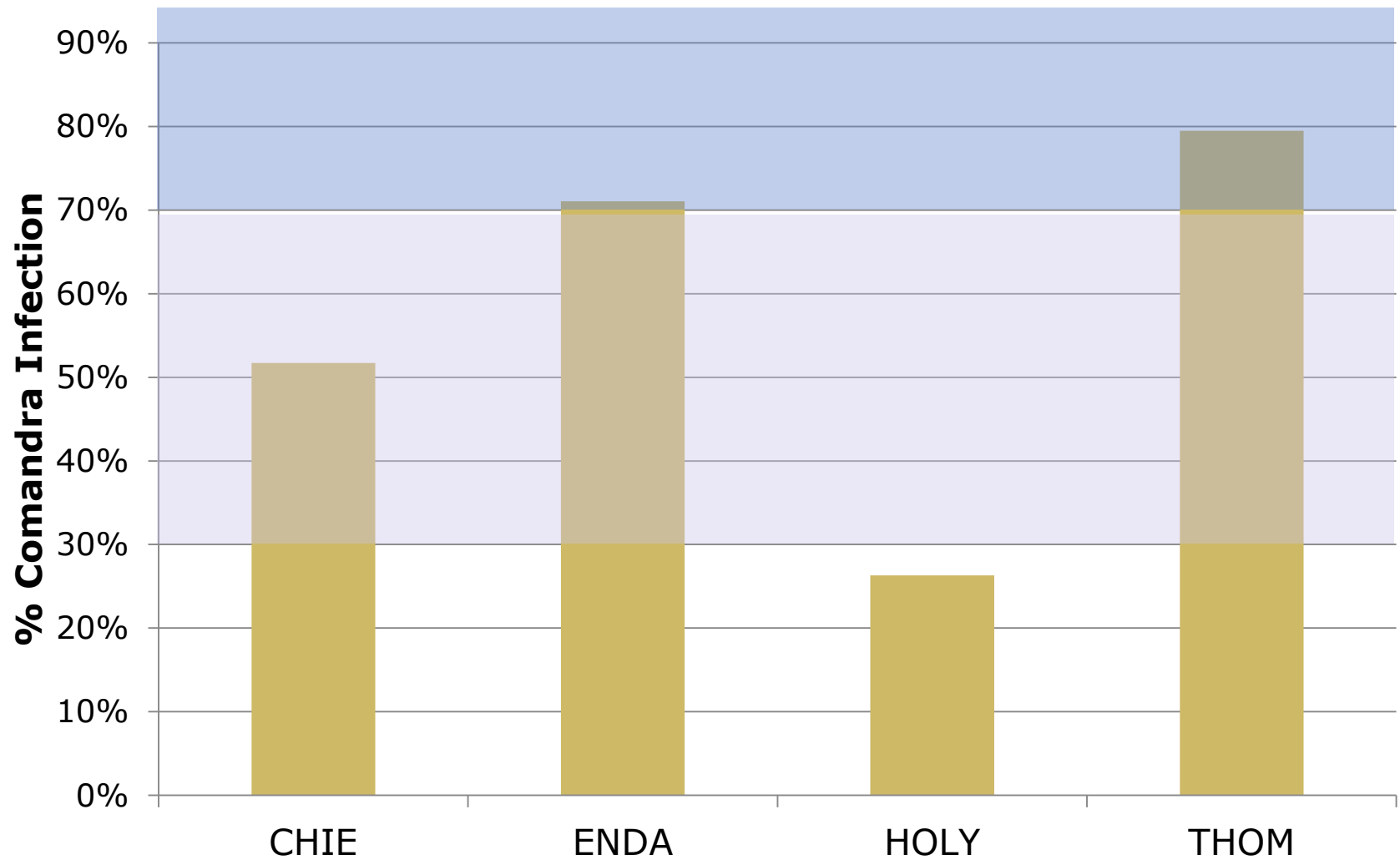


Comandra Resistance

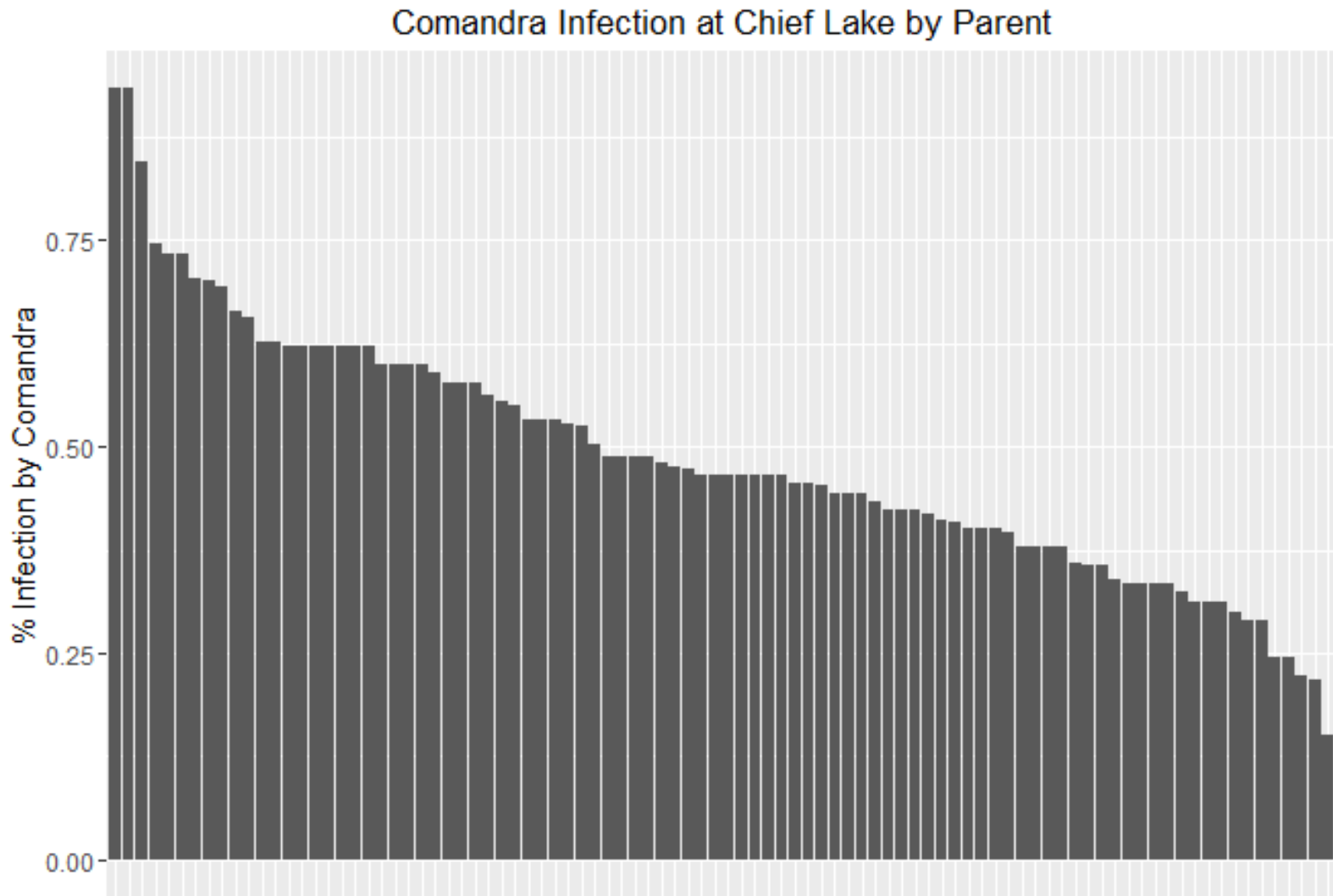
- Four sites
- 135 parent trees
- 28,000 trees



Comandra Resistance



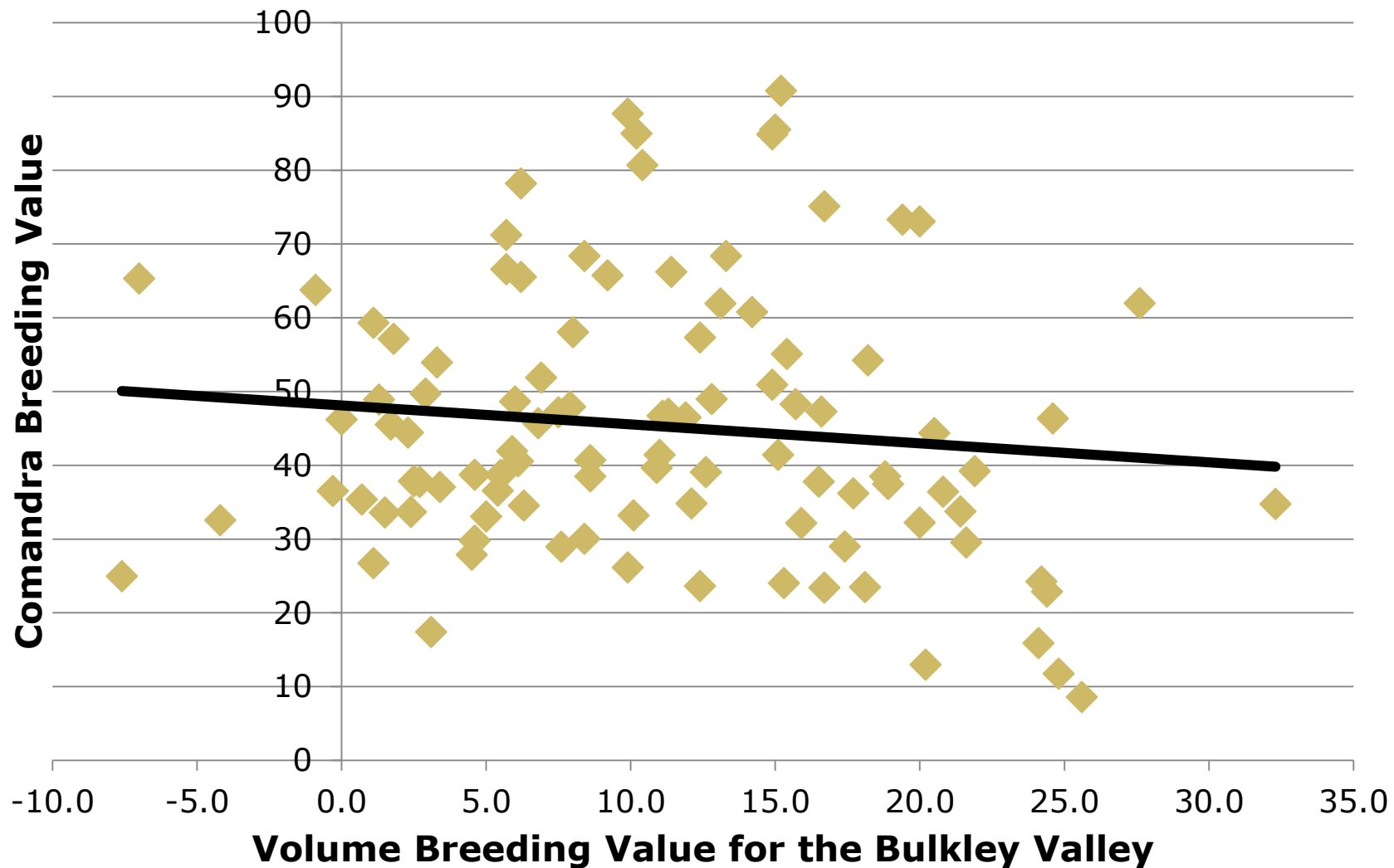
Comandra Resistance



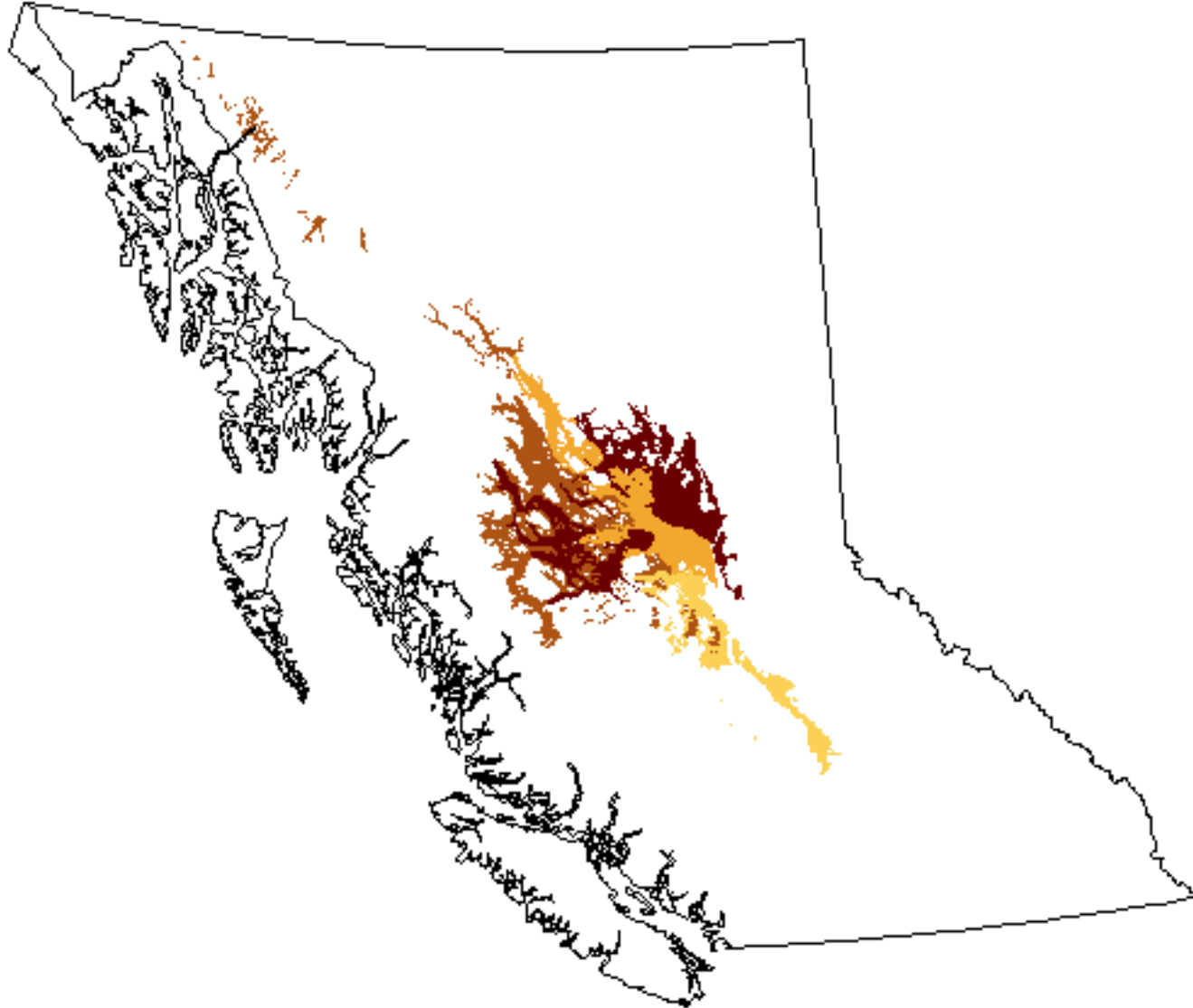
Comandra Resistance

- Q1: Is susceptibility or resistance heritable?
 - YES: heritability is 0.26
- Q2: Is susceptibility and resistance consistent across sites?
 - YES: Type B genetic correlation = 0.81
- Q3: What is the relationship with growth?
 - No strong relationship
- Q4: How much resistance?
 - Top 40 families: GWr = 71
 - Top 20 families: GWr = 79

Comandra Resistance



Comandra Resistance



Forest Health - Dothistroma



Forest Health - Dothistroma

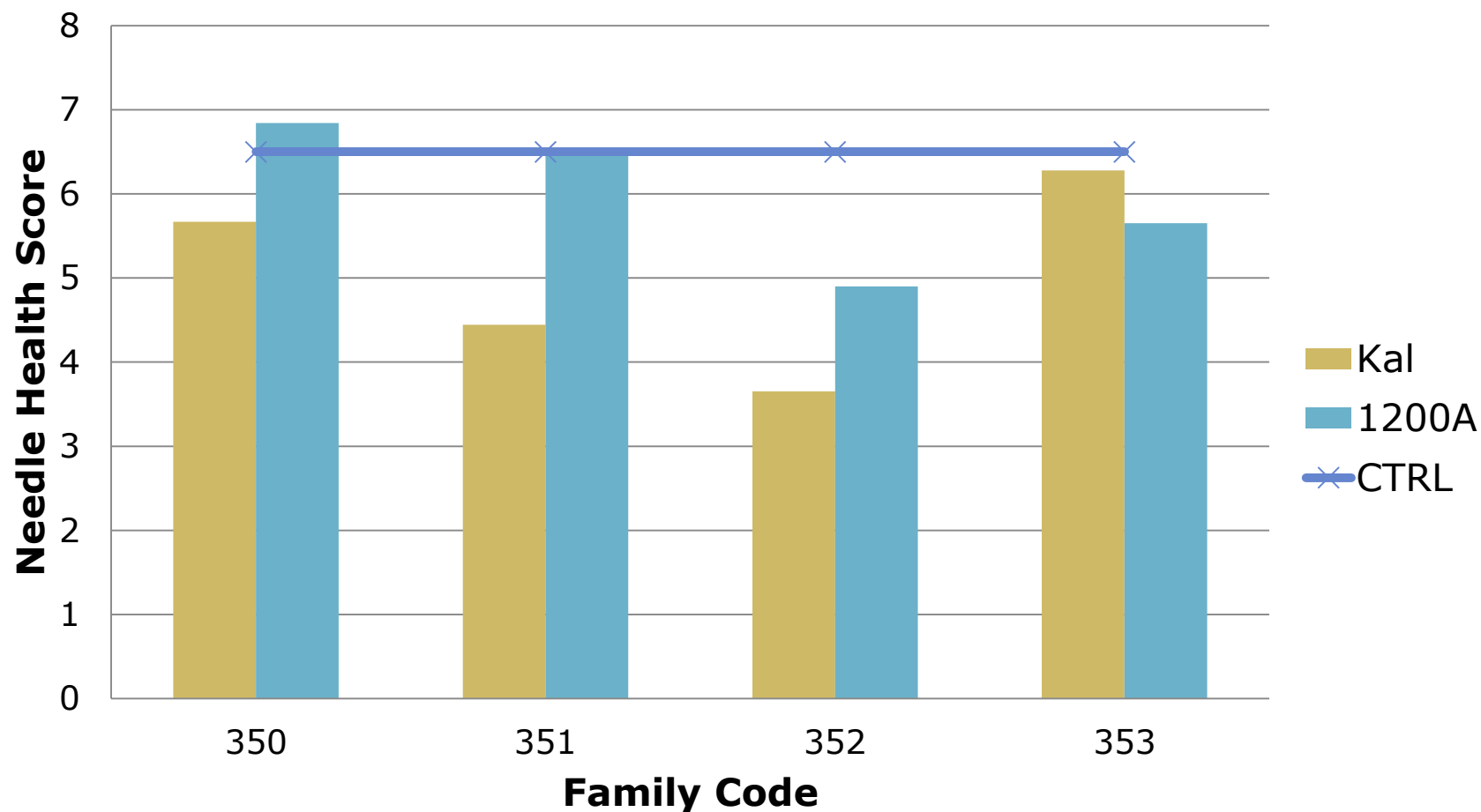


Forest Health - Dothistroma

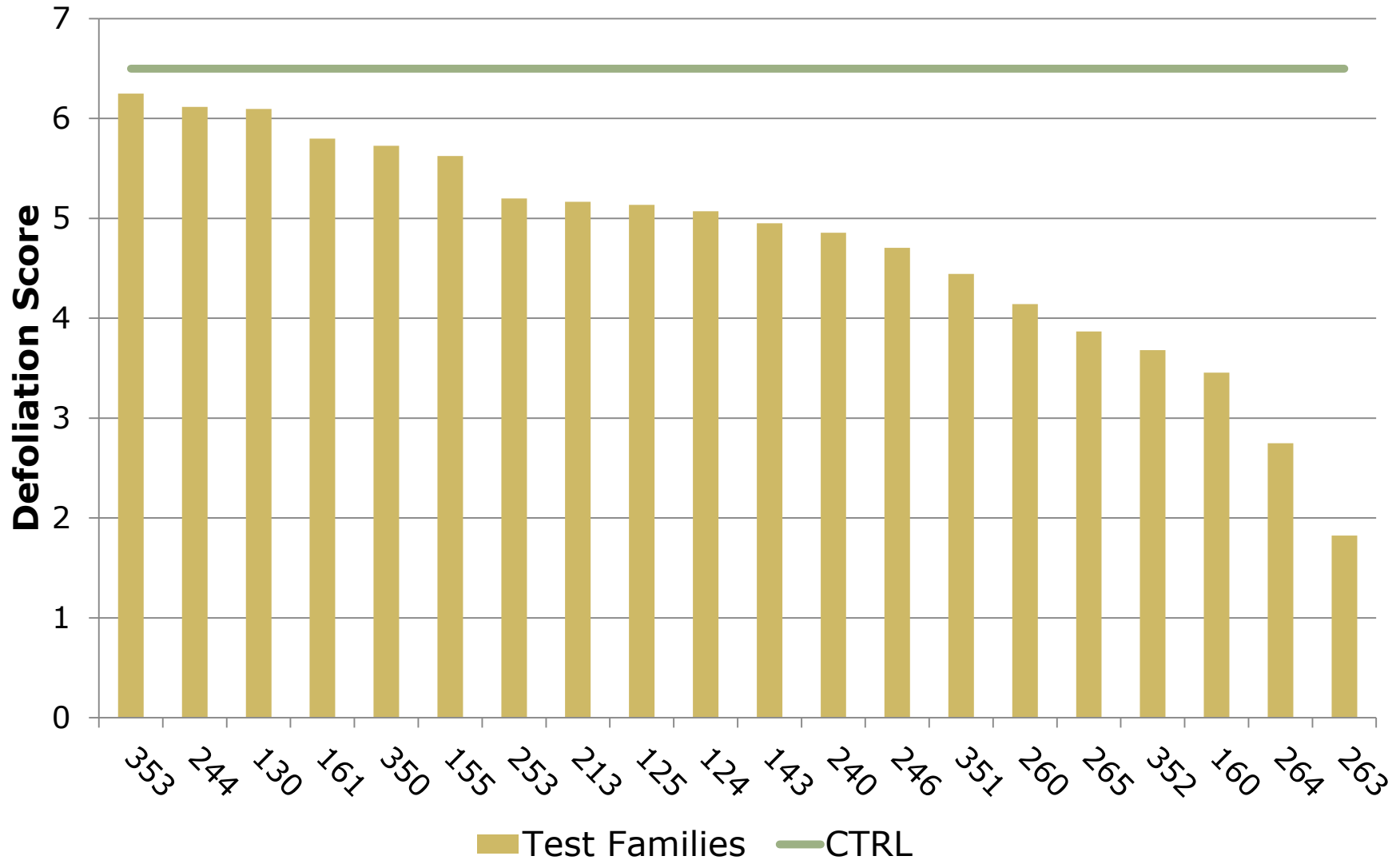


Forest Health - Dothistroma

Needle Health Score for Kal Inoculations and NST Field Trials



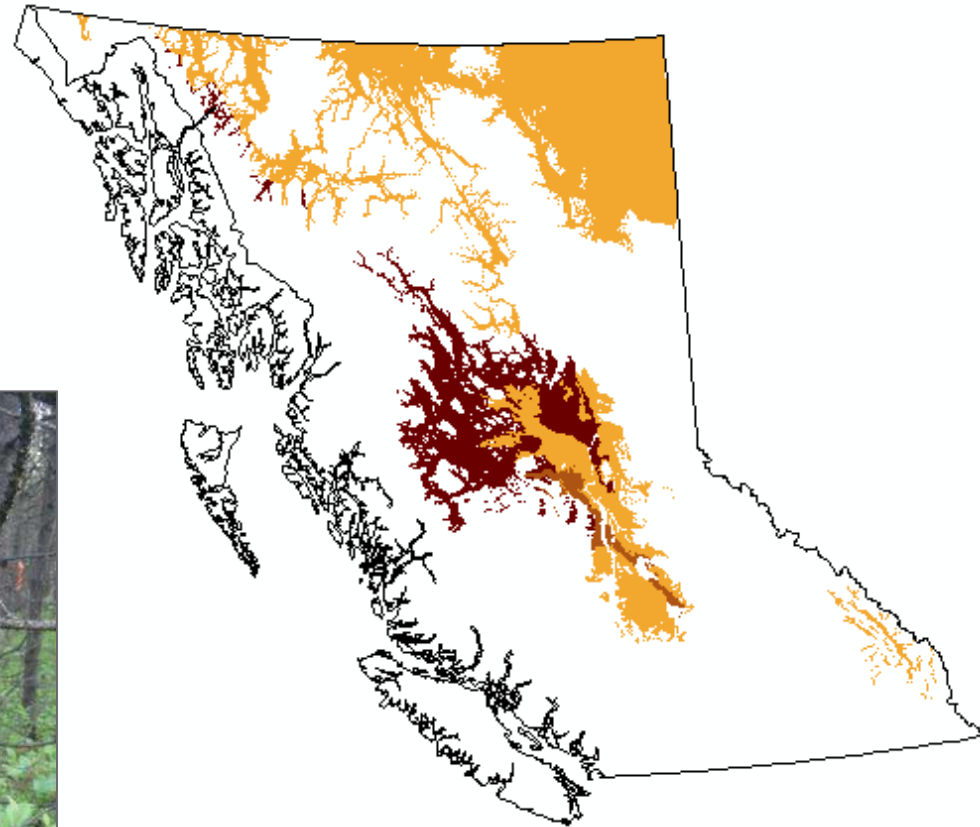
Forest Health - Dothistroma



Forest Health

Gall Rust:

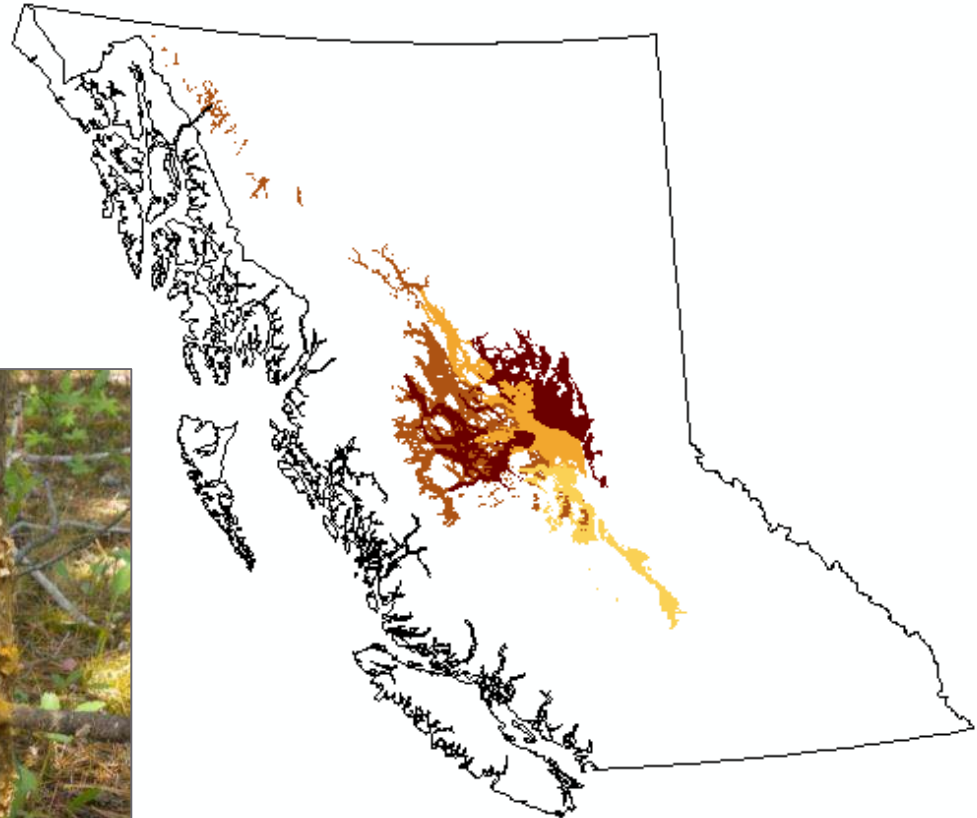
- > 700 parent trees ranked
- One seed orchard
 - GWr = 71



Forest Health

Comandra:

- 135 parent trees ranked
- 27 Forward Selections



Forest Health

Dothistroma:

- 111 Parents Ranked
- Screening methods




Forest Health

- 2017/2018 Budget: 61% of our expenditures have gone to disease resistance work
- Continue contract with CNC for disease surveys
 - Survey southern progeny tests
- Refine and perfect dothistroma screening protocol
- Establish field trials for comandra screening

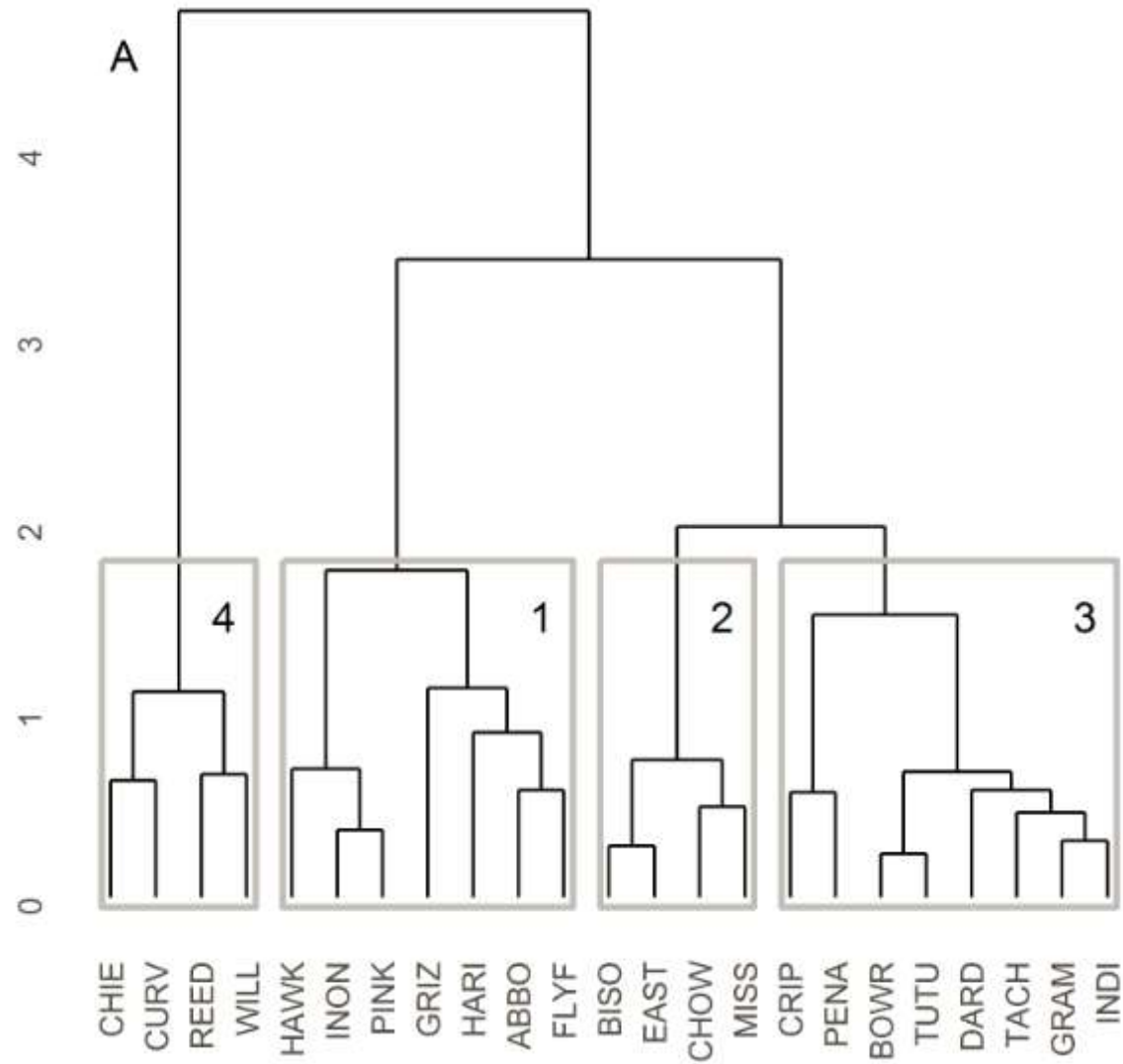
Lodgepole Pine New Breeding Zones



New Breeding Zones

1. Determine anchor sites
2. Align all sites to the anchor sites 
3. Finalize breeding groups
4. Allocate forward selections to breeding groups
5. Calculate breeding values
6. Align new breeding groups with CBST

New Breeding Zones

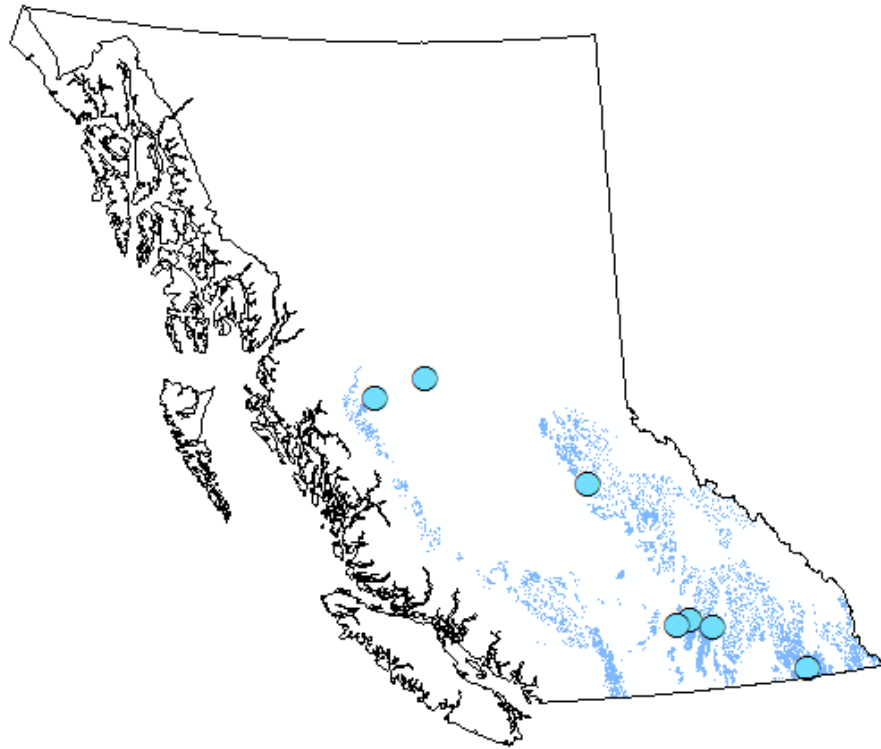


New Breeding Zones

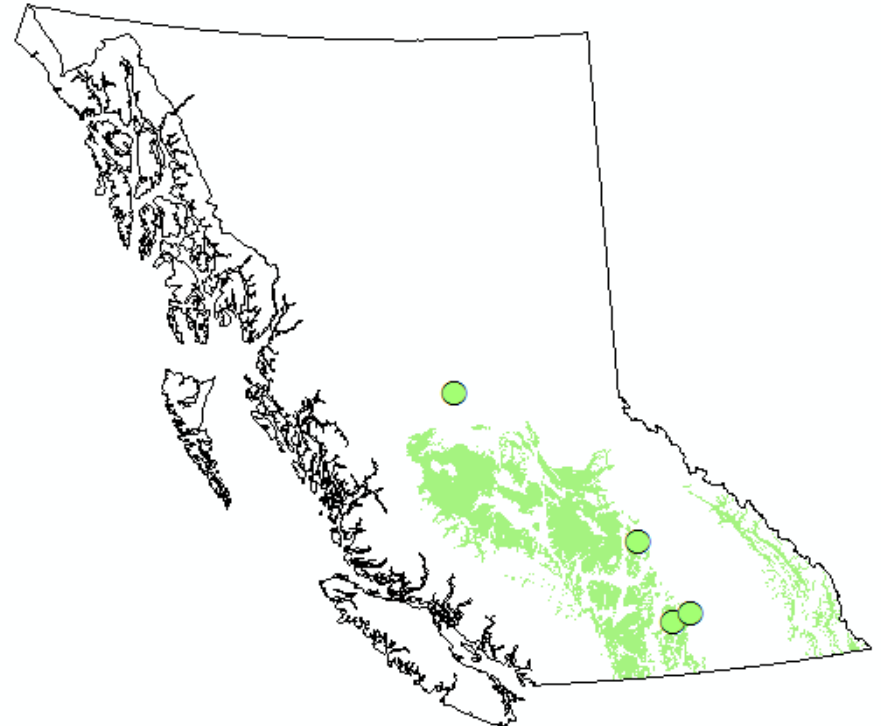
1. Dropped sites (OP and F1 progeny test sites)
2. Nass-Skeena (2 sites)
3. Big Bar-Chilcotin (~4 sites)
4. Thompson-Okanagan High (~5 sites)
5. East Kootenay Low (3 sites)
6. Comandra Resistance Trials (3 sites)

New Breeding Zones

Nelson High

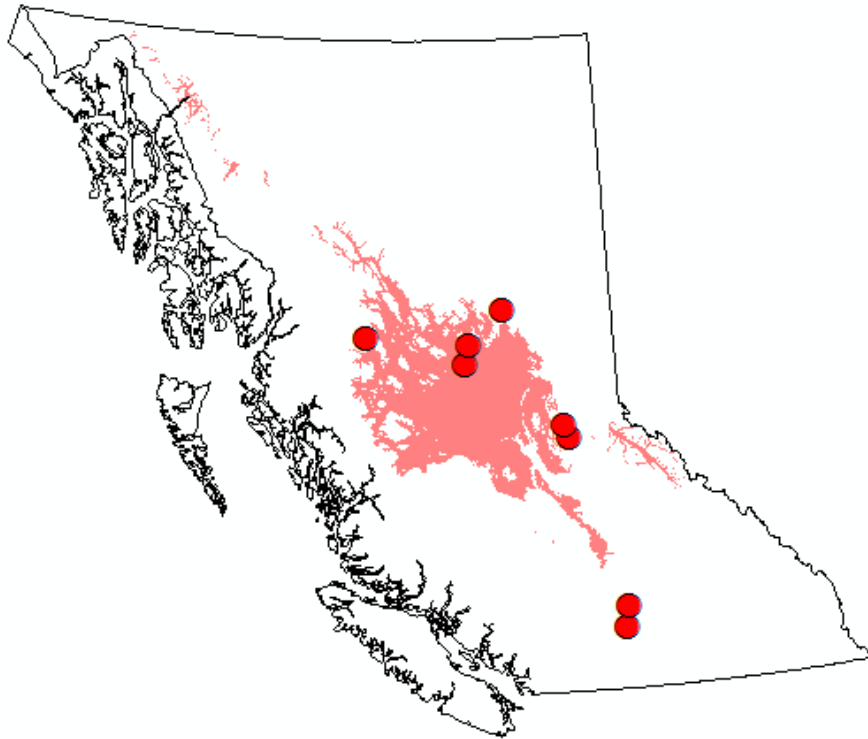


Thompson-Big Bar

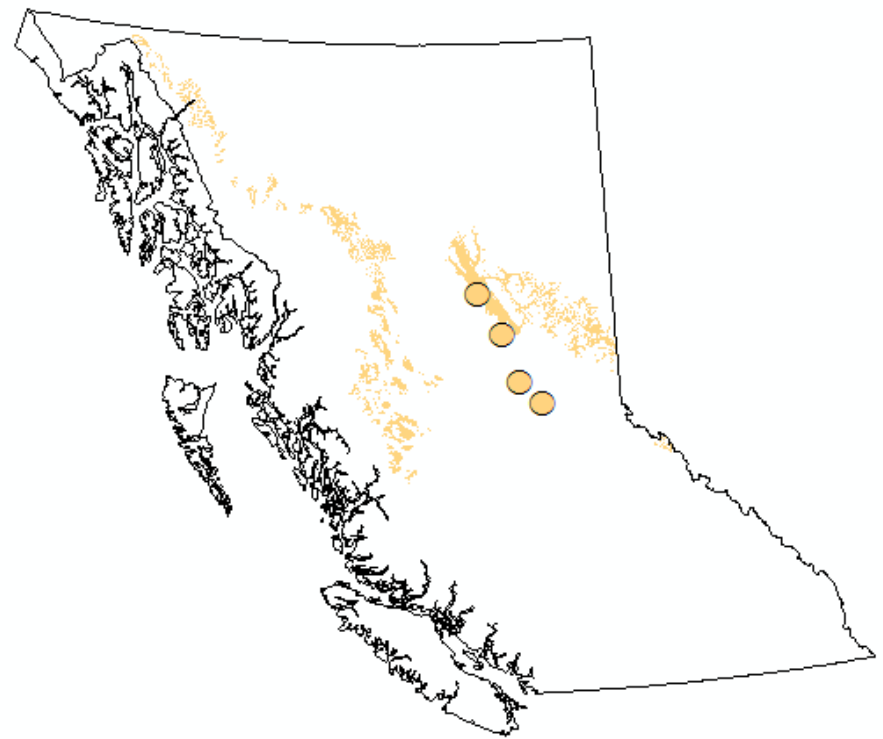


New Breeding Zones

Bulkley Valley



Central Plateau



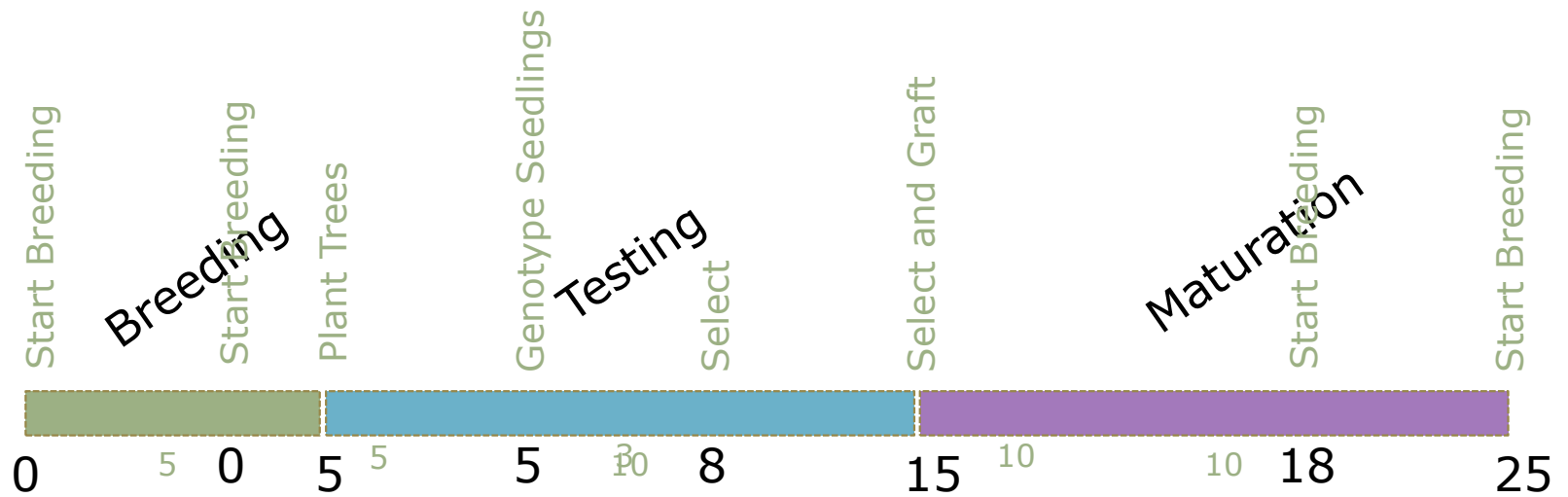
Lodgepole Pine Genomic Selection



Genomic Selection



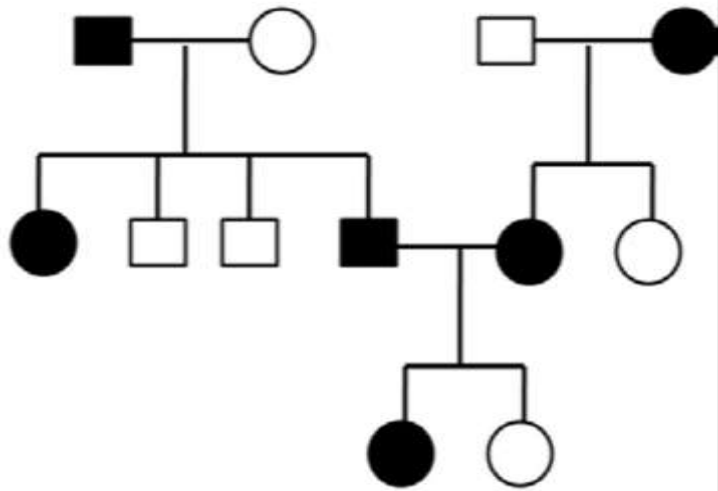
Genomic Selection



Genomic Selection

- Problem with conventional tree breeding... it takes a really long time!
 - Growth – 10 years
 - Wood quality > 15 years
 - Form traits >15 years
 - Disease resistance ???
- Genomic selection can increase gain per unit time

Genomic Selection

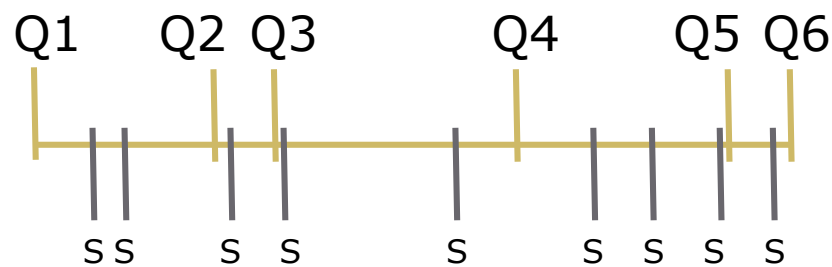


	1	2	3	4	5	101	102	103	104	105	106	107	108
1	1					0.5	0.5						
2		1				0.5	0.5			0.5	0.5		
3			1					0.5	0.5			0.5	0.5
4				1				0.5	0.5				
5					1					0.5	0.5	0.5	0.5
101	0.5	0.5				1	0.5			0.25	0.25		
102	0.5	0.5				0.5	1			0.25	0.25		
103			0.5	0.5				1	0.5			0.25	0.25
104			0.5	0.5				0.5	1			0.25	0.25
105		0.5			0.5	0.25	0.25			1	0.5	0.25	0.25
106		0.5			0.5	0.25	0.25			0.5	1	0.25	0.25
107			0.5	0.5				0.25	0.25	0.25	0.25	1	0.5
108			0.5	0.5				0.25	0.25	0.25	0.25	0.5	1

Genomic Selection

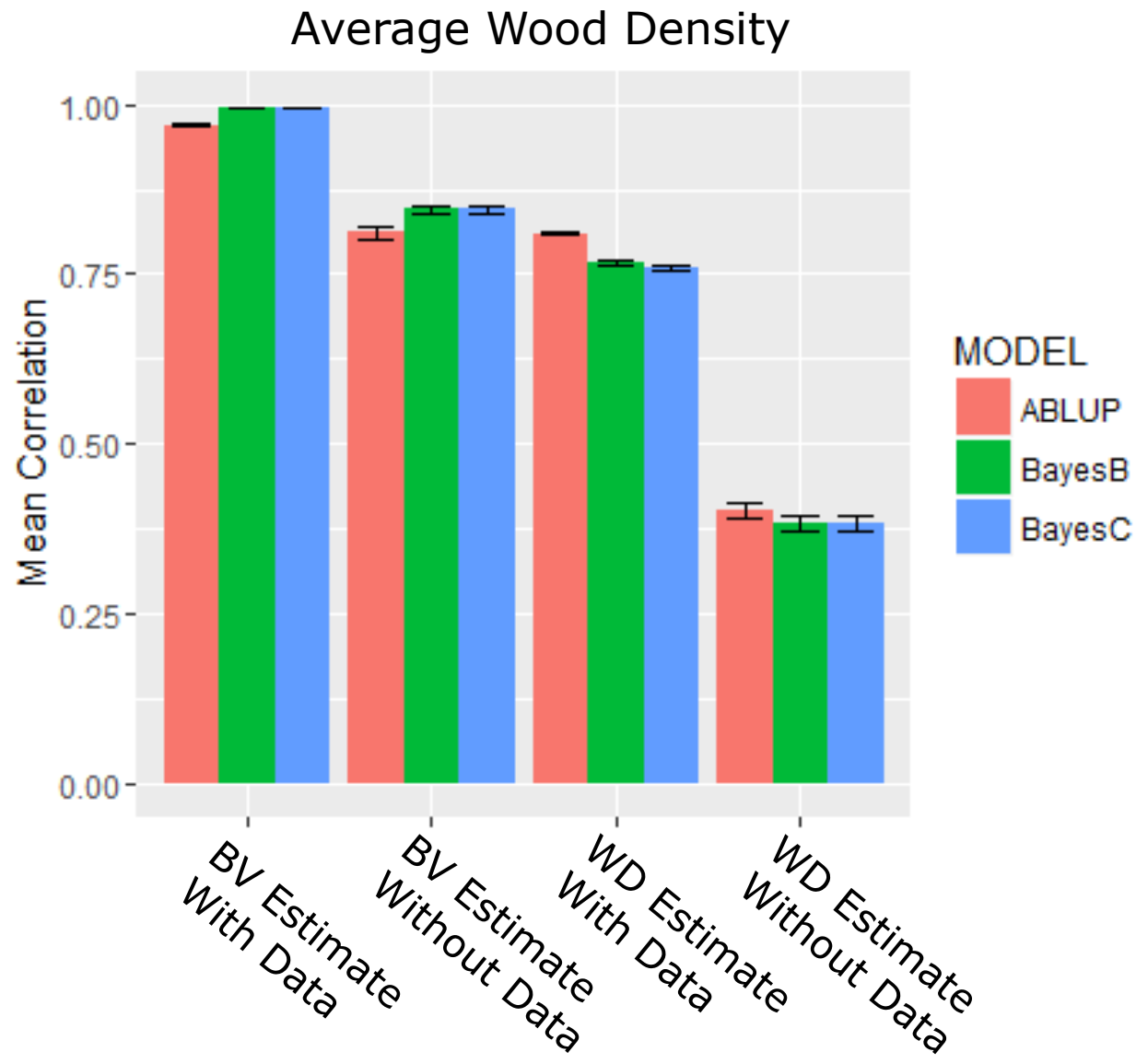
	101	102	103	104	105	106	107	108
101	1	0.5			0.25	0.25		
102	0.5	1			0.25	0.25		
103			1	0.5			0.25	0.25
104			0.5	1			0.25	0.25
105	0.25	0.25			1	0.5	0.25	0.25
106	0.25	0.25			0.5	1	0.25	0.25
107			0.25	0.25	0.25	0.25	1	0.5
108			0.25	0.25	0.25	0.25	0.5	1

Genomic Selection



	1	2	3	4	5	100	101	102	103	104	105	106	107	108	109	110
1	1.2000	0.0009	0.0010	0.0008	0.0009	0.4700	0.7300	0.4500	0.0004	0.0006	0.0008	0.0010	0.0009	0.4300	0.6300	0.0004
2	0.0005	0.9000	0.0007	0.0005	0.0008	0.0001	0.0003	0.0009	0.4900	0.7000	0.0006	0.0006	0.0001	0.0005	0.0010	0.5800
3	0.0007	0.0008	0.8000	0.0010	0.0007	0.5000	0.3600	0.5600	0.0010	0.0001	0.0002	0.0009	0.0010	0.3700	0.4200	0.0003
4	0.0009	0.0009	0.0008	0.9000	0.0004	0.0007	0.0001	0.0010	0.4600	0.4900	0.0003	0.0001	0.0001	0.0007	0.0004	0.5900
5	0.0005	0.0010	0.0009	0.0002	0.8000	0.0004	0.0006	0.0010	0.0001	0.0003	0.6500	0.2500	0.2900	0.0001	0.0008	0.0006
100	0.5800	0.0003	0.7400	0.0005	0.0008	1.1000	0.2800	0.3800	0.0003	0.0006	0.0003	0.0003	0.0008	0.3400	0.7200	0.0008
101	0.5300	0.0006	0.6800	0.0010	0.0008	0.3200	0.9000	0.5000	0.0004	0.0007	0.0006	0.0005	0.0004	0.5400	0.5800	0.0006
102	0.7200	0.0005	0.7100	0.0008	0.0006	0.6500	0.4100	1.1000	0.0004	0.0003	0.0002	0.0001	0.0001	0.5200	0.2500	0.0009
103	0.0009	0.3200	0.0006	0.5200	0.0006	0.0002	0.0002	0.0001	0.9000	0.7500	0.0004	0.0004	0.0010	0.0002	0.0006	0.7000
104	0.0009	0.3100	0.0006	0.2600	0.0003	0.0010	0.0002	0.0008	0.6800	1.1000	0.0005	0.0005	0.0009	0.0007	0.0005	0.6800
105	0.0002	0.0009	0.0003	0.0002	0.7100	0.0004	0.0009	0.0008	0.0010	0.0001	1.1000	0.1200	0.2300	0.0007	0.0006	0.0003
106	0.0001	0.0008	0.0009	0.0010	0.4100	0.0001	0.0002	0.0006	0.0004	0.0005	0.1400	0.8000	0.3100	0.0001	0.0003	0.0009
107	0.0010	0.0009	0.0004	0.0003	0.5000	0.0004	0.0006	0.0007	0.0007	0.0008	0.2400	0.1300	1.2000	0.0005	0.0003	0.0008
108	0.4200	0.0002	0.5400	0.0007	0.0007	0.3000	0.4500	0.7200	0.0003	0.0005	0.0004	0.0005	0.0010	0.9000	0.7400	0.0003
109	0.7400	0.0006	0.5400	0.0009	0.0004	0.2800	0.3300	0.4500	0.0004	0.0007	0.0002	0.0008	0.0010	0.2500	0.8000	0.0009
110	0.0005	0.3900	0.0007	0.6800	0.0001	0.0006	0.0007	0.0005	0.3500	0.6200	0.0002	0.0009	0.0008	0.0009	0.0008	1.0000

Genomic Selection



Genomic Selection

