



21st Biennial Conference on the Biology of Marine Mammals

13-18 DECEMBER 2015
HILTON SAN FRANCISCO UNION SQUARE
SAN FRANCISCO, CA USA

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Introgressive hybridization of Fraser's dolphin mitochondrial and nuclear DNA into Mariana Islands bottlenose dolphins

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Introgressive hybridization, in which genetic material from one species persists in the genome of another species following hybridization, can result in gene trees that do not match species trees and seriously mislead phylogenetic studies. This is particularly true in studies based solely on mitochondrial DNA, as introgression of maternally-inherited genomes is predicted to occur far more rapidly and persist longer than introgression of nuclear genomes. Introgressive hybridization has long been suspected as a source of taxonomic confusion in the Delphinidae. We detected mitochondrial introgressive hybridization in bottlenose dolphins (*Tursiops truncatus*) sampled around the southern islands of the Mariana Archipelago, where five out of 15 animals possess haplotypes characteristic of Fraser's dolphins (*Lagenodelphis hosei*). We used mitochondrial sequence data and genotypes from 14 nuclear microsatellite loci to further examine introgression of Fraser's dolphin DNA into the Mariana Islands population of bottlenose dolphins. We compared the Mariana Islands samples to bottlenose dolphin samples from elsewhere in the western Pacific and the Hawaiian Archipelago and to Fraser's dolphin samples from throughout the Pacific and Indian Oceans to investigate the extent and origin of hybrid ancestry in Mariana Islands bottlenose dolphins. We estimate that the Mariana Islands animals derive approximately 14% of their nuclear ancestry from Fraser's dolphins. The fact that every Mariana Islands sample showed evidence of nuclear introgression, combined with the fact that those exhibiting mitochondrial introgression all share the same Fraser's dolphin haplotype, suggests that there was a single hybridization event far enough in the past to allow Fraser's dolphin nuclear DNA to permeate the population. The Mariana Islands samples exhibited low genetic diversity compared to other bottlenose dolphin populations, suggesting that they represent a small, genetically isolated population.

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