Resolving management units of the spinner dolphin (*Stenella longirostris*) using population genetics to address ecotourism concerns in Hawai'i

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Abstract

Concern has grown over the last decade regarding the growing ecotourism industry focused on spinner dolphins (*Stenella longirostris*) in Hawai'i. This activity involves human interaction with free-ranging dolphins in sheltered (wave protected) daytime resting habitat, potentially disrupting diel behaviors. This resting area is essential habitat, as spinner dolphins do not consistently occur at islands within Hawai'i that lack these refuges. To aid in the development of effective regulations for this industry, we conducted a range-wide genetic survey of the Hawaiian spinner dolphin using mitochondrial DNA (mtDNA) control region sequences and 10 microsatellite loci (N=505). F-statistics, Bayesian cluster analyses, and assignment tests revealed population genetic differences between most islands/atolls (overall mtDNA F_{ST} = 0.086, P < 0.001, overall microsatellite F_{ST} = 0.015, P < 0.001), indicating that each island/atoll should be managed separately. A comparison of genetic structure with available data on habitat and social structure revealed a trend toward higher gene flow between populations inhabiting smaller islands/atolls and having higher group stability. Genetic comparisons to a South Pacific location (N=16) indicated that Hawaiian populations are genetically depauperate and isolated from other Pacific locations (mtDNA 0.216< F_{ST}<0.643, P <0.001; microsatellite 0.058< F_{ST}<0.090, P <0.001), providing evidence that populations in Hawai'i may be vulnerable due to genetic isolation and small population sizes. We conclude that limiting resources such as resting habitat may have a critical influence on spinner dolphin distribution, dispersal patterns, population isolation, and social structure in the Hawaiian Islands. If ecotourism activities are found to be disruptive to resting behavior of Hawaiian spinner dolphins, management actions must incorporate the recognition that these dolphins occur in small, isolated populations.

Background & Research Questions

- Spinner dolphin habitat and social structure vary across the Hawaiian Archipelago:
  - *Northwestern Hawaiian Islands:* low amounts of resting habitat, stable social structure
  - *Main Hawaiian Islands:* high amounts of resting habitat, "fission-fusion" social structure
- How does genetic structure relate to variation in habitat and social structure?
- How can data on genetic diversity, genetic structure, habitat, and social structure aid in defining stocks for management of the ecotourism industry in Hawai'i?

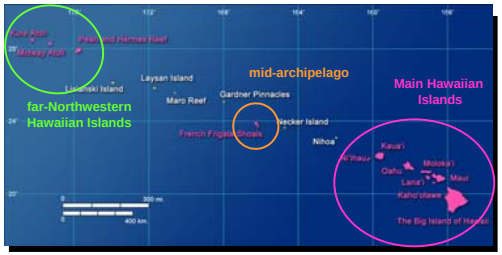

Figure 1. Hawaiian spinner dolphins are regularly seen at the islands colored in pink, and not at other islands or in open ocean.

Methods

Collected sloughed skin or biopsies (skin and blubber)

Genetic markers:

- mtDNA control region (417 base pairs)
- 10 Microsatellite loci

Photo: Cynthia Vanderlip

Photo: Leszek Karczmarski

Results:

Lower genetic diversity within Hawai'i than any other location yet sampled

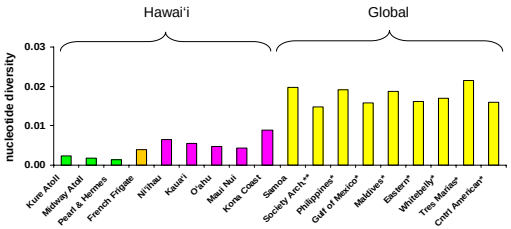

Figure 2. MtDNA control region diversity for spinner dolphins at each Hawaiian Island and nine other locations worldwide *Galver 2002, **Oremus *et al.* 2008

Shared haplotypes across Hawaiian Archipelago and Samoa

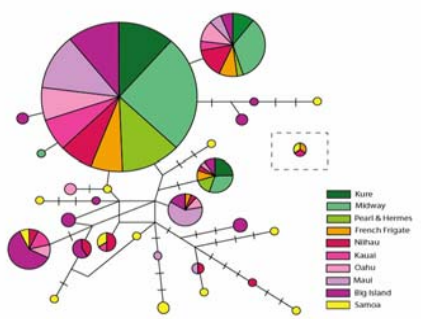

Figure 3. Parsimony network of mtDNA haplotypes. The haplotype within the dashed-line box was at least nine mutational steps from the closest haplotype and did not connect with ≥ 95% confidence anywhere in the network.

Genetically distinct populations across Hawaiian Archipelago and Samoa

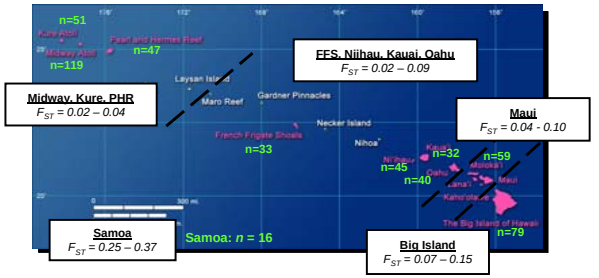

Figure 4. Summary of significant (p<0.05) pairwise F_{ST} values for microsatellite data. MtDNA pairwise F_{ST} tests gave similar results.

Photo: Susan Rickards • Oceanic Society • NMFS permit GA-LOC-10021622

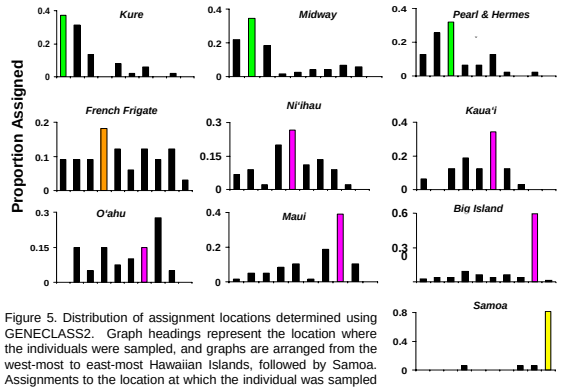

Figure 5. Distribution of assignment locations determined using GENECLASS2. Graph headings represent the location where the individuals were sampled, and graphs are arranged from the west-most to east-most Hawaiian Islands, followed by Samoa. Assignments to the location at which the individual was sampled are in color.

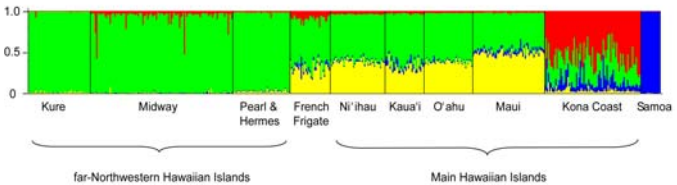

Figure 6. Assignment probabilities of individuals to putative population clusters at K = 4 using the program STRUCTURE 2.3.2. The highest average posterior probability occurred at K = 4 after five runs of the analysis for each K between 1 and 10.

Conclusions

- Genetic structure corresponds with resting habitat availability: smaller islands (far-Northwestern Hawaiian Islands, French Frigate, Niihau, Kauai, and Oahu) generally have less genetic structure
- Genetic structure corresponds with social structure: islands with stable social structure (Kure and Midway) have less genetic structure than the island with a fission-fusion social structure (Big Island)
- Genetic analyses support the designation of at least four management units (stocks) within the Hawaiian Archipelago (Fig. 3)
- Low genetic diversity within the Hawaiian Archipelago suggests stocks are vulnerable to environmental change

Literature Cited: *Galver LM (2002) *The molecular ecology of spinner dolphins, Stenella longirostris: genetic diversity and population structure* PhD thesis, University of California; **Oremus M, Poole MM, Steel D, Baker CS (2007) Isolation and interchange among insular spinner dolphin communities in the South Pacific revealed by individual identification and genetic diversity. *Marine Ecology-Progress Series* **336**, 275-289.

Acknowledgments: ***Permits:*** NMFS Scientific Research Permits No.'s 1007–1629 and 1000–1617, University of Hawai'i Animal Care Committee Protocol No. 01–014. ***Assistance with labwork:*** Tetsuya Hirano, Malia Rivera, Steve Karl, April Harlin, Malia Chow, Sarah Daley, Melinda Swanson, Kim Selkoe and members of the ToBo Lab and the Grau Lab. ***Assistance with sample collection:*** Bud Antonelis, Penny & Trevor Austin, Robin Baird, Jason Baker, Jay Barlow, Todd Buczyna, Suzanne Canja, Bruce Casler, Marie Chapla, Susan Chivers, Lisa Davis, Mark Deakos, Vinnie DePaolo, Sonok and Gerry Deutscher, Ania Driscoll-Lind, Jeff Eble, Chris Eggleston, Cari Eggleston, Beth Flint, Annie Gorgone, Nancy Hoffman, Stuart Ibsen, Dave Johnston, Patti and Bruce Jones, Randall Kosaki, Marc Lammers, Keith Larson, Amarisa Marie, Carl Meyer, Darlene Moegerle, Charles Moore, Rodrigo Moraga, Don Moses, Jan Östman-Lind, Yannis Papastamatiou, Robert Pitman, María José Pérez, Dick and Bonnie Robbins, Jim and Robin Roser, Tony Sarabia, Rob Shallenberger, Dave Smith, Robert Smith, Russel Sparks, Naomi Sugimura, Barbara Taylor, Kristen Taylor, Jen Tietjen, Jeff Walters, Daniel Webster, Birgit Winning, Bernd Würsig, Chad Yoshinaga, Hawai'i Department of Land and Natural Resources, Division of Forestry & Wildlife and Division of Aquatic Resources, USA Fish & Wildlife Service, Papahanaumokuakea Marine National Monument, Hawaiian Islands Humpback Whale National Marine Sanctuary, NMFS Southwest Fisheries Science Center, NMFS Pacific Islands Fisheries Science Center, Oceanic Society, Ko Olina Marina, the crew of the NOAA R/V Hialakai and Texas Institute of Oceanography. ***Funding:*** National Science Foundation Graduate Research Fellowship Program; National Geographic Society; Pacific Marine Life Foundation; National Fish and Wildlife Foundation; Anonymous Foundation; Maybelle Roth ARCS Scholarship; Jessie Kay Fellowship; University of Hawai'i Sea Grant College Program; University of Hawai'i Ecology, Evolution and Conservation Biology Program; Algalita Foundation; Sea Vision Foundation; American Museum of Natural History; Watson T. Yoshimoto Foundation; Animal Behavior Society Cetacean Behavior and Conservation Award; and Project AWARE Foundation. Research at Midway Atoll was partially sponsored by Oceanic Society. Most genetic analyses were conducted in the ToBo lab at Hawaii Institute of Marine Biology, which is supported by grants from the HIMB-NWHI Coral Reef Research Partnership (NMSP MOA 2005-008 / 6882), University of Hawaii Sea Grant College Program, National Science Foundation (OCE-0454873 to B.W.B., EPS 0554657 to University of Hawai, OCE-0623678 to R.J.T.).