Evaluation of marine zooplankton community structure through environmental DNA metabarcoding

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Introduction

An essential element of environmental conservation programs is biodiversity assessment. Traditional methods that characterize biodiversity are laborious and can be environmentally destructive (**1**). Genetic analysis of environmental DNA (eDNA), which contains DNA shed by organisms present in a given environment, offers a cheaper, more sensitive, and less destructive method for characterizing biodiversity (**2**).

Objective

Here we aim to assess methods for comparing net tow tissue sequencing (T-DNA) with eDNA for two different genetic markers (18S and COI) and comparing those to morphological assessment of net tow samples.

Methods

Seawater samples were collected onboard the R/V Walton Smith in May 2016 using a Conductivity Temperature Depth sensor fitted on a rosette with 12 Niskin bottles for water sampling. See Fig. 1 for laboratory and data workflow.

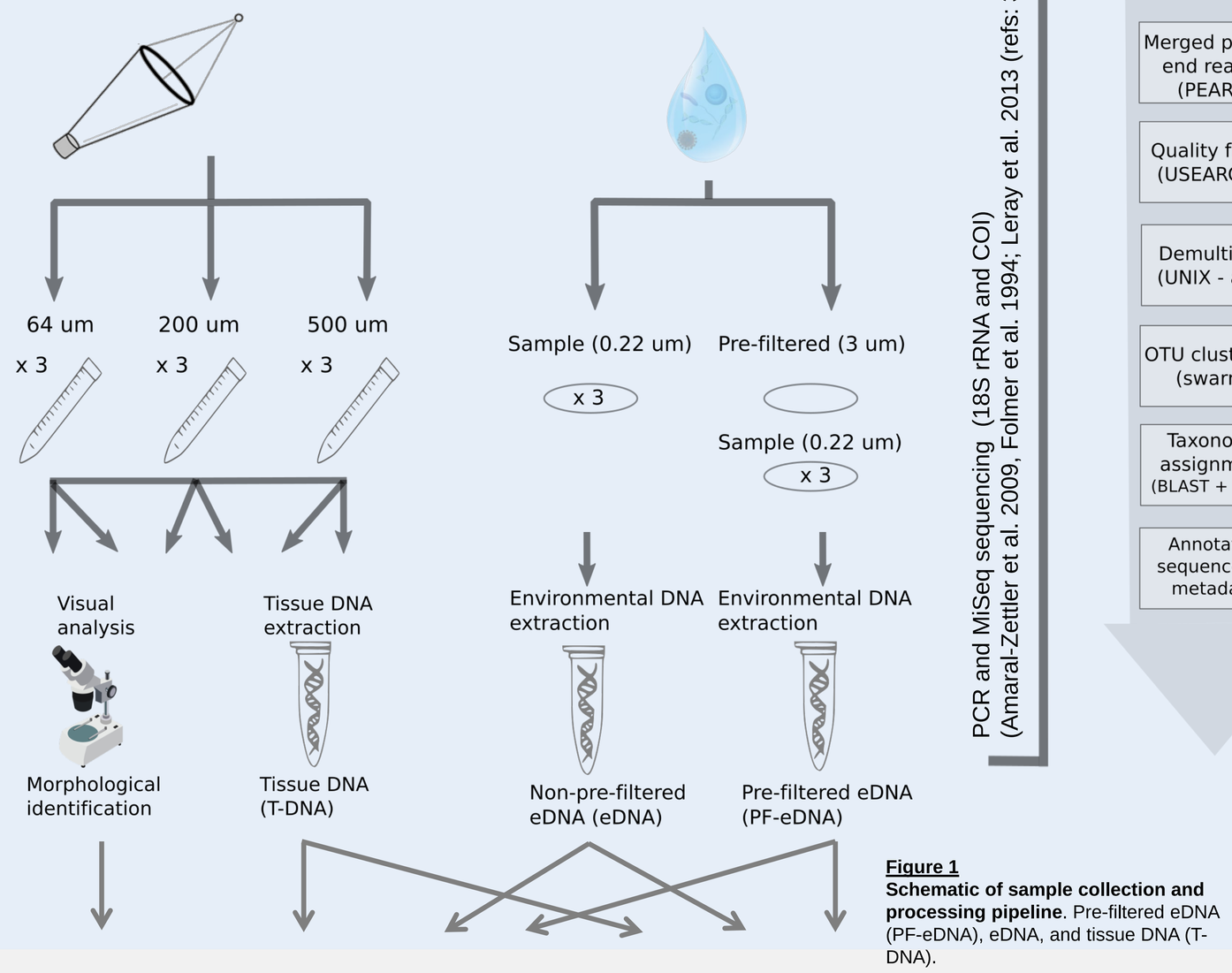

Figure 1
Schematic of sample collection and processing pipeline. Pre-filtered eDNA (PF-eDNA), eDNA, and tissue DNA (T-DNA).

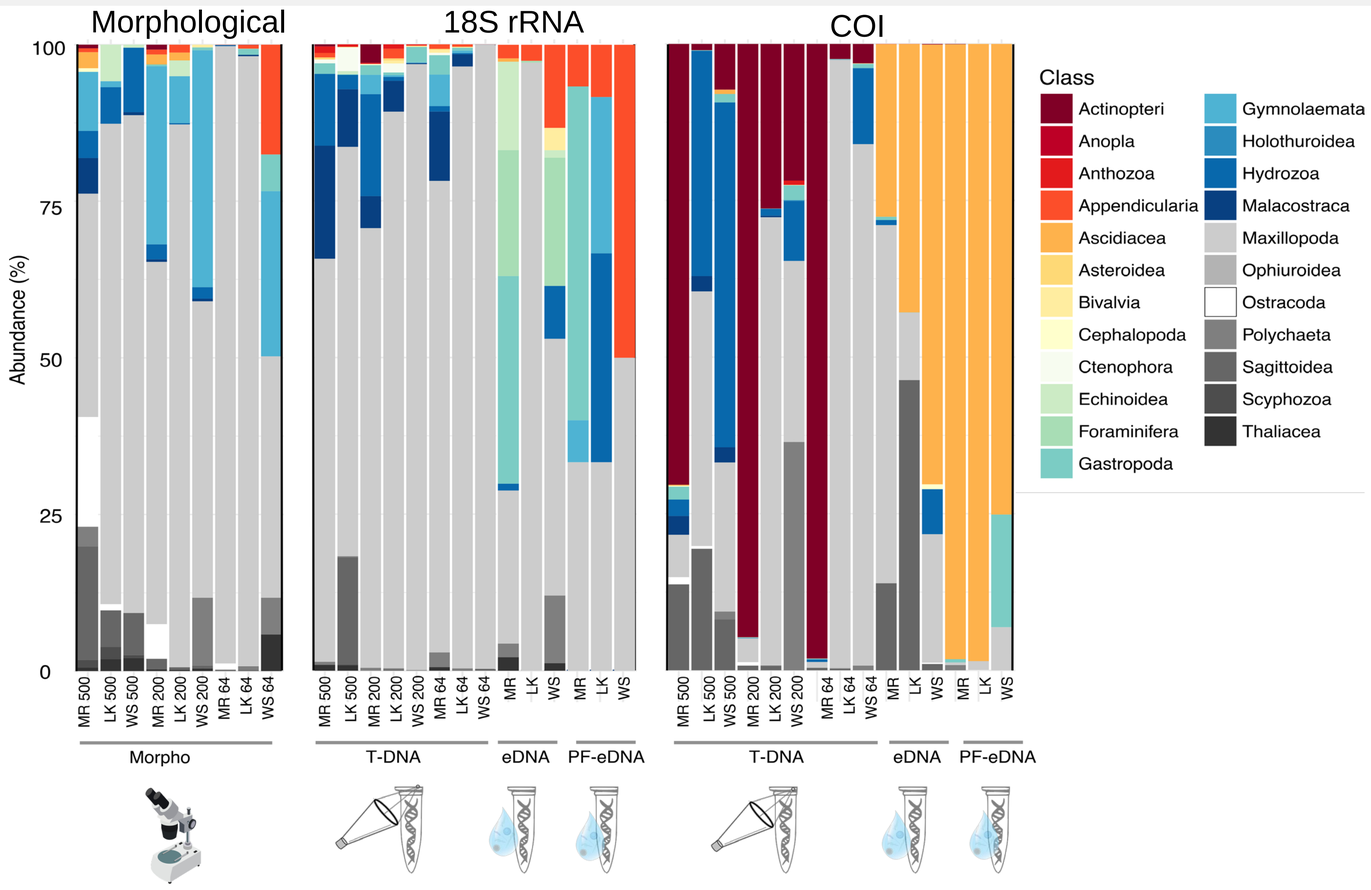

Figure 2
Barplot of all data at the Class level. The numbers on the labels for each bar refer to the mesh size (in µm) used in the net tows, and letters represent the sampling stations (Molasses Reef (MR), Looe Key (LK), and Western Sambo (WS)).

Results

- The two genetic loci (COI and 18S rRNA) recover different organisms on a Class level (i.e. chordates: ray-finned fishes (Class Actinopteri) and ascidians (Class Ascidiacea)) (Fig. 2).
- The tissue DNA (T-DNA) resembled the zooplankton taxonomic composition identified by microscopy more closely than the environmental DNA (eDNA) or pre-filtered environmental DNA (PF-eDNA).
- The morphologically identified taxa were more similar to the 18S rRNA taxonomy than to the COI.
- Both genes detected the same taxonomic groups but at different abundances (Fig. 2-3).
- The most abundant copepod genera were detected with all treatments (Fig. 3).

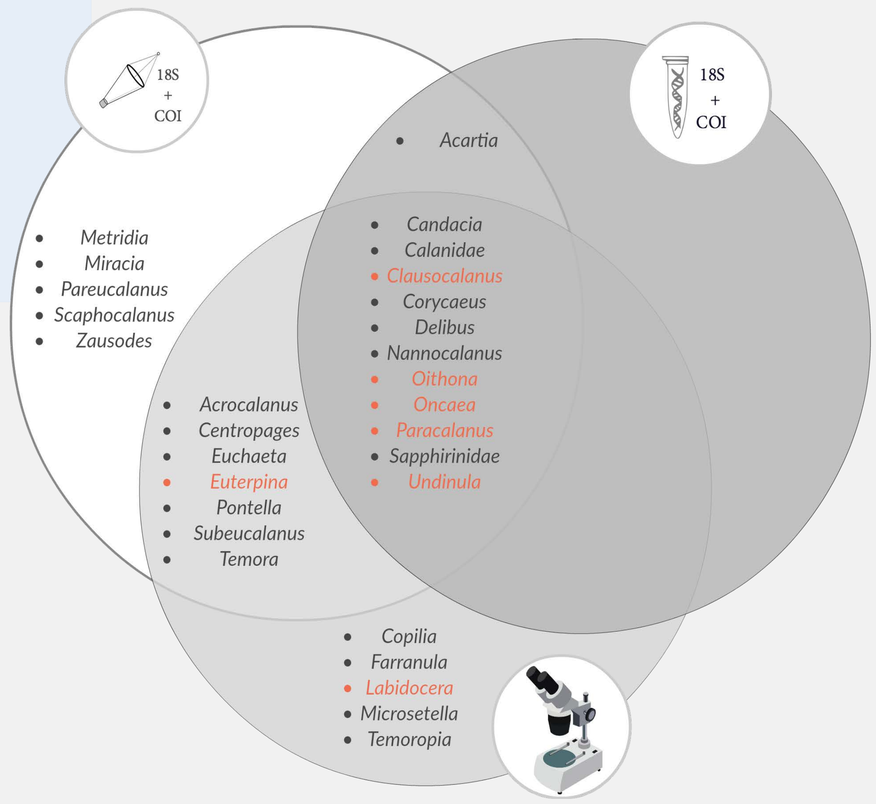

Figure 3.
Venn diagram of copepod genera detected using genetic markers in tissue DNA (T-DNA, left), environmental DNA (eDNA, right), and morphological assessments (bottom). Nearly all dominant (red, >5% of total abundance) copepod genera were identified by each treatment.

Acknowledgements

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