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How Do Marine Protected Area Strategies Influence Metapopulation Genetic Connectivity? A Modeling Study with Oysters

Daphne Munroe

Eric N. Powell

John M. Klinck
Old Dominion University, jklinck@odu.edu

Eileen E. Hofmann
Old Dominion University, ehofmann@odu.edu

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ABSTRACTS OF TECHNICAL PAPERS

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COMPARISON OF THE HEALTH STATUS OF THE COMMON COCKLE *CERASTODERMA EDULE* AT TWO SITES IN SOUTHERN IRELAND.

Emer Morgan, S.A. Lynch, R.M. O' Riordan, S.C. Culloty.
University College Cork, Cooperage, Distillery Fields, North Mall, Cork, Munster, Ireland.

Significant mortalities of the cockle *Cerastoderma edule* have been reported at a number of European sites over the past few years with complex and varied causes. In Ireland surfacing and subsequent mortality events are observed particularly over the summer months leading to an investigation of cockle health at two sites on the Irish Sea, southern Ireland. Over a 16 month period, March 2010–June 2011, 30 surfaced and 30 buried cockles were taken monthly from Flaxfort Strand, Co. Cork and Bannow Bay in Co. Wexford. Length, weight, age and sex were determined; tissues sections were screened for the prevalence of parasites or any pathogens. Cockles were larger in Bannow Bay, although the difference in mean age between sites was negligible. At both sites the prevalence of neoplasia was greater in surfaced rather than buried cockles; the advanced stages of the disease were more common in surfaced cockles. Trematode sporocysts and metacercriae showed seasonality, but peaks in their prevalences differed between sites. Prevalence of trematode metacercariae was higher at both sites in moribund cockles, being more pronounced at Bannow Bay. A range of other pathogens were identified including gregarines and copepods however unidentified haplosporidians were seen exclusively in Bannow Bay.

HOW DO MARINE PROTECTED AREA STRATEGIES INFLUENCE METAPOPULATION GENETIC CONNECTIVITY? A MODELING STUDY WITH OYSTERS.

Daphne Munroe[1], Eric Powell[1], John Klinck[2], Eileen Hofmann[3].
[1] Rutgers University, 6959 Miller Ave., Port Norris, NJ, 08349, USA.
[2] Old Dominion University, 4111 Monarch Way, Norfolk, VA, 23529, USA.
[3] Old Dominion University, 4111 Monarch Way, Norfolk, VA, 23529, USA.

Effective management of marine resources like oysters relies on understanding how populations are connected. Application of a modeling framework including distinct populations connected via larval transport is effective for examining complex metapopulation dynamics and how anthropogenic activities influence them. Here, our goal was to assess how various marine protected area (MPA) strategies alter genetic connectivity. An individual-based metapopulation model integrating population dynamics, dispersal, and genetics was used to examine mechanisms and dynamics of metapopulation genetic connectivity. The model was parameterized to simulate four eastern oyster (*Crassostrea virginica*) populations from Delaware Bay for two periods (1970's and 2000's). In our simulations, no fishing was allowed within MPA populations. Simulations included all possible combinations of MPA location (which population was protected) and fishing mortality rates for non-MPA populations (this included low (4%), medium (8%) and high (30%)). Results showed (i) MPAs can enhance genotypes originating within the protected area when surrounding fishing rates are relatively high (30%), and (ii) a strong temporal difference in the influence of MPA strategies on metapopulation genetic connectivity between the two time periods (1970 vs. 2000). Generally, these results suggest that MPA location, exploitation rates and regimes play a role in metapopulation genetic connectivity.

PREDICTING THE INFLUENCE OF SEED AND COMMERCIAL OYSTER FISHERIES ON METAPOPULATION GENETIC CONNECTIVITY USING MODEL SIMULATIONS.

Daphne Munroe[1], Eileen Hofmann[2], Eric Powell[1], John Klinck[2].
[1] Rutgers University, 6959 Miller Ave., Port Norris, NJ, 08349, USA.
[2] Old Dominion University, 4111 Monarch Way, Norfolk, VA, 23529, USA.

Previous research has demonstrated that changes in population demographics (mortality and abundance) can alter genetic connectivity among populations in an oyster metapopulation. Through increases in mortality rates and creation of mortality gradients in space, fisheries could potentially influence metapopulation genetic connectivity and source-sink dynamics. Our goal was to assess how various oyster seed and commercial fisheries alter metapopulation genetic connectivity. An individual-based metapopulation model integrating population dynamics, dispersal, and genetics was used to examine mechanisms and dynamics of metapopulation genetic connectivity. The model was parameterized to simulate four eastern oyster (*Crassostrea virginica*) populations from Delaware Bay for two periods (1970's and 2000's). Simulations included a range of fishing and seed fishing scenarios using rates currently observed in commercial oyster fisheries from Chesapeake and Delaware Bays and connectivity was tracked using population-specific neutral alleles. Results show (i) high rate (30%) seed fisheries can lead to loss of neutral alleles from exploited areas, (ii) relatively low rate fisheries (4%) affect minimal change in genetic connectivity, and (iii) a strong temporal difference between the two periods (1970 vs. 2000). These results suggest that fishery management, including size restrictions, and exploitation rate, can influence metapopulation genetic connectivity.