

Connectivity in Bivalve Populations: Assessing Sources of Larval Recruits

Lauren S. Mullineaux¹, Claudio DiBacco², Jim Lerczak¹, Simon R. Thorrold¹, Michael Neubert¹, Hal Caswell¹, Lisa A. Levin³, and John L. Largier³

¹Woods Hole Oceanographic Institution

²University of British Columbia

³Scripps Institution of Oceanography

NSF Biological Oceanography, 01 November 2003 – 31 October 2006

PROJECT SUMMARY

The early life history of most marine benthic invertebrate organisms involves a planktonic larval stage of development that acts as an agent for increased dispersal and gene flow between sessile or sedentary adult populations. There remains considerable debate as to the spatial scale and strength of the connections between populations. This proposal examines connectivity of bivalve populations (defined as the extent to which a local population receives recruits from external sources), the role of physical transport, and the metapopulation consequences. Because the larval stages are microscopic, it is all but impossible to follow individuals, or to track them with conventional tags.

Technological advances have facilitated the use of trace element analysis to evaluate origins and trajectories of some planktonic larvae. Spatial variability in environmental, trace elemental characteristics of different coastal water masses is recorded in the geochemistry of biogenic carbonates. Since shells are deposited throughout planktonic larval development, they effectively record changes in environmental characteristics of different habitats occupied by larvae through development. Analysis of larval shell retained by newly settled bivalves will provide information about their source locations.

We propose to use trace element fingerprinting methods to evaluate the spatial scale and strength of connectivity among bivalve populations on the Massachusetts and southern California coasts. Hypotheses will address (1) the relative contribution of remote larval sources versus local ones (self seeding), (2) the relationship between circulation-driven dispersal potential and realized connectivity among bivalve populations and (3) the roles of species spawning period, planktonic period, and spatial separation of sites in determining probabilities of larval exchange. Our approach involves laser ablation inductively coupled plasma mass spectrometry (LA-ICPMS) to resolve spatial changes in larval shell composition that reflect recruit origins and temporal patterns of larval transport. We will work with the clam *Mya arenaria* and the mussel *Mytilus edulis* in New England and the mussels *Mytilus galloprovincialis* and *M. californianus* in southern California. Population connectivities will be studied with two metapopulation approaches that estimate dispersal probabilities from hydrodynamic models. One involves habitat area as a proxy for fecundity and the other is a multiregional matrix model that uses a demographic framework to describe the dynamics of the metapopulation. We will test

realized population connectivity determined from trace elemental analysis of recruit origins against a priori predictions based on the circulation and metapopulation models.

Broader impacts: The resulting information about source populations and connectivities will enhance understanding of metapopulation dynamics in commercially valuable bivalve species. Connectivity information applicable to the east and west coasts of the USA will facilitate conservation of coastal resources through the improved design of marine protected areas and fisheries regulations. Key educational elements include the involvement of undergraduate, graduate, and postdoctoral students, as well as early-career scientists, in interdisciplinary research that integrates coastal ocean physics, larval ecology and metapopulation theory. There will be a transfer of trace element fingerprinting technology (from fish) into the realm of invertebrate dispersal and to collaborators in Mexico.