

Olavarria et al 2008_MEPS

Most known concentrations of humpback whales in the southern hemisphere were exploited by commercial whaling operations, first on tropical breeding grounds during the 19th century and then in Antarctic feeding areas and along migratory corridors during the 20th century. However, whaling logbooks of 19th century whalers show almost no records of catches in some regions of current concentration, notably eastern Polynesia, suggesting that humpback whales were formerly absent from these regions or that the locations of their primary concentrations were unknown to early whalers. Here we investigate the population structure of humpback whales across the South Pacific and eastern Indian oceans, with an interest in the origins of whales in eastern Polynesia, using an extensive collection of mitochondrial DNA (mtDNA) sequences obtained from living whales on 6 breeding grounds: New Caledonia, Tonga, Cook Islands, eastern Polynesia (Society Islands of French Polynesia), Colombia and Western Australia. From a total of 1112 samples we sequenced 470 bp of the mtDNA control region, revealing 115 unique haplotypes identified by 71 variable sites. We found significant differentiation, at both the haplotype and nucleotide level ($F_{ST} = 0.033$; $\sqrt{sT} = 0.022$), among the 6 breeding grounds and for most pairwise comparisons. The differentiation of the eastern Polynesia humpback whales is consistent with the hypothesis of a relic subpopulation, rather than vagrancy or colonization from known neighboring breeding grounds. Regardless of their origin, it seems probable that islands of eastern Polynesia are now the primary breeding grounds for humpback whales feeding in management Area VI (170 to 120° W) of the Antarctic, as defined by the International Whaling Commission.