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Theme Session K Poster # 109



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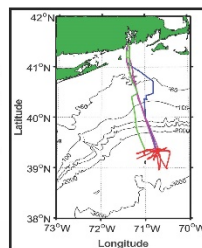
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Metabarcoding analysis of salp diets and trophic relationships in mesopelagic food webs

ABSTRACT

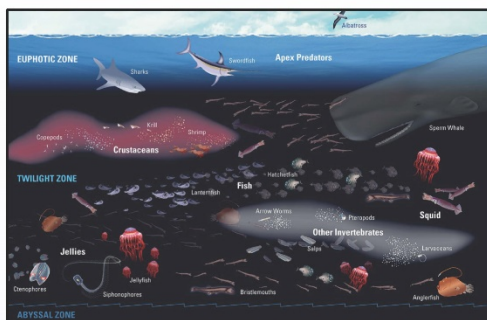
- Salps are among the most important and efficient grazers and diurnal migrators within the mesopelagic zone (200m-1,000m).
- In the NW Atlantic Ocean, seasonal and annual environmental variation drive changes in biodiversity and biomass of phytoplankton and zooplankton, altering dynamics of the mesopelagic food web.
- DNA from gut contents of salps collected from the Slope Water of the Northwest Atlantic Ocean (2018 and 2019) was sequenced for the V9 hypervariable region of the 18S rRNA gene using an Illumina MiSeq sequencer.
- Sequences and Operational Taxonomic Units (OTUs) were resolved and classified using custom scripts and reference databases



R/V Henry B. Bigelow cruise track (August 2018)

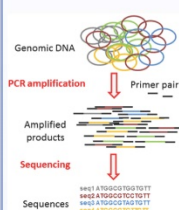
GOAL

DNA metabarcoding analysis of consumed prey will yield new insights into the trophic relationships of salps and their importance in particle and energy transfer in mesopelagic food webs.



<https://www.whoi.edu/oceanus/feature/mission-to-the-ocean-s-twilight-zone/>

METHODS

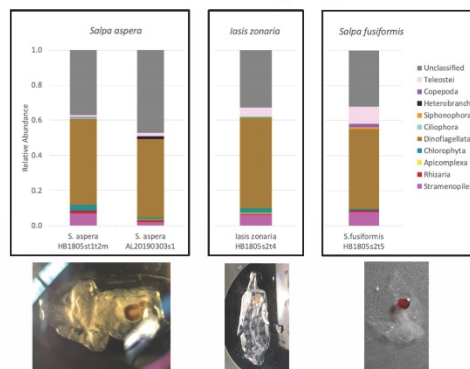


Salps were identified from the collected zooplankton samples, gut and tissue was dissected from each individual. Gut DNA was extracted following a salt-based protocol⁽¹⁾ followed by a Phenol:Chloroform purification. Amplicons for 18S region V9 were generated using 1389F and 1510R primers⁽²⁾ and KAPA HiFi. Library preparation was carried out following 16S Illumina's protocol for amplicon generation. Sequencing was carried out on an Illumina MiSeq Platform. Using 2X150bp paired-end (ver. 2 chemistry) reagents.

Bioinformatics was carried out in Mothur⁽³⁾ (Ver. 1.39.5) on UCHC Xanadu cluster using the SILVA 132 reference database

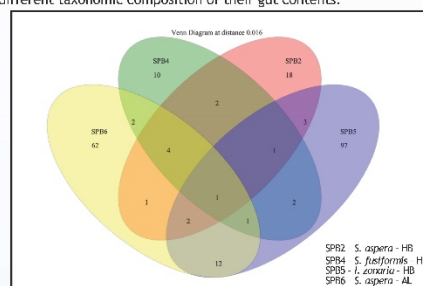


RESULTS - 18S V9 Metabarcoding of Salp Gut Contents



CONCLUSIONS

- Preliminary metabarcoding of 18S V9 data showed some differences in the plankton composition of gut content between *Salpa aspera*, *S. fusiformis* and *Isala zonaria* salp species.
- Based on 18S V9 sequences Dinoflagellata was the most abundant taxon in Salp gut content (after removing predator sequences).
- Siphonophores and Copepoda were detected in *S. fusiformis* gut content sequences.
- Salpa aspera* collected during summer 2018 and Spring 2019 showed different taxonomic composition of their gut contents.



Four-way Venn diagram illustrating the number of shared unique OTUs at the 0.015 cut off level between samples.

NEXT STEPS

- Salp species identification with long barcodes sequences (MinION)
- Metabarcoding of gut contents using 18S V4 and COI
- Comparisons between salp species/ seasons/ environments

ACKNOWLEDGEMENTS

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Metabarcoding analysis of salp diets and trophic relationships in mesopelagic food webs

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Abstract

Salps are among the most important and efficient grazers and diurnal migrators within the mesopelagic zone (200m-1,000m). In the NW Atlantic Ocean, the dynamics of these deep sea ecosystems are impacted by seasonal and annual environmental variation, driving changes in biodiversity and biomass of phytoplankton and zooplankton, and altering dynamics of the mesopelagic food web. DNA-based analysis of gut contents allows highly precise and broad coverage information about the diet of salps, and is yielding new insights into the energy flow through pelagic food webs. Salps were collected using mid water-trawls from the NW Atlantic Slope Water during the summers of 2016, 2017 and 2018. Selected specimens were removed from samples immediately on collection and flash-frozen in liquid nitrogen. Salps were partially thawed for dissection of gut contents and tissue for molecular species identification. *Salpa aspera* and *Iasis zonaria* were paired by species and stage for comparison of gut contents by metabarcoding analysis. Extracted DNA was sequenced for the V4 hypervariable region of the 18s rRNA gene using an Illumina MiSeq. Sequences and Operational Taxonomic Units (OTU's) were resolved and classified using custom scripts and reference databases. Multivariate statistical approaches were used to compare prey composition among different salp species over the 3 years. DNA metabarcoding analysis of consumed prey is yielding new insights into the trophic relationships of salps and their importance in particle and energy transfer in mesopelagic food webs.

Keywords:

mesopelagic food webs, salps, metabarcoding, trophic relationships

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