### Contemporary Genetic Diversity for the Kiwikiu (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 survivalARS 46%



## **Kiwikiu Population Range**

Historically on the islands of Maui and Molokai





Currently on the windward slopes of the island of Maui



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## **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?







# 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 Diversity**

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

Sample size (*n*), number of haplotypes (Hp), haplotype (gene) diversity (Hd), nucleotide diversity ( $\pi$ ) and the frequencies (*f*) of haplotypes A, B and C.



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## **Haplotype Diversity**



## **Haplotype Diversity**

Compared to other island populations:

- Kiwikiu  $H_d = 0.38$
- Hawaii Akepa H<sub>d</sub> = 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



# Population Genetics – Nuclear DNA - Microsatellites

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

#### Heterozygosity patterns



	Overall	Captive	East	West
Observed Heterozygosity	0.574 (0.052)	0.599 (0.099)	0.618 (0.081)	0.505 (0.096)
Expected Heterozygosity	0.534 (0.045)	0.512 (0.081)	0.605 (0.073)	0.485 (0.082)
Unbiased Expected Heterozygosity	0.550 (0.046)	0.541 (0.085)	0.609 (0.073)	0.500 (0.084)



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#### **Microsatellite Results**





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#### Private alleles found in both the east and the west

	Overall	Captive	East	West
No. of Different Alleles	4.878 (0.416)	3.818 (0.519)	6.727 (0.714)	4.090 (0.609
No. of Effective Alleles	2.770 (0.227)	2.512 (0.295)	3.386 (0.499)	2.413 (0.319

# Measuring Population Fragmentation

• How different are the subpopulations? F<sub>st</sub> and R<sub>st</sub> values

F <sub>IS</sub>	-0.044 (0.037)
FIT	0.014 (0.039)
F <sub>ST</sub>	0.056 (0.012)

	Captive	East	West
Captive			
East	0.031		
West	0.162	0.061	

East and west not significantly different but variation present

• Captive and west had the most, and the only significant, differentiation





### **Nakula Exclosure Restoration**







 Restoration trials currently being set up
 Planting to begin in 2013



#### Mahalo to: •MFBRP 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















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