

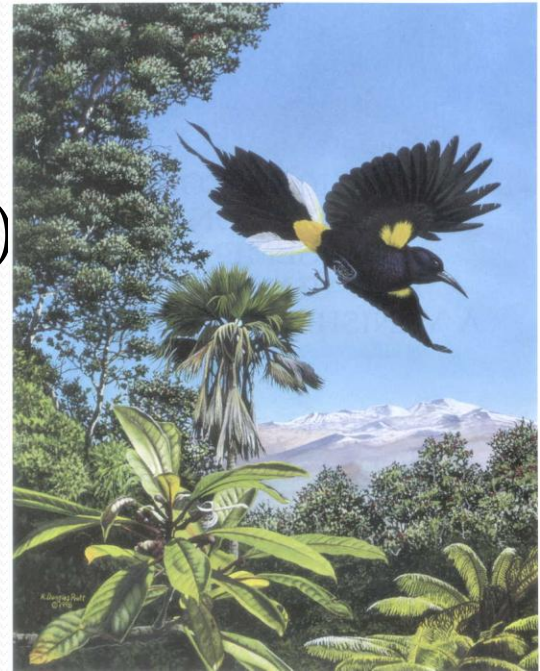


The Role of Genetics in the Conservation of Hawaiian Birds

**Sheila Conant
Department of Zoology
University of Hawai`i at Mānoa**

Hawaiian Birds: Vital Statistics

- 110+ native, endemic land-bird species before human arrival
- ~50 lost during Polynesian period; 26 more since 1778
- Of the remaining endemic forms, 32 listed as Endangered
- Most recent extinction 2004 – Po`o-uli
- 15 species “on the brink” (fewer than 500) some of these may be extinct
- 8 not seen in last ~20 years



Historical Distributions and Genetic Variation



- Discovery and reconstruction of Hawaiian bird distributions has been a combined effort by paleontologists (James and Olson) and geneticists (Fleischer, Paxinos, Rhymer, Cooper, others)
- Laysan Teal found on all main Hawaiian islands
- Laysan and Nihoa Finches found in main Hawaiian islands
- Loss of genetic variation: `Ālalā, Nēnē, Palila

These results guide both *ex situ* and *in situ* management

Genetics and Systematics

- Johnson, Fleischer *et al.*: Phylogenetic position of Drepanids
- Tarr and Fleischer: splitting the `Amakihi
- Fleischer and McIntosh: enumeration of founding lineages: 19 nonpasserine, 6 passerine colonists radiated into 36 and 72 species, respectively
- VanderWerf *et al.*: splitting the `Elepaio
- Yeung *et al.*: lumping the White Tern



Disease and Hawaiian Forest Birds

Avian malaria and pox, vectored by *Culex quinquefasciatus* are the biggest threats to continued existence of many forest bird species



- Molecular genetic studies of *Plasmodium*
- Molecular genetic studies of *Culex*
- Genetic signatures and disease resistance
 - Big Island `Amakihi (Foster *et al.* Eggert *et al.*)
 - O`ahu `Amakihi (Krend in prep)

Culex Genetics



- Fonseca *et al.*
 - Original *Culex* introduction was probably from New World
 - Original lineage has been replaced by South Pacific lineage, which is consistent with recent expansion of populations to higher elevations
 - Significant interisland and within island population structure exists
- Keyghobadi *et al.*
 - There is significant population structure in Big Island *Culex*
 - Low elevation *Culex* populations showed significantly greater genetic diversity than mid-elevation populations

Plasmodium Genetics

- Beadell, Fleischer, Atkinson, et al.
 - *Plasmodium* strain in Hawai`i represents a single lineage
 - This lineage has broad host range world wide
 - The lineage probably originated in Old World
 - The lineage is dominant on several other oceanic islands

Genetic characterization of disease resistant honeycreepers

Foster *et al.* and Eggert *et al.* found population structure in Big Island `Amakihi: high elevation populations differed from low elevation, malaria resistant populations

Foster *et al.*: no population structure in Big Island `Apapane or `I`iwi, both of which are more susceptible to malaria and are rare to extremely rare, respectively, at low elevations



Honeycreeper Major Histocompatibility Complex (MHC) variation (Jarvi *et al.*)

- Honeycreeper MHC sequences exhibit two distinct clusters, one variable, one nearly invariable
- Mitochondrial DNA non variable in malaria susceptible `I` iwi, but variable in malaria resistant, low elevation populations of `A` makihi
- Low variability in `I` iwi may be due to pre-disease population bottleneck



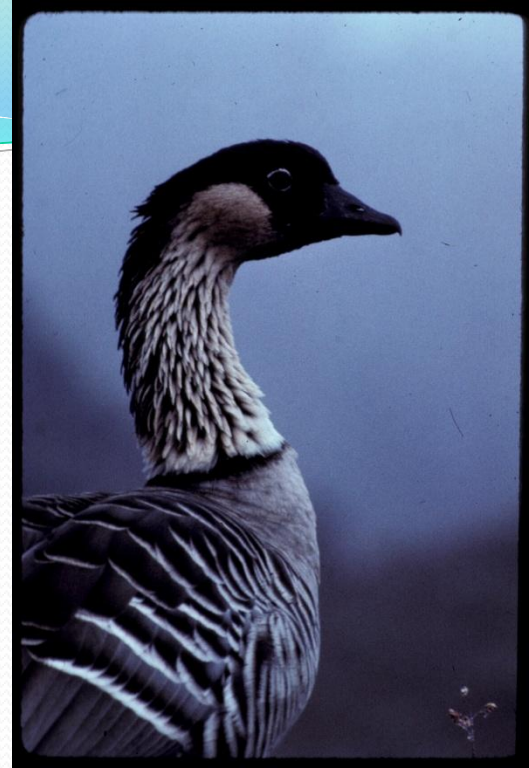
Population Genetics and Management

- Reding *et al.* – Hawai`i `Ākepa: little diversity lost despite recent declines from a population size about one order of magnitude greater than current population
- Foster *et al.*, Eggert *et al.* – Big Island Forest Birds: genetically diverse, low elevation `Amakihi exhibit disease resistance
- James *et al.* – Hawaiian Petrel: N_e , population structure
- Young *et al.* – Laysan Albatross: Identification of management units (ESUs)
- Yeung *et al.* – White Tern: Identification of management units



Captive Propagation

- Hawaii State captive propagation facilities released Nēnē and Koloa and bred the first `Ālalā in captivity
- 874 birds raised by Keauhou and Maui Bird Conservation Centers since 1993
- `Ālalā (75 adults, 10 chicks 2010)
- Nēnē: (400+ birds released; Kaua`i population robust, growing rapidly)
- Palila: (birds released 4 different years)
- Puaiohi (188 birds released since 1999)
- Kiwikiu (Maui Parrotbill): breeding
- `Ākohekohe

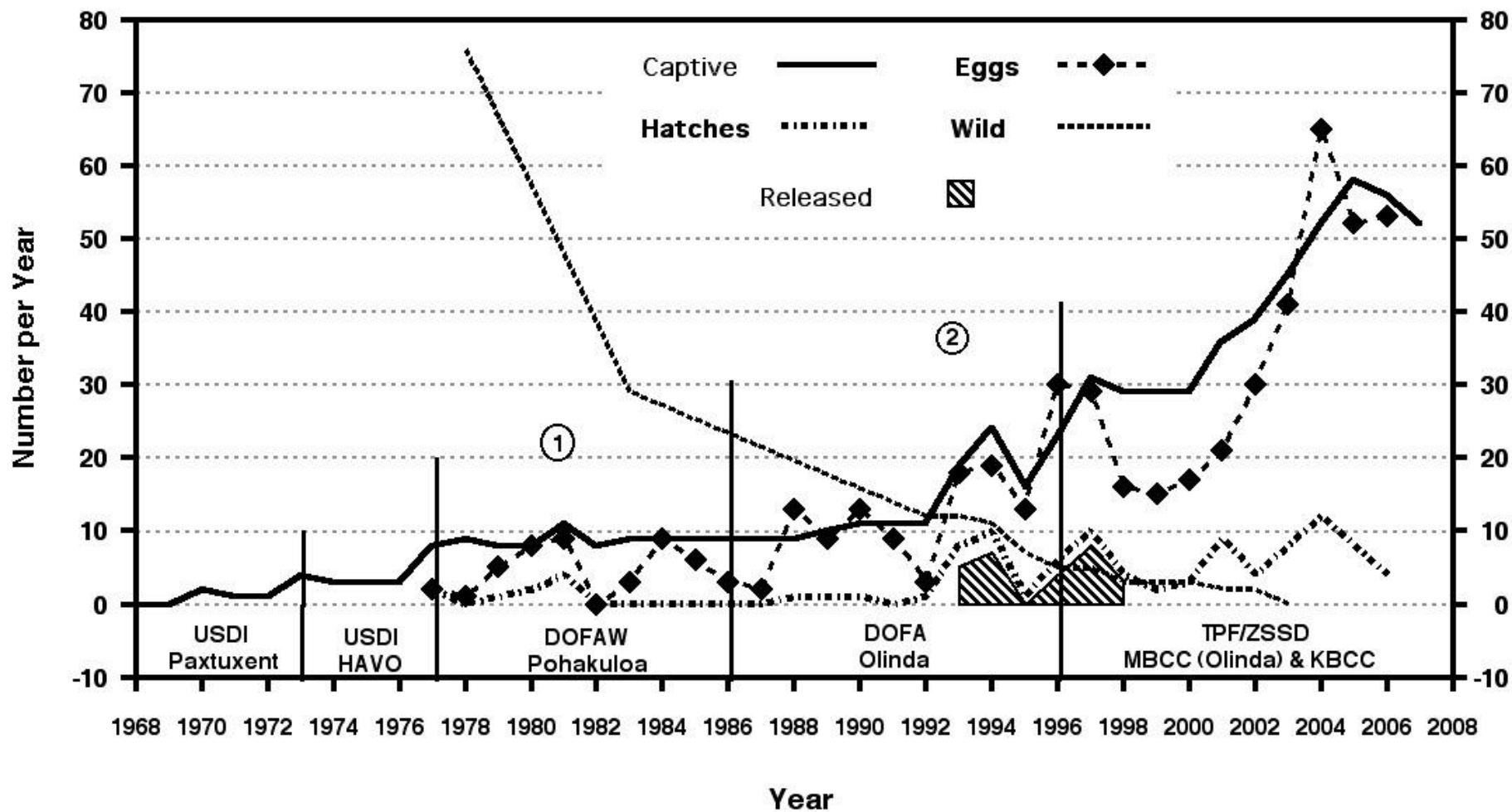


Captive Propagation

- Rapid sexing techniques for species lacking sexual dimorphism essential to establish new populations *in situ* (translocations) or captivity
- Assessment of genetic diversity
 - Rave and Fleischer: characterized genetic diversity; results guided captive propagation matings and releases
 - Fleischer, Jarvi: assessments of genetic diversity in Ālalā guide management of captive breeding program
 - Releases of Nēnē on Kaua`i guided by choice of birds with greatest range of diversity. This is now by far the most robust population of the species.



History of Alala: Captive and Wild



A manager's point of view



“...the best answer to your question about what has been the most important contribution to Hawaiian bird conservation has been our ability to track and use pedigrees for the captive management of the `Ālalā. Without the use of a pedigree we would be lost. Without the captive management of `Ālalā the species would be lost...”

Alan Lieberman

In situ Management



- Tarr *et al.*: Characterization of population structure and estimation of N_e in translocated populations of Laysan Finch
- Laysan Duck translocation to Midway Atoll – highly successful. Sex ratio a problem at first.
- Translocation of Nihoa Millerbird to Laysan Island (coming soon to an atoll near you). Sex determination will be critical.
- Planning for translocations of Nihoa and Laysan Finches to Kure and Lisianski—coming kind of soon to an atoll near you
- Selecting individuals to maximize genetic diversity and secure appropriate sex ratios in new populations is logistically very challenging for the Northwestern Hawaiian Islands passerine species

Summary

the simple things have helped most

- Clarification of taxonomic status of species, subspecies, populations, etc.
- Identification of ESUs
- Characterization of baseline genetic diversity in species and populations of birds, their diseases, their disease vectors
- Reconstruction of historical distributions and population sizes
- Understanding of how mating systems may affect maintenance of genetic diversity
- Genetic management of captive populations





The end