

# DEVELOPING A HIGH-THROUGHPUT GENETIC METHOD TO ELUCIDATE THE DIVERSITY AND ABUNDANCE OF ZOOPLANKTON FROM SOUTHERN-OCEAN CONTINUOUS PLANKTON RECORDER (CPR) COLLECTIONS

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### ZOOPLANKTON IN THE SOUTHERN OCEAN

- Zooplankton are important to Southern Ocean ecosystems and carbon flux
- · Climate Change Predictions:

Increased temperature

Acidification

Shifts in sea ice coverage

Increased upwelling

Marine Protected Area
 Climate change vs fishing pressure



Credit: BBC

### CURRENT METHODOLOGIES

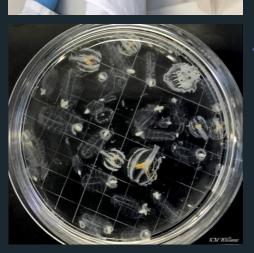
### **Sample Collection**

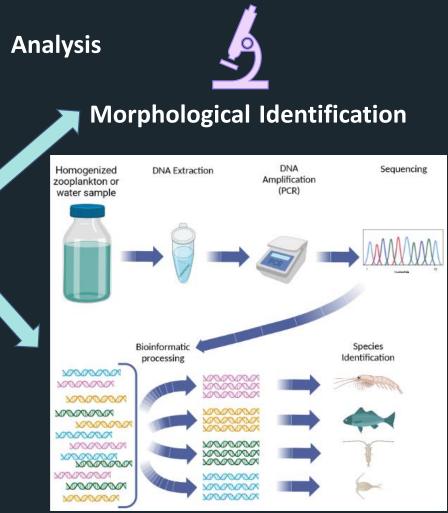


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Credit: Mary Sewell







Credit: NOAA

Credit: NOAA

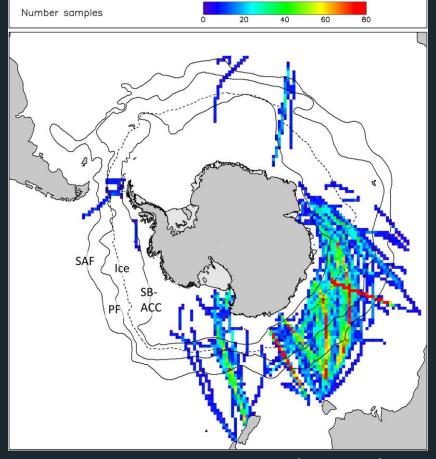
### CURRENT METHODOLOGIES - COMPARISON

Method	Advantages	Disadvantages	Best Uses
Morphological Identification	<ul> <li>Information about individuals</li> <li>Life stage</li> <li>Species abundance</li> </ul>	<ul> <li>Large proportion unidentifiable</li> <li>Specialized knowledge required</li> <li>Expensive</li> <li>Small sample sizes</li> </ul>	<ul><li>Species abundance</li><li>Developmental stages</li></ul>
Metabarcoding	<ul> <li>Identification irrespective of appearance</li> <li>Low cost</li> <li>High throughput</li> </ul>	<ul> <li>No information about individuals         <ul> <li>Not reliable for abundance</li> </ul> </li> <li>Biases can be introduced throughout process</li> <li>Databases         <ul> <li>Prior identification</li> <li>Misidentification</li> </ul> </li> <li>Unknown unknowns</li> </ul>	• Species presence/absence

### GOALS

- Current research limitations
  - Methods of analysis
    - Resource intensive
    - Introduce biases
  - Sample processing backlog
- · A new methodology is needed
  - Accurate
  - High throughput
  - Universal

### Number of CPR samples by area

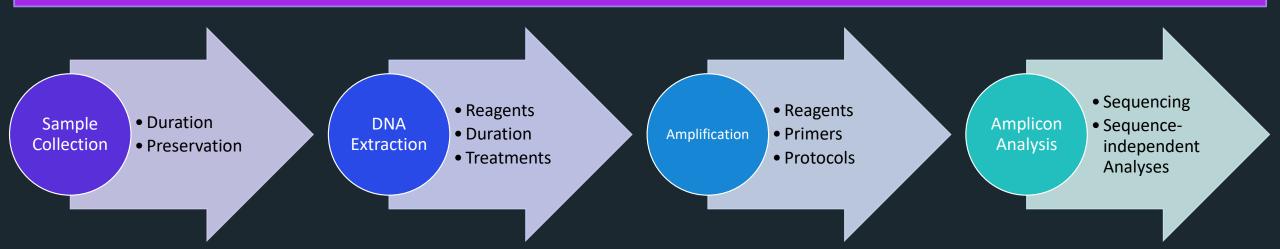


Pinkerton et al, 2020



### METHOD DEVELOPMENT OVERVIEW

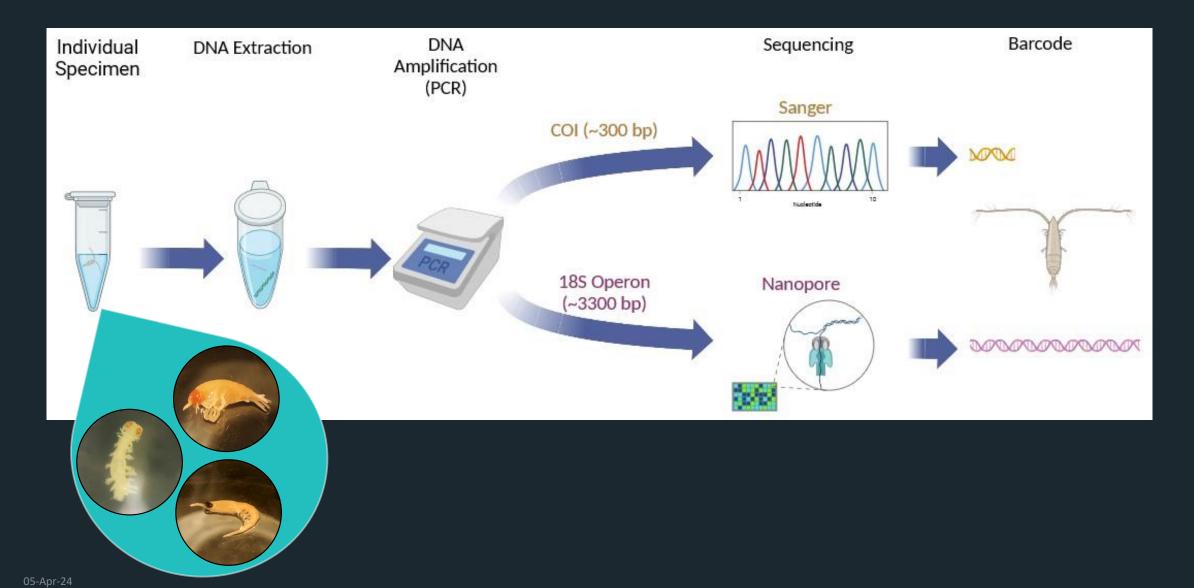
### Universal Procedure Across Zooplankton Taxa



### SAMPLE COLLECTION / IDENTIFICATION



### SPECIMEN PROCESSING



### SEQUENCE ANALYSIS







Check sequence quality and BLAST search sequences to confirm ID



Finalize reference sequences

Trimming



Generate sequence alignments

Southern Ocean sequence database

Barcodes and sample data



## 03 RESULTS

### RESULTS OVERVIEW

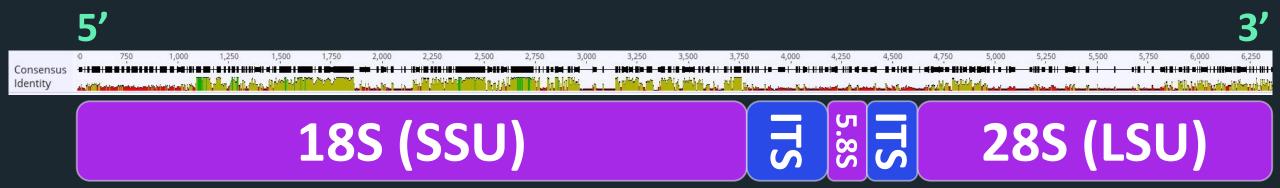
Amplicon	COI	18S Operon
# Taxa Sequenced	38	48

Phyla	COI Sequenced?	18S Operon Sequenced?
Annelida	Inconclusive	Yes
Arthropoda	Yes	Yes
Brachiopoda	No	No
Bryozoa	Yes	Yes
Chaetognatha	Yes	Yes
Chordata	Yes	Yes
Cnidaria	Inconclusive	Yes
Echinodermata	No	Yes
Foraminifera	Inconclusive	Yes
Hemichordata	No	No
Mollusca	Yes	Yes
Porifera	No	No
Radiozoa	No	Yes

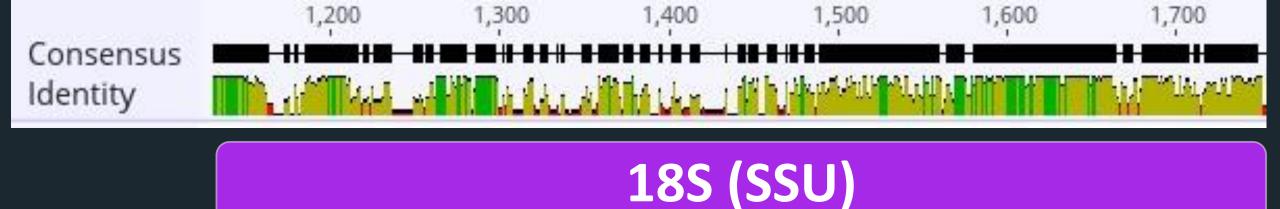
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### SEQUENCE ALIGNMENT - 18S OPERON

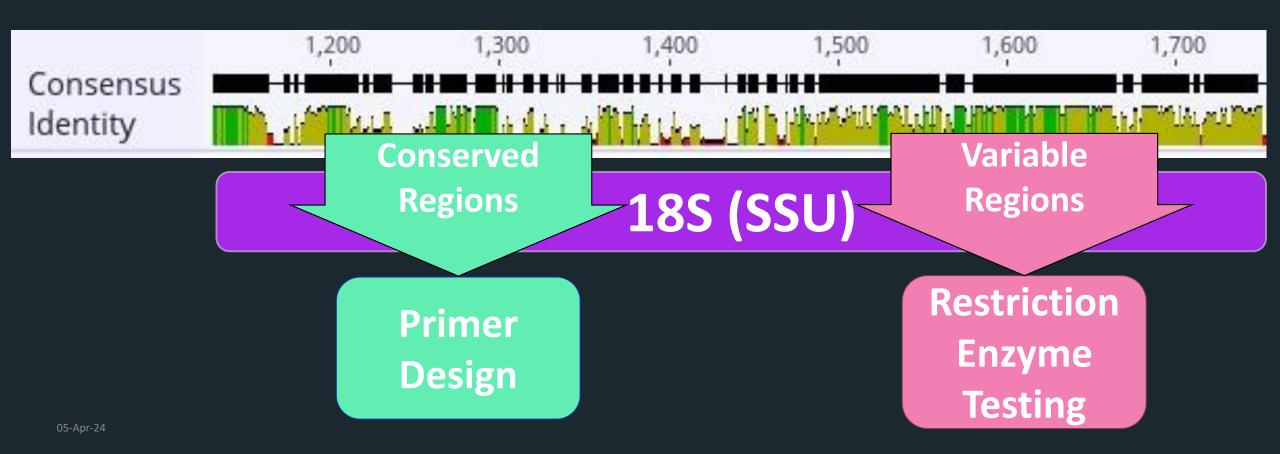
Alignment from 38 sequences, representing 32 taxa



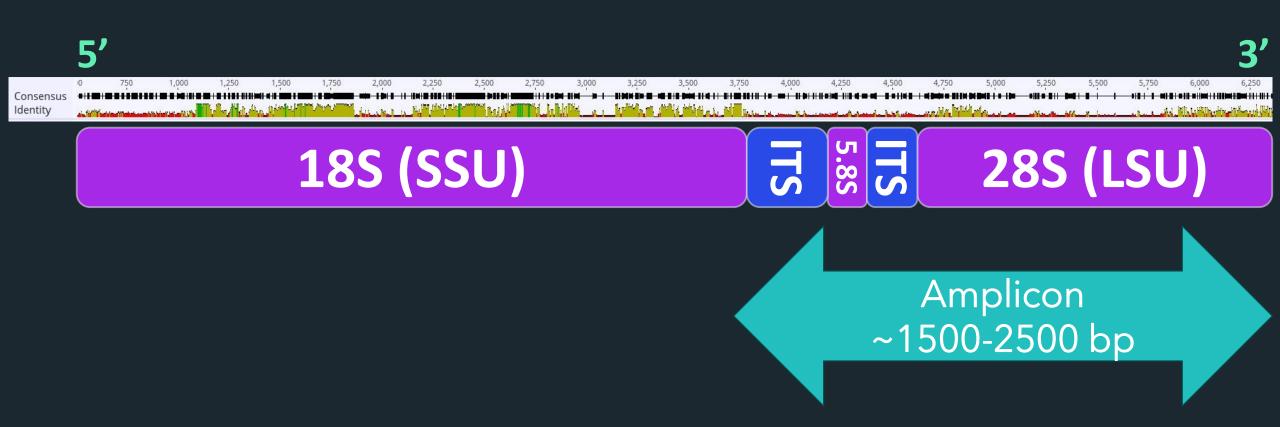
### SEQUENCE ALIGNMENT - 18S OPERON



### SEQUENCE ALIGNMENT - 18S OPERON



### PRIMER DESIGN - 18S OPERON



### RESTRICTION ENZYME TESTING

### GOALS

 Find 1 or more restriction enzymes that would differentially digest amplicons from different species to produce unique fingerprints

### PROBLEMS

- Co-amplification
- Unknown sequences

Decision: proceed with sequencing method

# 04 FUTURE WORK



### FUTURE WORK



- 1. Final determination of which primer set to use for this method
  - 1. COI or 18S operon
  - 2. Considerations:
    - 1. Amplification success across phyla
    - 2. Taxonomic resolution
- 2. Validation of the method versus morphological ID and metabarcoding
- 3. High-throughput processing of historical and recent ethanol samples

# IN MEMORIAM: PROF. CRAIG CARY

May 13, 1954-Feb 29, 2024

An exceptional scientist and mentor without whom this project would not have been possible.



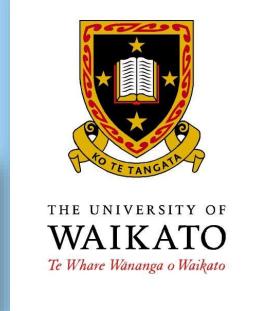


### THANK YOU

Special thanks to Karen Robinson and Dr. Svenja Halfter for providing samples







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