

# **Relationships Between Shell Height and Dry Tissue Biomass** for the Eastern Oyster (Crassostrea virginica)

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#### Introduction

Studies which attempt to evaluate the success of oyster restoration efforts, model oyster population dynamics or evaluate the ecosystem services provided by oysters often rely upon estimates oyster biomass, both for an individual oyster of a particular size and for an entire population. Determining dry tissue biomass (DTB) for large numbers of oysters can be time consuming and expensive. Consequently, it is more common to measure shell height (SH) and infer DTB from published relationships from other studies.

We explore the relationships of oyster (C. virginica) shell height and DTB for data collected from multiple studies and compare them with two published models. Finally, we apply these different models to estimating the oyster populationlevel biomass within a tributary of Chesapeake Bay to explore their potential impacts on population/ecosystem models.

#### Study Area

Development of our SH-biomass models come from five studies that differ in both time and space (Fig 1). Over multiple years and seasons, oysters were sampled from a variety of salinities, habitats and inundation regimes (Table 1 & Fig 2). All study sites were in tributaries of the Chesapeake Bay, with the exception of the Chincoteague Bay location (Fig 1).



Red stars indicate study sites in the Chesapeake Bay region on the mid-Atlantic seaboard of USA (inset)



FIGURE 2. Examples of oyster habitats sampled for our models. Top Row: subtidal reefs (enhanced aerial photo and profile schematic) Bottom Row (1 to r): intertidal patch reefs, riprap and aquaculture floats

#### TABLE 2. Summary of relationships between shell height and dry tissue biomass for several groupings of our data. Equations and R<sup>2</sup>-values refer to best-fit power functions where W=v dry tissue biomass (i.e. Ash-free Dry Weight) and L=mm shell beight

Grouping	Sub-grouping	Equation	R <sup>2</sup> -value
All	All	W=0.00003 x L <sup>2.3952</sup>	0.80
Chincoteague Aquaculture	All	W=0.000006 x L <sup>2.6704</sup>	0.78
Rivers with subtidal oyster reefs (Gr. Wicomico, Rappahannock & Piankatank data combined)	All		0.90
	Spring	W=0.00004 x L <sup>2.4257</sup>	0.78
	Summer	W=0.00007 x L <sup>2.1704</sup>	0.71
	Fall	W=0.00001 x L <sup>2.6497</sup>	0.94
Lynnhaven Basin	All	W=0.00006 x L <sup>2.2809</sup>	0.68
	Intertidal Patch Reefs	W=0.0003 x L <sup>1.9352</sup>	0.76
	Subtidal Patch Reefs	W=0.00003 x L <sup>2.3465</sup>	0.74

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Chincoteague Aquaculture	All	W=0.000006 x L <sup>2.6704</sup>	0.78
	All	W=0.00002 x L <sup>2.5988</sup>	0.90
Rivers with subtidal oyster reefs (Gr. Wicomico, Rappahannock & Piankatank data combined)	Spring	W=0.00004 x L <sup>2.4257</sup>	0.78
	Summer	W=0.00007 x L <sup>2.1704</sup>	0.71
	Fall	W=0.00001 x L <sup>2.6497</sup>	0.94
	All	W=0.00006 x L <sup>2.2809</sup>	0.68
Lynnhaven Basin	Intertidal Patch Reefs	W=0.0003 x L <sup>1.9352</sup>	0.76
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#### Results

Best-fit models developed from our data were power-functions with R2-values ranging from 0.68 to 0.90 and some differences between regions/tributaries and within datasets for season and habitat type were observed (Table 2). Variation in the relationship between oyster size and dry tissue biomass increased with shell height (e.g. Fig 4).

- · Predicting individual oyster biomass Data source specific models were only rarely better predictors than more general models (see Table 3) either from our pooled data or the Mann and Evans model derived from ovsters in the Chesapeake Bay region; however, they were better predictors than the White et al. model derived from Gulf oysters
- · Estimating the total biomass of a group of oysters with known biomass Based on a sample of Lynnhaven River oysters, our data source-specific model was much more accurate than the other models (Table 5). All models based on Chesapeake Bay oysters tended to underestimate total biomass to varying degrees, whereas, the Gulf model severely overestimated total biomass.
- · Estimating the total biomass of a large-scale population of oysters (Lynnhaven River) with known size distribution (Figure 5) and size-specific abundance - The choice of model for computing oyster biomass in the Lynnhaven River has a very substantial impact on the estimate (Fig. 6), with some models estimating more than double the biomass of

#### Methods

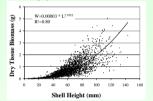
Oysters were collected utilizing standard sampling techniques depending on the study and habitat sampled (Fig 3). Shell height was measured to the nearest mm as the longest hinge-to-lip distance. Sub-samples of oysters representing the entire size range present for a given study were processed to determine ash-free dry tissue biomass (AFDW). Individual shucked meats were dried to a constant weight at 90°C and placed in a muffle furnace at 538 °C for 5 hours. The difference between the dried weight and the remaining ash weight was used to determine AFDW. A best-fit power function was then computed relating shell height to dry tissue biomass.

Model Comparisons - Several of our resulting models, as well as two published relationships, were compared in

- · Predicting individual oyster biomass;
- · Estimating the total biomass of a group of oysters with known biomass: and
- · Estimating the total biomass of a large-scale population of oysters with known size distribution and size-specific abundance.

To accomplish the latter, AFDW was computed for the midpoint of each size bin of oysters in the Lynnhaven River and multiplied by the total number of oysters for that hin. Results were then summed to estimate the total dry tissue biomass of the oyster population in the system.

FIGURE 4. Relationship between oyster dry tissue biomass and shell height for "Pooled" data. A bestfit power function trend line is fitted to the data with the resulting equation and R<sup>2</sup> value.



Sampling ovsters (Clockwise From Top Left)

aquaculture floats, intertidal patch reef, bulkhead

and subtidal patch reef

TABLE 3. Models used to estimate oyster dry tissue biomass based on shell height for further comparisons (W=dry tissue weight in g and L=shell height in mm)

Based on	Equation	
Lynnhaven River (Ches. Bay)	W=0.00006 x L <sup>2.2809</sup>	
Multiple areas and habitats (see Table 1)	W=0.00003 x L <sup>2.3952</sup>	
James River (Ches. Bay)	W=0.000423 x L <sup>1.7475</sup>	
Texas (Gulf of Mexico)	W=0.148 x (0.0000008958 x (L <sup>3</sup> ) <sup>1.27</sup> )	
	Lynnhaven River (Ches. Bay)  Multiple areas and habitats (see Table 1)  James River (Ches. Bay)  Texas (Gulf of	

- Data pooled for all the studies in Table 1.
- b Equation taken from Mann and Evans, 1998 (see literature cited)
- c Equation taken from White et al. 1988 (see literature cited)

Shell Height (2 mm intervals)

FIGURE 5. Overall size distribution (shell height)

of oysters in the Lynnhaven Basin. This distribution

was used to calculate total estimated biomass for the

model comparisons in Figure 6.

FIGURE 6. Total dry tissue biomass (kg) in the Lynnhaven Basin as estimated by four different size-biomass models (see Table 5 for an estimation of their relative accuracy).

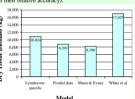


TABLE 4. Comparison of the ability of several oyster size-biomass models to predict dry tissue biomass of oysters from different regions, seasons and inundation regimes. Numbers are R2-values for linear regression of observed versus predicted biomass for individual ovsters

	Model				
Data Source	Data Source Specific	ESL Pooled	Mann & Evans	White et al	
Chinc. Aquaculture	0.58	0.59	0.61	0.51	
Subtidal Ches. Bay	0.61	0.61	0.66	0.46	
Spring	0.75	0.75	0.74	-	
Summer	0.64	0.62	0.66	-	
Fall	0.74	0.62	0.66	-	
Lynnhaven Basin	0.59	0.58	0.60	0.49	
Intertidal Patch Reefs	0.71	0.71	0.73	-	
Subtidal Patch Reefs	0.58	0.57	0.59	-	

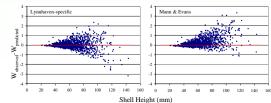
TABLE 5. Measured (highlighted in red) and calculated total dry tissue biomass for a sample of oysters in the Lynnhaven River. The differences between the calculated and measured values for several models are reported as % difference. Negative and positive values indicate underestimates and overestimates, respectively

Total Dry	0/ D:00
Tissue Biomass for Dataset (g)	% Difference from Observed
1,135	
1,097	-3%
900	-21%
777	-31%
1,980	+74%
	1,135 1,097 900 777

#### TABLE 1. Summary of projects from which the data for our models were derived, including the "Pooled Model" (all data summarized below) and "Lynnhaven-specific Model" (only includes data below from NOAA Lynnhaven

Project	Year for Biomass Data	Tributary/ Region	Salinity Regime (psu)	Inundation Regime	Sample Size	Size Range (shell ht., mm)	Notes
Aquaculture	2000	Chincoteague	28-32	Subtidal (in floats)	365	24-133	Aquaculture stocks in floats
Rappahannock River VA Sea Grant	2001- 2002	Rappahannock River, Ches. Bay	14-22	Subtidal	133	5-63	Recruits to restoration reefs
VA Oyster Heritage Program	2004	Multiple rivers, Ches. Bay	14-22	Subtidal	338	14-114	Recruits to restoration reefs
NOAA Restoration Monitoring	2005	Multiple rivers, Ches. Bay (inc. Lynnhaven)	10-25	Subtidal	597	21-145	Recruits to restoration reefs
NOAA Lynnhaven Assessment	2006	Lynnhaven Basin, Ches. Bay	10-25	Intertidal	951	25-143	Multiple habitats

FIGURE 7. Plots of observed minus predicted oyster dry tissue biomass for two models applied to a sample of Lynnhaven River oysters. The Lynnhaven-specific model hints at overestimating biomass at oyster sizes > 100 mm while the Mann & Evans model consistently underestimates biomass at sizes > 40 mm



#### Literature Cited

**Discussion & Conclusions** 

The observed differences in power function relationships for our data are to be

expected since they were developed from oysters from varying temporal and

environmental backgrounds. Differences in the size-biomass relationship

between seasons and between varying habitats (or tidal inundation regimes)

at larger scales for broader and more complex modeling efforts where size-

specific or overall oyster biomass is an important input. Based on the R2

values of various models when computing individual oyster biomass, one

therefore, money and time could be saved by using existing relationships to estimate ovster biomass rather than sampling ovsters in the field (e.g. see

However, these results do not provide insight into any inherent model bias, hints of which are seen in the actual plots (Figure 7). Model bias becomes fully apparent and magnified when predicting the total biomass of a

population, however (e.g. Table 5 & Figure 6). This suggests that for complex

modeling efforts where oyster biomass is a critical, multiplicative input,

population-specific size-biomass relationships should be developed.

would assume that any general regional relationship would suffice and,

Table 4 for the Lynnhaven Basin data source).

make biological sense. The question is which size-biomass models to utilize

Mann, R. and D.A. Evans. 1998. Estimation of oyster, Crassostrea virginica, standing stock, larval production and advective loss in relation to observed recruitment in the James River, Virginia. Journal of Shellfish Research, 17(1):239-253.

White, M.E., E.N. Powell and S.M. Ray. 1988. Effect of parasitism by the Pyramidellid gastropod Boonea impressa on the net productivity of oysters (Crassostrea virginica). Estuarine, Coastal and Shelf Science, 26:359-377.

Acknowledgements: We greatly appreciate the assistance provided by many individuals over several years including Alan Birch, Edward Smith, Sean Fate, Peter Kingsley-Smith, Jamie Wheatley, Matt Foley, Ben Hammer, Trish Wagner, Andrew Wilson and Ben Wilson.