Proposal for Methodology Review of

Developing fish abundance and ecosystem indices from environmental DNA (eDNA)

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Background and purpose:

Fisheries-independent surveys form the foundation of fisheries stock assessments worldwide. On the West Coast, data collected from multi-species surveys such as the West Coast Groundfish Bottom Trawl Survey (WCGBTS) and the Integrated West Coast Pelagics Survey (IWCPS) inform abundance indices and thereby support stock assessments for dozens of species. However, there are tens of additional fish species that are missed or inconsistently measured by these surveys. For example, the WCGBTS cannot provide information for species associated with high relief bottom habitats that are untrawlable and bottom trawl methods inadequately quantify semi-pelagic species. Similarly, the acoustic-trawl IWCPS cannot currently be used to quantify pelagic rockfish species or additional abundant ecosystem components such as myctophids. With limited ship time and constrained budgets, expanding or adapting existing NOAA-led trawl surveys to target species that are sampled inconsistently is impractical. Thus, innovative and cost-effective methods that can extract additional information about a broader swath of marine species and ecosystem components without expanding the survey footprint or increasing survey days at sea are a critical need.

Over the past two decades, rapid advancements in molecular technologies have unlocked new methods for observing ocean ecosystems. In particular, environmental DNA (eDNA), in which residual genetic material is collected from environmental media such as water, air, or soil, has developed as a method for non-invasively detecting and quantifying a wide range of taxa in diverse habitats (e.g., Dougherty et al. 2016, Keller et al. 2020, Shelton et al. 2019, 2022). This methodology review will describe currently available eDNA samples for the US West Coast, the types of eDNA observations that can be derived from these samples, and how metrics of abundance of individual fish species and ecosystem components can be derived from these observations.

Methods:

This methodology review will encompass three components. First, as this topic is entirely new to the PFMC process, we propose to provide an introduction to the theory and practice of eDNA including a summary of the supporting literature outlining the processes underlying the production, transport, and loss of eDNA, the types of observations that can be derived from eDNA samples, and the theoretical and experimental support for a strong connection between eDNA concentrations and fish biomass. Second, we will detail the application of eDNA approaches to building an abundance index for Pacific hake. We will use a very large set of eDNA samples collected during the 2019 - 2025 IWCPS (and predecessor hake surveys) to illustrate these methods. This analysis will include practical details of building an index (which was included as a sensitivity analysis in the 2025 Pacific hake stock assessment), comparisons with indices derived from acoustic-trawl methods, and a discussion of a range of important technical issues (e.g., Catchability, Selectivity) which have potentially novel complications with regard to eDNA data. Third, we will discuss how the same samples collected and analyzed for hake can be repurposed to examine the abundance and distribution of a wide range of groundfish and coastal pelagic species. We will propose how such indices can inform upcoming stock assessments and other science that supports a range of PFMC management objectives.

References:

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