

# Staying close to home: Mitochondrial DNA analysis reveals insular population structure for the pelagic dolphin *Steno bredanensis*

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## BACKGROUND

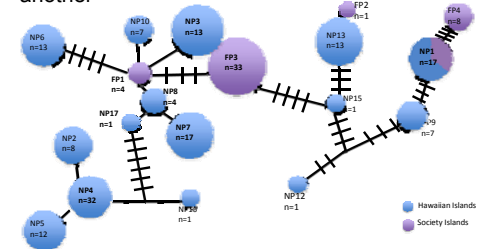
Rough-toothed dolphins have a worldwide tropical and subtropical distribution<sup>1</sup>. Although it has been assumed that pelagic dolphins move widely due to the lack of apparent barriers in the open-ocean, recent photo-identification evidence suggests rough-toothed dolphins exhibit fidelity to some oceanic islands<sup>2</sup>. Opportunities to study these elusive dolphins may be greatest around oceanic islands where deep-water populations may be found with higher frequency and relatively close to shore simplifying data collection and minimizing costs<sup>2</sup>. Current anthropogenic threats include drive kills, known interaction with fisheries and bycatch in pelagic longlines<sup>3</sup>. Unrecognized population structure can have serious implications for conservation, therefore determining the scale of population differentiation is imperative for proper management<sup>2,3,4</sup>.

## OBJECTIVES

- Examine phylogenetic structure within and between ocean basins.
- Investigate mtDNA diversity and maternal gene flow of *Steno bredanensis* between and within the Hawaiian and Society Islands.

## REGIONAL DIFFERENCES

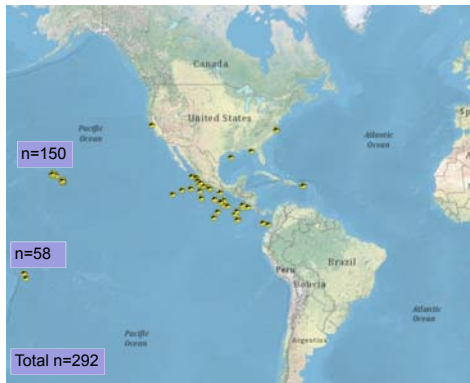
- One shared haplotype exists between island groups
- High diversity found in the Hawaiian Islands
- Society Islands haplotypes are distant from one another



There are 19 unique haplotypes defined by 36 variable sites for the Hawaii and the Society Islands. Bars represent number of mutational steps.

## METHODS

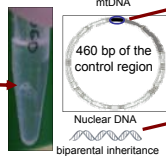
### Sample locations



### Step 1: Sample Collection



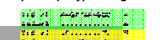
### Step 2: DNA Extraction



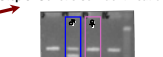
### Step 3: mtDNA sequencing



### Step 4: Haplotype Assignment



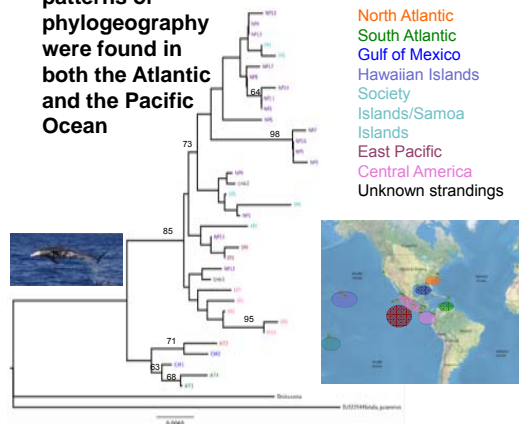
### Step 5: Genetic sex identification



We examined genetic differentiation using  $F_{ST}$  and  $\Phi_{ST}$ <sup>4</sup>. Phylogeographic relationships were reconstructed using a Neighbor-Joining tree as implemented in MEGA<sup>5</sup>.

## PHYLOGENETIC RELATIONSHIPS

- Phylogeographic clades identified between ocean basins
- Regional patterns of phylogeography were found in both the Atlantic and the Pacific Ocean



A neighbor-joining tree<sup>5</sup> illustrating phylogenetic relationships among 36 haplotypes identified by 51 variable sites for *Steno bredanensis*.

## ACKNOWLEDGEMENTS

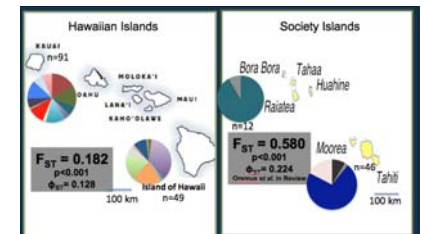
Funding for fieldwork in French Polynesia was provided by New Zealand Marsden Fund. Additional funding provided by the Ministry of the Environment of French Polynesia and Dolphin and Whale Watch Expeditions. Special thanks to Southwest Fisheries Science Center and the Pacific Islands Region Office for providing funding for the archiving and DNA extraction of all samples outside of French Polynesia and Samoa. National Marine Fisheries Service, U.S. Navy (NAES, Office of Naval Research NAVAC/PAC), and Wild Whale Research Foundation provided funding for main Hawaiian Islands fieldwork. Main Hawaiian Islands fieldwork was conducted by Cascadia Research Collective. Photos by G. R. Albertson unless otherwise noted.

## REFERENCES

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## PARALLEL STRUCTURE BETWEEN ISLAND GROUPS

- Significant genetic differentiation found within island groups
- High  $F_{ST}$  values within each island group, illustrating low migration rate between islands



Mitochondrial DNA haplotype frequencies illustrated in pie charts.  $F_{ST}$  values are within each island group.

## CONSERVATION IMPLICATIONS



The Island of Hawaii is genetically differentiated and demographically isolated from Kaua'i/Ni'ihau, suggesting a local and relatively closed community structure.



Genetic evidence suggests that rough-toothed dolphins may form stable communities around the islands of Moorea and Raiatea.



Distinct clades at the oceanic scale indicate limited dispersal of females.



Contrary to previous assumptions, rough-toothed dolphins may exist in relatively small genetically differentiated populations throughout their range.