Contemporary Genetic Diversity for the Kiwikipi (Maui Parrotbill; *Pseudonestor xanthophrys*)

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Kiwikiu Sp. Biology

- Population ~500
- Insectivorous
- Usually raise one HY
- Long juvenile dependency
- Long term monogamous

- High adult and low juvenile survival
- ARS 46%
Kiwikiu Population Range

Historically on the islands of Maui and Molokai

Currently on the windward slopes of the island of Maui
Why Conservation Genetics?

- Are there genetic factors affecting the extinction risk for the Kiwikiu?
- Can we make management decisions to minimize inbreeding and loss of genetic diversity?
- How can we relate these to plans for reintroduction of a second population?
Blood and Feather Sampling

120 individuals
(92 East, 17 West, 11 Captive)
Ko’olau Gap
Population Genetics
– Mitochondrial DNA

- Control-region
  - Non-coding, highly variable
  - Inherited maternally
  - Not under selection
- 552 bp (base pairs, sites) examined
- 85 individuals
- 3 population groups
HAPLOTYPE A (Most Common)

HAPLOTYPE B (Common)

HAPLOTYPE C (Rare)
## Haplotype Diversity

<table>
<thead>
<tr>
<th>Population Groups</th>
<th>n</th>
<th>Hp</th>
<th>Hd</th>
<th>± SD</th>
<th>π</th>
<th>f (A)</th>
<th>f (B)</th>
<th>f (C)</th>
</tr>
</thead>
<tbody>
<tr>
<td>East</td>
<td>56</td>
<td>3</td>
<td>0.350</td>
<td>± 0.067</td>
<td>0.001</td>
<td>0.786</td>
<td>0.196</td>
<td>0.018</td>
</tr>
<tr>
<td>West</td>
<td>18</td>
<td>2</td>
<td>0.425</td>
<td>± 0.099</td>
<td>0.001</td>
<td>0.722</td>
<td>0.278</td>
<td>0.000</td>
</tr>
<tr>
<td>Captive</td>
<td>11</td>
<td>2</td>
<td>0.509</td>
<td>± 0.010</td>
<td>0.001</td>
<td>0.636</td>
<td>0.364</td>
<td>0.000</td>
</tr>
<tr>
<td>Total</td>
<td>85</td>
<td>3</td>
<td>0.382</td>
<td>± 0.050</td>
<td>0.001</td>
<td>0.753</td>
<td>0.235</td>
<td>0.012</td>
</tr>
</tbody>
</table>

Sample size (n), number of haplotypes (Hp), haplotype (gene) diversity (Hd), nucleotide diversity (π) and the frequencies (f) of haplotypes A, B and C.
Haplotype Diversity

CAPTIVE n = 11

[Diagram showing haplotype diversity with pie charts and map]
Haplotype Diversity

- Compared to other island populations:
  - Kiwikiu $H_d = 0.38$
  - Hawaii Akepa $H_d = 0.98$ (common)
  - Pink Pigeon $H_d = 0.45$ (bottleneck of ~12)
  - Seychelles Paradise Flycatcher $H_d = 0.00$ (bottleneck of ~40)
  - Nihoa Millerbird $H_d = 0.22$ (bottleneck of >200)

- Single female of Haplotype C, no known offspring found
- Captive population may need new individuals to match frequencies found in the wild
Microsatellites are favored for evaluating diversity due to high variability and co-dominant inheritance.

Species specific microsatellites identified and primers optimized by Genetic Identification Services.

- Found 13 polymorphic and 11 monomorphic markers on 5 MAPA samples.
- Tested 15 of these markers across all DNA samples.
  - Resulted in 12 useable polymorphic markers.
Chromosome locations in the zebra finch (*Taeniopygia guttata*) genome of the 12 microsatellite loci characterized in the Kiwikiu
Microsatellite Results

- Sample sizes differ yet represent equivalent % of populations
- Higher levels of heterozygosity in the east

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<th>Overall</th>
<th>Captive</th>
<th>East</th>
<th>West</th>
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</thead>
<tbody>
<tr>
<td>Observed Heterozygosity</td>
<td>0.574 (0.052)</td>
<td>0.599 (0.099)</td>
<td>0.618 (0.081)</td>
<td>0.505 (0.096)</td>
</tr>
<tr>
<td>Expected Heterozygosity</td>
<td>0.534 (0.045)</td>
<td>0.512 (0.081)</td>
<td>0.605 (0.073)</td>
<td>0.485 (0.082)</td>
</tr>
<tr>
<td>Unbiased Expected Heterozygosity</td>
<td>0.550 (0.046)</td>
<td>0.541 (0.085)</td>
<td>0.609 (0.073)</td>
<td>0.500 (0.084)</td>
</tr>
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</table>
**Microsatellite Results**

- Private alleles found in both the east and the west

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<th>East</th>
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<tbody>
<tr>
<td><strong>No. of Different Alleles</strong></td>
<td>4.878 (0.416)</td>
<td>3.818 (0.519)</td>
<td>6.727 (0.714)</td>
<td>4.090 (0.609)</td>
</tr>
<tr>
<td><strong>No. of Effective Alleles</strong></td>
<td>2.770 (0.227)</td>
<td>2.512 (0.295)</td>
<td>3.386 (0.499)</td>
<td>2.413 (0.319)</td>
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Measuring Population Fragmentation

- How different are the subpopulations? $F_{ST}$ and $R_{ST}$ values

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<tr>
<td>$F_{IS}$</td>
<td>-0.044 (0.037)</td>
<td></td>
<td></td>
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<tr>
<td>$F_{IT}$</td>
<td>0.014 (0.039)</td>
<td></td>
<td></td>
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<tr>
<td>$F_{ST}$</td>
<td>0.056 (0.012)</td>
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- East and west not significantly different but variation present
- Captive and west had the most, and the only significant, differentiation
Reintroduction Plans
Nakula Exclosure Restoration

- Restoration trials currently being set up
- Planting to begin in 2013
Mahalo to:

• MFRBP Field Teams and Volunteers
• DLNR/Division of Forestry & Wildlife
• Natural Area Reserve System
• US Fish & Wildlife Service
• Pacific Cooperative Studies Unit
• Pacific Helicopters
• Windward Aviation
• Haleakala National Park
• Haleakala Ranch
• The Nature Conservancy
• The University of Kent
• Tri-Isle RC&D