

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



Matthew B. Ogburn, Katrina P. Lohan, Anson H. Hines



Smithsonian Environmental
Research Center



@fishinvertlab

Goals and objectives

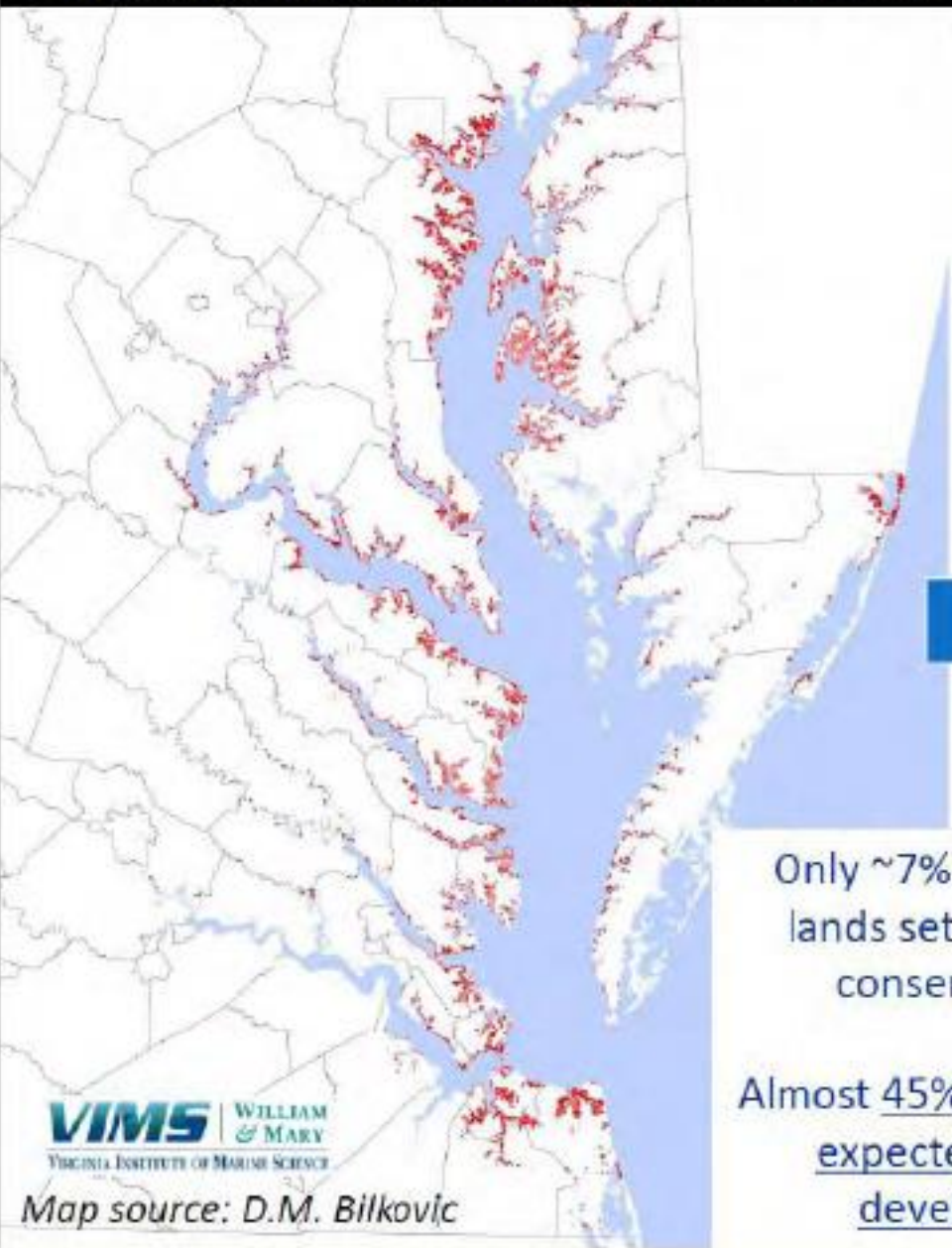
Project goals: To quantify the quality of shallow tributary habitats of Chesapeake Bay as foraging habitat for Striped Bass and to identify key prey species in those habitats across life-history stages.

Objectives:

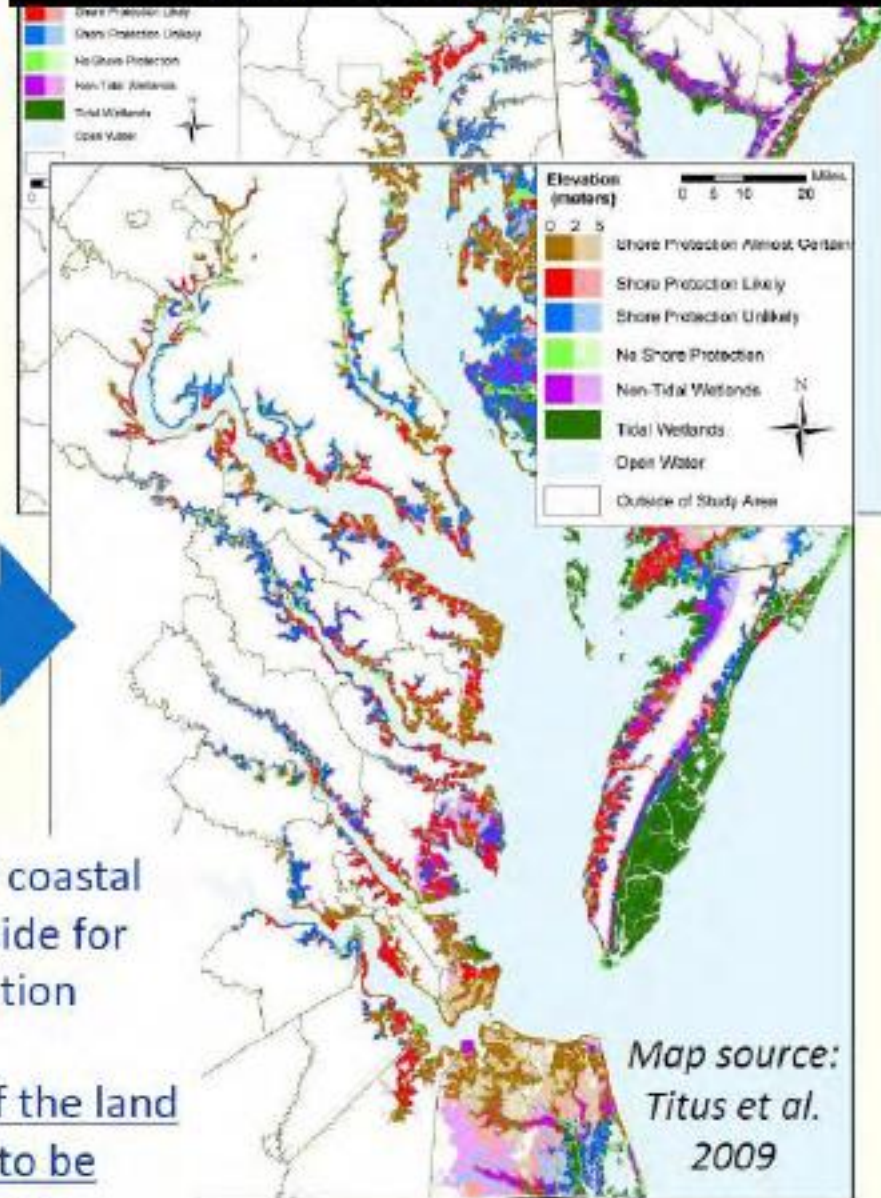
1. Collect Striped Bass at 5 sites in early summer, late summer, fall
2. Assess age and size structure, condition, growth, and parasites
3. Quantify diet and nutrition (morphology, genetics, isotopes)
4. Relate diet, condition, growth, parasitism, and environmental variation to assess habitat quality

Coastal Development: Status and Future Trends

Current shoreline hardening – Bulkhead/Riprap



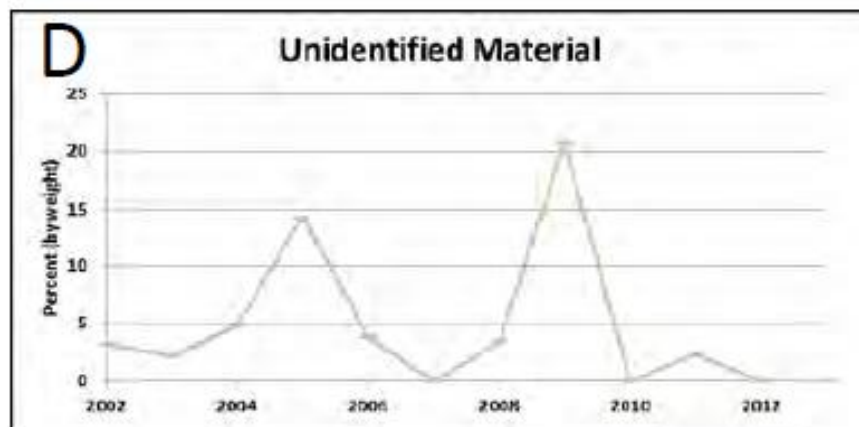
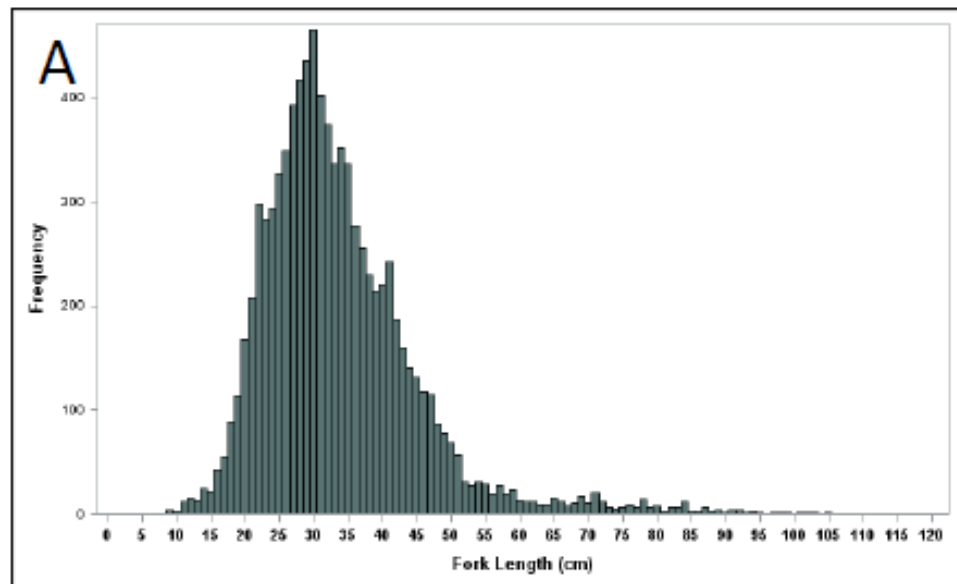
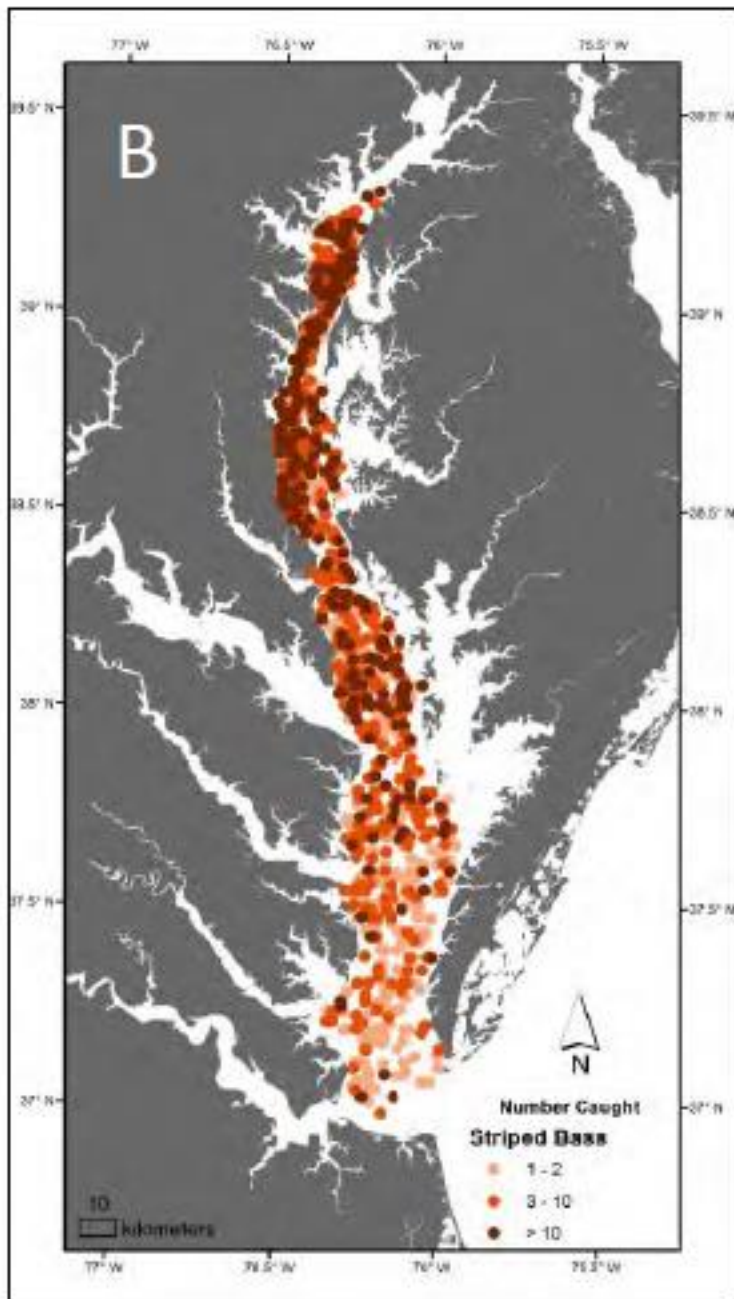
Future shore protection



Only ~7% of coastal lands set aside for conservation

Almost 45% of the land expected to be developed

Map source: Titus et al. 2009



Methods

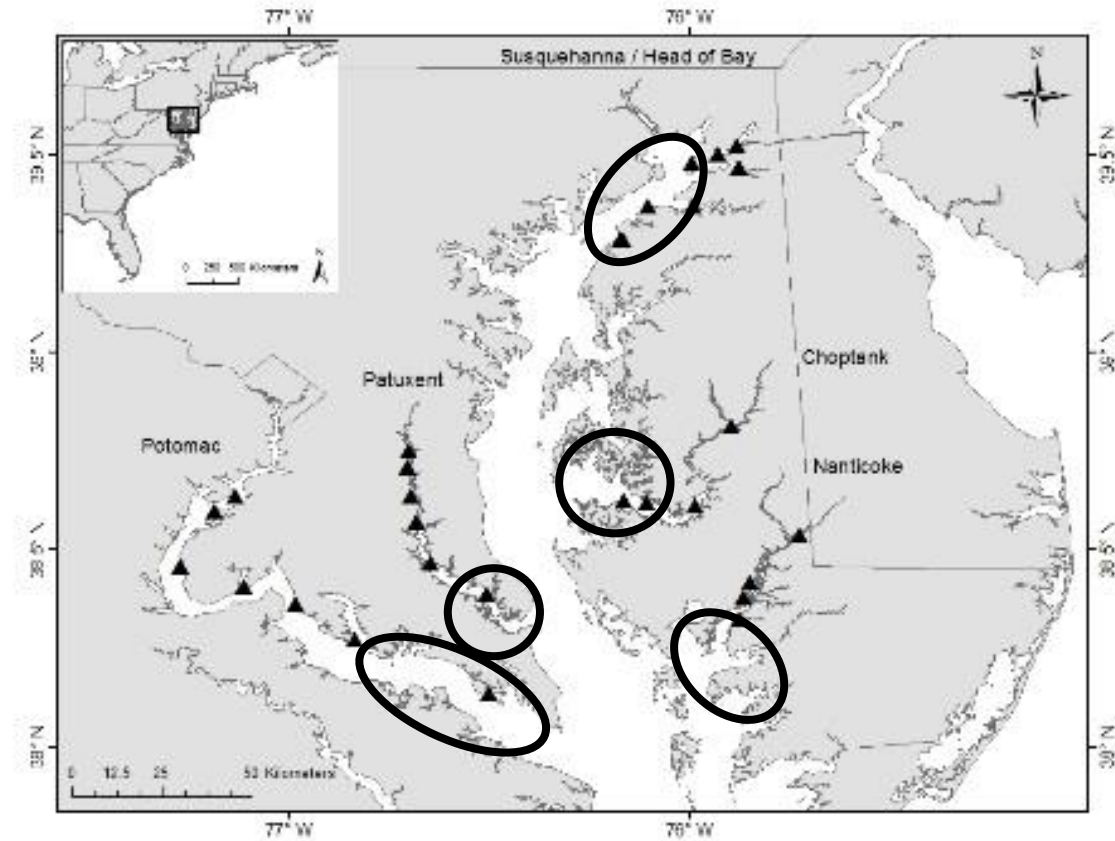
Collect young-of-year (YOY), juvenile, and subadult fish using gillnets and fish provided by the Maryland DNR Striped Bass Seine Survey (N=50 per collection)

Up to 30 adult fish will also be accepted that suffer incidental mortality during 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

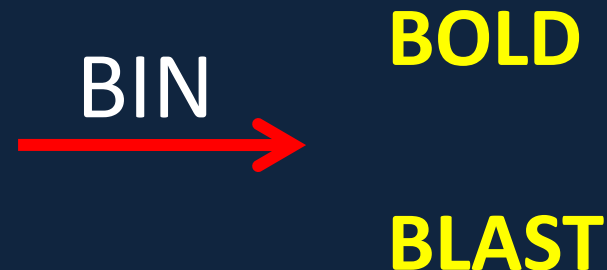
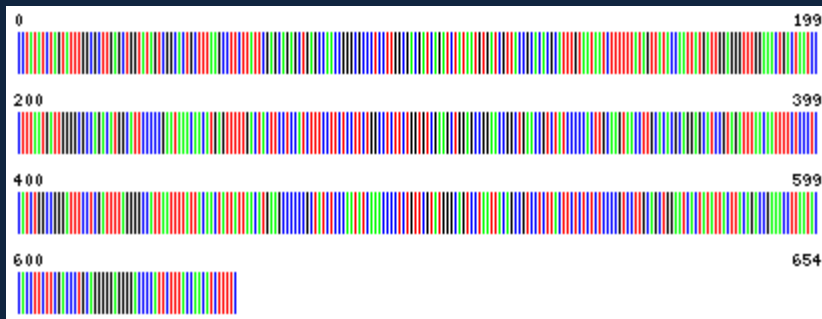
Otolith ageing for growth rate



Species Identification using Genetic Barcoding

Sequence: 655bp

CCTATATCTAGTATTTGGCGCTTGAGCTGGTATAGTCGGCACTGCTTTAAGCCTTCTTAT
TCGAGCAGAGCTGAGCCAACCGGGCGCCCTCCTTGGCGACGATCAGATCTATAATGTGAT
CGTTACCGCACACGCATTGTATAATCTTTTTTATAGTTATACCAATTATGATTGGAGG
GTTTGGAAACTGACTAATCCCTTTAATGATTGGGGCGCCAGACATGGCATTCCCCCGAAT
AAACAACATGAGTTTTGACTACTTCCTCCATCTTTCCTTCTCCTTCTGGCCTCTTCTGG
TGTCGAAGCTGGAGCCGGAACCGGCTGAACCGTCTATCCCCCACTTGCAAGTAACCTTGC
ACACGCAGGAGCATCCGTAGATTTAACAATTTTCTCCCTCCATCTGGCCGGGATTTCCTC
GATTTTAGGGGCCATTAATTTTATTACAATATTATTAACATGAAGCCCCCGCTATCTC
CCAATATCAAACCCCTCTGTTTCGTATGGGCAGTCCTAATTACAGCCGTCCTCTTACTTCT
CTCTCTCCCCGTCCTTGCAGCTGGAATCACTATATTACTTACAGACCGAAACCTTAATAC
CACCTTCTTCGACCCTGCAGGGGGAGGGGACCCCATTCCTTACCAACATCTTTTC



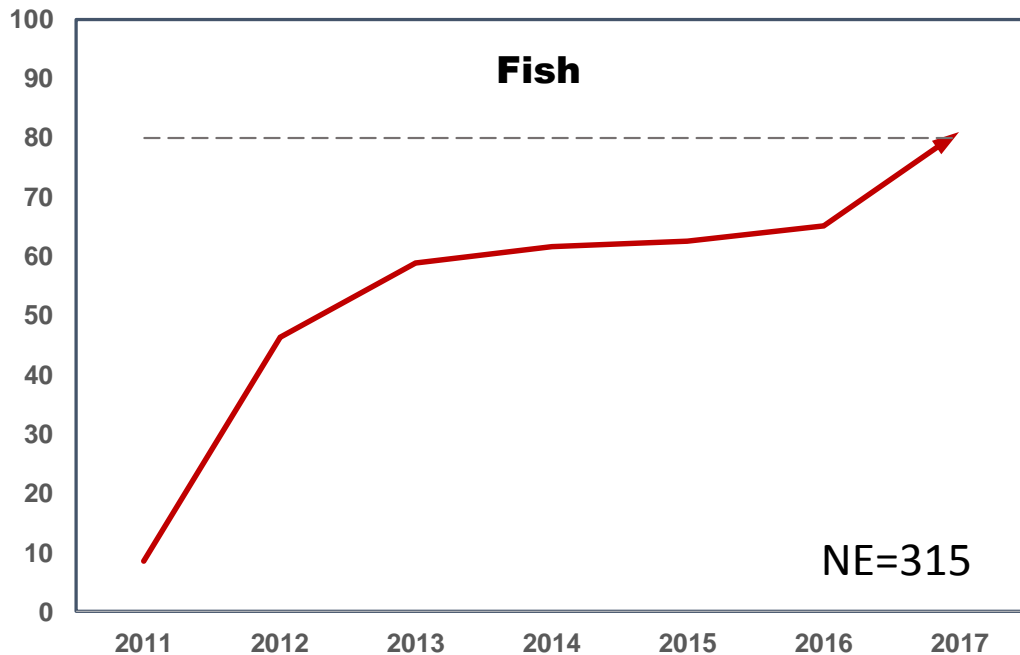


Chesapeake Bay Barcode Initiative

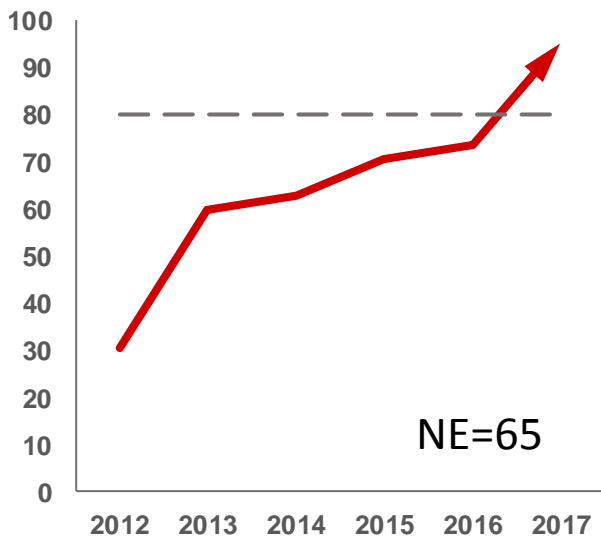
<https://serc.si.edu/projects/species-diversity-chesapeake-bay>



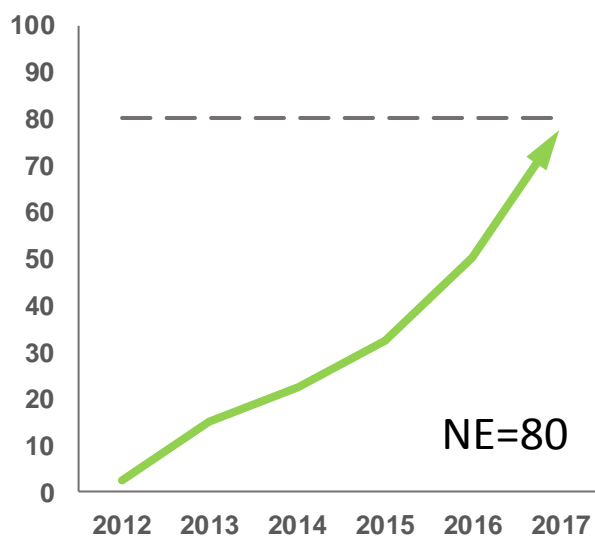
Percentage of Expected Species Collected



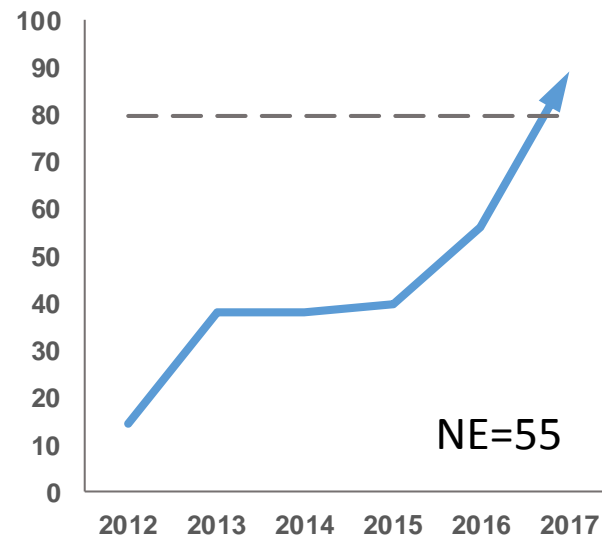
Decapoda



Gastropoda



Bivalvia

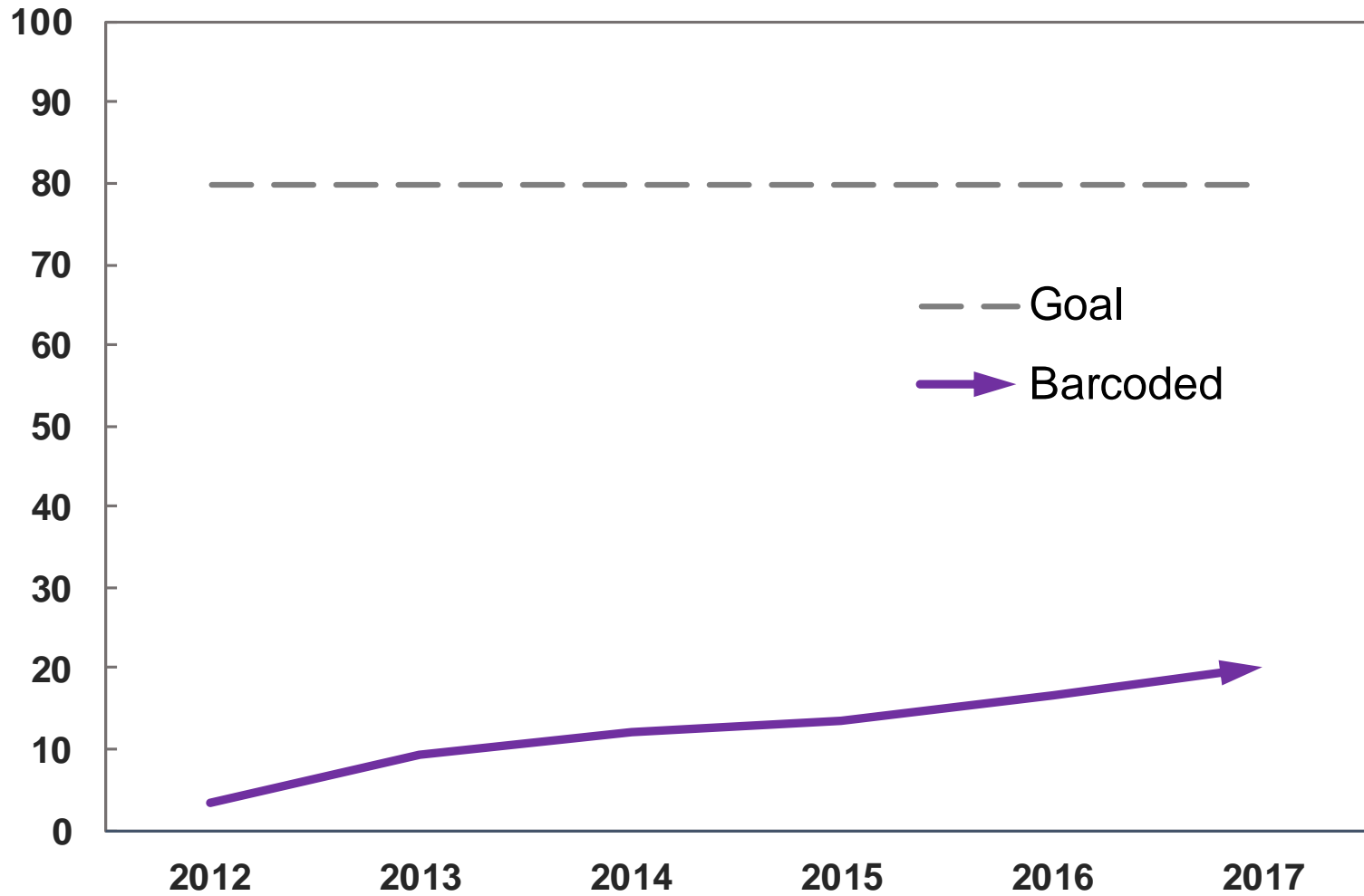


→ Barcoded — — Goal

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Percent of Other Inverts



Based on estimated 800 species (not including decapods and mollusks)

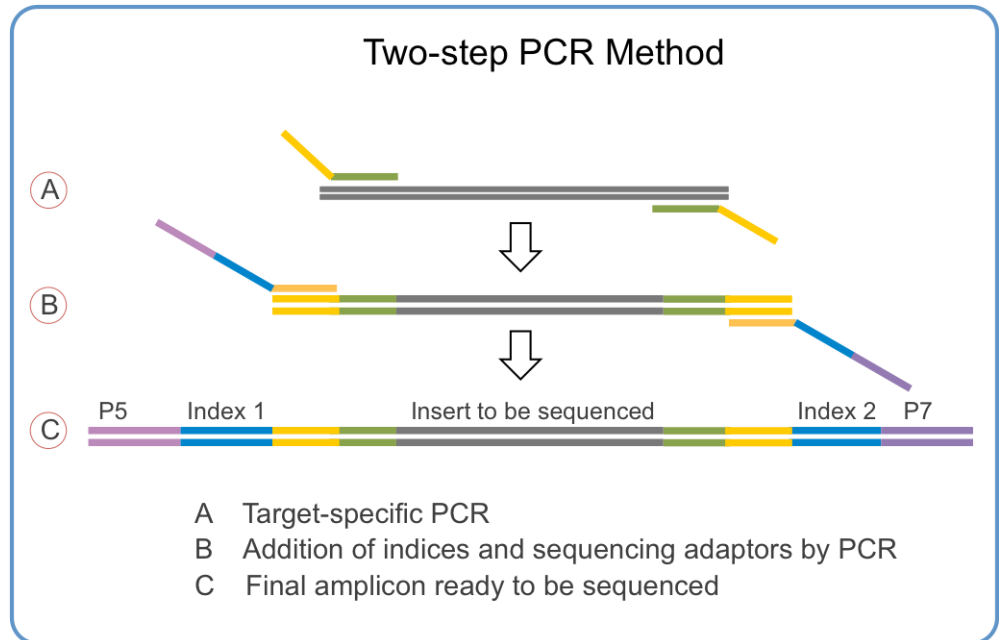
Methods

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



Methods

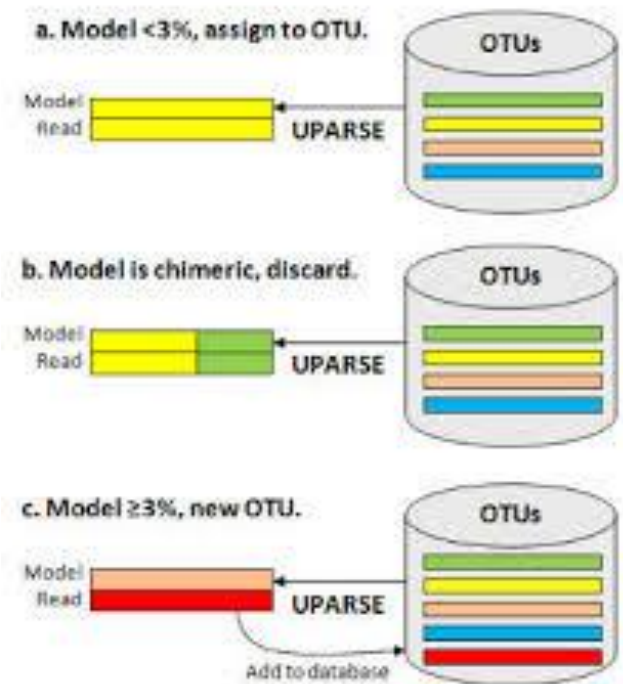
Generate OTU tables using USEARCH pipeline

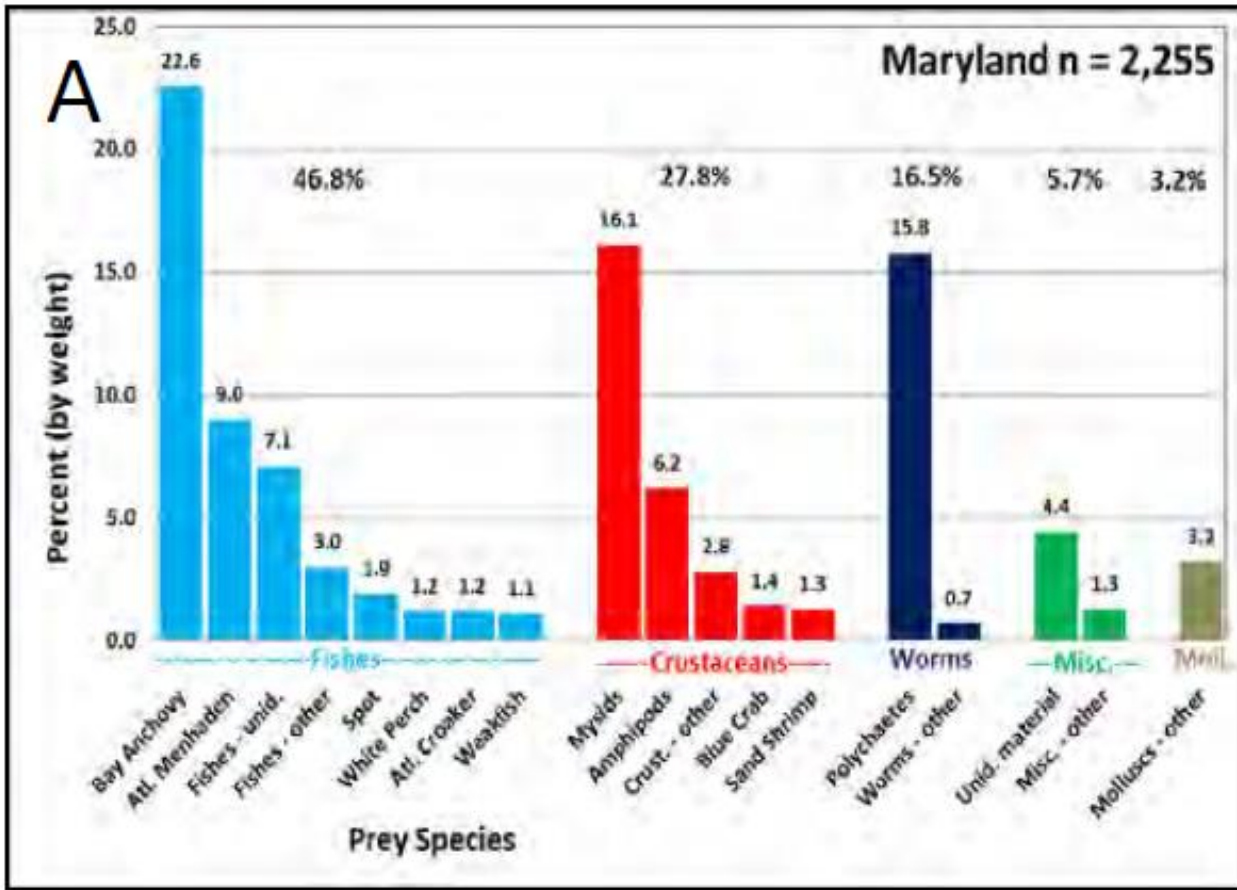
Includes UPARSE for removing chimeras and clustering OTUs

-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





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