GENETIC SIGNATURES of SELECTION & ASSOCIATION ANALYSIS of the DOMESTICATION EVENT in SOUTH AFRICAN ABALONE, HALIOTIS MIDAE

Rhode C., Dale-Kuys R., Vervalle J., Bester- Van der Merwe A., Roodt-Wilding R.
Department of Genetics, Stellenbosch University, Private Bag X1, Matieland, 7602 South Africa.
E-mail: clintr@sun.ac.za
Introduction: Abalone

• Gastropod mollusc, genus *Haliotis*, with approximately 56 extant species, globally

• Five endemic species in South Africa
  • a) *H. midae*; b) *H. spadicea*; c) *H. alfredensis*; d) *H. parva*; e) *H. queketti*

*Figure taken from Bester-van der Merwe et al. 2012*
Introduction: Abalone

- *Haliotis midae, i.e. Perlemoen*
  - Local species of commercial importance
  - Fisheries and aquaculture

% Tonnage of total aquaculture production (Figure taken from DAFF, 2012)

% Revenue of total aquaculture production (Figure taken from DAFF, 2012)
Introduction: Domestication as an Evolutionary Process

• Selection
  • Relaxed natural selection for survival in the wild
  • Increased natural selection for adaptation to “humanised environment”
  • Increased artificial selection

• Demography
  • Founder effect, reduction in effective population size
    • Greater influence of random drift
    • Increased inbreeding
    • Unequal parental contribution
Introduction:
General Observation for South African Abalone

Figure adapted from Rhode et al., 2012
Research Question

How is selection shaping the observed patterns of genetic variation in cultured populations of abalone?
Identifying Signatures of Selection

• Study populations:

[Map of South Africa with stars indicating wild and culture populations]
Identifying Signatures of Selection

- Molecular markers
- 150 microsatellite markers
- Genome-wide distribution
- On average 10cM interval

![Figure](image)

Figure adapted from Vervalle et al., 2012
Identifying Signatures of Selection

- Frequentist (LOSITAN) and Bayesian (BayeScan) $F_{st}$-outlier analysis
Identifying Signatures of Selection

% Loci under selection

<table>
<thead>
<tr>
<th></th>
<th>Across cultured populations</th>
<th>Across wild populations</th>
<th>Across all populations</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Directional</strong></td>
<td>2-4</td>
<td>3-13</td>
<td>~9</td>
</tr>
<tr>
<td><strong>Balancing</strong></td>
<td>4-12</td>
<td>2-3</td>
<td>6-18</td>
</tr>
</tbody>
</table>
Identifying Signatures of Selection

- Variance explained due to directional selection

**AMOVA based on neutral loci (\(P < 0.05\))**

- Among groups, FCT: 0.00447*
- Among populations within groups, FSC: 0.01605*
- Within populations, FST: 0.02045*

- 98%
- 0.4%
- 1.6%

**AMOVA based on loci under directional selection (\(P < 0.05\))**

- Among groups, FCT: 0.17707*
- Among populations within groups, FSC: 0.05207*
- Within populations, FST: 0.21992*

- 78%
- 18%
- 4%
Marker Association with Growth

• Growth rate currently selected trait

• Artificial phenotypic selection causative to molecular signature of selection?

• Correlation of genetic variants with growth?
Marker Association with Growth

• Commercial cohort of 661 F1 animals phenotyped

• Top and bottom ±15% selected for genotyping
  • 13 loci under directional selection

• Parentage analysis to correct for family size bias (final cohort: 80)
Marker Association with Growth

• Association tests:
  • Case/Control analysis
  • Quantitative analysis

• Simple correlation analysis
  • Allelic correlations with size

• BLAST – putative functional analysis
## Marker Association with Growth

### Locus-by-locus AMOVA: Large vs Small

<table>
<thead>
<tr>
<th>Marker</th>
<th>SSD (^a)</th>
<th>Df</th>
<th>Variance</th>
<th>% Variation</th>
<th>F(_{st})</th>
<th>G(^{''})(_{st})</th>
</tr>
</thead>
<tbody>
<tr>
<td>HmidILL-087955T</td>
<td>0.3091</td>
<td>1</td>
<td>0.0004</td>
<td>0.1179</td>
<td>0.0064</td>
<td>0.0051</td>
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<tr>
<td>HmLCS5M</td>
<td>0.1293</td>
<td>1</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0024</td>
<td>-0.0330</td>
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<tr>
<td>HmLCS48M</td>
<td>0.1453</td>
<td>1</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0036</td>
<td>-0.0200</td>
</tr>
<tr>
<td>Hm-NS18M</td>
<td>0.5574</td>
<td>1</td>
<td>0.0055</td>
<td>1.4459</td>
<td>0.0117*</td>
<td>0.0355*</td>
</tr>
<tr>
<td>HmidILL-146360P</td>
<td>1.4740</td>
<td>1</td>
<td>0.0133</td>
<td>3.2478</td>
<td>0.0232*</td>
<td>0.1569*</td>
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<tr>
<td>HmidILL-064192P</td>
<td>0.0264</td>
<td>1</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0005</td>
<td>-0.0313</td>
</tr>
<tr>
<td>HmNR106D</td>
<td>0.3132</td>
<td>1</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0026</td>
<td>-0.0577</td>
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<tr>
<td>HmidPS1.559</td>
<td>0.2919</td>
<td>1</td>
<td>0.0020</td>
<td>1.8547</td>
<td>0.0238*</td>
<td>0.0395*</td>
</tr>
</tbody>
</table>

\(^a\) SSD: Sum of Squares Deviation
Marker Association with Growth

**HmidILL-087955T**

- \( r = 0.3043 \)
- \( P = 0.0064 \)
- \( R^2 = 0.0926 \)

**HmidILL-146360P**

- \( r = 0.2426 \)
- \( P = 0.0302 \)
- \( R^2 = 0.0588 \)
Marker Association with Growth

HmidILL-087955T & HmidILL-146360P
Marker Association with Growth

• HmidILL-087955T :
  • 3’ UTR of retinol dehydrogenase 14a gene
  • Activation of retinol (vitamin A) to retinoic acid
  • Associated with development

• HmidILL-146360P :
  • 3’ UTR of malectin gene
  • N-linked glycosylation / carbohydrate binding
  • Carbohydrate metabolism / transmembrane / signalling
Conclusions

• Rapid divergence between wild progenitor and cultured populations
  • Role of selection
  • Artificial vs Natural selection

• Application in marker assisted breeding
  • Confirm in independent and larger cohorts
  • Larger genome project in future
Acknowledgements
Thank You!

Questions?