Integrative Assessment of the Quality of Shallow Tributary Forage Habitats for Striped Bass in Chesapeake Bay

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Goals and objectives

Project goals: To quantify the quality of shallow tributary habitats of Chesapeake Bay as foraging habitat for Striped Bass and to identify key prey species in those habitats across life-history stages.

Objectives:

1. Collect Striped Bass at 5 sites in early summer, late summer, fall
2. Assess age and size structure, condition, growth, and parasites
3. Quantify diet and nutrition (morphology, genetics, isotopes)
4. Relate diet, condition, growth, parasitism, and environmental variation to assess habitat quality

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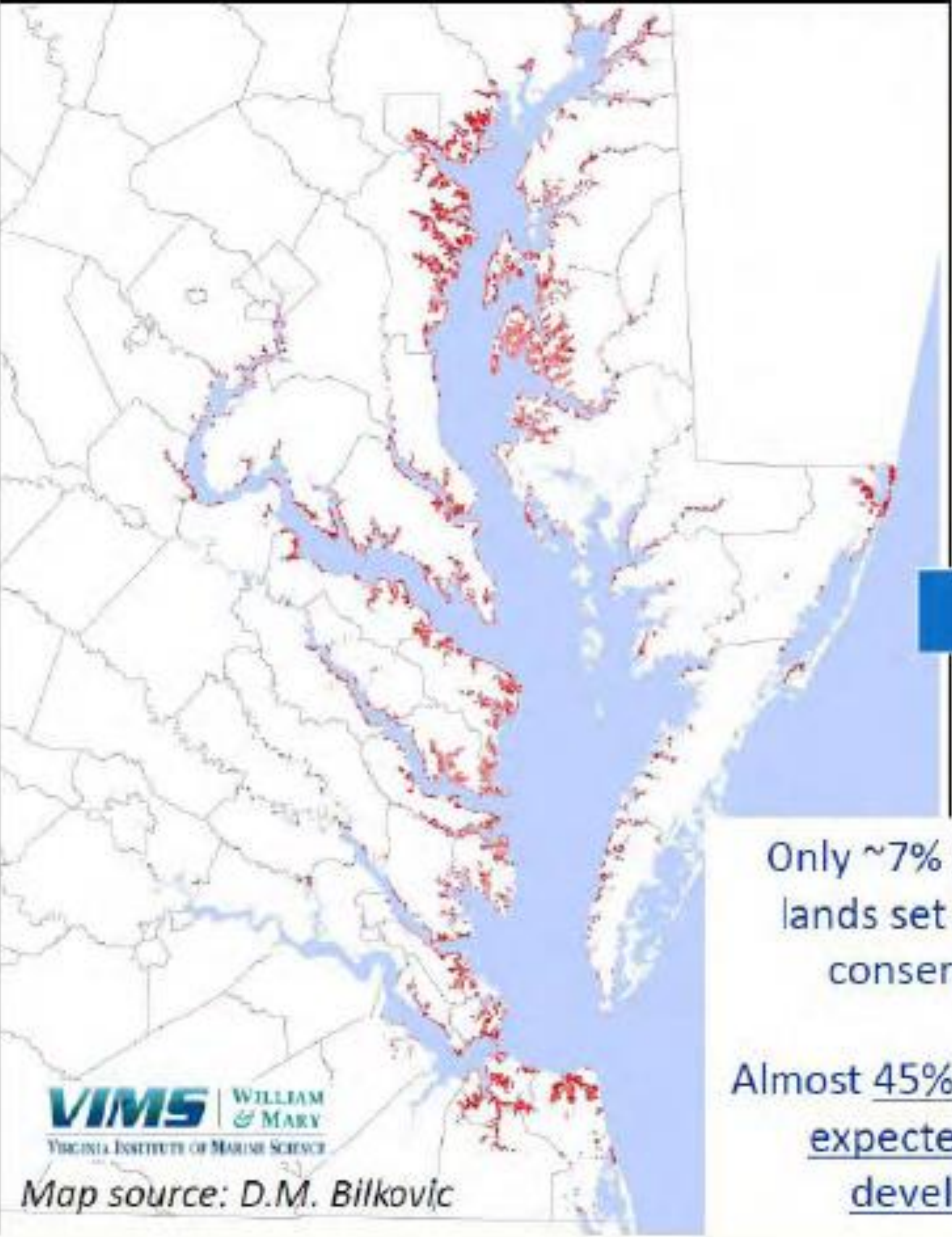
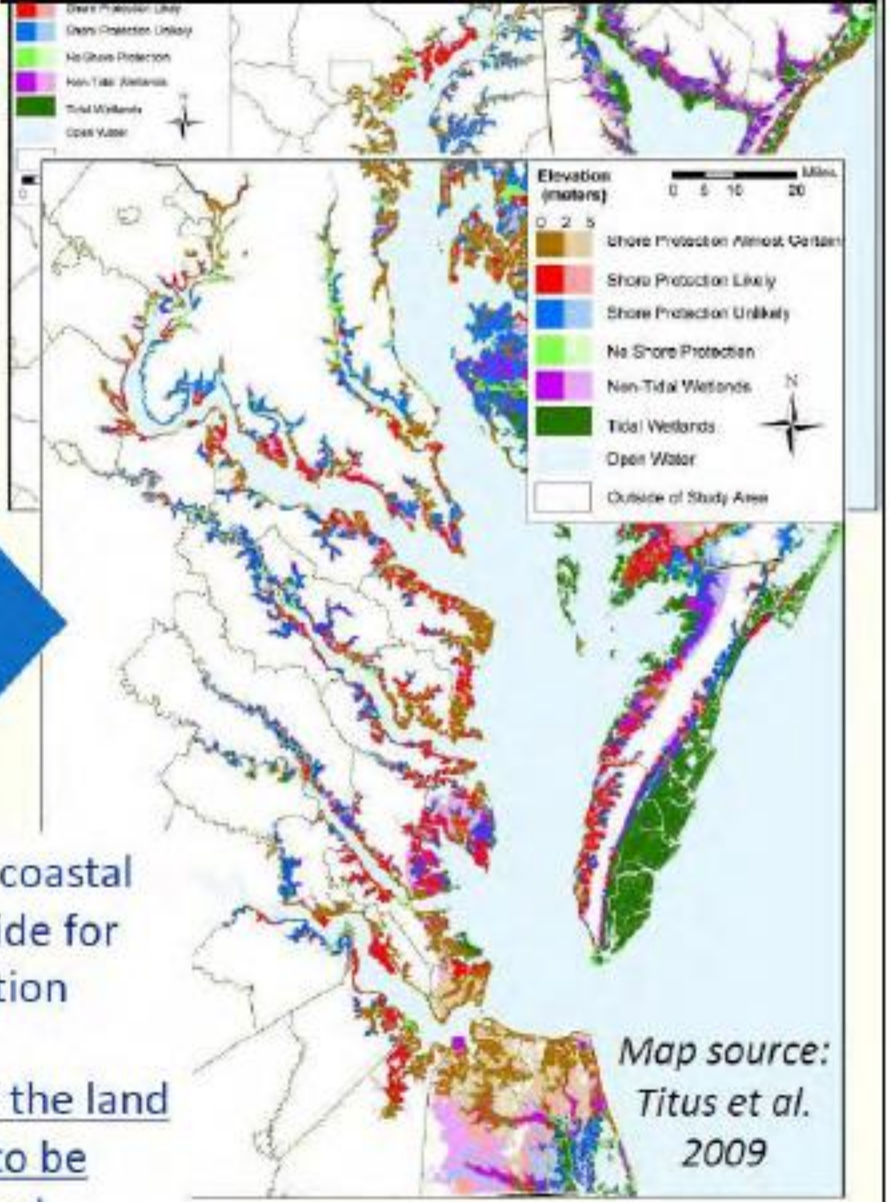
Coastal Development: Status and Future Trends

Current shoreline hardening – Bulkhead/Riprap



Map source: D.M. Bilkovic

Future shore protection

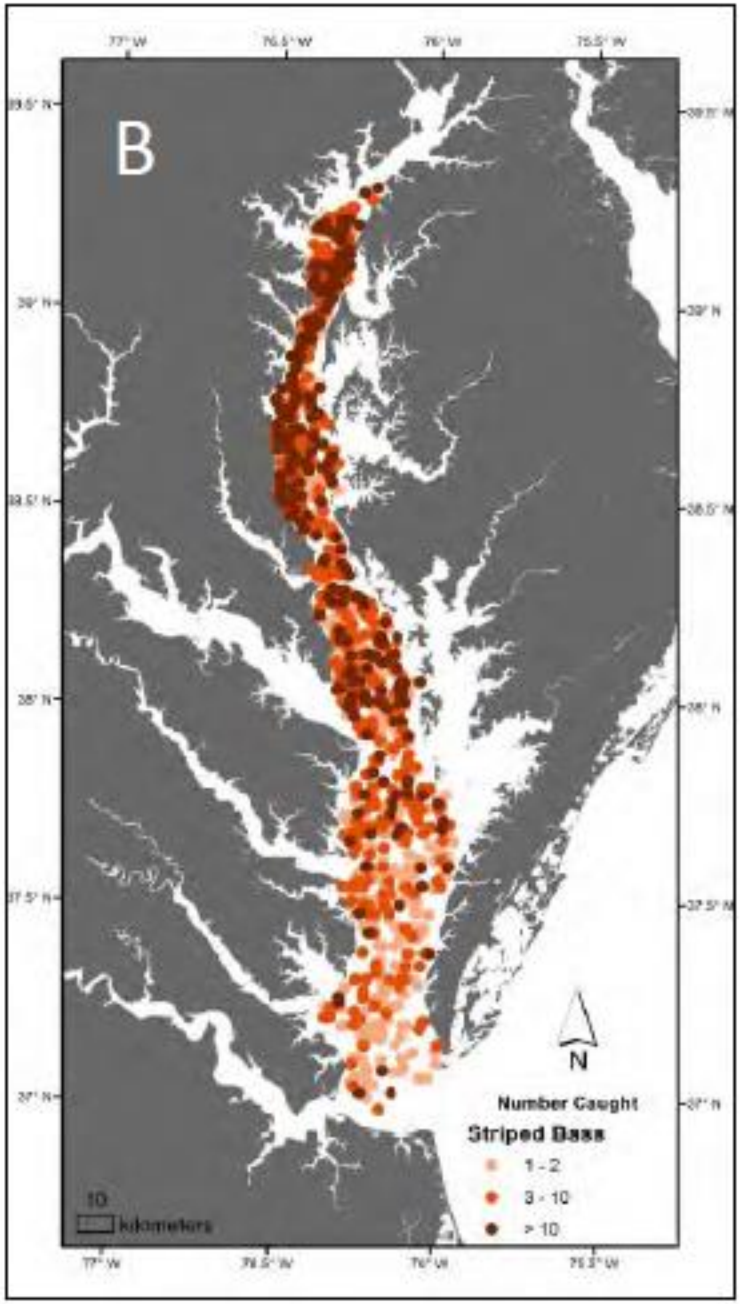


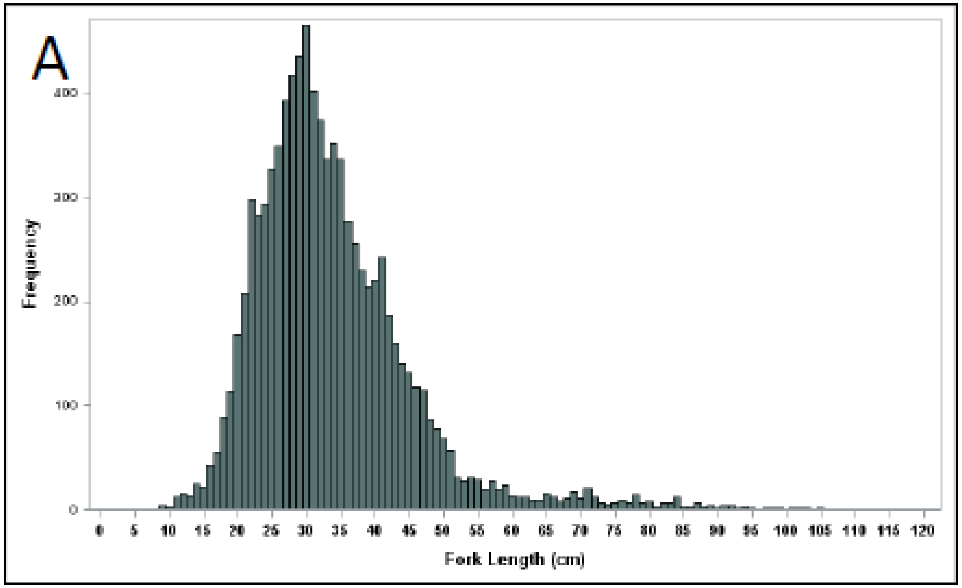
Map source: Titus et al. 2009

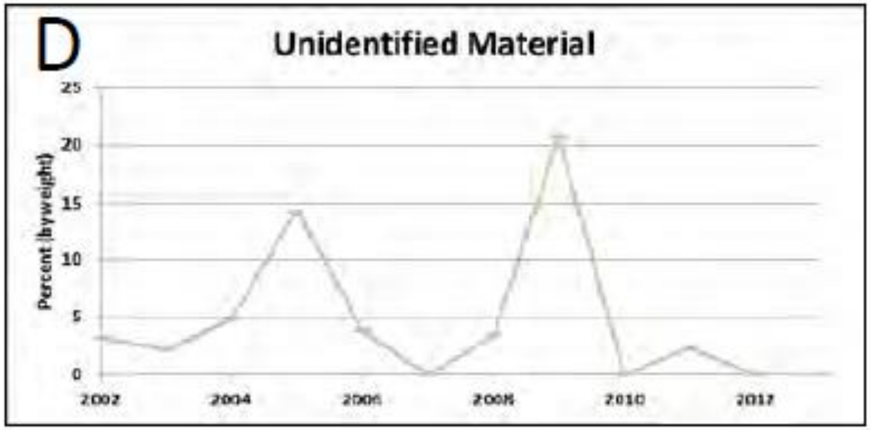
Only ~7% of coastal lands set aside for conservation

Almost <u>45% of the land expected to be developed</u>

Ihde et al. 2015







Ihde et al. 2015

Methods

Collected fish in tributaries using gillnets and from MD and VA seine surveys

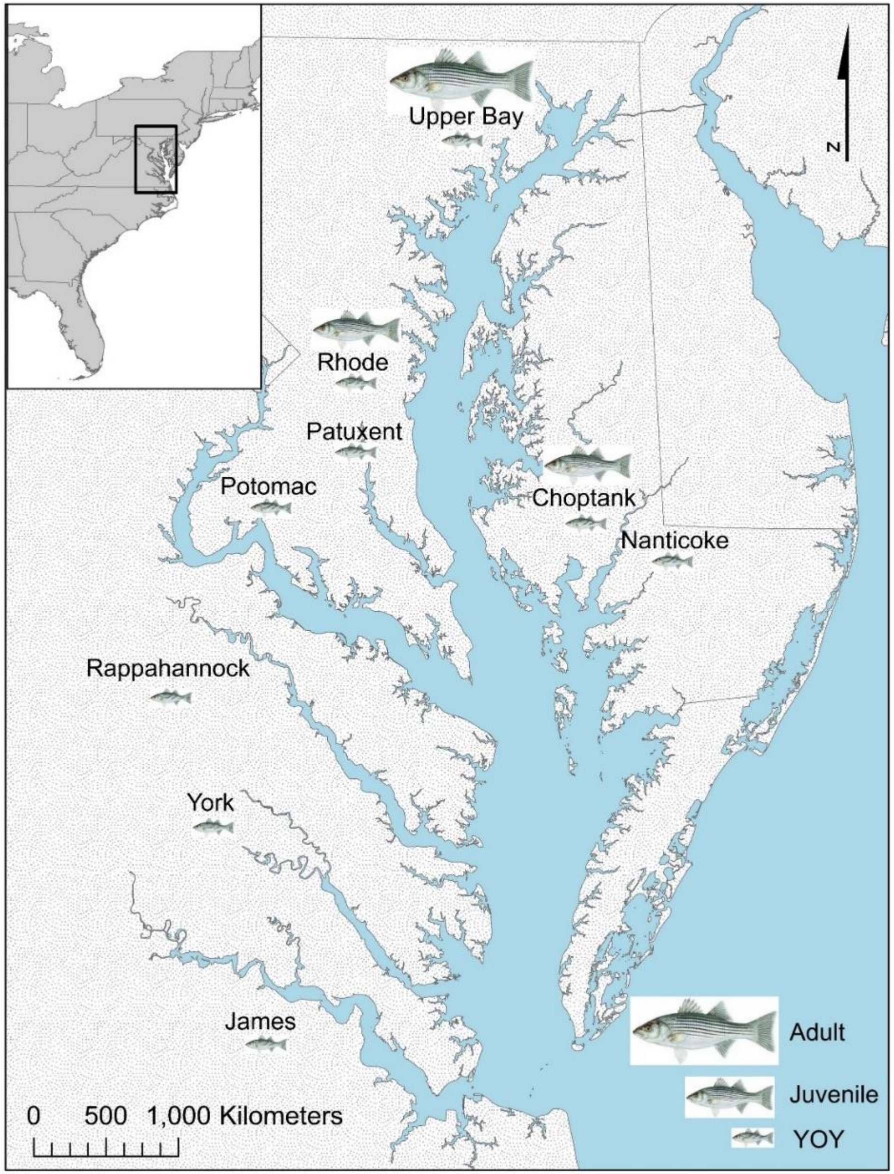
- young-of-year (YOY) – N=9 tributaries
- Age 1-4 – N=2 tributaries
- Adults – Upper Bay only (Maryland Striped Bass Spawning Survey)

Morphological gut content analysis for 50% of fish, genetic analysis for the rest

Visual inspection for body condition and parasites

Otolith ageing planned to determine growth rate for selected YOY (TBD)

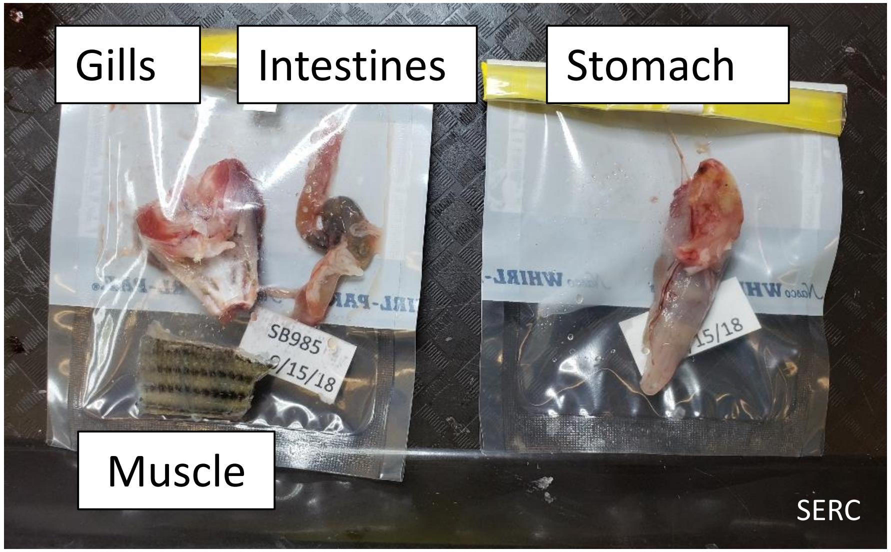

SERC



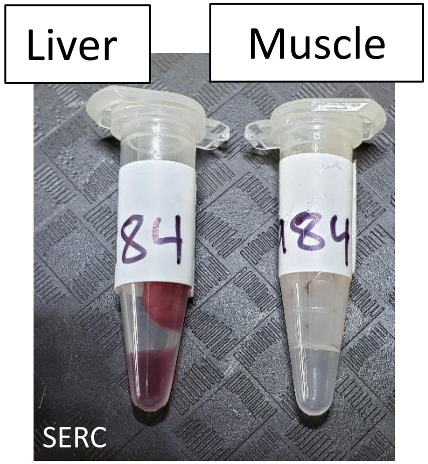
Methods

Parasite Analysis

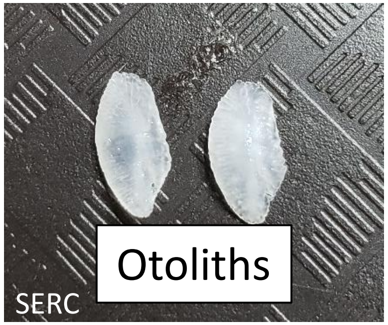
Diet Study



Stable Isotopes



Age and Growth



Gut Content Identification using Genetic Barcoding

Sequence: 655bp
CCTATATCTAGTATTTGGCGCTTGAGCTGGTATAGTCGGCACTGCTTTAAGCCTTCTTAT
TCGAGCAGAGCTGAGCCAACCGGGCGCCCTCCTTGGCGACGATCAGATCTATAATGTGAT
CGTTACCGCACACGCATTTGTAATAATCTTTTTTATAGTTATACCAATTATGATTGGAGG
GTTTGGAAACTGACTAATCCCTTTAATGATTGGGGCGCCAGACATGGCATTCCCCCGAAT
AAACAACATGAGTTTTTGACTACTTCCTCCATCTTTCCTTCTCCTTCTGGCCTCTTCTGG
TGTCGAAGCTGGAGCCGGAACCGGCTGAACCGTCTATCCCCCACTTGCAAGTAACCTTGC
ACACGCAGGAGCATCCGTAGATTTAACAATTTTCTCCCTCCATCTGGCCGGGATTTCCTC
GATTTTAGGGGCCATTAATTTTATTACAACTATTATTAACATGAAGCCCCCGCTATCTC
CCAATATCAAACCCCTCTGTTCGTATGGGCAGTCCTAATTACAGCCGTCCTCTTACTTCT
CTCTCTCCCCGTCCTTGCAGCTGGAATCACTATATTACTTACAGACCGAAACCTTAATAC
CACCTTCTTCGACCCTGCAGGGGGAGGGGACCCCATTCTTTACCAACATCTTTTC

BIN →

BOLD

BLAST

Chesapeake Bay Barcode Initiative

https://serc.si.edu/projects/species-diversity-chesapeake-bay

Methods

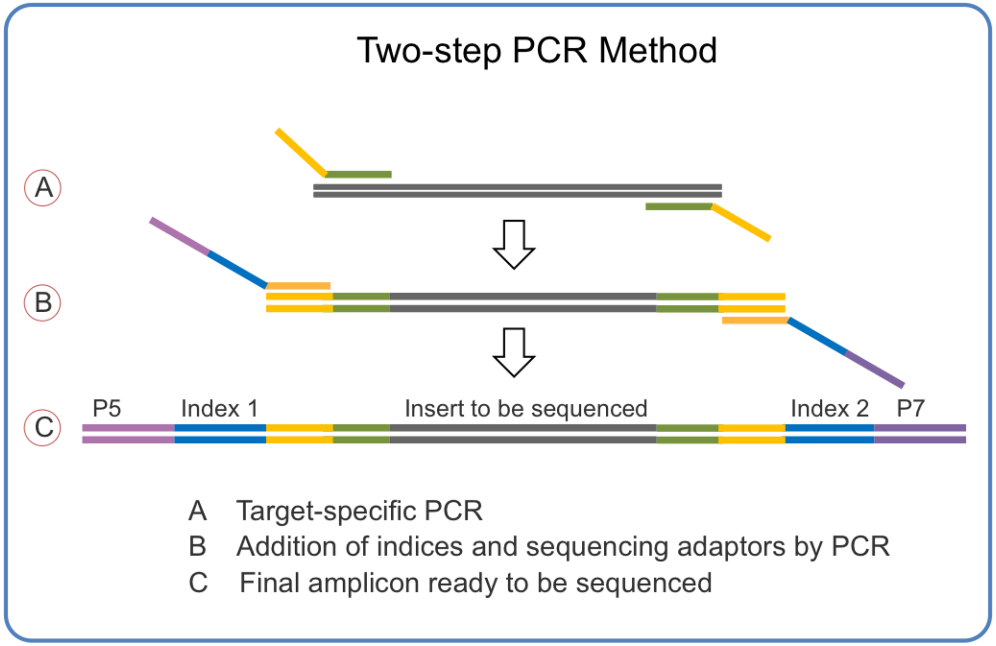
Homogenize gut contents, then extract genomic DNA using standard DNA Extraction kit

Use two-step PCR method to generate amplicon libraries

  - COI and 18S genes for comprehensive assessment of prey items present

Dual-indexing to increase # of samples we can put on single run

Sequencing on Illumina Miseq platform



Two-step PCR Method

A Target-specific PCR
B Addition of indices and sequencing adaptors by PCR
C Final amplicon ready to be sequenced

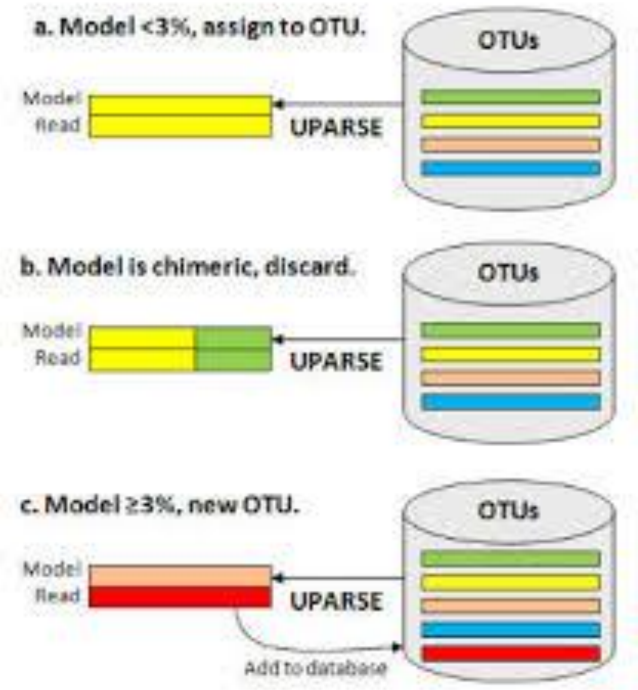
Methods

Generate OTU tables using USEARCH pipeline

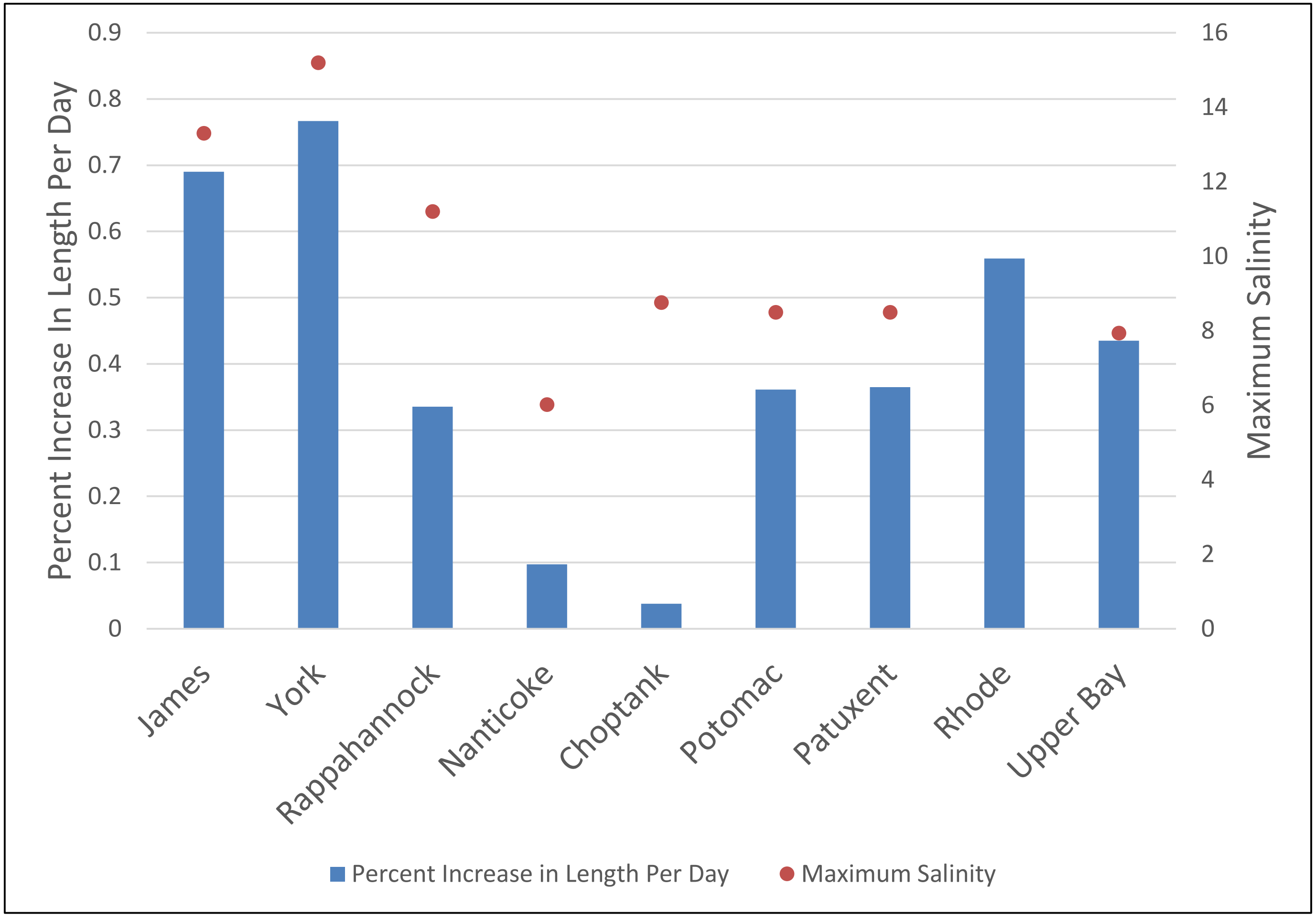
Includes UPARSE for removing chimeras and clustering OTUs
	-parameters changed for the two amplicon types

Taxonomy will be assigned first with the RDP classifier using Chesapeake Bay Barcode Initiative sequences, then with GenBank for the COI sequences and the RDP classifier with the PR2 database for the 18S sequences

QIIME and R will be used for analyses of the OTU table to compare the diversity and connectivity of OTUs across sites, individuals, and size classes



Preliminary results: Length



South → North

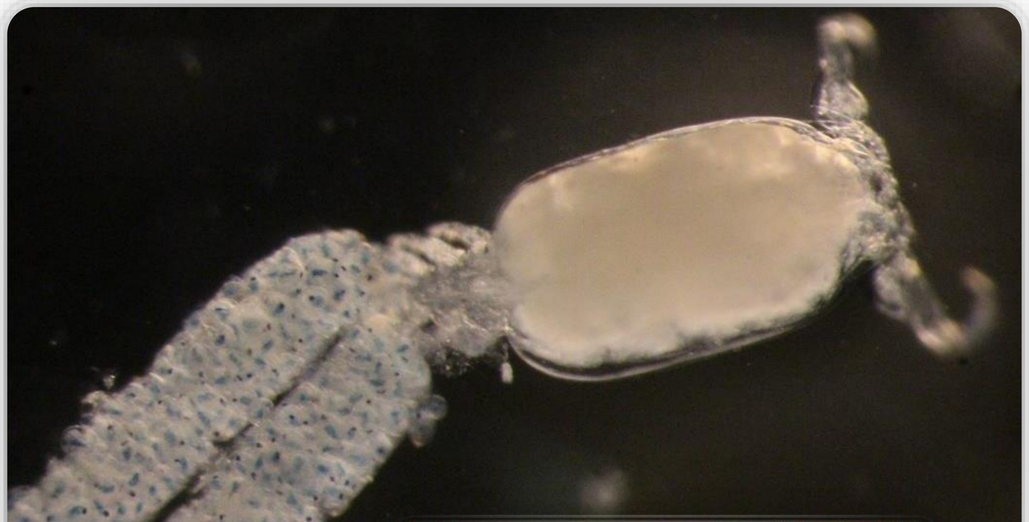
Ogburn, unpublished data

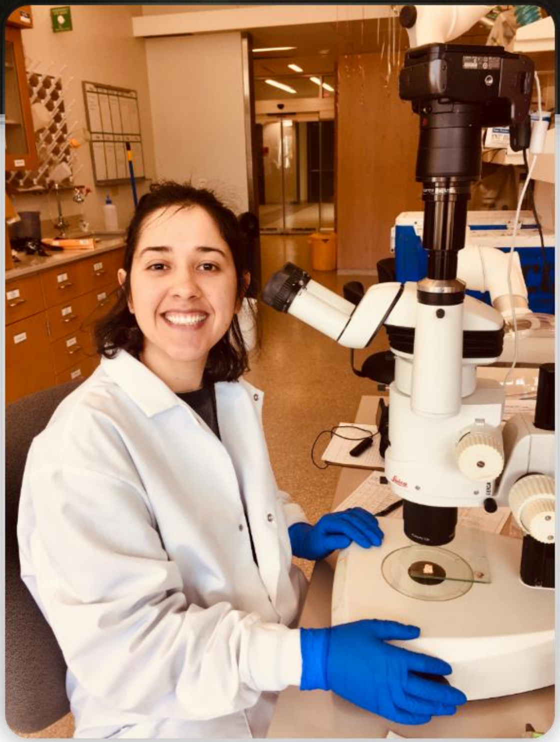
Preliminary results: Parasites

Intestine

Muscle

Gills





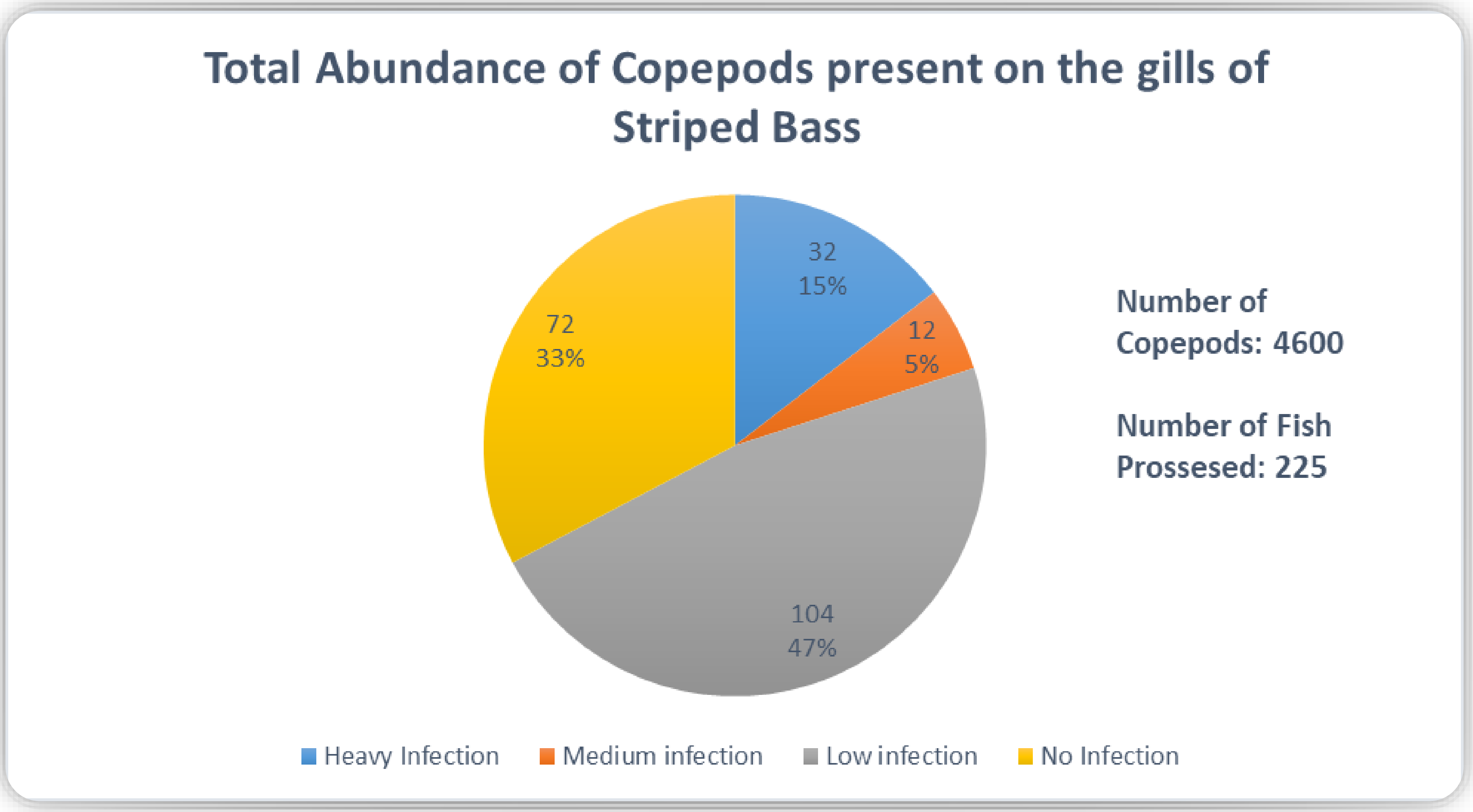
Ergasilidae

- Grasp with Antennae
- Fresh and Marine Habitats

Pathogenesis:

- Hyperplasia and Necrosis

Preliminary results: Parasites



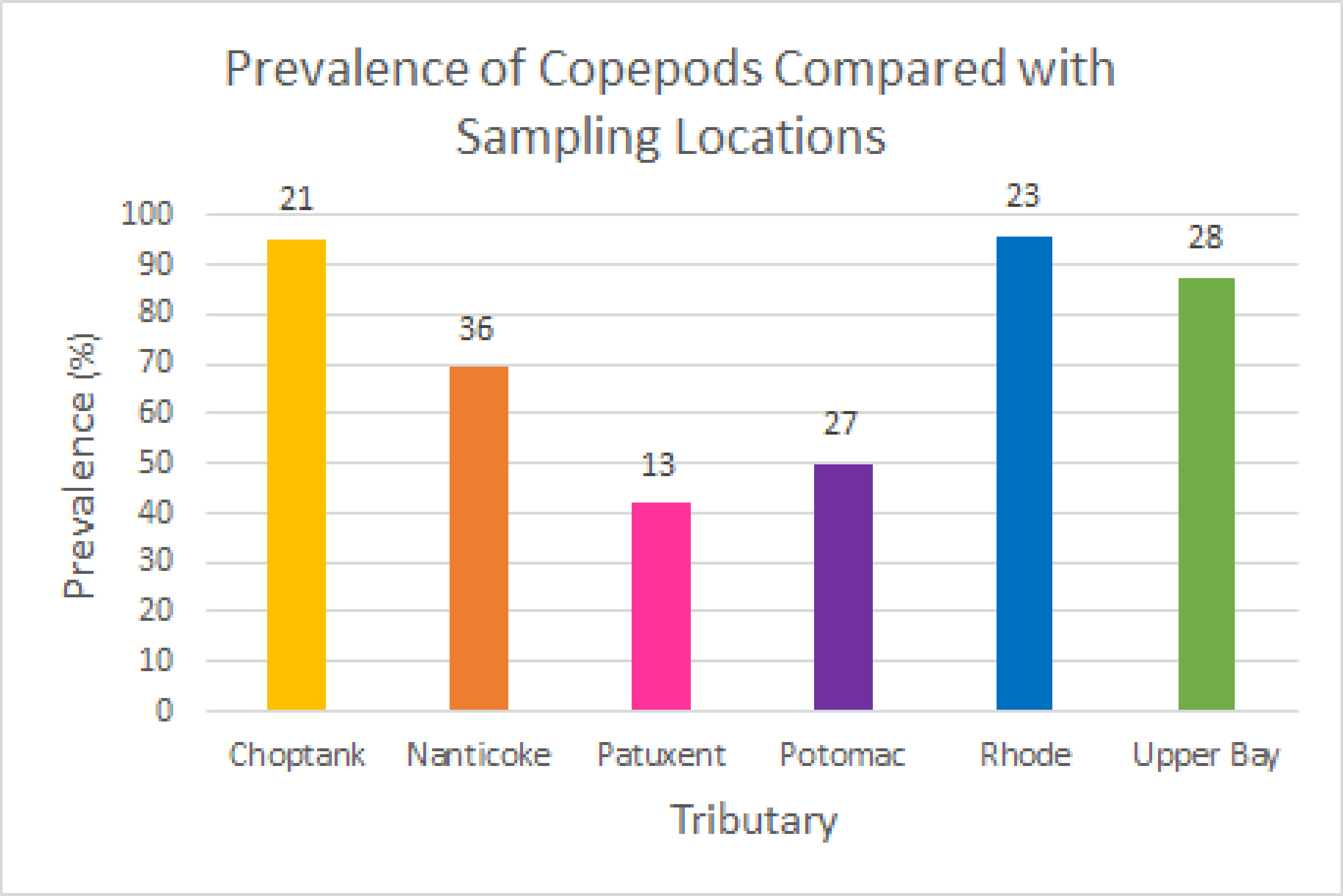
Total Abundance of Copepods present on the gills of Striped Bass

Number of Copepods: 4600

Number of Fish Prossesed: 225

Lohan, unpublished data

Preliminary results: Parasites



Lohan, unpublished data

Project impacts

Identify key forage species for Striped Bass in tributary forage habitats, especially YOY fish

First comprehensive diet analysis in Chesapeake Bay using DNA barcoding and Chesapeake Bay Barcode Initiative database

Test the hypothesis that metabarcoding increases efficiency in diet studies

Provide the first comprehensive data on diversity and importance of free-living protists and parasites in the Striped Bass food web in Chesapeake Bay