Genetics for productivity

» 3-4 years to flowering
» 10 years breeding to production cycle
» Progeny test + RRS
» Backcross / inbreeding /sex
Genetics for productivity

- Volume (m$^3$)
- Wood quality
  - Wood density
  - Spiral Grain
  - Stiffness
- Dothistroma

- Yield (trays/ha)
- Fruit Quality
  - Dry Matter
  - SSC
  - Flavour
- Psa
Genetics for productivity

» Longevity
» Climate change
» n=12
  » *Fitzroya cupressoides* (4x)
  » *Sequoia sempervirens* (6x)

» Longevity
» Climate change
» n=29
  » *Actinidia chinensis* (2x, 4x)
  » *A. arguta* (2x, 4x, 8x)
  » *Actinidia deliciosa* (6x)
Germplasm

Ferguson and Datson
"The killer awoke before dawn, he put his boots on he took a face from the ancient gallery And he walked on down the hall"
Quantitative and non-ordinal trait
<table>
<thead>
<tr>
<th>Year</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>1995</td>
<td>Tetraploid <em>Actinidia chinensis</em> breeding programme begins</td>
</tr>
<tr>
<td>2000</td>
<td>Breeding team selects 6 females and 7 males as promising parents</td>
</tr>
<tr>
<td>2002</td>
<td>2800 seedlings, including Gold3, are planted out in the research orchard</td>
</tr>
<tr>
<td>2004</td>
<td>Gold3 produces its first four fruit, identified as having superior dry matter and texture characteristics</td>
</tr>
<tr>
<td>2006</td>
<td>Ten selections, including Gold3, are selected for clonal trials</td>
</tr>
<tr>
<td>2008</td>
<td>Gold3 is transferred from the clonal development programme to pre-commercial block trials after sensory trials indicate high consumer preference</td>
</tr>
<tr>
<td>2009</td>
<td>Approximately 11.5 hectares of Gold3 established across the North Island and top of the South Island</td>
</tr>
<tr>
<td>2010</td>
<td>206 hectares of Gold3 is released to growers. Psa is identified in New Zealand</td>
</tr>
<tr>
<td>2011</td>
<td>An additional 250 hectares of Gold3 is released to growers</td>
</tr>
<tr>
<td>2012</td>
<td>An additional 1,750 hectares of Gold3 to be released to growers to replace Hort16A</td>
</tr>
<tr>
<td>2015</td>
<td>7,600 hectares of Gold3 planted</td>
</tr>
</tbody>
</table>
### Forecast ‘GOLD’ Production by Supply Year

<table>
<thead>
<tr>
<th>Year</th>
<th>Volume (million trays)</th>
<th>GOLD 3</th>
<th>Hort16A</th>
</tr>
</thead>
<tbody>
<tr>
<td>2011</td>
<td>29</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2012</td>
<td>26</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2013</td>
<td>16</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2014</td>
<td>23</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015</td>
<td>36</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2016</td>
<td>49</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2017</td>
<td>56</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2018</td>
<td>61</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2019</td>
<td>63</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2020</td>
<td>63</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

‘Gold3’
Message

1. Importance of pipeline concept
2. Understanding that breeding a new cultivar was going to take a few years
3. A new cultivar needs to be developed fast(er)
November 2010: Now what?
Breeding post-Psa
We cannot make progress only by increasing numbers.
Genomics pocket

» Automated DNA extraction, genotyping and scoring
» High resolution melting
Genomics of red and Psa tolerance

» Database
  » Pedigree
  » Ent

» Accurate phenotyping
» Genetic architecture
» Structure, trial design, population size
Pedigrees and database
Database

Everything? How far back? What data?
Accurate phenotyping
Accurate phenotyping

Whole fruit

Core

Inner pericarp

Outer pericarp

Peter McAtee 2015
Genetic architecture

Male parent

Female parent

Canhong Cheng, Paul Datson
Tightly-Linked Myb Genes are Associated with Red Petal Colour in \( A. \) \( e r i a n t h a \) x \( A. \) \( c h i n e n s i s \) Back-cross Families

Fraser \textit{et al}
Round 1 Marker Design

<table>
<thead>
<tr>
<th>List of Candidate Genes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transcription Factors</td>
</tr>
</tbody>
</table>

Map Genomic Sequence

- BWA/Samtools
- ‘Red 5’ Scaffolds

Filter out Non-Synonymous Variants

- Ensembl VEP
- ‘Red5’ Gene Models

Design Small-Amplicon HRM

https://github.com/cfljam/galaxy-PCR-markers
Whole Genome Sequencing - Myb210
Improved assembly of *A. chinensis* ‘Red5’ for Genetic Analysis

Ross Crowhurst
Round 2 marker design

BamH1 GBS
12E Factorial

Map to ‘Hong Yang’

Tassel

GS

Logistic Regression

WGS
12 chinensis

Map to ‘Hong Yang’

Freebayes/VCFtools

Fst/Phasing

Taqman/HRM
Organisation of Myb Genes on Red5 Pseudo-Sanger Pseudomolecule Chromosome 9
Transient expression in tobacco suggests Myb210/110b may act as a repressor.
GBS for Red Flesh Score

Canhong Cheng, Paul Datson
Psa, ploidy and bioassay

The New Zealand Institute for Plant & Food Research Limited
Mapping in a susceptible x tolerant population

- 2x CK 52 seedlings clonally propagated and 200 bioassayed
- Detailed phenotyping
- Good reads aligned to HY and PFR reference genome assembly
- 30,797 SNP sites detected; 11,211 polymorphic filtered to 6,608
- Draft genetic map comprised 3,364 SNPs spanning 4,295 cM
- SSR analysis at QTL peaks
Sus x Res mapping

Sue Gardiner, John McCallum
PSA Survival in Genotyped Commercial Red x Gold Families

- rOC_287: 36%
- rOD_287: 53%
- rOE_287: 49%
- rOF_287: 80%
Directions

» Quantitative phenotypes with image analysis
» Tagging markers for MAS
» Integration of red with Psa
  » Validation
  » Bioassay
Wise monkeys?
» Qualitative measurement
» Low heritability
» Expensive
» Negatively correlated
Germplasm universe, the lungs of new breeding

Cooper M. et al 2014
Acknowledgements

» KRIP
» Zespri
» Breeding and Genomics
  (Te Puke, MARC, Kerikeri, Motueka, Palmerston North, Lincoln)
» Plant pathology team
  (Te Puke, Ruakura)