A cross-shelf eDNA survey of Southern California midwater ecosystems

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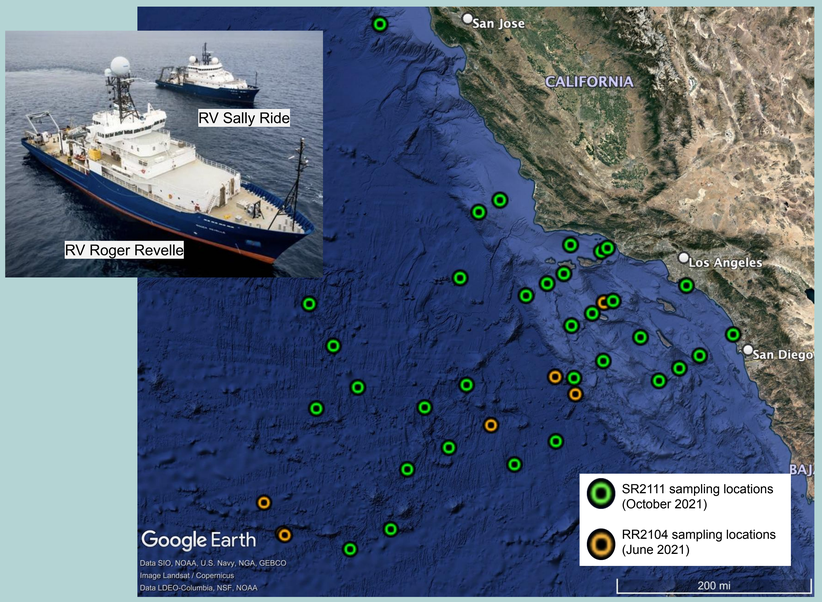
Study Design and Motivation

Using ships of opportunity to conduct eDNA surveys can greatly expand the scope and quality of biodiversity observing programs. To better understand the impacts of opportunistic eDNA sampling the Global eDNA Marine Collection and Analysis Program (GEMCAP) conducted a pilot study in collaboration with CalCOFI cruise 2111SR (Oct. 2021). To minimize impact on core science operations, GEMCAP provided a technician from the UNOLS Marine Technician Pool. The technician was given approximately two hours of training before the vessel departed and provided with a detailed protocol and log sheets. 2111SR samples were supplemented with samples from cruise RR2104, collected by M. Dan along CalCOFI Line 90 in June 2021.

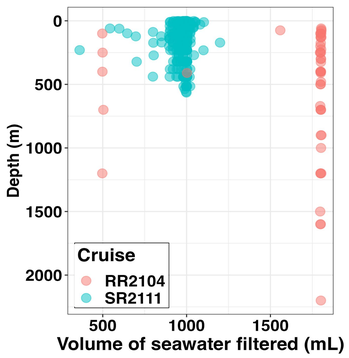


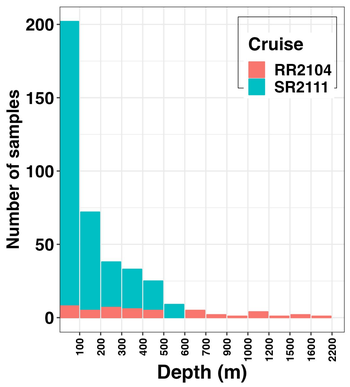
Methods

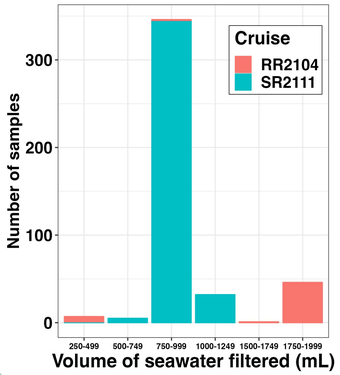
Water was collected by vacuum filtration whenever a sufficient volume was left after the completion of core science activities. Nominally 1L of water was filtered through 0.2 micron filters. Sterile blanks were used at intervals throughout the cruise to constrain crossover and contamination. DNA was extracted on a KingFisher Flex robot. Library preparation and sequencing was carried out at the Argonne National Lab Environmental Sample Preparation and Sequencing Facility.

The GEMCAP scientific steering committee selected three primers based on previous work to cover vertebrates (12S: Riaz et al., 2011), invertebrates (CO1: Leray et al., 2013), and marine mammals (mitochondrial control region: Baker et al., 2021). Sequence reads were denoised and classified using dada2 (Callahan et al., 2016).

Preliminary Results: Sample Coverage

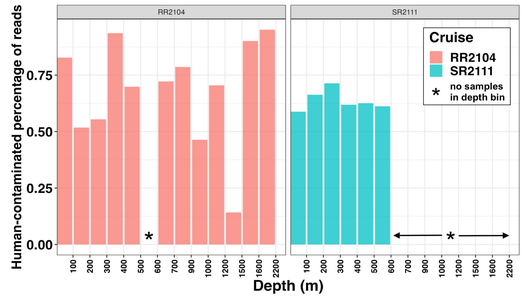






By dedicating a technician fully to this task, and utilizing only water volume remaining after core science activities were complete, we obtained 437 samples representing 34 stations on 2111SR and 4 stations on RR2104. Most 2111SR and RR2104 samples consisted of 900 and 1800 mL water, respectively.

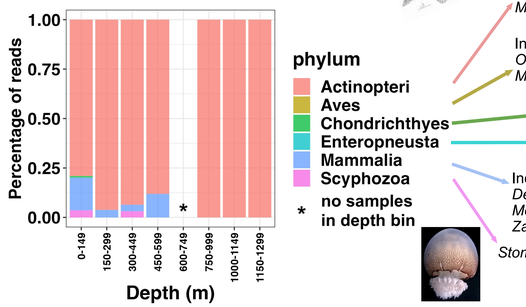
Preliminary Results: 12S primers



Reads resulting from human contamination are observed in a significant proportion of 12S samples. These reads, along with contamination from other, non-midwater species, were removed for subsequent analyses

Representation of Phyla by Depth

Likely dominated by fishes due to vertebrate-specificity of 12S primers



Including:
Triphoturus mexicanus (Mexican lampfish)
Argyropelecus sladeni (Sladen's hatchetfish)
Malacosteus niger (black dragonfish)
Mola mola (ocean sunfish)

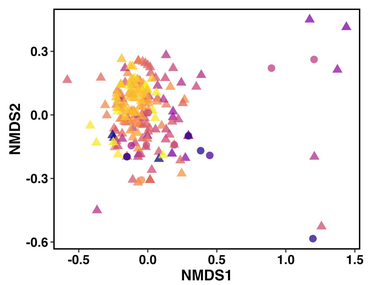
Including:
Oceanites oceanicus (Wilson's storm petrel)
Melanitta perspicillata (surf scoter)

Chimaeridae

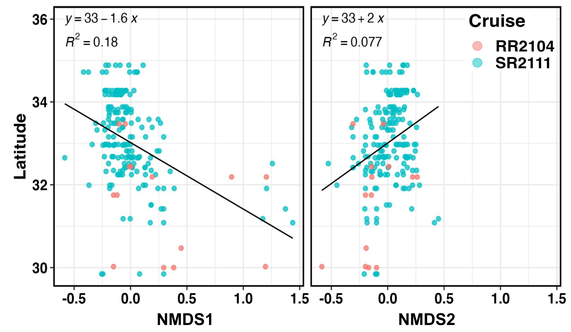
Schizocardium brasiliense (acorn worm)

Including:
Delphinus delphis (common dolphin)
Megaptera novaeangliae (Humpback whale)
Zalophus californianus (California sea lion)

Stomolophus meleagris (cannonball jellyfish)



Non-metric multidimensional scaling (NMDS, left) and linear regression (below) of ASV reads across samples shows a weak association between latitude (of sample collection) and overall community structure. Associations were not found with other environmental variables (depth, longitude) or volume filtered



Future Analysis

Our project will continue toward three analysis goals:

1) Determine the cost, feasibility, and likely products from an opportunistic eDNA collection program collaborating with CalCOFI and other cruises of opportunity.
2) Evaluate distributions of key taxa across CalCOFI study regions.
3) Determine the level of agreement between taxonomic surveys conducted by traditional methods and by eDNA analysis.

Acknowledgements

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