Drivers of forage population trends and consumption patterns:

environmental, spatial and temporal patterns in Chesapeake Bay forage population distributions and predator consumption

Update to the Forage Action Team – February 16th 2017

Ryan Woodland¹, Edward Houde¹, Andre Buchheister², Robert Latour³, Carlos Lozano¹, Christopher Sweetman³

¹Univ. Maryland Center for Environmental Science, Chesapeake Biological Laboratory, Solomons, MD 20688

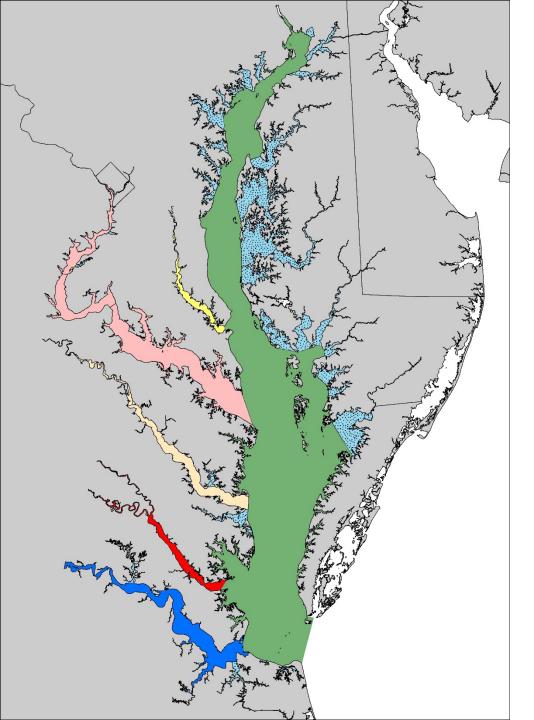
²Humboldt State University, Arcata, CA 95521

³Viginia Institute of Marine Science, Gloucester Point, VA 23062

Project goals

Objective 1 – Identify environmental gradients
 associated with spatial and temporal patterns in
 relative abundance of forage taxa in Chesapeake Bay

 Objective 2 — Explain how spatial and temporal gradients in environmental variables control consumption of forage taxa, and quantify the effect of forage abundance on consumer populations



Spatial scales and areas of interest

- Baywide
- Regional
 - 1. Mainstem
 - 2. Tributaries:

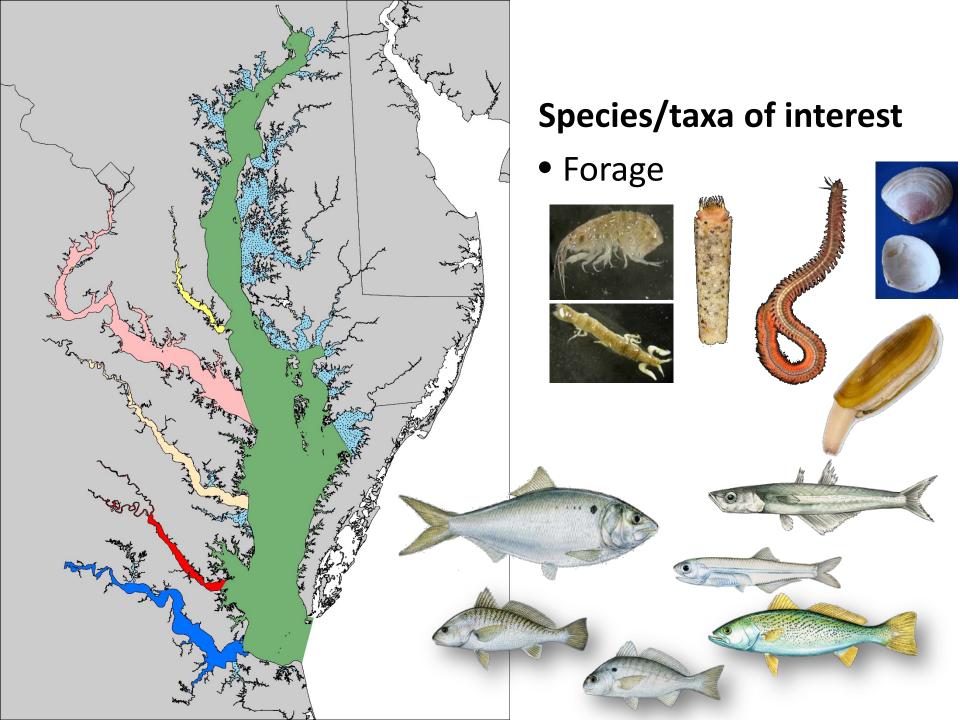
 Patuxent River

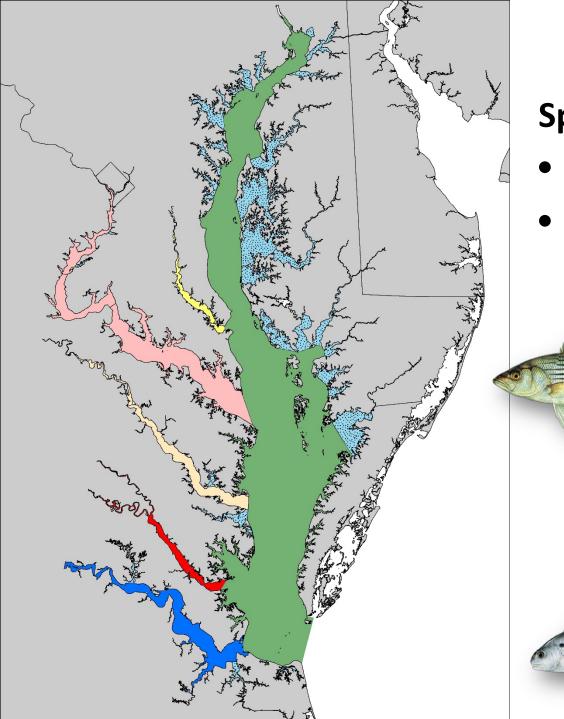
 Potomac River

 Rappahannock River

 York River

 James River





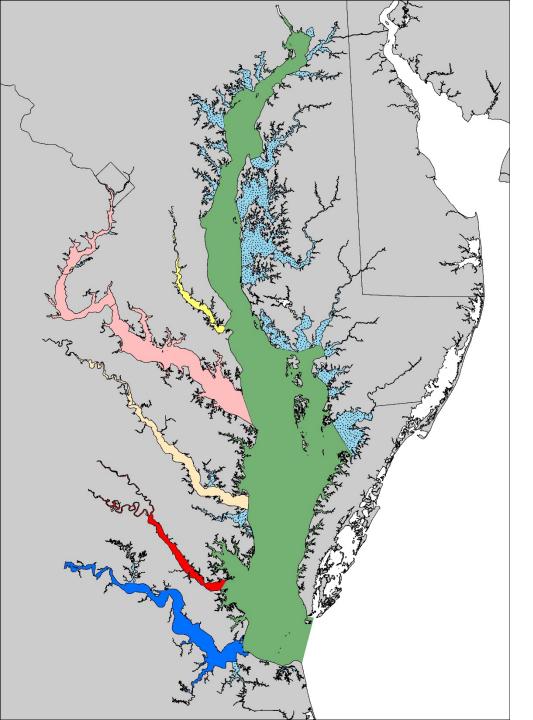
Species/taxa of interest

Forage

Consumers

Multiple size-classes





Species/taxa of interest

- Forage
- Consumers
 - Multiple size-classes

Multiple surveys

- Chesapeake Bay Program Benthic Survey/WQ monitoring survey
- MD DNR/VIMS juvenile striped bass index seine surveys
- MD DNR/VIMS trawl surveys
- CHESFIMS/TIES midwater trawl survey
- ChesMMaP trawl survey

Project methods

Project Objective	Indices	Patch-scale	Large-scale	Time-series
Forage				
Environment	Delta-GLM	GAM/GAMM	GLM/GLMM	DFA
Predators				
Consumption-Environment	Evacuation model		GLM	DFA
Diet-Environment		Delta-GAMM		
Diet-density dependence			GLM	

Models-

- 1. GLM: generalized linear model
- 2. GAM: generalized additive model
- 3. Delta-GLM: delta-generalized linear model
- 4. Delta-GAM(M): delta-generalized additive (mixed) model
- 5. DFA: dynamic factor analysis

Forage-environment analysis

GAMs: patch-scale patterns

$$y_i = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + s_1(x_1) + s_1(x_1) ... \beta_n x_n + s_n(x_n)$$

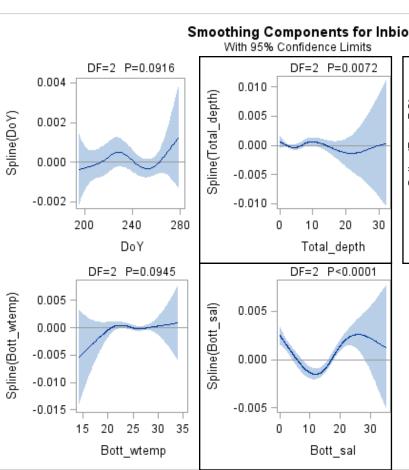
- **Taxonomic resolution** Species (n=8), Genus/Family (n=5), Functional (n=5)
- Response variable In(biomass per square meter[AFDW])
- Explanatory variables
 - *Class*: region, year
 - Continuous: dissolved oxygen, salinity, temperature, depth (CBP survey)
 - Interactions (depth*DO, depth*salinity, temperature*DO)

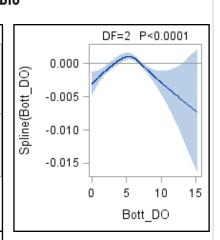
GLMs: large-scale patterns

$$y_i = \beta_0 + \beta_1 x_1 + \beta_2 x_2 ... \beta_n x_n$$

- Response variable In(biomass per square meter[AFDW])
- Explanatory variables (all continuous)
 - Teleconnections/climate indices (NOAA)
 - Susquehanna River flow (USGS)
 - Cumulative 5°C water temperature degree (CBL/VIMS pier dataset)
 - Ordinate DoY at which cumulative 5°C DD > 500 (CBP survey)
 - Chlorophyll concentration (CBP WQ survey)
 - Hypoxic volume (UMichigan)

Example: trumpet worm (*Pectinaria gouldii*)

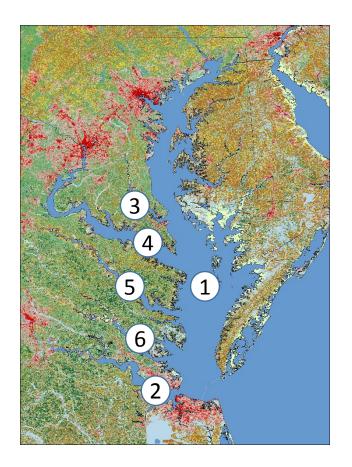




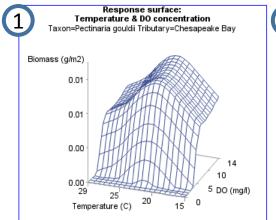


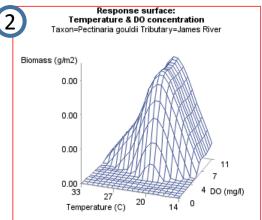
Linear term	Estimate	SE	t-value	р			
Day of year (d)	-0.00003	0.00002	-1.55	0.12			
Depth (m)	0.0007	80000.0	7.94	<.0001			
DO (mg/l)	0.0009	0.0002	5.90	<.0001			
Temperature (C)	-0.0003	0.0002	-1.79	0.07			
Salinity	0.0006	0.00006	11.20	<.0001			

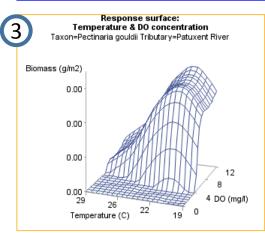
Pectinaria gouldii (trumpet worm)

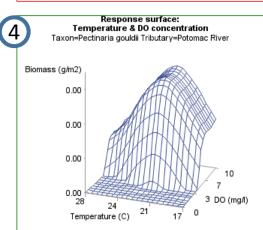


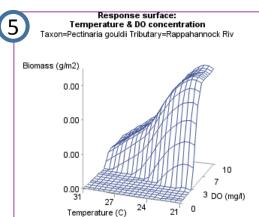
Response surface: temperature & DO

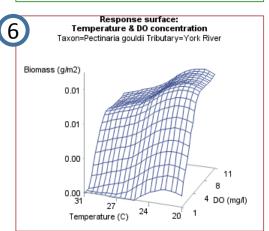




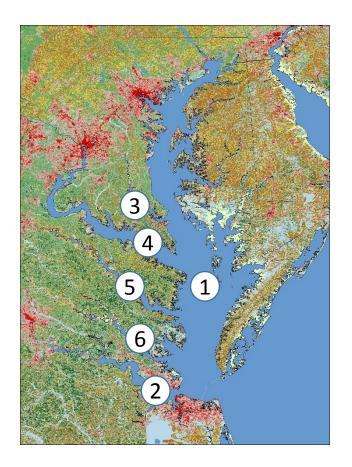




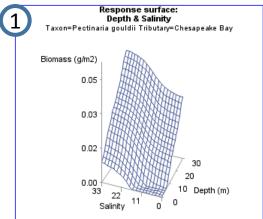


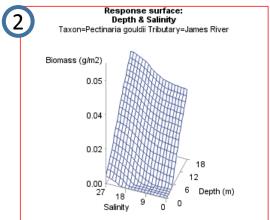


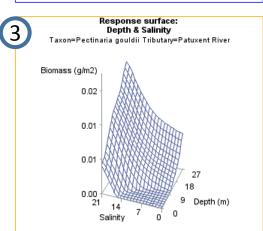
Pectinaria gouldii (trumpet worm)

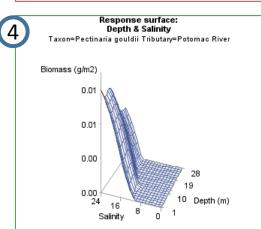


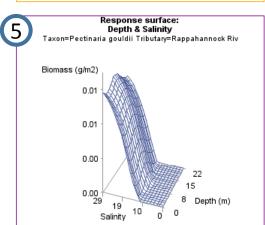
Response surface: depth & salinity

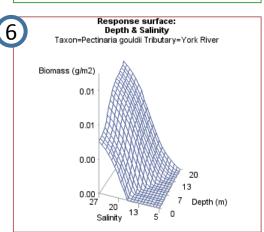






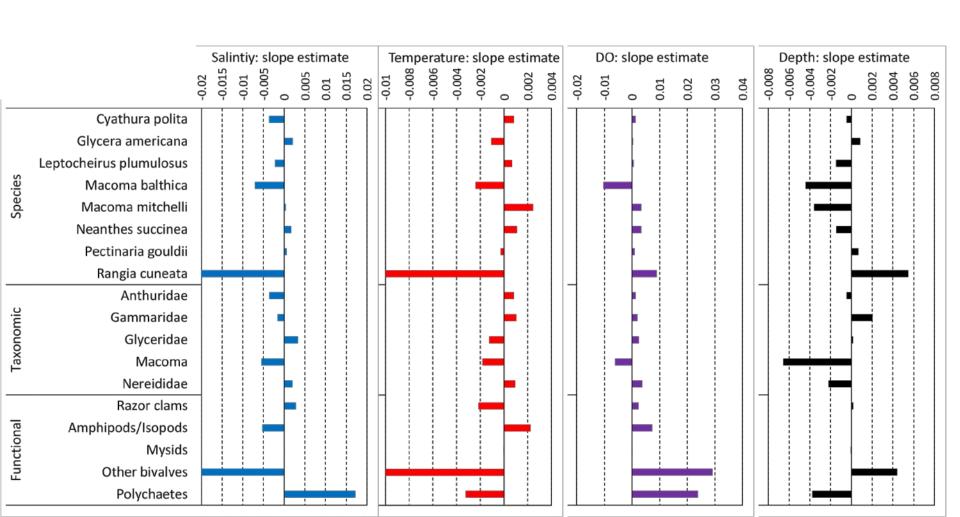






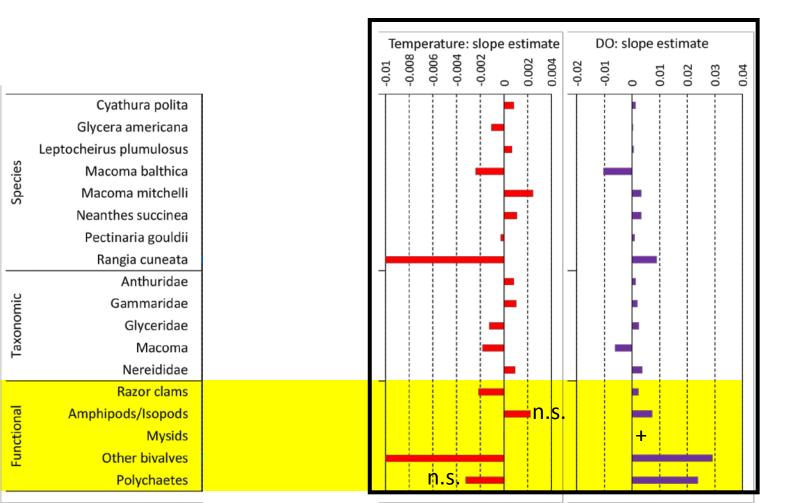
Forage-environment analysis

1. Strong differences among invertebrate groups, even within genera (e.g., Macoma spp.)

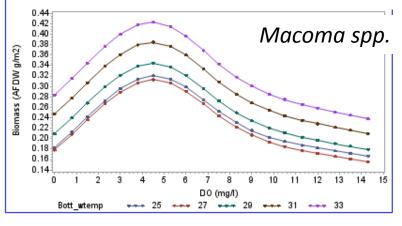


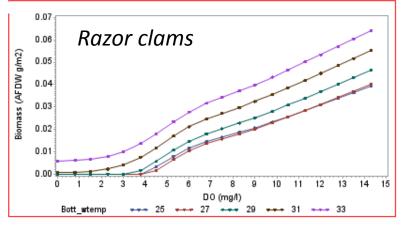
Forage-environment analysis

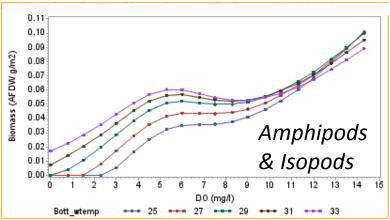
- 1. Strong differences among invertebrate groups, even within genera (e.g., Macoma spp.)
- 2. At level of 'Functional' group, significant linear effect of both Temperature and DO

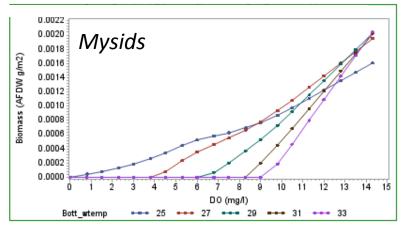


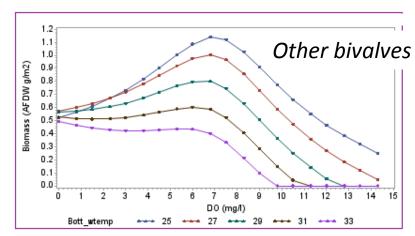
Functional groups (and Macoma): Modeled effect of DO at different Temperatures on biomass

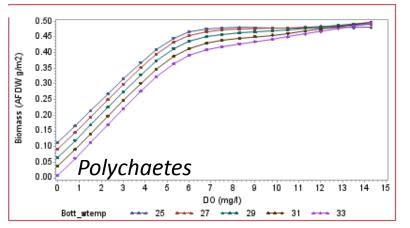












Forage-environment analysis

- 1. Model performance evaluated using information criterion AICc
- 2. Variables most consistently occurring in best performing models: salinity, spring Chla, degree day 'phenology', large-scale climate patterns

		Average water quality				Degree o	day varia	ables	_	Climate patterns			
Group	Taxon	Salinity	Temp	DO	Chla	Cumulative	Timing	Flow	Нурохіа	AMO	NAO		
Species	Leptocheirus plumulosus	-0.58**									0.37*		
	Macoma balthica					-0.42							
	Macoma mitchelli				0.21		0.26	0.71***	;				
	Neanthes succinea				0.34						0.41*		
	Pectinaria gouldii						0.38*			-0.47*			
	Rangia cuneata	0.45*			-0.38								
Taxonomio	c Anthuridae				0.49*	-0.29				-0.29			
	Glyceridae	-0.5*							-0.61**				
	Масота					-0.59							
	Nereididae				0.33						0.42*		
Functional	Amphipods & Isopods						0.6***			-0.47**			
	Polychaetes	0.38			0.35*		0.58**			-0.28			
	Other bivalves												

P-values provided for information – grey text: p = 0.2-0.1, black text, no asterisk: p = 0.1-0.05, *: p = 0.05-0.01, **: p = 0.05-0.01, **: p = 0.05-0.01

Forage-environment preliminary results (invertebrates)

- Local densities major forage groups influenced by dissolved oxygen availability and temperature (some groups)
 - Groups such as *Macoma* spp., razor clams and polychaetes show negative relationships with temperature
 - A positive relationship with water column DO was observed in all functional groups
- Interannual patterns in density of several forage groups
 - timing of water temperature warming
 - spring phytoplankton production
 - Large-scale climate patterns (positive NAO, negative AMO)

Project timeline (updated to include extension)

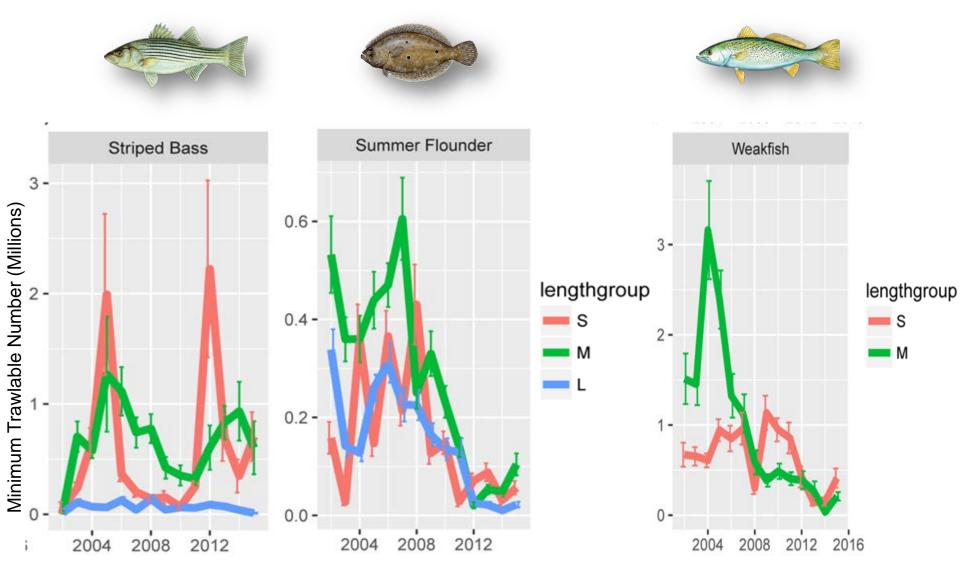
	2016							2017										
	Mr	Ар	Ma	Jn	Jl	Au	Se	Oc	No	De	Ja	Fe	Mr	Ар	Ma	Jn	Jl	Au
Logistics and planning																		
Data verification/validation																		
Objective 1																		
Expanding forage indices																		
Forage abundance vs enviro.																		
Objective 2																		
Predator consumption vs environment																		
Density dependent foraging																		
Variance dampening																		
Project deliverables																		
Presentations (Forage Act. Team/Fisheries GIT)																		
Reports (quarterly)																		
Scientific presentations (Tidewater x 2)																		
Peer-review manuscript draft																		



Questions?

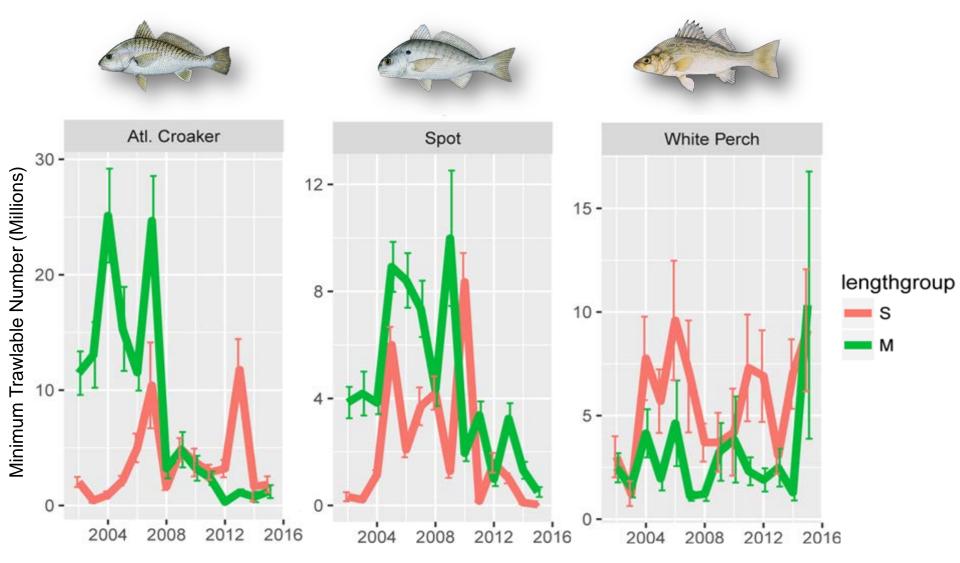


Abundance Indices



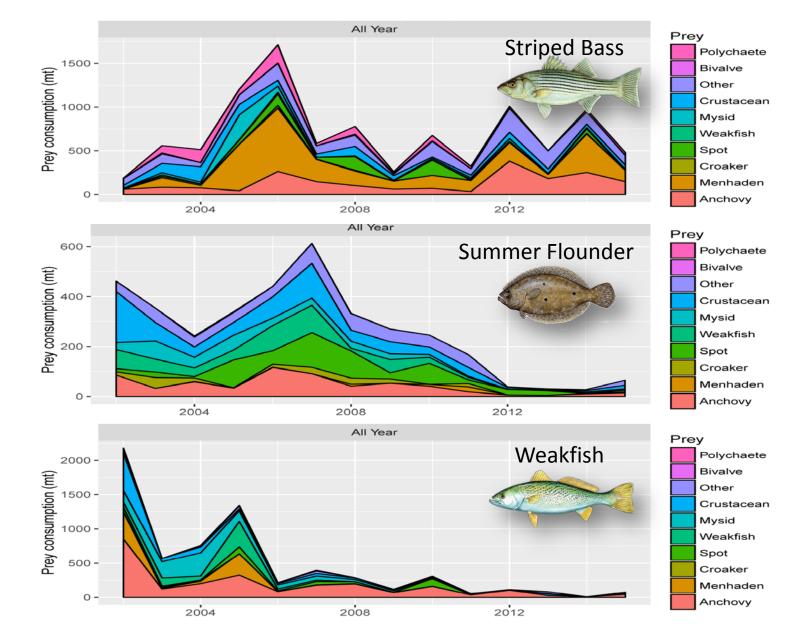


Abundance Indices



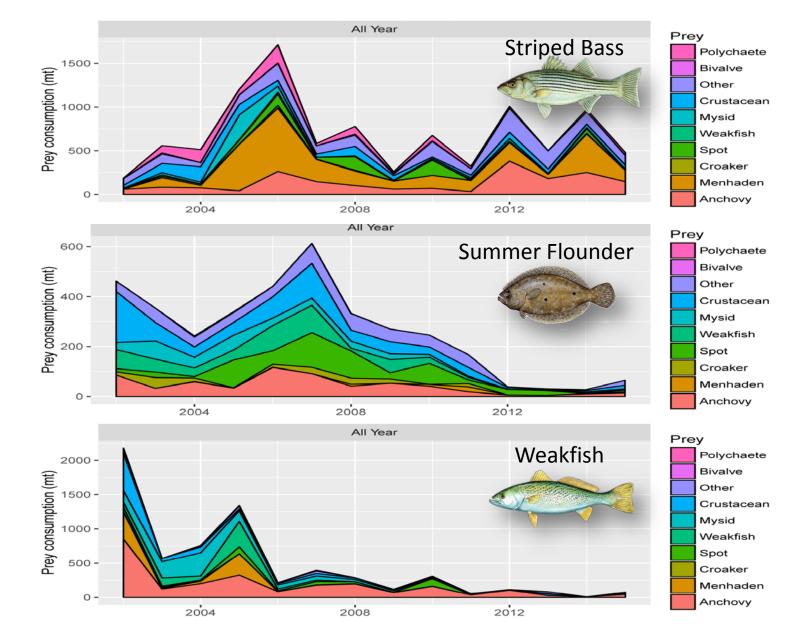


Population-level Consumption





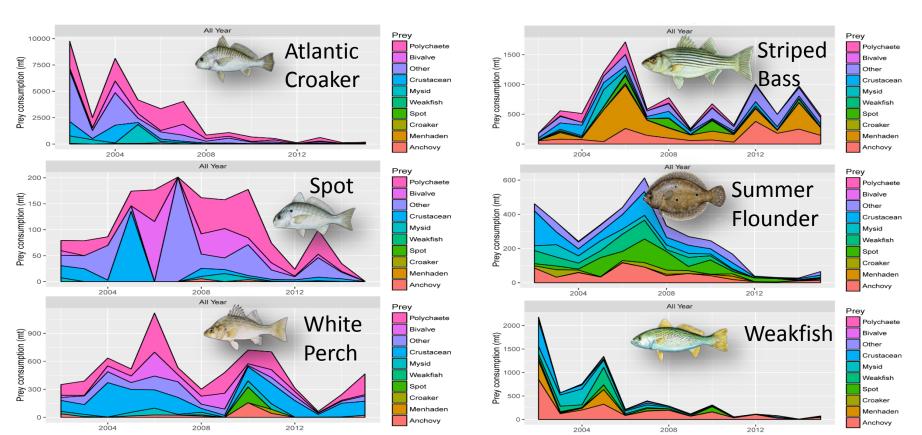
Population-level Consumption



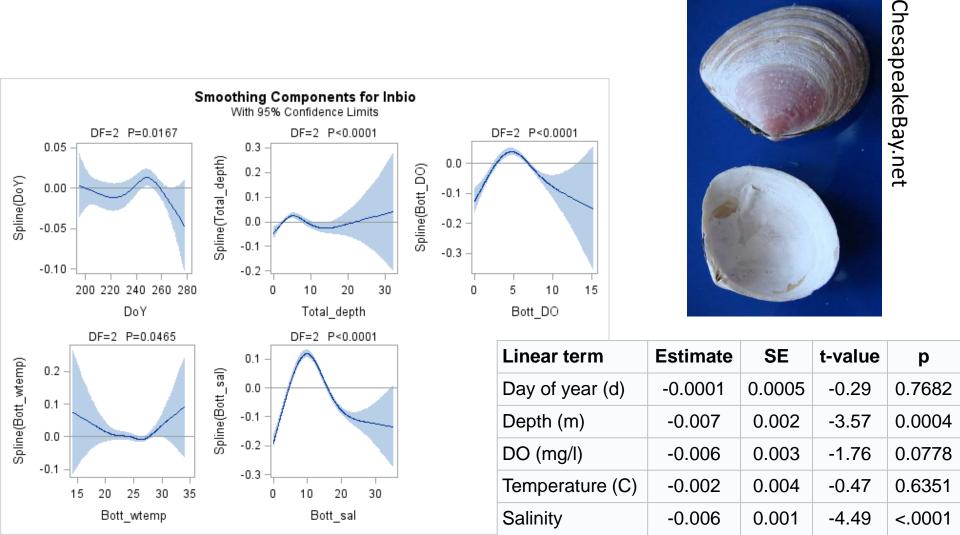


Predator-environment & -forage analysis

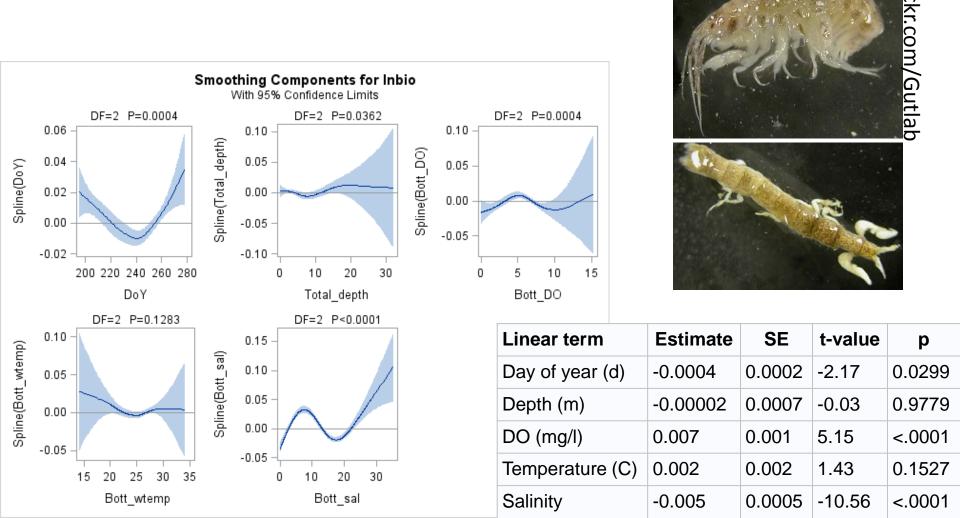
- Consumption indices have been updated to include most recent years in ChesMAPP survey
- Analysis of multivariate diet composition, diet-forage and consumption-environment underway
 - assessing potential for spatial analysis within mainstem of Chesapeake Bay

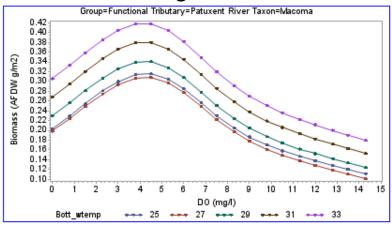


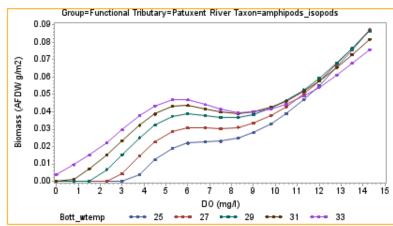
Taxonomic group: Macoma spp.

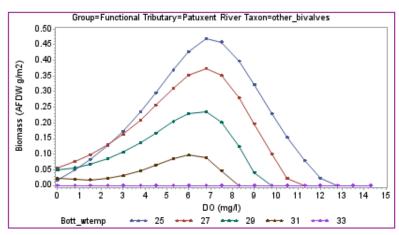


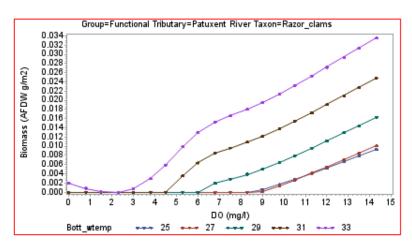
Functional group: Amphipod/Isopods

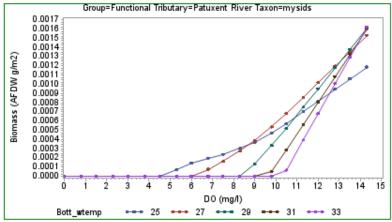


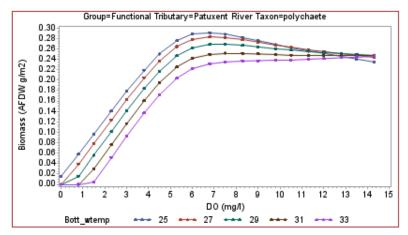






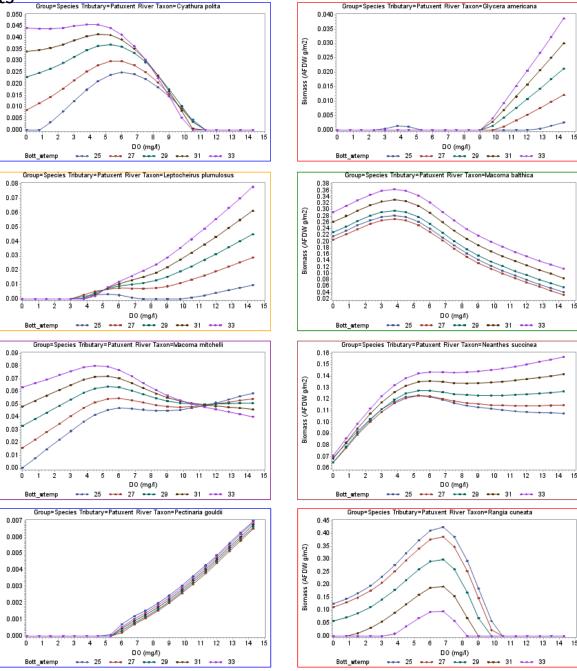


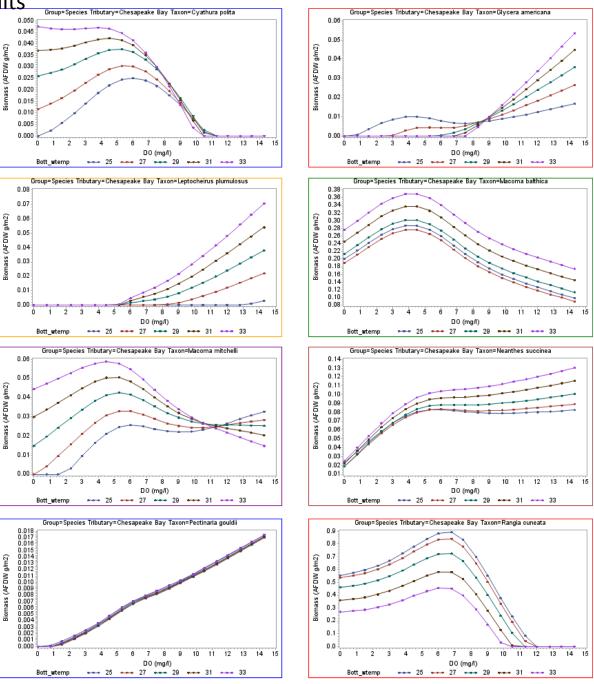


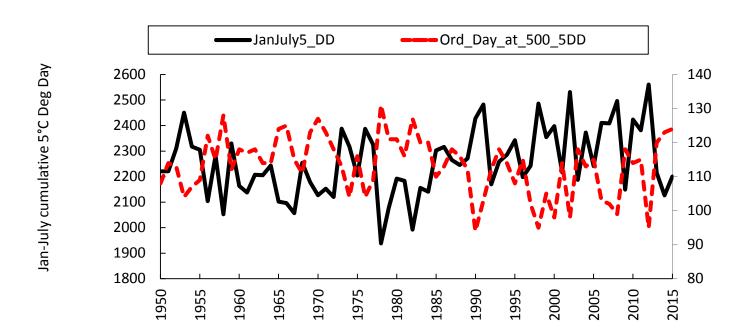


(AFDW

Š

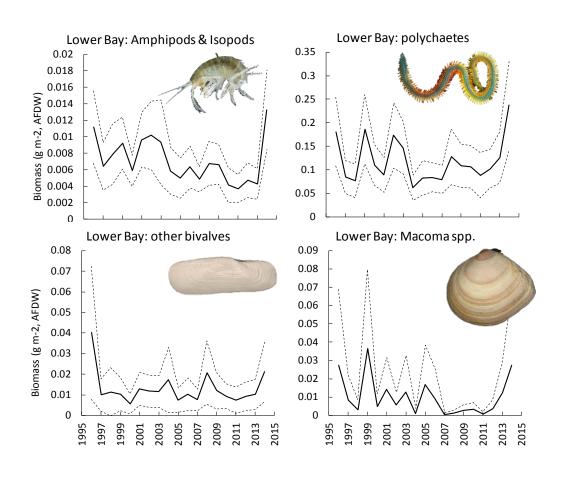






Ordinate DoY at which cumulative 5°C DD > 500

DATA – Forage



Chesapeake Bay Hypoxic Volume Forecasts

Donald Scavia¹, Isabella Bertani¹ and Mary Anne Evans²

¹University of Michigan

²US Geological Survey – Great Lakes Science Center

June 13, 2016

