An update on CSIRO research into AGD in Tasmania

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FOOD FUTURES FLAGSHIP
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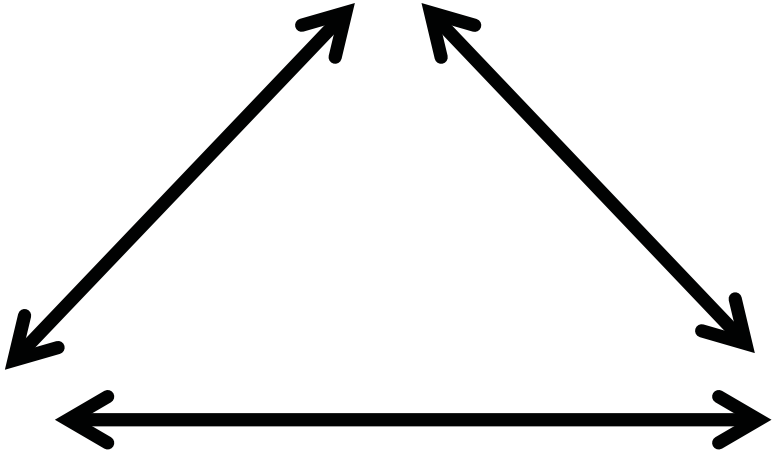
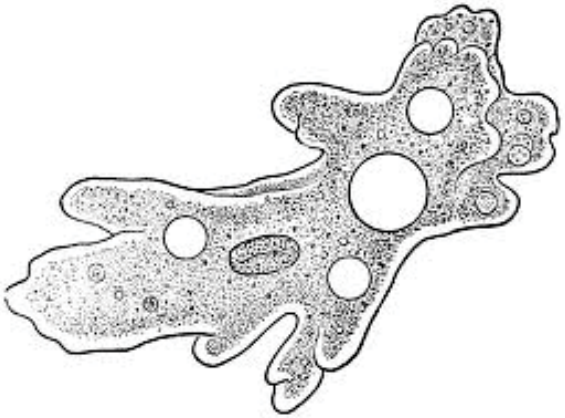
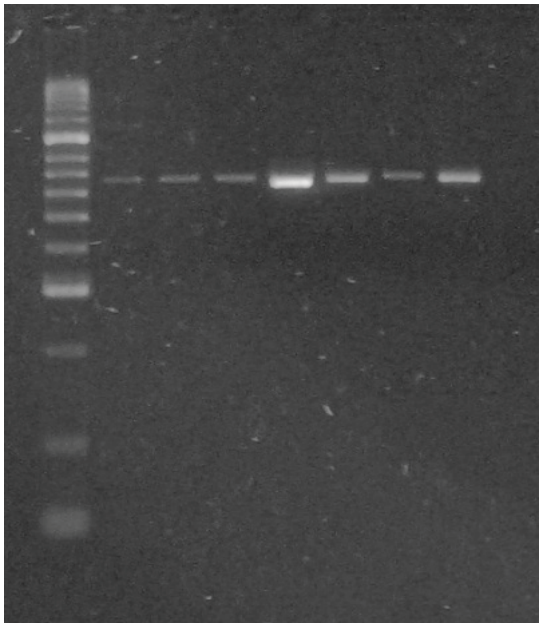




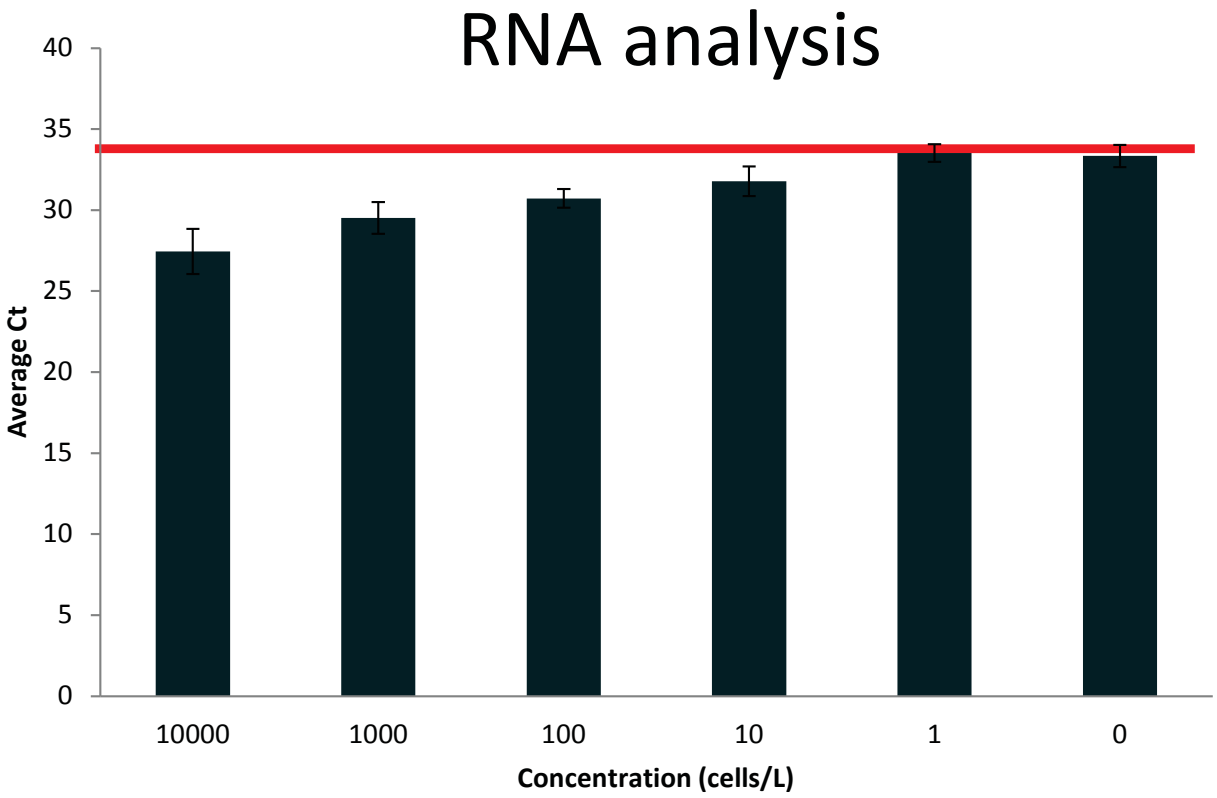
Environment – water sampling, traditionally labour intensive and replication difficult

Semi-automatic sampling in situ

Results – Semi-automated water sampling



DNA Analysis

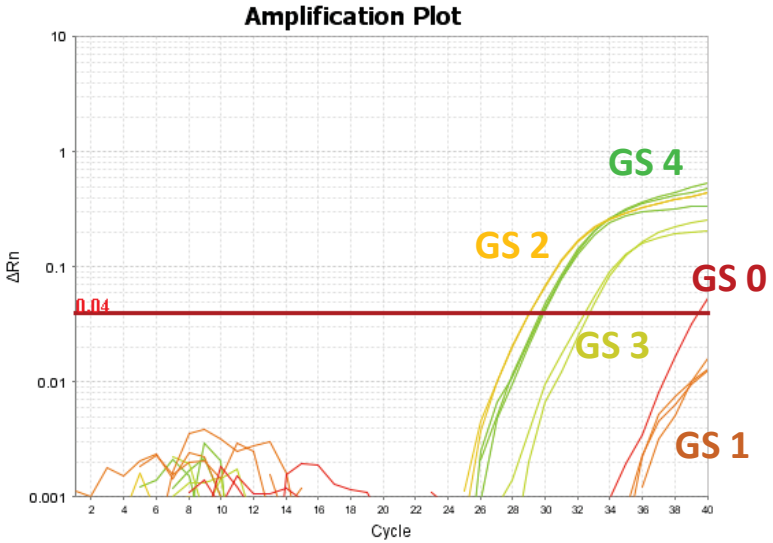


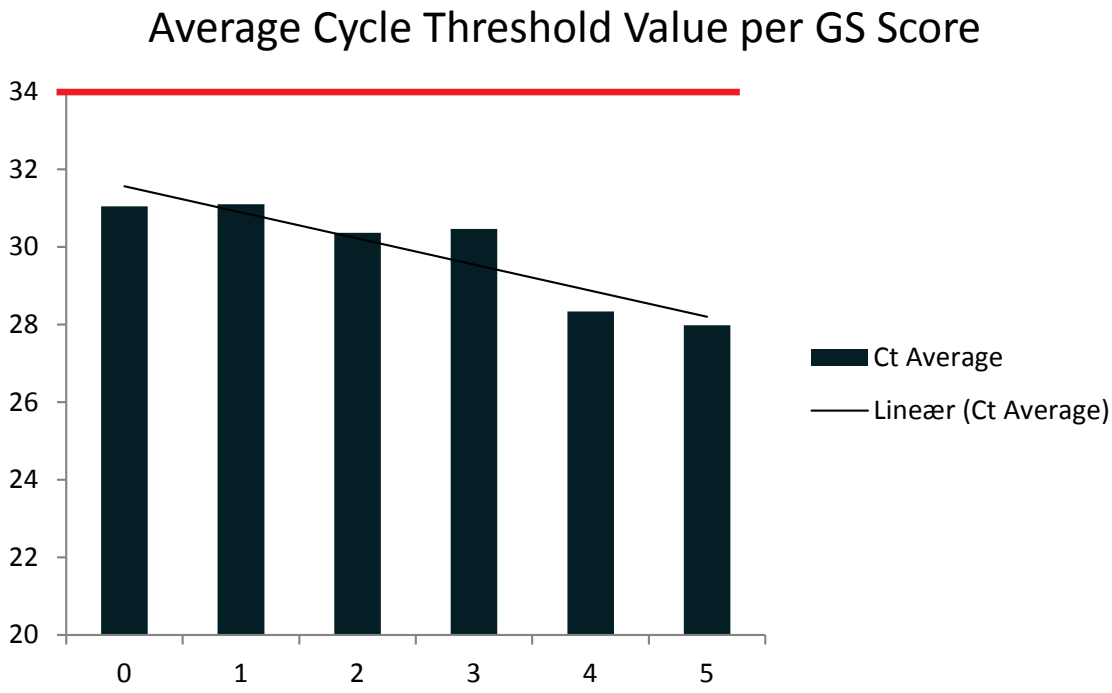
2nd Generation sampler

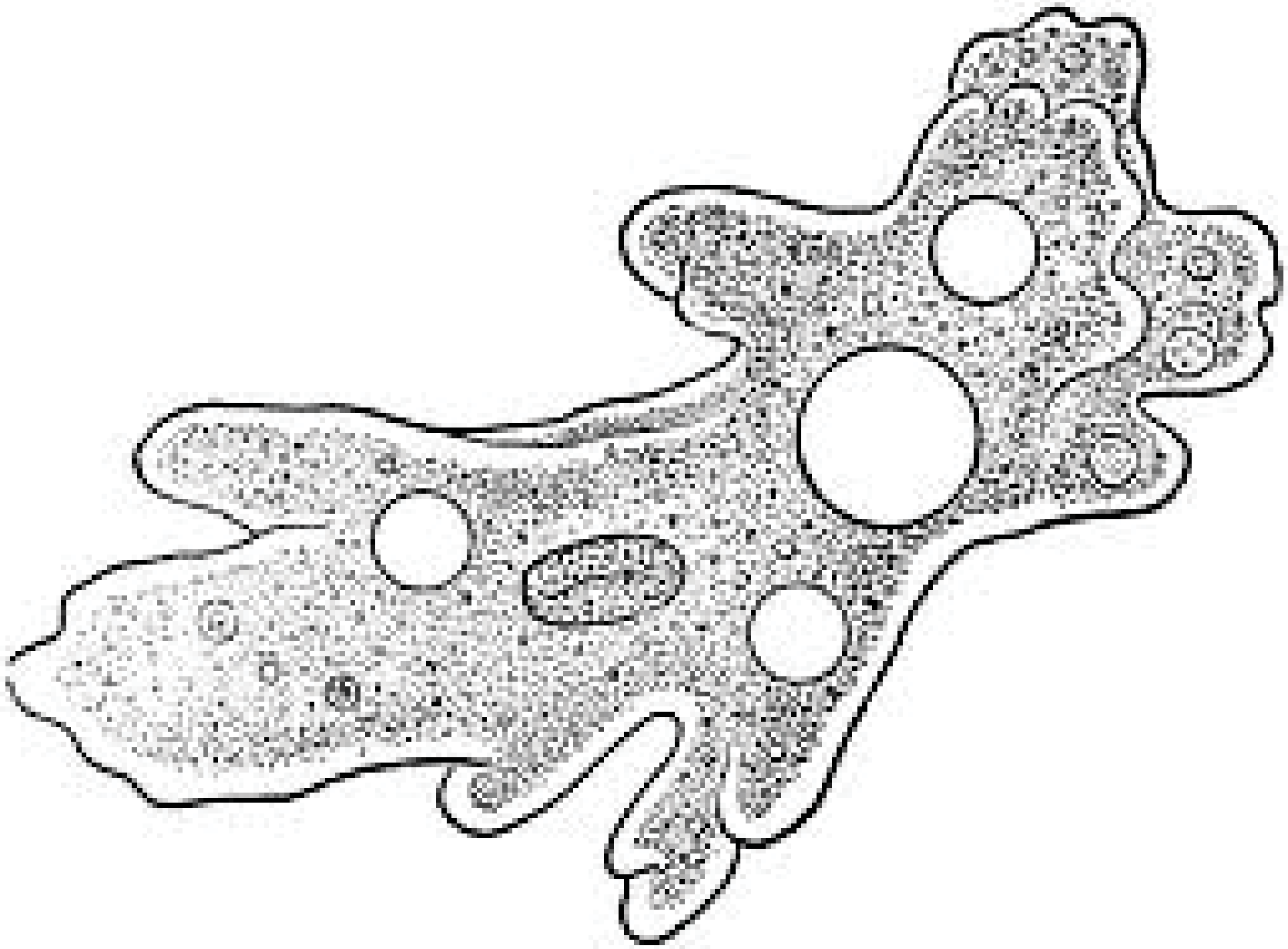
- Computer controlled – set and forget
- Capable of taking and archiving 24 samples
- Pumps water across filter and then ‘floods’ with appropriate buffer
- Will be deployed 2nd ½ of 2014

Non-destructive sampling of gills - swabs

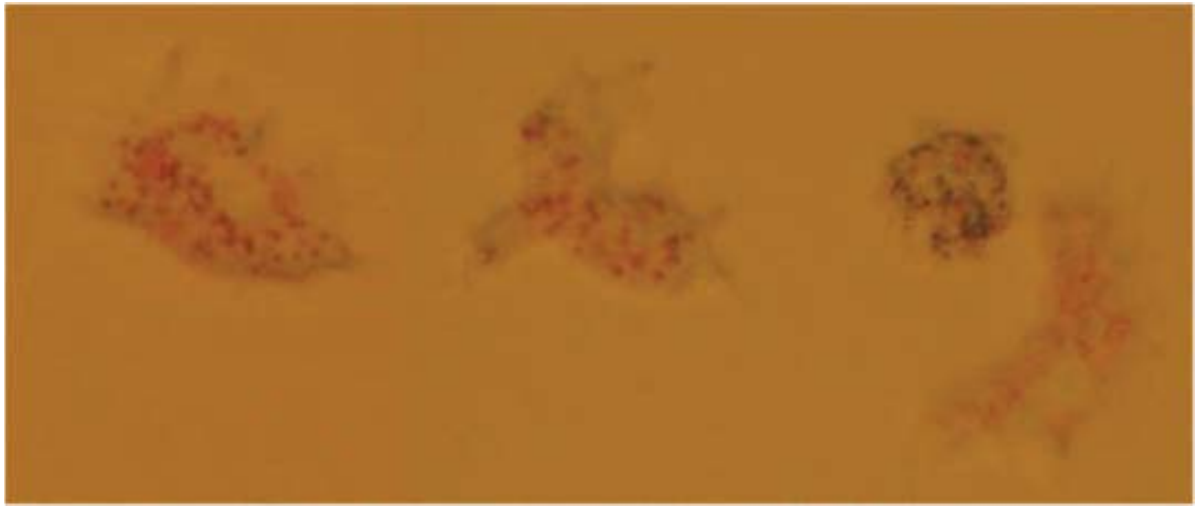
RNA vs DNA results





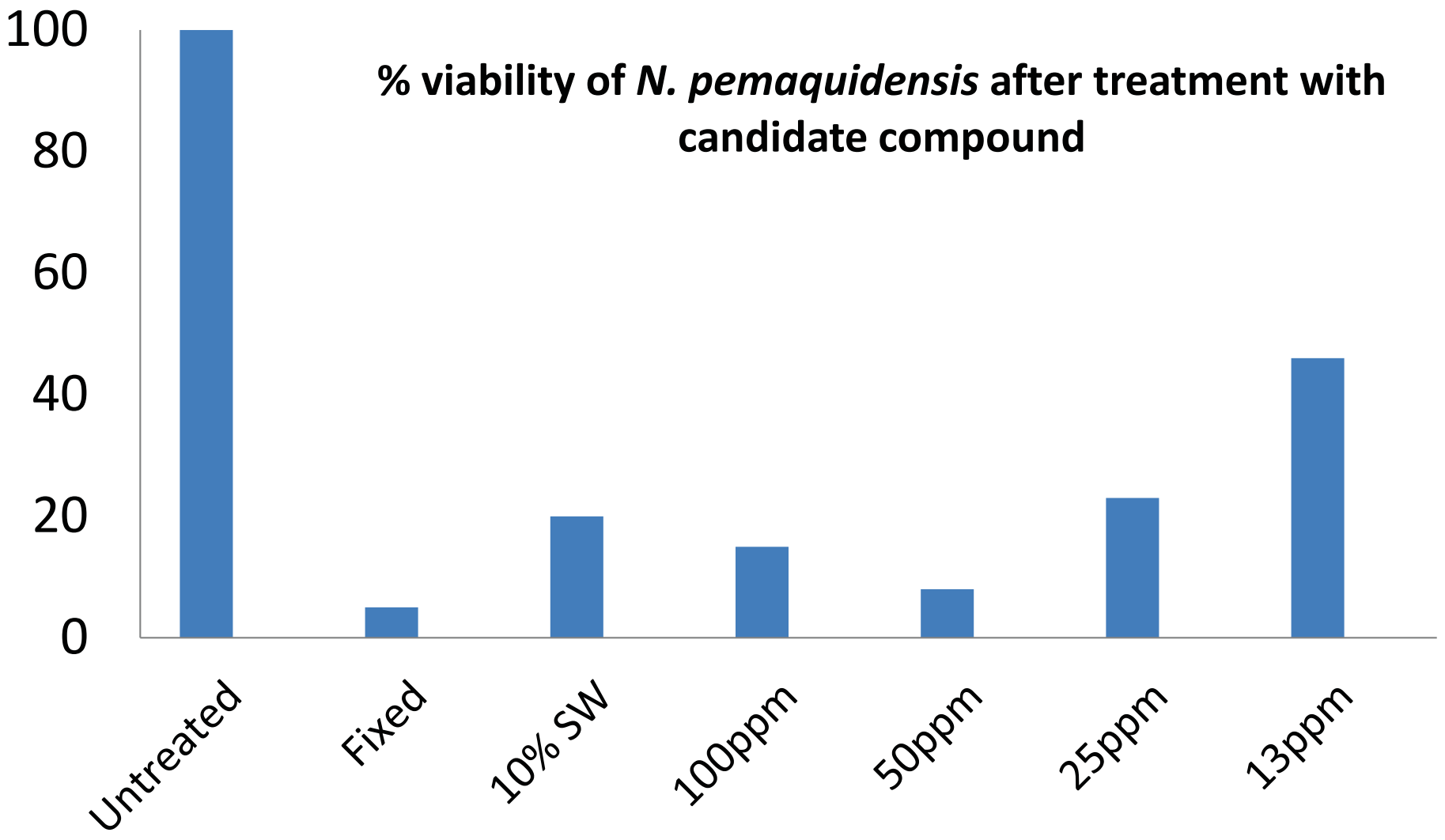


Development of Amoebae Bioassay



- Assay based on the observation that P. perurans actively ‘takes up’ Neutral red dye
- Apply treatments to observe ‘uptake’
- Requires appropriate controls (+ve and –ve)

Indicative results



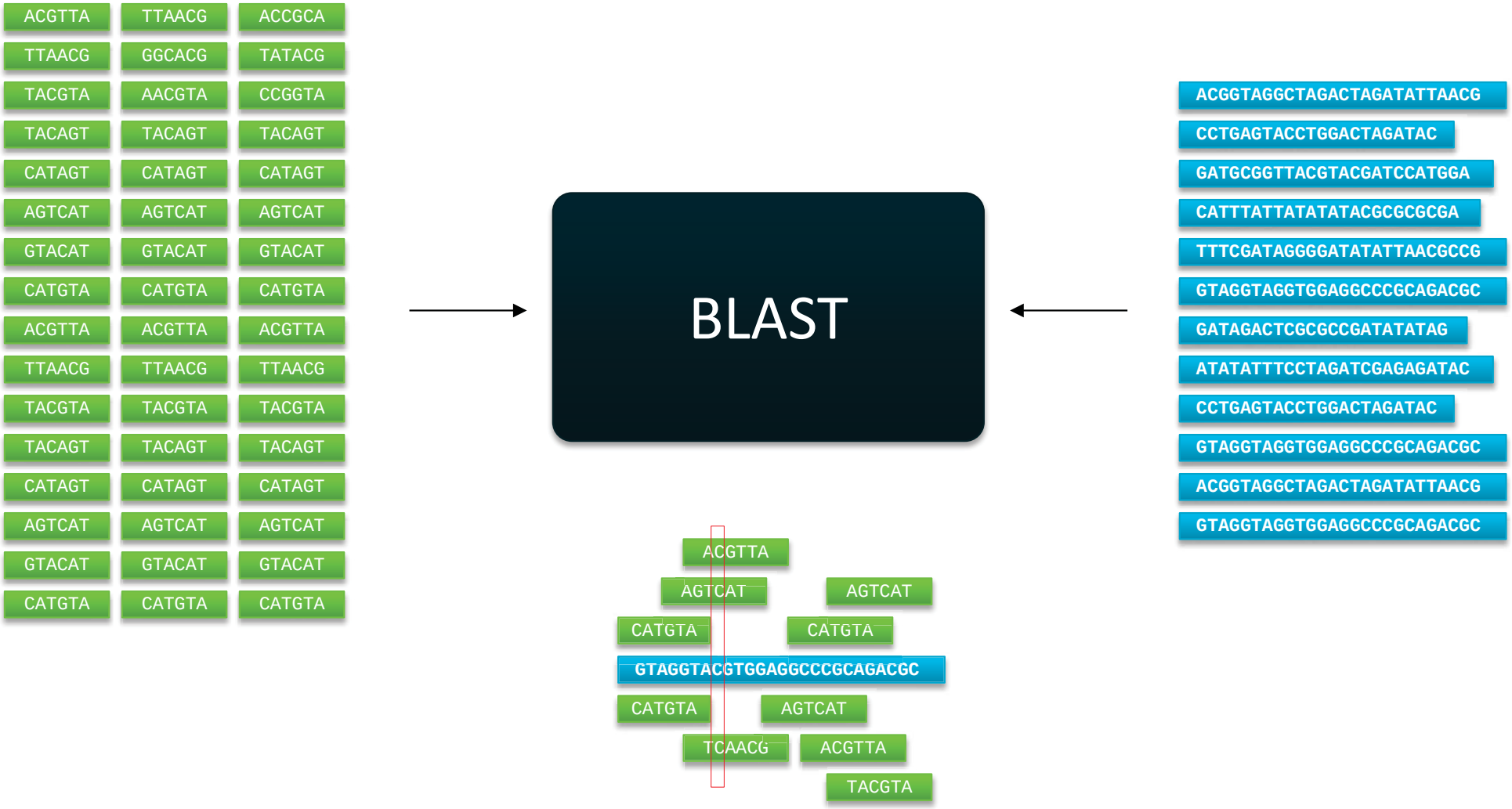
Transcriptomic analysis

Compare genetic information of amoeba ***P. Perurans*** (infective) and closely related species ***P. Pemaquidensis*** (non-infective) to identify differences.

Compare the two datasets to identify:

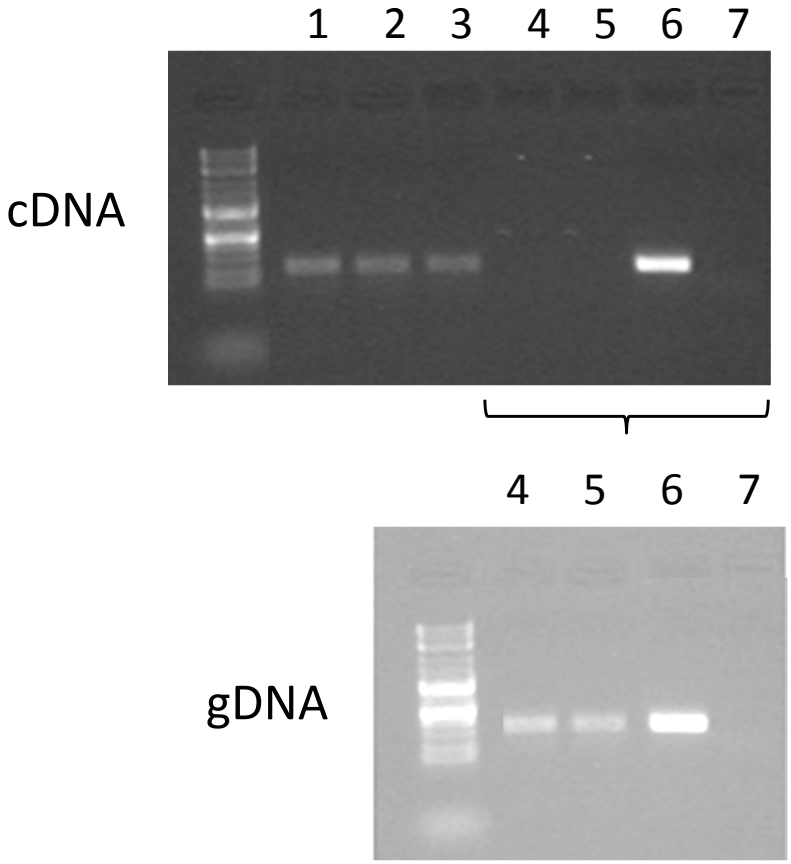
1. Transcripts (i.e., ***functionality***) present in one dataset that are "missing" in the other dataset?
2. Of those transcripts that are similar, how similar are they?

Raw Read Support



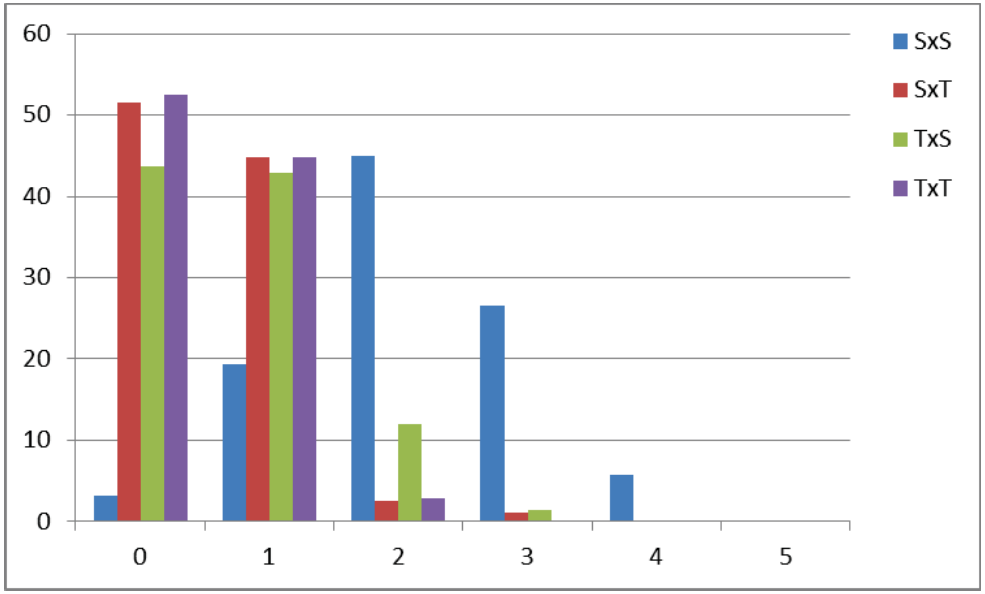
We can turn off genes in P. perurans

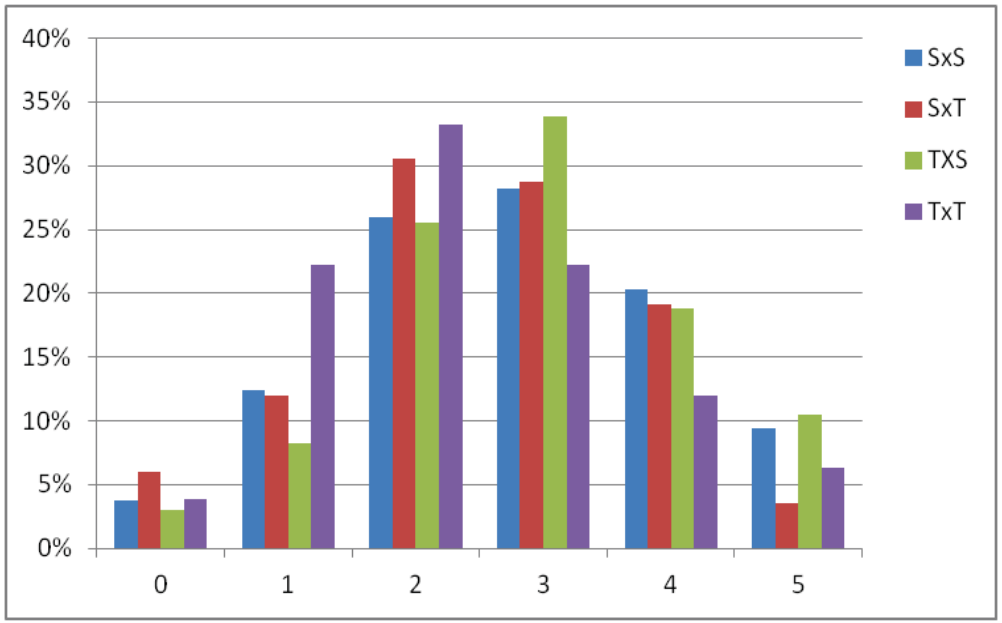
GSP for ‘Target’

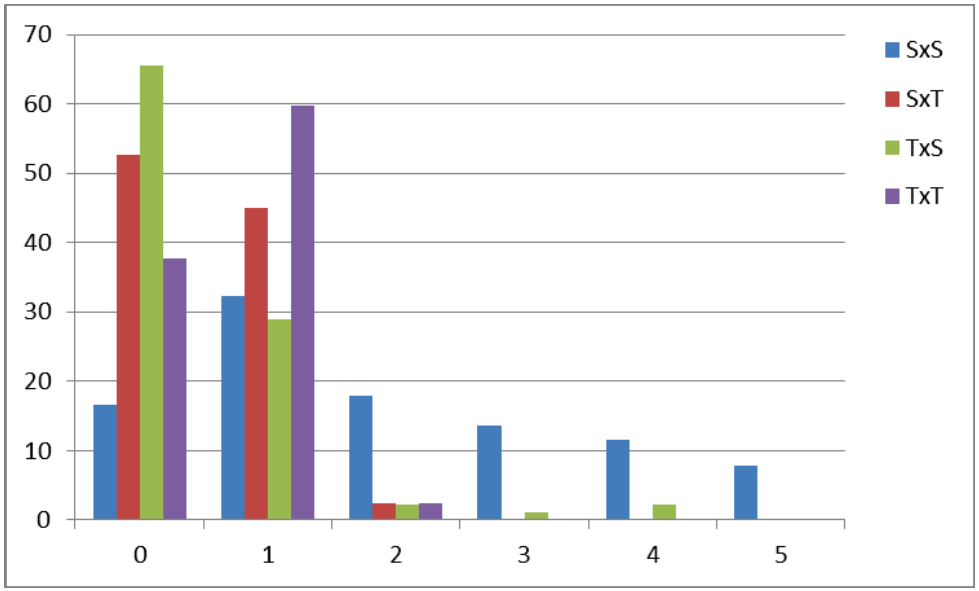


	Average Ct	
time	Target	18S
Untreated	28.2	22.5
24hr	28.7	22.9
48hr	29.8	23.6
72hr	32	23.9
1week	31.7	24.9
NTC	**32.5**	**34.4**

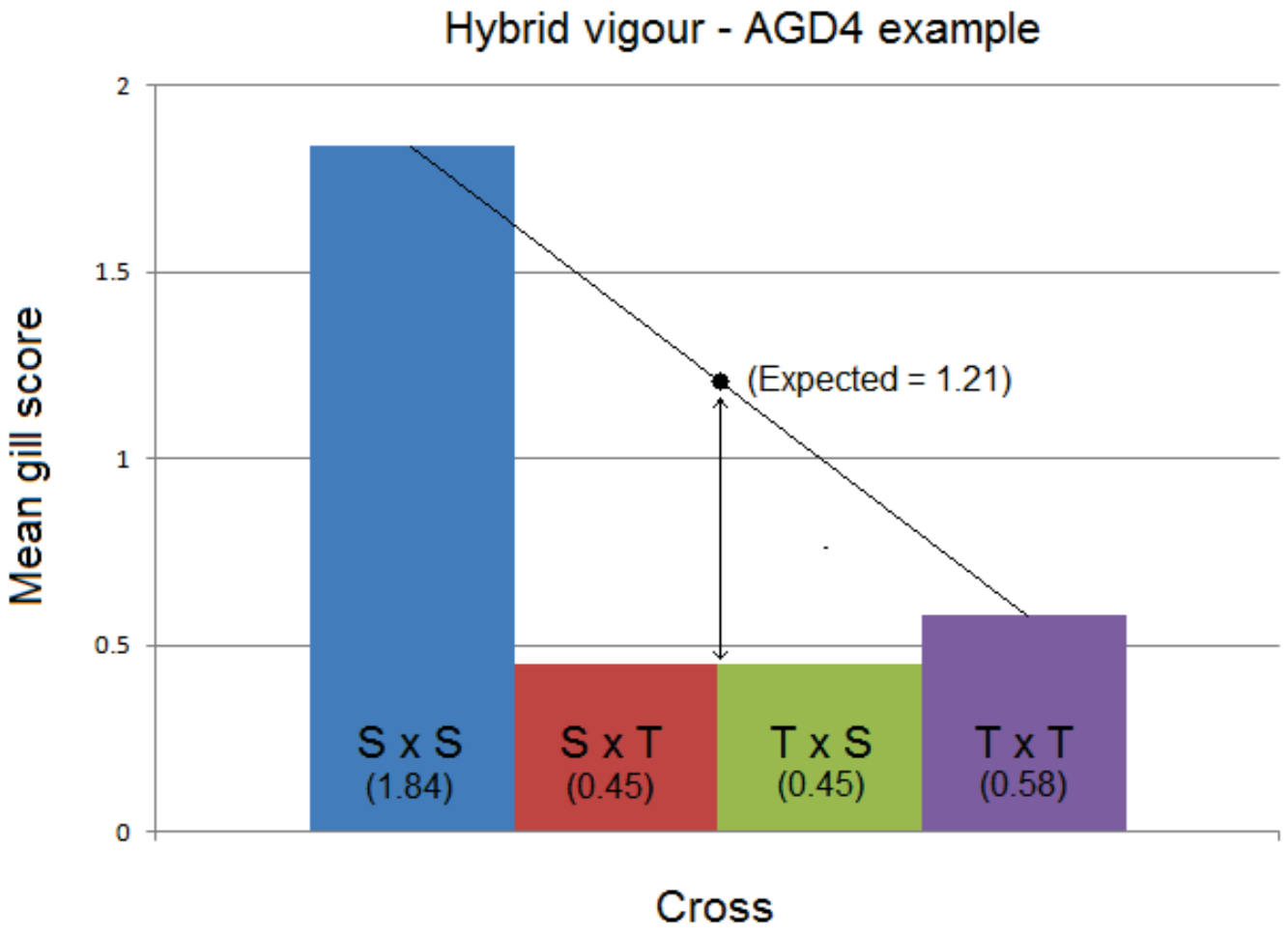
Hybrids – can we unlock the ‘key’ to resistance


60
50
40
30
20
10
0
0
1
2
3
4
5
SxS
SxT
TxS
TxT


40%
35%
30%
25%
20%
15%
10%
5%
0%
0
1
2
3
4
5
SxS
SxT
TXS
TxT


70
60
50
40
30
20
10
0
0
1
2
3
4
5
SxS
SxT
TxS
TxT

Hybrid vigour



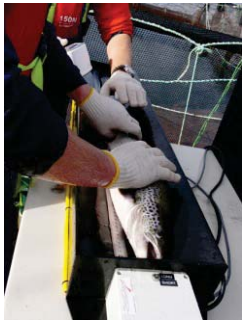
- 63% hybrid vigour observed at AGD4
- “Best parent” performance

Breeding for AGD Resistance

Broodstock never go to sea

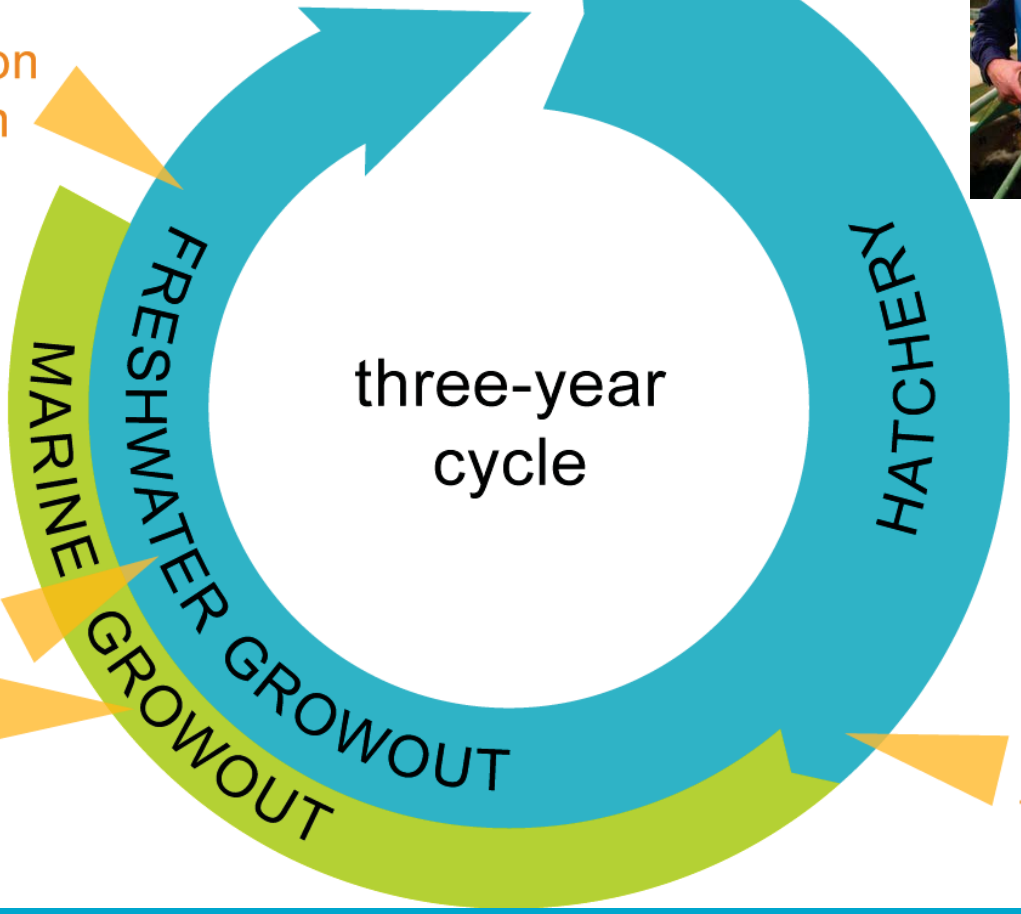
genetic evaluation and selection

spawn selected broodstock



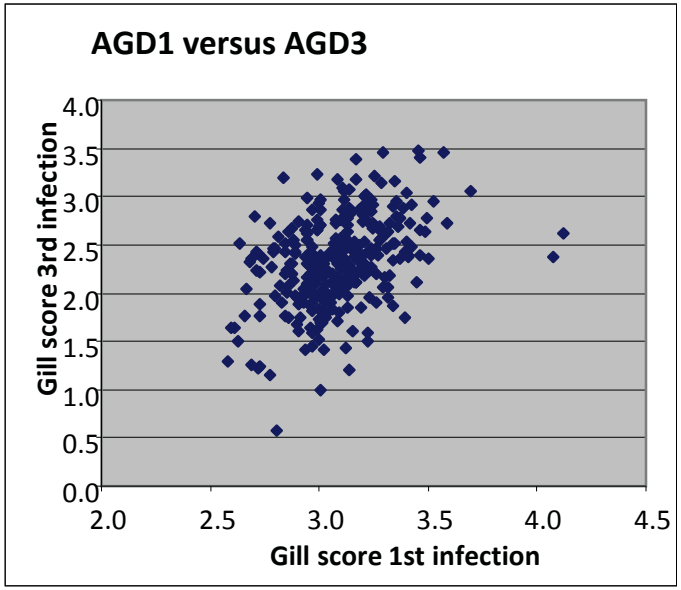
measurements

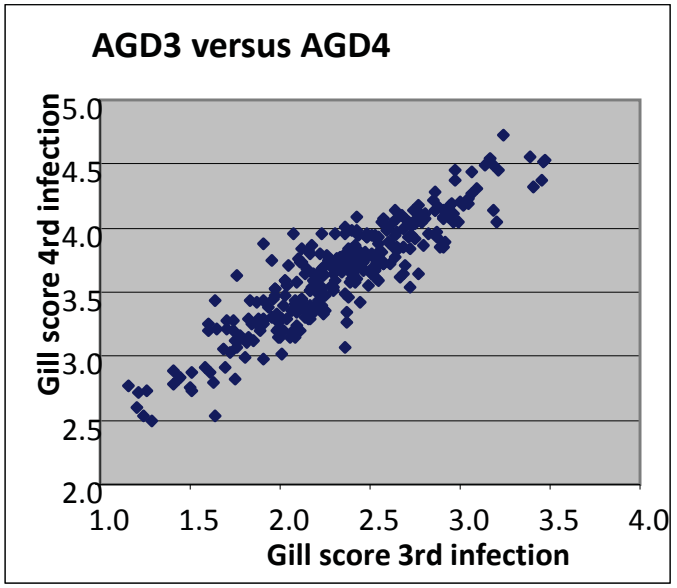
tag and DNA fingerprint



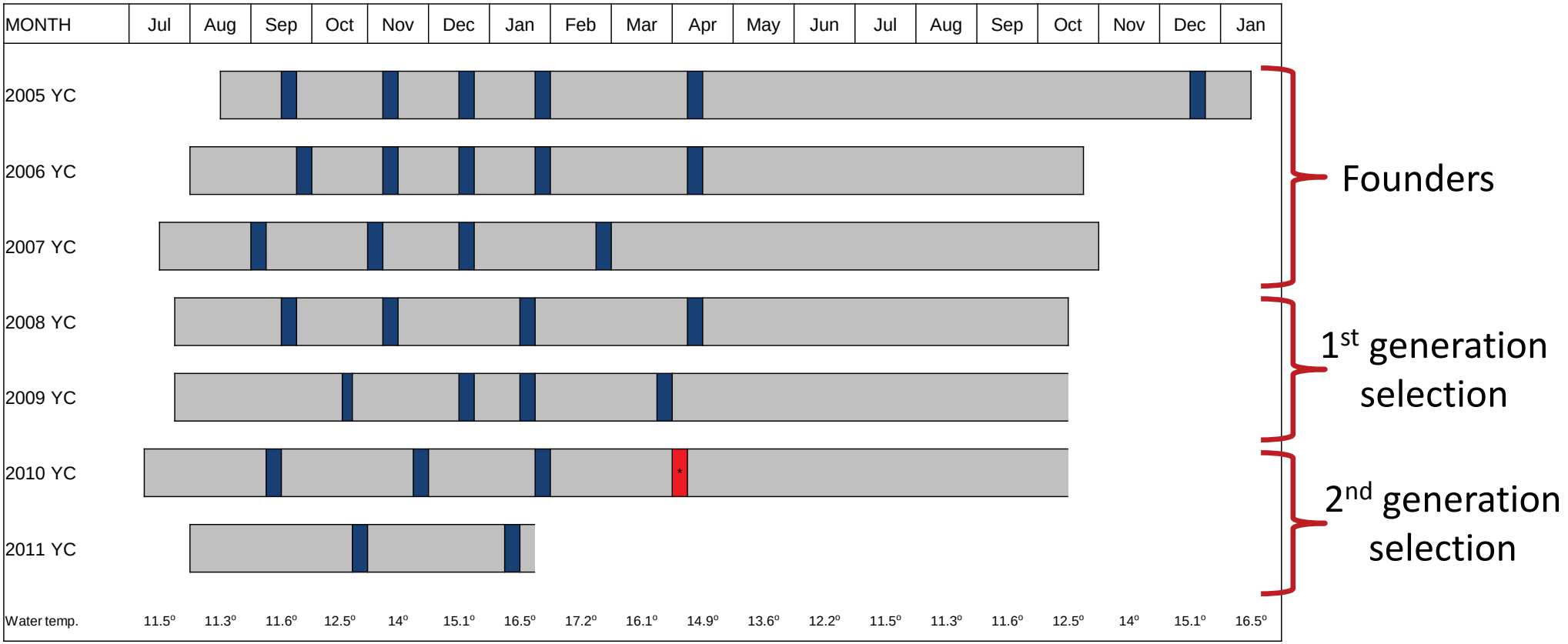
Gill Score is a consistent heritable trait

- All infections have significant genetic variation
  - (heritability range is h2 = 0.14±0.02 to 0.40±0.03)
- Two distinct traits, one is measured at first infection and the other at all subsequent infections
- First infection has lower genetic variation (h2 = 0.14)
- Subsequent infections have stronger genetic expression, especially when measured during summer





Selection is reducing the number of bathes

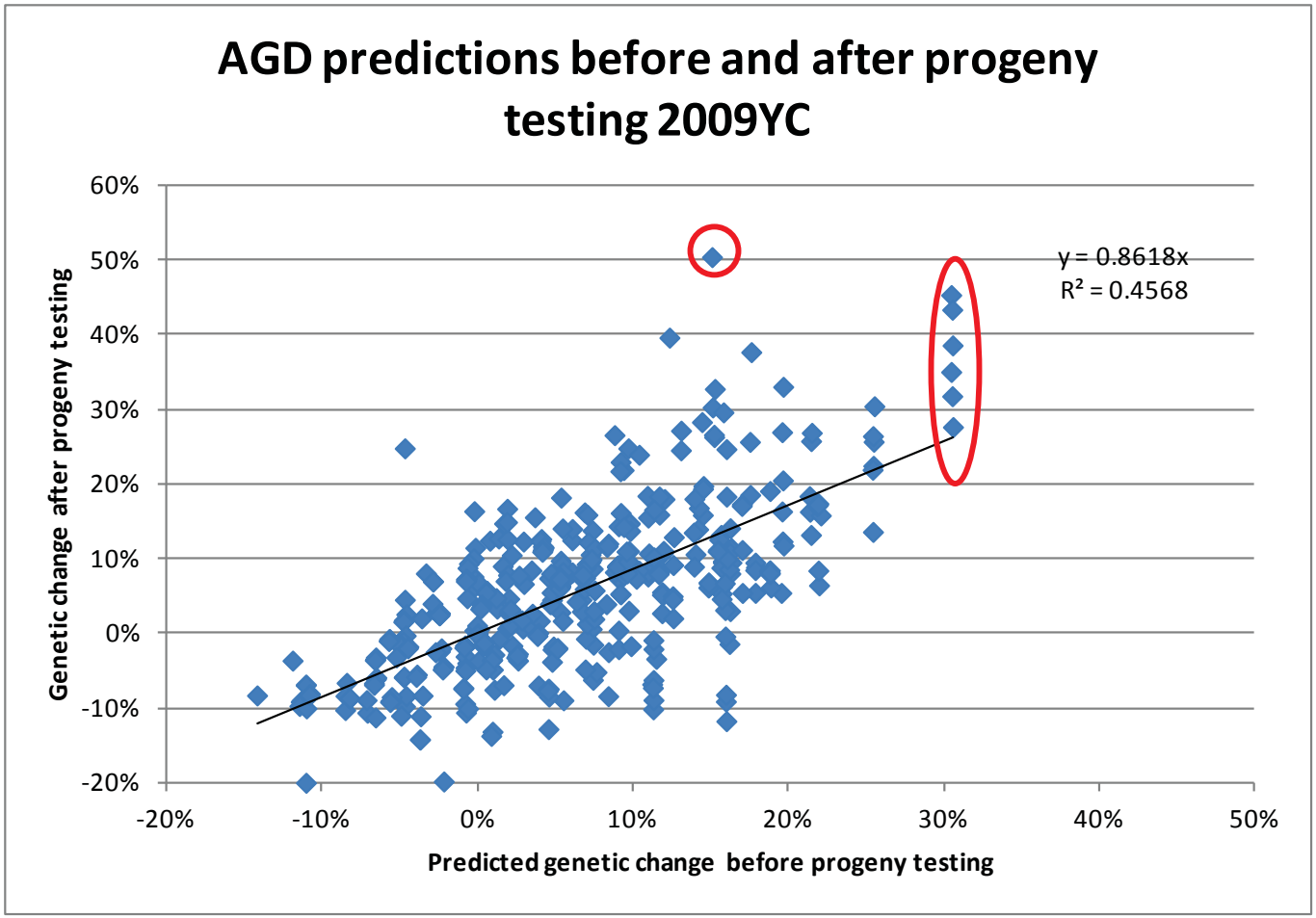


Selection is working – A deliberate 'Bad' family

AVERAGE FAMILY VALUES 2012 YC (SBP COHORT)			
	SBP families	BAD AGD family	Best AGD family
EBV AGDac (Bath interval) *	25%	-12%	49%
Mean AGD1 Gill score	1.4	1.8	1.2
Mean AGD2 Gill score	3.1	4.5	1.2

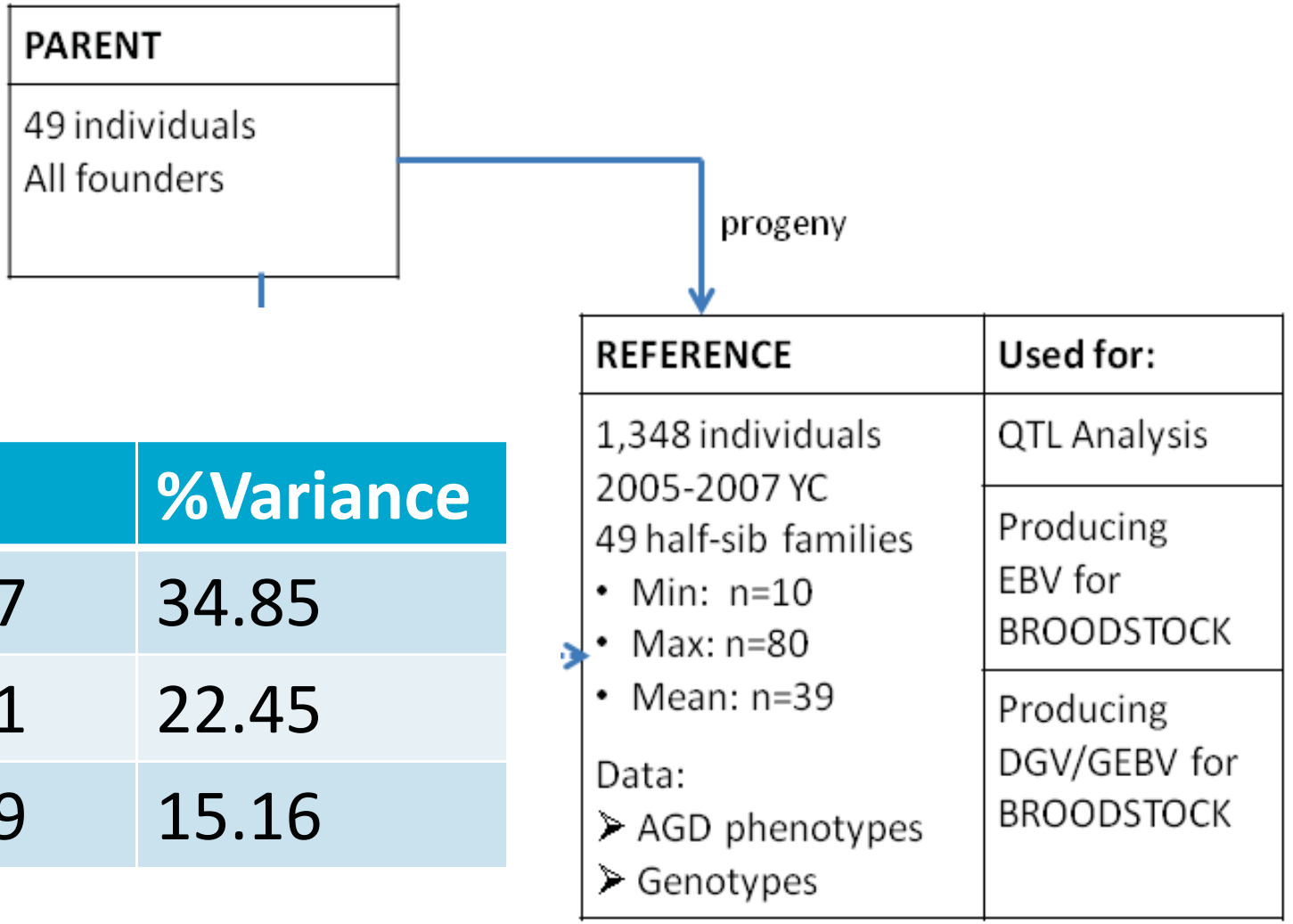
NB: Following GS2, Best AGD Family >75% ≤ GS1

Within vs between family variation



- Highlights the power of whole genome selection (WGS) to increase genetic gains as the broodstock remain in freshwater (biosecurity)

Can SNP explain some of the AGD resistance observed?



SNP #	LG	%Variance
1	Ssa-07	34.85
2	Ssa-01	22.45
3	Ssa-19	15.16

Summary

- Activities are focused on ‘HOST’, ‘PATHOGEN’ and ‘ENVIRONMENT’
- Focus is on delivering solutions/information to assist in alleviating the issue
- Partnership with the end users (industry) is crucial
- AGD R&D needs to be dynamic to adjust to changing priorities
- International collaboration is key – no need to reinvent the wheel

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Funding bodies and Industry and Academic collaborators

Thank you

CSIRO Food Futures Flagship
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