Monitoring Spawning Activity in Cabo Pulmo National Park
Using Molecular Identification of Fish Eggs and Larvae

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Introduction

Located in southern Baja California, Mexico, Cabo Pulmo National Park's 27 square miles of teeming waters is a shining example of a well-managed marine protected area. A recent study determined that in just 14 years fish biomass increased by 463%, the largest measured in a marine reserve worldwide.[1] While there is an abundance of data collected via traditional monitoring techniques such as diver surveys, little is known about the species specific spawning activities that occur in Cabo Pulmo. This study monitors the fish spawning activity through molecular identification of eggs and larvae collected in the park.

[1]Aburto-Oropeza O, B. Erisman, G.R. Galland, I. Mascarenas-Osorio, E. Sala., E. Ezcurra. 2011. Large Recovery of Fish Biomass in a No-Take Marine Reserve. PLoSONE 6: 23601.

Why Ichthyoplankton? Why Genetics?

• Reveal the species composition, timing and location of spawning activities
• Complement diver-conducted surveys
• Can be used as a baseline to compare shifting populations and spawning patterns
• Provide evidence of the success of marine protected areas
• Aid in the assessment and management of marine ecosystems
• Molecular identification is more accurate and reliable than traditional morphological methods
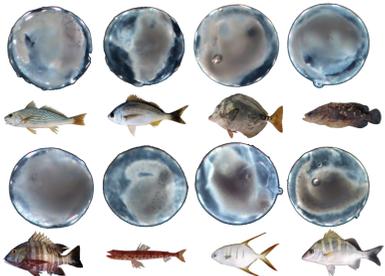
Eggs identified morphologically as one species; genetics revealed 8 different species

Methods

• Weekly plankton tows in CPNP conducted by David Castro, divemaster from Cabo Pulmo
• Biologists at CICIMAR-IPN in La Paz, BCS separate eggs from zooplankton, make preliminary morphological identifications, and send eggs and larvae to SIO for analysis
• Universal fish primers are used to amplify cytochrome oxidase subunit 1 (COI) or 16S ribosomal RNA through polymerase chain reaction (PCR)
• Successfully amplified samples sent offsite for sequencing
• Results compared to sequences in GenBank and FishBOL, online databases of sequences from vouchered specimens
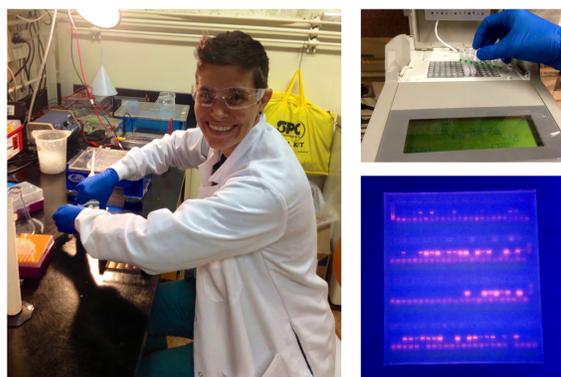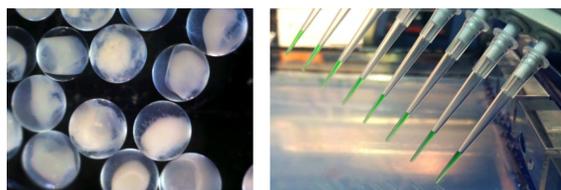
Results

• Identified 112 species from 16 orders, 49 families and 94 genera
• An additional 51 sequences did not match to existing voucher specimens in online databases, revealing even greater diversity
• Identified species from diverse natural histories including reef-associated species and highly migratory pelagic species
• Captured rare, understudied mesopelagic species such as *Regalecus glesne* (giant oarfish), revealing new information regarding spawning location and timing
• Several popular recreational fishery species were present, including *Nematistius pectoralis* (roosterfish) and *Coryphaena hippurus* (dolphinfish)
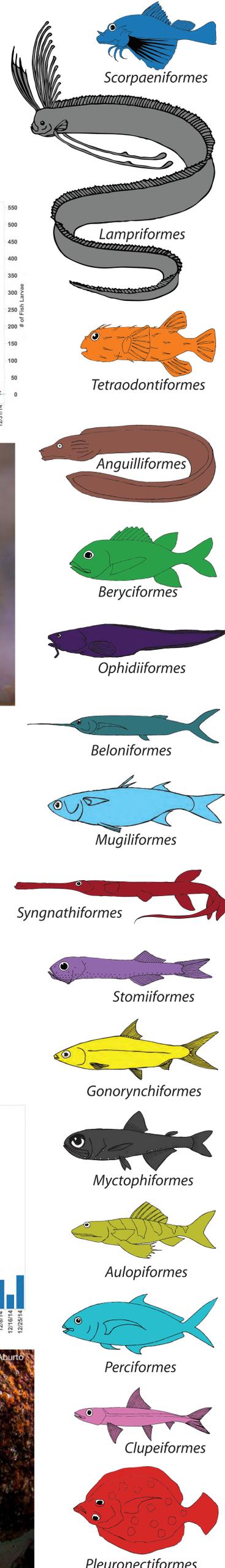
Regalecus glesne egg

Total Number of Fish Eggs and Larvae Collected

Rarefaction Curves
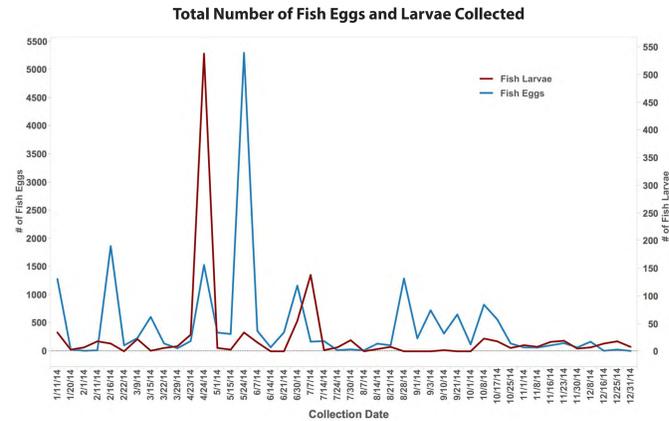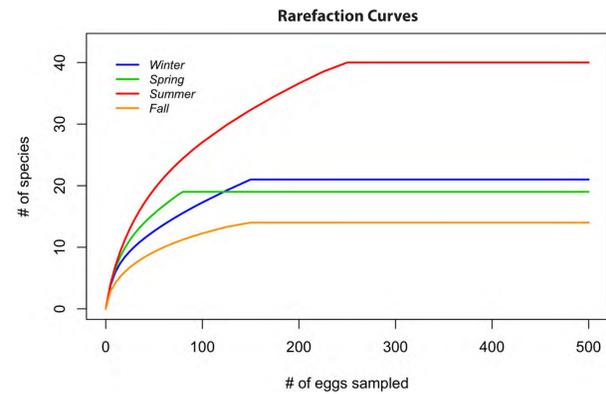
• Distinctive peaks in spawning activity were revealed for several species, potentially triggered by full moons
• Eggs of some species were present throughout the time series whereas others showed restricted spawning seasons
• Revealed inaccuracy of morphological identification
• Captured species and activities that would be missed in traditional survey methods utilized in Cabo Pulmo

Number of Species in Each Collection
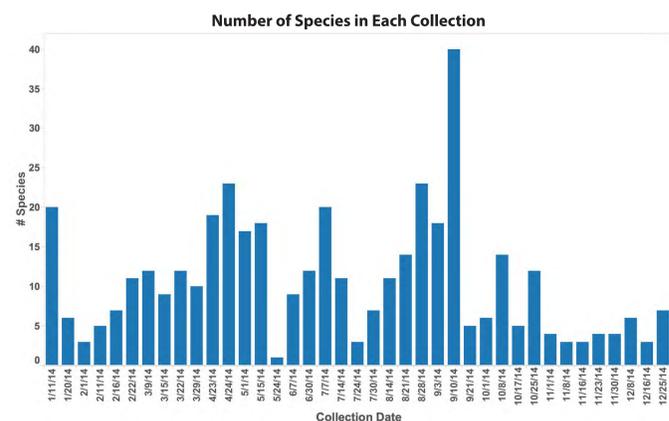
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44369 COLLECTED

4870 ANALYZED

2929 SEQUENCED

16 ORDERS

49 FAMILIES

94 GENERA

162 SPECIES

Scorpaeniformes

Lampriformes

Tetraodontiformes

Anguilliformes

Beryciformes

Ophidiiformes

Beloniformes

Mugiliformes

Syngnathiformes

Stomiiformes

Gonorynchiformes

Myctophiformes

Aulopiformes

Perciformes

Clupeiformes

Pleuronectiformes