

Population Structure of Pantropical Spotted Dolphins Near the Main Hawaiian Islands: Evidence of Multiple Genetic Stocks

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Introduction

- Our study focuses on gene flow among pantropical spotted dolphins near the main Hawaiian Islands
- Only one stock currently recognized within Hawaiian EEZ
- Understanding gene flow is important—localized depletions can reduce genetic diversity when gene flow is limited
- Results useful for identifying stocks requiring separate management
- Spotted dolphins affect and are affected by multi-million dollar ecotourism and fishing industries
- Of special concern are commercial and recreational troll fisheries that are unregulated and troll through groups of dolphins to catch tuna, occasionally hooking individuals, disturbing groups, and likely resulting in vessel collisions (Fig 1)

Methods

- Regions defined for separate analysis as Hawai'i, 4-islands area, O'ahu, and Kaua'i/Ni'i'hau (Fig 2)
- Analyzed 176 skin samples collected by remote biopsy 2002-2008, for 11 microsatellites and mtDNA sequence
- Compared among and within regions (putative populations); and between sexes to investigate sex-biased dispersal



Fig 1. Spotted dolphin with wounds caused by a boat propeller, possibly associated with fishing.

Results

- Analyzed 75 males and 101 females from 70 groups (encounters)
- 10 mtDNA haplotypes (sequences): 77 type "A" (most common), 9 type "B" (second most common), 7 type "C," rest are unique
- High genetic diversity, among-region difference in haplotype diversity (Table 1); fixation indices show significantly reduced gene flow (Table 2)
- Mean migration rates range from $Nm=1.405$ (95%SI±0.202) to $Nm=1.873$ (95%SI±0.0129) (often <2 is considered separate pops)
- Analyses of microsats show support for 3 significant clusters (Fig 3)
- Kaua'i/Ni'i'hau clusters with Hawai'i (Fig 3), but sample size is small and high diversity in mtDNA (Table 1) suggests regional differences
- No differences found between sexes

Table 1. Region	Mean Microsat Allele Diversity	n	Mean mtDNA Haplotype Diversity	n
Hawai'i	0.835 (SD±0.430)	74	0.376 (SD±0.098)	38
Kaua'i/Ni'i'hau	0.841 (SD±0.457)	16	0.750 (SD±0.139)	8
4-islands area	0.826 (SD±0.429)	52	0.527 (SD±0.097)	27
O'ahu	0.794 (SD±0.413)	52	0.145 (SD±0.090)	27

Table 2. Top: Microsatellites Rst above diagonal, Fst below diagonal Bottom: MtDNA Φ_{st} above diagonal, Fst below diagonal Bold and italicized are significantly different from zero Kaua'i/Ni'i'hau is not included due to low sample size

	Hawai'i	4-islands	O'ahu
Hawai'i		<i>0.046</i>	<i>0.055</i>
4-islands	<i>0.028</i>		
O'ahu	<i>0.038</i>	<i>0.037</i>	
Hawai'i		0.017	0.005
4-islands	0.011		<i>0.105</i>
O'ahu	0.016	<i>0.112</i>	

Conclusions

- Support for genetic differentiation among the four island regions
- Differences support management as separate stocks
- Separate management could affect fisheries & ecotourism
- No evidence to support sex-biased dispersal
- Differentiation may be mediated by behavior adapted to differing habitat types, such as shallow (4-islands) & deep (Hawai'i) waters

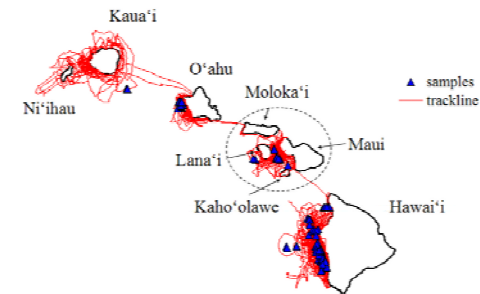


Fig 2. Map showing locations of samples (blue triangles) and search effort (red lines). The 4-islands area is shown with the dotted line.

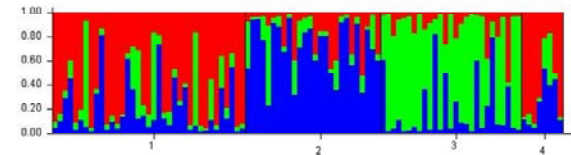


Fig 3. Assignment to clusters for microsatellites. 1=Hawai'i, 2=O'ahu, 3=4-islands area, 4=Kaua'i/Ni'i'hau. Each color represents a different cluster assuming three populations. Note Hawai'i is mostly red, O'ahu mostly blue, & 4-islands area mostly green.

Acknowledgments: Fieldwork supported by the Southwest Fisheries Science Center, Wild Whale Research Foundation, and the U.S. Navy through grants and contracts to Cascadia Research Collective and the Hawai'i Wildlife Fund. For sample collections we thank Daniel Webster, Allan Ligon, Greg Schorr, and Dan McSweeney. Samples collected under NMFS Scientific Research Permit No. 774 (issued to Southwest Fisheries Science Center). We also thank Dr. Mitch Cruzan, Dr. Suzanne Estes, Dr. Eric Routman, Ron Nelson, Bia Wahl, Eli Pursifull, and William A. Jackson III. Funding for genetic analyses and student support was provided by EPA GRO Fellowship, Rogue Ales Foundation Scholarship, Frank L. Roberts Scholarship, Elsa Jorgenson Scholarship, Forbes Lea Fund, Zale Parry Scholarship, Lerner Gray Marine Research Fund, Mensa J.F. Shimer Scholarship, Mensa Henry Lustig Memorial Award, Seaspace Scholarship, International Women's Fishing Association, Sigma Xi GIAR, American Society of Mammalogists GIAR, and Oregon Sports Lottery Scholarship.