The Genetic Basis for the Propensity to Migrate in a Sequestered Population of Rainbow and Steelhead Trout

Ben Hecht
Columbia River Inter-Tribal Fish Commission
March 19, 2013
Migration

• Cultural, ecological, and economic benefits and services
• Migratory species declining globally
• Migratory species purported to have common syndrome (Dingle 2006)
Anadromy

Oncorhynchus mykiss

Freshwater Saltwater

smoltification
Smoltification

Genetic component

Parr

Environmental cues

Physiology

Morphology

Behavior

Smolt
Objectives

• Identify regions of the genome associated with migration
  – in a wild population of *O.mykiss* which maintains connection to ocean
  – in a wild population of *O.mykiss* sequestered for last 50 years behind barrier dam

• Are the same genetic regions associated with migration in both populations?
  – Is migration a derived trait?
  – Is migration locally adapted?
Genetics of Anadromy

Genome-Wide Association Study (GWAS)

• Samples
  – *Wild* populations of segregating individuals

• Genetic Markers
  – Thousands distributed throughout the genome

• Statistics
  – Marker/Trait associations
Samples

Washington

Idaho

Oregon

Columbia R.

N. F. Teanaway R.

M. F. Teanaway R.

Teanaway River

Yakima R.

Snake R.

WDFW

Brownlee Dam (est. 1958)

Upper Mann Creek

Holecek et al. (2012)

Barrier Dam
Samples

Yakima River, WA
- Electrofishing by WDFW
- PIT tagged in Spring 2008 recovered in Summer/Fall
- Resident RBT = mature w/ gametes
- Smolt = PIT array detection at downstream dam

Upper Mann Creek, ID
- Screw trap (March-June 2009)
- Parr = fish >1 yo with gametes and/or parr marks
- Smolts = silver fish >1 yo w/out parr marks
## Samples

<table>
<thead>
<tr>
<th>Location</th>
<th>Smolts</th>
<th>Residents</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yakima R.</td>
<td>29</td>
<td>98</td>
<td>127</td>
</tr>
<tr>
<td>Upper Mann Cr.</td>
<td>28</td>
<td>27</td>
<td>55</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>57</strong></td>
<td><strong>125</strong></td>
<td><strong>182</strong></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Gender</th>
<th>Smolts</th>
<th>Residents</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female</td>
<td>45</td>
<td>28</td>
<td>73</td>
</tr>
<tr>
<td>Male</td>
<td>12</td>
<td>97</td>
<td>109</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>57</strong></td>
<td><strong>125</strong></td>
<td><strong>182</strong></td>
</tr>
</tbody>
</table>
Genetic Markers

- Restriction-site Associated DNA (RAD) tag sequencing
  - Thousands of markers distributed throughout the genome
- OmyY1 – molecular sex marker
Genetic Markers

- 12,073 Polymorphic RAD-tag SNPs
- 8,219 (68%) SNPs aligned perfectly to loci from Miller et al. (2012) and Hecht et al. (2012)
- 1,148 (14%) SNPs had been assigned to a linkage group.
Statistics

Phenotype

Genotype

A/A  A/T  T/T

No Association
Statistics

**GLM**

\[ y = X\beta + S\alpha + Qv + e \]

*Life-History = SNP + sex + STRUCTURE + e*

**MLM**

\[ y = X\beta + S\alpha + Qv + Zu + e \]

*Life-History = SNP + sex + STRUCTURE + kinship + e*
## Results - GWAS

<table>
<thead>
<tr>
<th>Population</th>
<th># Loci</th>
<th># Sig. Loci GLM</th>
<th># Sig. Loci MLM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Global</td>
<td>5,019</td>
<td>58</td>
<td>219</td>
</tr>
<tr>
<td>Yakima River</td>
<td>4,338</td>
<td>107</td>
<td>50</td>
</tr>
<tr>
<td>Upper Mann Creek</td>
<td>6,039</td>
<td>22</td>
<td>138</td>
</tr>
</tbody>
</table>

**504 loci detected overall**

**267 loci detected in Global analyses**

**123 loci detected in Yakima River analyses**

**157 loci detected in Upper Mann Creek analyses**
Results - Marker Overlap

Significant Loci
Linkage map adapted from Miller et al. (2012)
Nichols et al. (2008)
Wringe et al. (2010)
Le Bras et al. (2011)
Martínez et al. (2011)
Hecht et al. (2012)

Linkage map adapted from Miller et al. (2012)
Linkage map adapted from Miller et al. (2012)
Linkage map adapted from Miller et al. (2012)
Conclusions

• Identified 504 loci associated with the propensity to migrate in two wild populations of *O.mykiss*

• Several mapped loci localize to QTL regions previously detected suggesting some conserved mechanisms between populations

• Some loci are unique to each population, suggesting locally adapted mechanisms
Conclusions

• UMC continues to exhibit genetic variation for propensity to migrate despite 50 years sequestration above a barrier dam

• Does this mean if passage to the ocean is restored anadromy in Upper Mann Creek would be reestablished???
Genome-wide association reveals genetic basis for the propensity to migrate in wild populations of rainbow and steelhead trout

BENJAMIN C. HECHT,*† NATHAN R. CAMPBELL,† DEAN E. HOLECEK‡ and SHAWN R. NARUM†

*Hagerman Fish Culture Experiment Station, Aquaculture Research Institute, University of Idaho, 3059-F National Fish Hatchery Road, Hagerman, ID 83332, USA, †Hagerman Fish Culture Experiment Station, Columbia River Inter-Tribal Fish Commission, 3059-F National Fish Hatchery Road, Hagerman, ID 83332, USA, ‡Department of Fish and Wildlife Resources, University of Idaho, PO Box 441136, Moscow, ID 83844-1136, USA
Thank You

Scott M. Blankenship
Cherril Bowman

Alex Lipka

Mike Miller
Doug Turnbull
GCF

Contact: Ben Hecht
Email: hecb@critfc.org

Dennis Scarnecchia
Rob Lyon
IBEST CRC

Garrett McKinney

Megan Moore
Travis Jacobson
Andrew Matala
Results - Structure

Estimated using programs STRUCTURE and CLUMPP using a subset of 1,000 SNPs with 100% genotype frequency and MAF $\geq 0.10$. Figure generated by program DISTRUCT.
RADseq

DNA

sbfi digestion

P1 Ligation

Sonication

Size Select

P2 Ligation

PCR
Genotyping by sequencing

L1^A/A^, L6^C/G^ (ID001)

L1^T/T^, L6^C/G^ (ID002)
Results - RAD

- 5 RAD libraries
- 38-39 barcoded samples per library
- Avg. 185M raw & 123M QF reads per library

- 189 total individuals sequenced
- Avg. 2.8M QF reads per individual
- 12,073 polymorphic loci detected
### Linkage group assignment of significant loci

<table>
<thead>
<tr>
<th>Linkage group</th>
<th>Global</th>
<th></th>
<th>Yakima</th>
<th>Upper Mann Creek</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>GLM</td>
<td>MLM</td>
<td>GLM</td>
<td>MLM</td>
<td>GLM</td>
</tr>
<tr>
<td>OmySex</td>
<td>2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Omy1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>Omy2</td>
<td>2</td>
<td>4</td>
<td>2</td>
<td>1</td>
<td>9</td>
</tr>
<tr>
<td>Omy3</td>
<td>4</td>
<td>1</td>
<td>1</td>
<td></td>
<td>6</td>
</tr>
<tr>
<td>Omy4</td>
<td>2</td>
<td></td>
<td></td>
<td>1</td>
<td>3</td>
</tr>
<tr>
<td>Omy5</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0</td>
</tr>
<tr>
<td>Omy6</td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Omy7</td>
<td>1</td>
<td></td>
<td></td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Omy8</td>
<td>5</td>
<td>2</td>
<td></td>
<td></td>
<td>7</td>
</tr>
<tr>
<td>Omy9</td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Omy10</td>
<td>1</td>
<td>2</td>
<td></td>
<td>1</td>
<td>4</td>
</tr>
<tr>
<td>Omy11</td>
<td>1</td>
<td>8</td>
<td>3</td>
<td>2</td>
<td>14</td>
</tr>
<tr>
<td>Omy12</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>1</td>
<td>5</td>
</tr>
<tr>
<td>Omy13</td>
<td>2</td>
<td></td>
<td>1</td>
<td>1</td>
<td>4</td>
</tr>
<tr>
<td>Omy14</td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Omy15</td>
<td>2</td>
<td></td>
<td>1</td>
<td></td>
<td>4</td>
</tr>
<tr>
<td>Omy16</td>
<td>1</td>
<td></td>
<td>3</td>
<td>2</td>
<td>6</td>
</tr>
<tr>
<td>Omy17</td>
<td>1</td>
<td></td>
<td>1</td>
<td></td>
<td>2</td>
</tr>
<tr>
<td>Omy18</td>
<td>1</td>
<td></td>
<td>4</td>
<td>1</td>
<td>6</td>
</tr>
<tr>
<td>Omy19</td>
<td>1</td>
<td></td>
<td></td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Omy20</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>4</td>
</tr>
<tr>
<td>Omy21</td>
<td>1</td>
<td></td>
<td></td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Omy22</td>
<td>1</td>
<td></td>
<td></td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>Omy23</td>
<td>2</td>
<td></td>
<td></td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>Omy24</td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Omy25</td>
<td>1</td>
<td></td>
<td>6</td>
<td></td>
<td>7</td>
</tr>
<tr>
<td>Omy26</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0</td>
</tr>
<tr>
<td>Omy27</td>
<td>1</td>
<td></td>
<td>1</td>
<td>1</td>
<td>5</td>
</tr>
<tr>
<td>Omy28</td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>12</td>
<td>49</td>
<td>22</td>
<td>11</td>
<td>7</td>
</tr>
</tbody>
</table>

Linkage group assignment based on alignment of RAD markers to Miller et al. (2012) and Hecht et al. (2012)