

Evaluation of Larval Sources and Connectivity in Mid-Atlantic Sea Scallop Populations

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Background:

The U.S. sea scallop (*Placopecten magellanicus*) fishery is the most valuable fishery in the U.S.; its ex-vessel value in 2011 was over \$580 million. This fishery has shown a remarkable recovery from a severely overfished state in early 1990s; biomass increased by a factor of about 12 between 1994 to 2009, and landings have more than tripled (NEFSC 2010). While these increases are due to a combination of a number of management measures and ecological factors (Hart & Rago 2006;

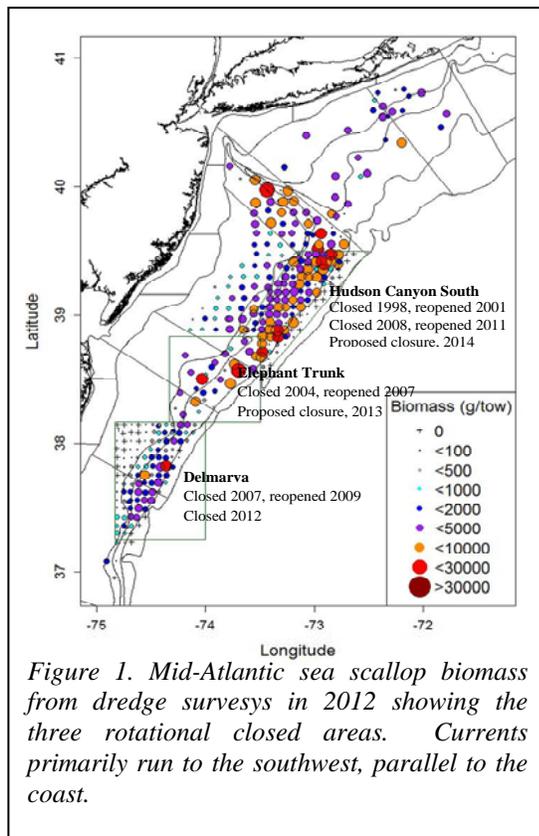


Figure 1. Mid-Atlantic sea scallop biomass from dredge surveys in 2012 showing the three rotational closed areas. Currents primarily run to the southwest, parallel to the coast.

Shank et al., in press), one important contributor to the recent successes is the system of rotational closures that has evolved in the Mid-Atlantic Bight region (Fig 1). These closures were primarily designed to improve yield-per-recruit (Hart 2003), but by allowing the buildup of spawning biomass, they may be contributing to increased recruitment that has been observed in the southern Mid-Atlantic region. Not only is biomass and egg production unusually high inside the rotational closures, but egg fertilization success may be greatly improved (Hart 2003; Smith & Rago 2004). Sea scallops naturally aggregate, and fishermen target these aggregations, so that fished populations may have lower egg fertilization rates because sea scallops are dioecious broadcast spawners that depend on females and males being in close proximity for successful spawning. Thus, closed areas may be contributing even more to larval production than would be inferred by the increases in biomass.

Empirical evidence suggests that these rotational closures may have induced increased recruitment. The Hudson Canyon South area was closed to scallop fishing in 1998, and biomass there peaked in 2001, when it was reopened to fishing (Fig 2). An extremely large 2001 year class was observed in the Elephant Trunk area, directly “downstream” of the Hudson Canyon South area. As Hudson Canyon South was fished down, recruitment was weak in the Elephant Trunk area. Hudson Canyon South was closed again for three years in 2008, and a strong 2010 year class and even stronger 2011 year class were observed on the 2012 NEFSC sea scallop survey in the Elephant Trunk. To a lesser extent, strong recruitment was observed downstream of the Elephant Trunk area during the time that area was closed.

There would be profound management and assessment implications if indeed the rotational areas have induced

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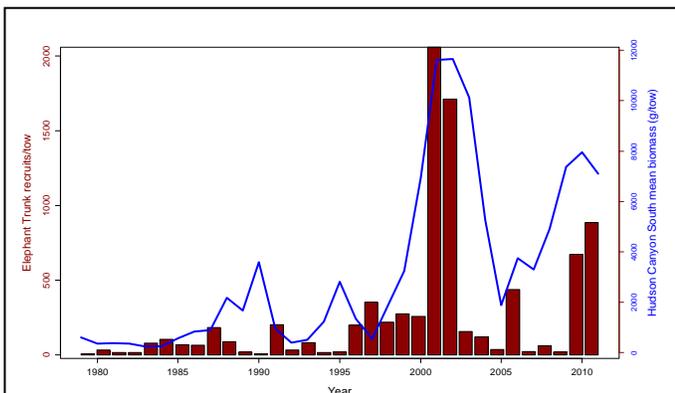


Figure 2. Relationship of recruitment in Elephant Trunk (by year spawned) and biomass in Hudson Canyon South. Note that this does not include potential fertilization success effects of the closures.

increased recruitment. It would suggest that managers should increase the frequency and perhaps the duration of closures, and should consider extending the system of rotational areas further upstream to the north. The estimated MSY for sea scallops strongly depends on the assumed stock-recruit relationship (NEFSC 2010; Hart submitted). Currently, a simple Beverton-Holt relationship is used, but the above discussion suggests that a metapopulation approach may be better, where each area seeds the area directly to the south.

Estimates of larval transport distances are required to confirm or refute the idea that the rotational areas are seeding areas directly to the south. While there have been a number of studies modeling sea scallop larval transport on Georges Bank (Tremblay et al. 1994; Tian et al. 2009a; Gilbert et al. 2010) and one that evaluated transport of larvae from Georges Bank to the Mid-Atlantic (Tian et al. 2009b), no published studies have modeled transport within the Mid-Atlantic. The purpose of this proposal is to construct such a sea scallop larval transport model in the Mid-Atlantic Bight and to examine the possibility that rotational areas are enhancing recruitment.

Approach:

To examine the linkage between increased adult abundance and potential for increased recruitment downstream, a circulation model (**R**egional **O**cean **M**odeling **S**ystem, ROMS, Haidvogel et al. 2000; Shchepetkin & McWilliams, 2005) will be coupled to a scallop larval model to simulate larval dispersal dynamics and connectivity for the scallop stock. To examine the possibility of enhanced fertilization success, larvae initiated in the coupled model will be calculated based on (i) a simple biomass based fecundity relationship and (ii) a fertilization model that assumes increases egg production with decreased nearest-neighbour distance (Smith & Rago, 2004). Simulations will specifically examine the trajectories of larval dispersal from areas of increased scallop biomass resulting from management actions and will allow us to address the following questions:

1. Did scallop larvae from broodstock in harvest area closures settle in the high recruitment events following the closure?
2. What are the patterns of general connectivity and larval sources and sinks along the Middle Atlantic Bight (MAB)?
3. Is there evidence that area closures facilitate improved recruitment and fertilization success?

Circulation Model

The circulation model to be used for this study is the Regional Ocean Modeling System (ROMS; Haidvogel et al. 2000; Shchepetkin & McWilliams 2005). ROMS solves the three-dimensional hydrostatic primitive equations in terrain-following vertical coordinates using split-explicit time stepping. Computational features of importance to the simulations described below include greatly reduced pressure gradient error arising from the terrain-following coordinate, a quasi-monotone advection algorithm for the temperature and salinity fields, alias-ent free coupling of the barotropic and baroclinic model, and a Lagrangian particle tracking sub-model. ROMS has been developed for, and successfully applied to, a wide variety of marine applications, including many studies of coastal and estuarine circulation (*e.g.*, Warner *et al.*, 2005; Liu *et al.*, 2009; Zhang *et al.*, 2009).

In particular, ROMS has been successfully implemented for the estuaries and continental shelf regions of the U.S. east coast (*e.g.*, Fennel et al. 2006; Wang et al. 2012; Zhang pers comm) with funding from the NASA Interdisciplinary Science (IDS) and NSF Ecology of Infectious Diseases (EID) and Coupled Natural and Human Systems (CNH) programs. The present configuration - covering the Middle Atlantic Bight, Gulf of Maine, and the adjacent deep ocean - has 10-km horizontal resolution, 30 vertical levels, and may be embedded alternatively within the

eddy-resolving North Atlantic models maintained by the HyCOM (hycom.rsmas.miami.edu) or Mercator (www.mercator.com.fr) projects. The model exhibits recognized features of local and remotely-forced circulation, including: wind-driven upwelling in the MAB, buoyancy-driven river plumes, low salinity on the MAB inner shelf, retention of passive particles in the shelf-slope front, and interactions of Gulf Stream warm rings with the slope region (Hofmann et al. 2008).

Scallop Larval Submodel:

The individual-based scallop larval submodel, which will be developed as part of this proposal, will be based on extensive experience in the development of larval models including eastern oysters and surfclams. The specific application we propose will be based on Dekshenieks et al. (1993, 1996, 1997) and Bochenek et al. (2001). The submodel will simulate the growth, vertical behaviour and settlement of scallop larvae. Growth will depend on food, temperature and body size. Vertical movement will include Stokes law (sinking), and size and temperature relationships for upward and downward swimming. Settlement is successful for modeled larvae that attain sufficient body size and reach suitable settlement locations within a realistic larval life span. As part of an ongoing NSF-funded CNH project, this larval model structure has been embedded in ROMS and used to simulate dispersal of surfclam larvae in the Mid Atlantic Bight (Zhang, pers comm), and a previous NSF-funded EID project used this coupled circulation-larval model structure study dispersal and connectivity in oyster larvae in the Delaware Bay oyster fishery (Narváez et al. 2012; Munroe et al. 2012). The larval submodel will be reformulated and parameterized for Atlantic sea scallops using available studies of growth (Hurley et al. 1986; Manuel & Dadswell 1991,1993), temperature effects (Tremblay & Sinclair 1988, 1990; Manuel et al. 2000; Pearce et al. 2004), and metamorphosis (Culliney 1974; Pernet et al., 2003). Additionally, a larval mortality term will be included in the larval submodel. Larval mortality has no available studies with which to parameterize this term, therefore we will use a range of larval mortality rates to evaluate the influence of this uncertainty on simulation outcomes, potentially linked to temperature and observed chlorophyll levels. We emphasize that the basic model structure is well tested, already coupled to ROMS and utilized in a number of applications, so that only reparameterization for sea scallops is necessary to support the proposed application.

Coupled Model:

The current implementation of ROMS for the MAB provides simulated circulation distributions that can be used to perform Lagrangian particle tracking experiments. The particle tracking module relates the trajectory of the particles ($\vec{\chi}$) to particle velocity (\vec{v}) for each time step (∂t) following:

$$\frac{\partial \vec{\chi}}{\partial t} = \vec{v}(\vec{\chi}, t) \quad 1$$

The larval submodel is coupled with the vertical particle displacement by adding larval behaviour (V_{bio}) to the vertical component of equation 1 ($\omega(z, t)$) as follows:

$$\frac{dz}{dt} = \omega(z, t) + V_{bio}(z, t) \quad 2$$

ROMS interpolates temperature for each particle location. Larval vertical behaviour (sinking and swimming) depends on larval size;

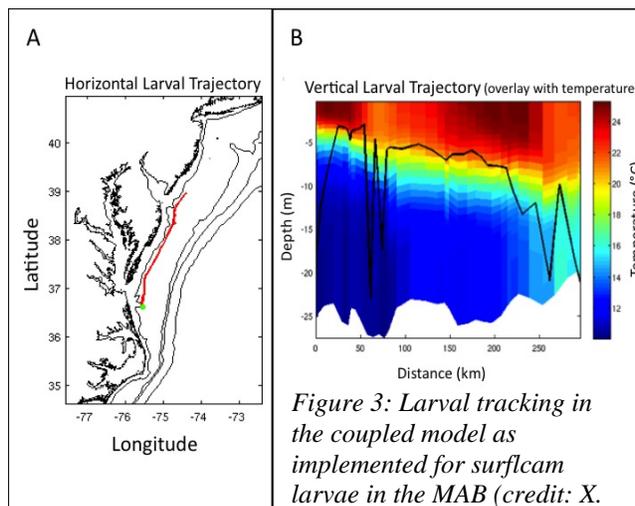


Figure 3: Larval tracking in the coupled model as implemented for surfclam larvae in the MAB (credit: X.

therefore, temperature dependant growth equations are solved simultaneously with equation 2 at each timestep. The particle tracking capability of ROMS coupled with the individual-based larval model provides a powerful tool for understanding larval connectivity in scallop metapopulations (Fig 3) and can be validated against observed larval distributions such as Tremblay & Sinclair (1992).

Larval Initiation:

Larval particles initiated in the coupled model will be calculated based on observed densities and biomass of scallops from the NEFSC sea scallop surveys and potentially other surveys when available (NEFSC 2010). Calculations will be made in two ways; (i) using simple shell height to gonad weight relationship (Hennen & Hart, 2012) and (ii) with a fertilization model that assumes increases egg production with decreased nearest-neighbour distance (Smith & Rago, 2004). Comparison of simulations using each of these larval particle initiations will allow consideration of the hypothesis that by accumulation of spawning biomass, rotational closures may be contributing to increased recruitment not only through increased biomass and egg production, but by improved egg fertilization success (Hart 2003, Smith & Rago 2004).

Simulations:

Our initial simulations (Case 1) will compare the likely distribution of larvae spawned from harvest closure regions with observed high recruitment events subsequent to those closures. This will answer research question 1, allow validation of the coupled model and provide a preliminary assessment of scallop larval transport in the MAB. In year 2, further simulations will be run to examine larval dispersal of scallops along the MAB during the past (1980's and 1990's) and into the future (where adequate physical forcing functions are available) addressing research question two. We will also add larval and post-settlement mortality terms that will be based on food supply (from SeaWiFS data) and benthic predators (from NEFSC sea scallop data) that can be fit from the comparison of predicted larval settlement with observed scallop recruitment from survey data. Phytoplankton and predator distributions have been already estimated during a previous FATE-funded project and will be available for this project. Project milestones and timelines are outlined in Table 1.

Benefits:

The results of this proposal would have direct impact on sea scallop management; if the results are consistent with a downstream seeding effect, then this would argue for more frequent, longer closures as well as extending rotational management to the rest of the Mid-Atlantic Bight. The understanding of sea scallop connectivity in the Mid-Atlantic will greatly assist developing metapopulation stock-recruit models rather than a simple whole stock dynamic pool relationship. The results of Case 1 simulations will be prepared in time for presentation at the next sea scallop stock assessment in 2014 (SAW 59), and will be presented to the New England Fishery Management Council Sea Scallop Plan and Development Team. More broadly, while numerous larval transport models have been constructed, there is rarely an opportunity to validate these models due in part to lack of reliable information regarding the locations of spawning and/or settlement. Because sea scallops are sedentary, and have a time series from a dedicated survey, there is good knowledge of spawning and recruitment locations. In addition, the large increases and decreases in spawning biomass from the rotational closures and openings are effectively an almost unique large-scale experiment which can aid the validation of the larval transport model.

Deliverables:

This project will provide key comparisons of larval dispersal from closed areas with known abundances of recruitment to the fishery as well as identification of larval source and sink regions for the stock. This will allow management strategies to be optimized for maximal recruitment resulting from area closures. Results of Case 1 simulations will be presentation at SAW 59, and results of the remaining simulations will be shared with scallop fishery management councils. Further, we will endeavor to produce peer-reviewed manuscript(s) discussing the larval connectivity patterns for this species. Results will be presented at the annual FATE science meetings.

Table 1: Project Timeline (ODU: Old Dominion University; RU: Rutgers University; WH: Woods Hole)

Timeline	Activity	Comments
May 2013	Meeting (ODU): Project Initiation & Larval Submodel Parameterization	Investigators will discuss relevant literature and begin work on larval submodel parameterization.
May – July 2013	Larval Submodel Parameterization.	
July 2013	Meeting (ODU): Larval Submodel Parameterization	Investigators will evaluate performance of the larval submodel and plan necessary changes and adjustments.
July – Sept. 2013	Finalize Larval Submodel	
Sept. 2013	Meeting (RU): Full Model Parameterization	Larval submodel will be embedded within the physical model. Investigators will discuss relevant literature and plan simulations for Case 1 simulations.
Sept. 13– Feb.14	Run Case 1 Simulations	
Feb. 2014	Meeting (WH): Review of Case 1 Simulations and Full Simulation Planning	Investigators will review Case 1 simulations, discuss implications and plan full suite of simulations based on biological and physical data availability.
Spring 2014	Present Case 1 results at SARC 59 .	SARC 59 will focus on scallops and results of this study will be directly relevant at this meeting.
Feb. – June 2014	Run Full Set of Simulations	
June 2014	Meeting (RU): Review of Full Set of Simulation Results	Investigators will review all simulations with respect to implications to larval connectivity and recruitment dynamics.
June – Dec. 2014	Analysis of simulation results and report writing.	
Other:		
August 2015	Present Results at AFS 2015 Meeting	
2014 and 2015	Attend FATE Science Meetings	

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Roles and Responsibilities of Principal Investigators

Dr. Daphne M. Munroe (Rutgers University, RU) – project coordination; evaluation and summarization of results; report writing; larval submodel parameterization; literature review.

Dr. Dvora Hart (Northeast Fisheries Science Center, NEFSC) – assist in development and parameterization of the sea scallop larval IBM; evaluation and summarization of results; report writing; interpretation of relevance to fishery and management; integration of results into stock assessment and management.

Dr. Burton Shank (Northeast Fisheries Science Center/Integrated Statistics) – assist in development and parameterization of the sea scallop larval IBM; integration of SeaWiFS and benthic predator data into the modeling; report writing.

Dr. John Klinck (Old Dominion University, ODU) – larval submodel programming; larval submodel parameterization; coupling of larval submodel and ROMS.

Dr. Dale Haidvogel (Rutgers University, RU) - coupling of larval submodel and ROMS; coupled model simulations; identification of physical forcing data.

Dr. Eric Powell (University of So. Mississippi, USM) - evaluation and summarization of results; report writing; larval submodel parameterization; interpretation of relevance to fishery and management.