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DNA Barcoding is the identification of organisms through the use of a standardized portion of the genome, a concept first suggested by Hebert, et al (2003) and since developed to include standard databases and many campaigns internationally to identify and barcode all species in the world. Because DNA barcoding uses molecular data, rather than morphology, to identify organisms, it allows for the identification of organisms that are morphologically similar or have been processed to the point of unrecognizability. Barcoding has the potential to streamline and enhance conservation efforts drastically. Its "quick and easy" identification process allows better fisheries management, market regulation to ensure vendors are selling what they say they're selling (no more horsemeat burgers or dolphin sushi), and greater enforcement of regulations against the killing and selling of endangered animal products (Minhos et al., 2013).

In my work this summer, I've been using DNA barcoding to examine the dynamics of a community of larval fish off the coast of Oahu through a seven-year longitudinal barcoding study. Fish larvae are very hard to identify morphologically because they lack obvious identifying characteristics. For this reason, barcoding is essential for accurately understanding the community structure of such fish.

In my work, I analyze a set of sequences from the 5-prime region of the mitochondrial gene *cytochrome oxidase subunit 1,* widely used as a barcode in the animal kingdom, gathered from fish larvae collected off the coast of Oahu by the University of Hawaii Manoa Biology 301L class. The sampling consisted of a series of oblique plankton tows taken at three depths (5m, 25m, and 50m) between January and April every year from 2007 to 2013. During this period, a total of 833 fish larvae were sampled and sequenced. Using the Barcode of Life Data Systems (BOLD Systems) Identification Engine, I was able to identify 78% of all specimens to family-level or better, representing about 25% of the 202 families of shore fishes known to occur in Hawaiian coastal waters. The data stratification consisted of 7 years, each with three depths and 56 family groups, a 21 by 56 data matrix. In order to see the patterns of the matrix, I used Principal Components Analysis, a form of ordination, which distills multidimensional data to a form that is more easily visualized. This ordination revealed that 2009 and 2011 had highly anomalous community structure in which there were large increases in abundance (greater than three (3) Standard Deviations from the mean) of 12 family groups in each year, indicating concerted change in the structure of ichythoplankton in those years, though the families may be represented by a low number of specimens in the sample. Because these families had little to no representation in other years, we are able to rule out the possibility of results being skewed by a couple of families that showed up in our nets by chance that don't reflect the actual community structure. In these years, the highly anomalous families did not overlap, indicating that the factors causing the anomalies were non-identical. In 2009 there were eight families that deviated from the mean by over four (4) Standard Deviations, and in 2011 there were ten. Though the biggest groups of deviant families in both years were reef fish and mesopelagic fish, tropical habitat ranged from shallow water benthic (sea-bed) fish such as *Ophichthidae*, to bathypelagic (deep sea) fish such as the anglerfish family *Ceratiidae*.

In my last few weeks working on this project I am exploring what environmental factors may have had a hand in such anomalies. El Niño cycles may have had a hand, as there was a weak La Niña (slightly cooler waters) anomaly leading into 2009, and a very strong La Niña (drastically cooler waters) anomaly leading into 2011 ("Cold and Warm Episodes by Season," 2014). The differences in community structure I detected had different signs, that is the co-variance of fish families was different for each of these years. This suggests that water temperature itself may not be causing these ecological patterns. A more likely hypothesis links the effects of El Niño/La Niña on oceanographic circulation throughout the Pacific and even near-shore in the Hawaiian Islands. These changes can drive differences in the delivery of larvae to the islands, as well as advection away from the islands. Further research in the remainder of the summer will attempt to gather more information on what may have caused the community structure anomalies.

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