

How should DNA metabarcoding based food web data be integrated into marine ecosystem models?

Authors: Naiara Rodríguez-Ezpeleta, Anders Lanzen, Iñaki Mendibil, Eneko Bachiller, Eider Andonegi, Unai Cotano

Abstract

Understanding predator-prey interactions is key for a successful ecosystem approach-based fisheries management. Yet, comprehensive datasets on fish diets are lacking, mostly due to the difficulty and high economic cost of taxonomically characterizing fish stomach contents, composed of preys of a broad range of organismal groups, which are often semi-digested and/or in early life stages. DNA metabarcoding has been shown as a promising tool for inventorying gut contents, but technical challenges, such as the presence of large amounts of predator DNA or the difficulty of relating number of reads to biomass, as well as the suitability of DNA metabarcoding data to feed ecosystem models have yet to be addressed. Here, we have developed alternative metabarcoding assays for analysing the diet of five commercially important fish species (anchovy, sardine, hake, mackerel and horse mackerel) and have tested them in mock community samples mimicking stomach contents and in real stomach samples, some of which were previously analysed under the microscope. Our analyses based on about 300 samples have allowed to define guidelines for studying trophic interactions in commercial fish species and for integration of metabarcoding based diet data into ecosystem models.

Keywords:

DNA metabarcoding, small pelagics, hake, trophic webs, gut contents, ecosystem-based approach, ecosystem models

Contact author:

Naiara Rodríguez-Ezpeleta; AZTI, Txatxarramendi ugarte 48395
Bizkaia, Spain

Twitter usernames (in order): @naiara_re, @ambulanzen, n/a, n/a, @EAndonegi, n/a