

## Assessment of Ichthyoplankton Metabarcoding for Routine Monitoring

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### EXECUTIVE SUMMARY

Existing marine monitoring programs in the Southern California Bight (SCB) include evaluation of demersal (bottom-dwelling) and rocky reef/kelp-associated fish communities. The pelagic (water column) fish communities are ecologically and commercially important, but difficult to assess due to large scale and extreme variability. When pelagic communities are included, only the adult organisms are evaluated. Quantification of early life stages, including larvae and eggs (commonly referred to as ichthyoplankton), is a useful way to understand the composition of the pelagic community, as well as provide insight into levels of reproduction and recruitment. Such assessments provide important insight to condition, impacts, and efficacy of management actions.

Traditional study of ichthyoplankton is laborious and expensive, and requires highly specialized technical expertise. Over the past decade, DNA-based identification, known as metabarcoding, has been used to more accurately identify morphologically indistinguishable species. Although already proven effective in concept, this method still requires refinement for application to ichthyoplankton to allow it to yield accurate, useful results, and be easily integrated into routine monitoring and assessment programs.

The overall goal of this project was to develop a framework for cost-effective and informative ichthyoplankton monitoring within the coastal waters of Santa Monica Bay (SMB) and beyond. The main objectives for this study were to compare traditional approaches to metabarcoding results to determine whether metabarcoding is a viable alternative to traditional methods and could be used for a meaningful status and trends monitoring program in the SMB or SCB. The scope of this project is related to a larger regional effort aimed at developing and evaluating molecular methods for ichthyoplankton assessment.

A total of 74 ichthyoplankton samples were collected from 37 stations in May and June of 2016 in collaboration with three partners: City of Los Angeles Environmental Monitoring Division (CLAEMD), Los Angeles County Sanitation Districts (LACSD), and the University of California at Santa Barbara Marine Biodiversity Observation Network (MBON). Samples from each station were sorted, enumerated and identified to lowest possible taxonomic level by expert taxonomists at the Southwest Fisheries Science Center in La Jolla, California. After morphological identification, samples were homogenized and extracted using universal primers for COI and 12s ribosomal DNA, and then sequenced. Concordance between metabarcoding and traditional approaches was then evaluated by comparing the number of taxa with matching identification to the total number identified in each sample, and then averaging across all the samples in each group.

Traditional morphological analysis showed that crustaceans, largely copepods and euphausiids, comprised the majority of the plankton in each sample. Samples ranged from zero to 21 individual ichthyoplankton, with a mean of 4.1 individuals across all samples (Table ES-1). Traditional barcoding identified 29 different species of ichthyoplankton among the samples, comprising 13 families. Of the 180 individuals previously identified via morphology, 177 of them were corroborated with barcoding results, with increased resolution within the rockfish complex, which were only morphologically identified to *Sebastes* sp.

**Full Text**

[http://ftp.sccwrp.org/pub/download/DOCUMENTS/TechnicalReports/1031\\_IchthyoplanktonMeta\\_barcoding.pdf](http://ftp.sccwrp.org/pub/download/DOCUMENTS/TechnicalReports/1031_IchthyoplanktonMeta_barcoding.pdf)