



University of New Hampshire

NEW HAMPSHIRE SEA GRANT

Clam gene expression and climate change

Background

The soft-shell clam (*Mya arenaria*) fishery has a landings value of more than \$20 million annually with more than 3.9 million pounds harvested largely from the state of Maine. In New Hampshire, the soft-shell clam fishery is an important recreational activity with hundreds of local and vacationing participants annually. In 1997, researchers estimated a harvestable soft-shell clam population in N.H.'s Hampton/Seabrook Harbor of 25,000 bushels, but that

number has since fallen to only 5,400 bushels. Clams are far from their peak abundance in N.H. coastal environments and many scientists from Maine and Massachusetts have reported similar declines.



This loss of productivity has caused considerable concern among both scientists and commercial fishermen.

Environmental changes

As water temperatures rise, biologists have observed that clam abundance is significantly impacted by seasonal and regional coastal acidification coupled with predation on juvenile clams by green crabs. The dual environmental stressors (temperature and pH) occur in a background of retroviral infection that impacts clams at two years of age when they are first reproductive.

What will be investigated?

Charles Walker, UNH professor of molecular, cellular, and biomedical science, is working with other researchers to investigate contributors to the etiology of clam leukemia including a possible retrovirally induced infection associated with increasing seawater temperature with and without ocean acidification. Linkages between specific environmental parameters and cancer are often difficult to demonstrate for lack of an appropriate model system.

Clam leukemia provides an opportunity to develop such a model. The genetic analysis of clam hemocyte leukemia using transcriptomics (methods to determine which genes are being expressed in an organism's cells at a given time

period) will indicate changing expression of stress-related genes and gene products during initiation and progression of this disease in the soft-shell clam. Ideally, results from this analysis will identify unique gene expression patterns that can be traced to the environmental stressors of sea water temperature and acidification.

Results to date

Ongoing laboratory studies are analyzing the effects of projected increases in temperature and salinity in the Gulf of Maine on the development and severity of clam leukemia at different clam life stages. Additionally, reference transcriptomes generated from hemocytes in field-collected normal and 100% leukemic clam hemocytes will allow comparison between gene expression patterns related to temperature and salinity stress and any related gene expression patterns that characterize the disease.

Currently, we know that several relevant genes are expressed at significantly higher levels in leukemic versus normal clam hemocytes. Expression of one of these proteins actually blocks the ability of cells to check for damaged DNA before cell division



and leads to immortalization of clam hemocytes (or clam leukemia) in adult sexually mature clams at two years of age. We expect to continue to identify the full suite of uniquely expressed leukemia-related genes for this disease. These data can be correlated with field observations from clam aquaculturists and fishermen to develop strategies for sensible out-planting and harvesting of New England soft-shell clams. As environmental conditions change, results of these analyses may vary significantly and adjustments can be made.

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