DETERMINING THE MOLECULAR TAXONOMY OF CIGUATOXIN VECTORS IN HAWAIIAN WATERS

A THESIS SUBMITTED TO
THE GLOBAL ENVIRONMENTAL SCIENCE
UNDERGRADUATE DIVISION IN PARTIAL FULFILLMENT
OF THE REQUIREMENTS FOR THE DEGREE OF

BACHELOR OF SCIENCE

IN

GLOBAL ENVIRONMENTAL SCIENCE

AUGUST 2011

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Abstract

Ciguatera fish poisoning is a seafood-borne illness caused by the consumption of fish which have ingested and accumulated ciguatoxins. Ciguatoxins travel up the marine food web from primary producers, *Gambierdiscus* sp, to herbivorous and carnivorous fish that are consumed by humans. In the United States, ciguatera is responsible for the highest reported incidence of food-borne illness outbreaks attributed to finfish and is thought to hold this distinction worldwide. However, little is known about the process of bioaccumulation or the vectors that deliver ciguatoxin to humans. The aim of this study was to gain a better understanding of the species that make up the food web that vector ciguatoxin to humans by more precisely identifying the organisms involved. To this end, molecular taxonomic techniques centered on the cytochrome c oxidase gene were employed to develop phylogenetic trees. Results indicate that a frequently ciguatoxic high-level carnivore in Hawaii's coral reef ecosystem, the *Cephalopholis argus*, differs from the type specimen of *C. argus* that is in the National Center for Biotechnology Information nucleotide sequence database. The COX-1 sequences from various local prey species were also studied and demonstrated the congruence of molecular and morphological data.