Annual Report for Period: 05/2009 - 04/2010 **Submitted on:** 04/29/2010

Principal Investigator: Stegeman, John J. **Award ID:** 0430724

Organization: Woods Hole Ocean Inst

Submitted By:

Stegeman, John - Principal Investigator

Title:

The Woods Hole Center for Oceans and Human Health

Project Participants

Senior Personnel

Name: Stegeman, John

Worked for more than 160 Hours: Yes

Contribution to Project:

Dr. Stegeman is responsible for the oversight of all of the activities of the Center, and for facilitating communication within and among the Centers.

Name: McGillicuddy, Dennis

Worked for more than 160 Hours: Yes

Contribution to Project:

Dr. McGillicuddy's responsibilities include overall project oversight for Project 2. Design of population dynamics models for the various A. fundyense genotypes, and execution of the physical oceanographic component of large-scale survey operations.

Name: Hahn, Mark

Worked for more than 160 Hours: No

Contribution to Project:

Senior Scientist and Director of the Pilot Project Program.

Name: Anderson, Donald

Worked for more than 160 Hours: Yes

Contribution to Project:

Senior Scientist and PI, is responsible for project oversight, and management.

Name: Erdner, Deana

Worked for more than 160 Hours: Yes

Contribution to Project:

Research Associate and Co-PI, is responsible for technical oversight of experimental work and sampling efforts, project management, and
data review and interpretation.

Name: Gast, Rebecca

Worked for more than 160 Hours: Yes

Contribution to Project:

Co-PI, supervised the pathogen detection,cultured amoebas from sediment samples.

Name: Amaral Zettler, Linda

Worked for more than 160 Hours: Yes

Contribution to Project:

Co-PI, supervised the microbial community surveys, participated in sample collection and processing.

Name: Polz, Martin

Worked for more than 160 Hours: No

Contribution to Project:

PI supervises and coordinates the project and participates in data analysis as well as dissemination of results.

Name: Lercczak, James

Worked for more than 160 Hours: No

Contribution to Project:

Co-PI is overseeing the collection and analysis of the physical measurements within Plum Island Estuary and is responsible for providing the physical estuarine context for the interpretation of Vibrio population dynamics.

Name: Sogin, Mitchell

Worked for more than 160 Hours: Yes

Contribution to Project:

Dr. Sogin directs activities in the Genomics Core including phylogenetic and associated bioinformatics activities. Directed the development of a new massively high-throughput tag sequencing approach for characterizing microbial populations in marine environments.

Name: Morrison, Hilary

Worked for more than 160 Hours: Yes

Contribution to Project:

Co-director of the Core Facility, Morrison has directed the sequencing service activities of the COHH genome core, participated in the tag sequencing project, and developed genomic sequencing protocols for the GS-FLX instrument. Dr. Morrison is also working with Dr. Sogin on a method of sampling two discontinuous variable regions from microbial rRNA genes; an expansion of the tag sequencing approach.

Name: Mark Welch, David

Worked for more than 160 Hours: Yes

Contribution to Project:

(Ellison GID program-no charge to COHH) has continued to participate in development of the bioinformatics analysis of the high-throughput tag sequencing project

Name: Huber, Julie

Worked for more than 160 Hours: Yes

Contribution to Project:

(Microbial Evolution program-no charge to COHH) has provided samples from Axial Seamount and has participated in the bioinformatics analysis of the high-throughput tag sequencing project. Dr. Huber is also working with Dr. Sogin on a pilot project that seeks to use comprehensive microbial population surveys afforded by tag sequencing protocols to examine anthropogenic impacts on a saltwater marsh that experience seasonal elevated levels of coliforms.

Name: Smith, Keston

Worked for more than 160 Hours: Yes

Contribution to Project:

Seagoing participation in the large-scale survey cruises and assimilation of A. fundyense data into models.

Post-doc

Name: Kirkup, Benjamin

Worked for more than 160 Hours: No

Contribution to Project:

Responsible for strain characterization, metabolic and physiological diversity, and pathogenicity determinant gene distribution.

Name: Hackett, Jeremiah

Worked for more than 160 Hours: No

Contribution to Project:

Worked on Alexandrium genomics, with a focus on the identification of genes involved in saxitoxin biosynthesis. Hackett was supported by a WHOI Postdoctoral Scholar award, but supplies and other support were provided by the COHH grant.

Name: Ralston, David

Worked for more than 160 Hours: No

Contribution to Project:

Investigation of the influence of vertical migration on the vertical distribution of A. fundyense.

Name: Carr, Jennifer

Worked for more than 160 Hours: No

Contribution to Project:

Responsible for sampling and development of genetic system for model organisms.

Name: Wildschutte, Hans

Worked for more than 160 Hours: No

Contribution to Project:

Responsible for genomics and O-antigen characterization of the vibrios.

Name: Aretxabaleta, Alfredo

Worked for more than 160 Hours: Yes

Contribution to Project:

Investigation of the mechanisms controlling the Bay of Fundy gyre system, the retentive characteristics of which are key to regional population dynamics of A. fundyense.

Name: Rose, Julie

Worked for more than 160 Hours: No

Contribution to Project:

Name: First, Matt

Worked for more than 160 Hours: No

Contribution to Project:

Name: Boucher, Yan

Worked for more than 160 Hours: No

Contribution to Project:

characterization of V. cholerae populations; discovery of populations of newly described pathogen ('V.pseudocholerae')

Name: Richlen, Mindy

Worked for more than 160 Hours: No

Contribution to Project:

General supervision of all microsatellite studies.

Graduate Student

Name: Brosnahan, Michael

Worked for more than 160 Hours: No

Contribution to Project:

Graduate Student, responsible for characterization and application of microsatellite markers used for population studies.

Name: Koid, Amy

Worked for more than 160 Hours: No

Contribution to Project:

REU student

Name: Osborn, Deborah

Worked for more than 160 Hours: No

Contribution to Project:

Hollings Fellow

Name: Willard, Eric

Worked for more than 160 Hours: No

Contribution to Project:

Northeastern University co-op student

Name: Blossom, Hannah

Worked for more than 160 Hours: No

Contribution to Project:

Northeastern University co-op student

Name: Tully, Benjamin

Worked for more than 160 Hours: No

Contribution to Project:

REU student, summer 2006.

Name: Hunt, Dana

Worked for more than 160 Hours: Yes

Contribution to Project:

Examines environmental distribution of vibrios in the water column.

Name: Preheim, Sarah

Worked for more than 160 Hours: Yes

Contribution to Project:

Researching the environmental distribution of vibrios among animal hosts.

Name: Xue, Xong

Worked for more than 160 Hours: No

Contribution to Project:

Identification of isolates, growth dynamics of vibrios over tidal cycles.

Name: Hasegawa, Yuko

Worked for more than 160 Hours: No

Contribution to Project:

Working on the development of PCR primers for the V-tag sequencing studies.

Name: Halliday, Elizabeth

Worked for more than 160 Hours: Yes

Contribution to Project:

Graduate Student working in PI Gast's lab. WHOI/MIT Joint program student 2007

Name: Kauffman, Kathryn

Worked for more than 160 Hours: No

Contribution to Project:

isolation and characterization of vibriophages

Name: Kauffman, Kathryn

Worked for more than 160 Hours: Yes

Contribution to Project:

isolation and characterization of vibriophages

Name: Takemura, Alison

Worked for more than 160 Hours: Yes

Contribution to Project:

genetics of habitat adapatations in vibrios

Name: Zhan, Minshu

Worked for more than 160 Hours: Yes

Contribution to Project:

MIT student
All undergraduates participated under the auspices of the MIT UROP program; they were involved with strain characterization, environmental sampling and sequence analysis.

Undergraduate Student

Name: Bobb-Semple, Aisha

Worked for more than 160 Hours: No

Contribution to Project:

Sophomore, biology. Participated under the auspices of the MIT UROP program; involved with strain characterization, environmental sampling and sequence analysis.

Name: Han, Jing

Worked for more than 160 Hours: No

Contribution to Project:

Sophomore, EECS. Participated under the auspices of the MIT UROP program; involved with strain characterization, environmental sampling and sequence analysis.

Name: Buchwald, Carolyn

Worked for more than 160 Hours: No

Contribution to Project:

Senior, EAPS. Participated under the auspices of the MIT UROP program; involved with strain characterization, environmental sampling and sequence analysis.

Name: Ngo, Lynn Ly

Worked for more than 160 Hours: No

Contribution to Project:

Graduated 2006, CE. Participated under the auspices of the MIT UROP program; involved with strain characterization, environmental sampling and sequence analysis.

Name: Chang, Sarah

Worked for more than 160 Hours: No

Contribution to Project:

Wellesley junior, history. Participated under the auspices of the MIT UROP program; involved with strain characterization, environmental sampling and sequence analysis.

Name: Proehl, Sarah

Worked for more than 160 Hours: No

Contribution to Project:

Sophomore, chemistry. Participated under the auspices of the MIT UROP program; involved with strain characterization, environmental sampling and sequence analysis.

Name: Smith, Sarah

Worked for more than 160 Hours: No

Contribution to Project:

Sophomore, chemistry. Participated under the auspices of the MIT UROP program; involved with strain characterization, environmental sampling and sequence analysis.

Name: Schieffer, Stella

Worked for more than 160 Hours: No

Contribution to Project:

Sophormore. Participated under the auspices of the MIT UROP program; involved with strain characterization, environmental sampling and sequence analysis.

Name: Yuen, Grace

Worked for more than 160 Hours: No

Contribution to Project:

Participated under the auspices of the MIT UROP program; they were involved with strain characterization, environmental sampling and sequence analysis.

Name: Cutler, Jennifer

Worked for more than 160 Hours: Yes

Contribution to Project:

REU Undergraduate

Name: Taylor, Holly

Worked for more than 160 Hours: No

Contribution to Project:

Participated through Northeastern University cooperative program.

Name: Selwyn, Jason

Worked for more than 160 Hours: No

Contribution to Project:

Participated through Northeastern University cooperative program.

Name: Roney, Catherine

Worked for more than 160 Hours: Yes

Contribution to Project:

Participated through Northeastern University cooperative program. Responsible for laboratory and analyses pertaining to cyst isolation and germination, and microsatellite genotyping.

Name: Fazan, Shahla

Worked for more than 160 Hours: Yes

Contribution to Project:

Name: Adams, Jillian

Worked for more than 160 Hours: Yes

Contribution to Project:

Participated through Northeastern University cooperative program. Responsible for laboratory and analyses pertaining to microsatellite genotyping.

Name: Fischer, Alexis F

Worked for more than 160 Hours: Yes

Contribution to Project:

Wellesley student

Technician, Programmer

Name: Keafer, Bruce

Worked for more than 160 Hours: No

Contribution to Project:

Research Associate, is responsible for field work planning and execution, as well as with sampling and sample analysis.

Name: McCauley, Linda

Worked for more than 160 Hours: Yes

Contribution to Project:

Research Assistant, is responsible for testing and application of molecular methods for the population genetic studies, phytoplankton culture and characterization, and data review and analysis.

Name: Kosnyrev, Valery

Worked for more than 160 Hours: Yes

Contribution to Project:

Research Associate and is assisting Dr. McGillicuddy in processing and analysis of the various data sets, seagoing operations, running the coupled models, and visualizing the results.

Name: Anderson, Laurence

Worked for more than 160 Hours: No

Contribution to Project:

Research Associate and has significant seagoing experience, and will participate in the large-scale survey cruises and will support post-cruise processing of the data.

Name: Dennett, Mark

Worked for more than 160 Hours: Yes

Contribution to Project:

Assisted with sample collection and processing.

Name: Moran, Dawn

Worked for more than 160 Hours: Yes

Contribution to Project:

Processed samples and ameba cultures, pathogen detection, cloning, and sequencing.

Name: Rocca, Jennifer

Worked for more than 160 Hours: Yes

Contribution to Project:

Works in the core facility preparing DNA templates and sequencing reactions for members of the COHH team.

Name: Huse, Susan

Worked for more than 160 Hours: Yes

Contribution to Project:

Susan, Research Associate, has been developing methods to evaluate error rates associated with pyrosequencing technology and has been assessing the correlation of variable region distances with full-length 16s distances.

Name: Libera, Katherine

Worked for more than 160 Hours: No

Contribution to Project:

Responsible for testing and application of molecular methods for the population genetic studies, phytoplankton culture and characterization, and data review and analysis.

Name: del Castillo, Erika

Worked for more than 160 Hours: No

Contribution to Project:

Responsible for microbial community survey library construction and analysis.

Name: Kosnyrev, Olga

Worked for more than 160 Hours: Yes

Contribution to Project:

Seagoing participation in the large-scale survey cruises and support for post-cruise processing of the data.

Other Participant

Name: Rossi, Dianne

Worked for more than 160 Hours: Yes

Contribution to Project:

Assists with grant management, report and proposal preparation, coordination of meetings, record-keeping, and other administrative duties. Support is from NSF and NIH as well as institutional funds from the Woods Hole Oceanographic Institution.

Research Experience for Undergraduates

Organizational Partners

Massachusetts Institute of Technology

Marine Biological Laboratory

Other Collaborators or Contacts

University of Washington

Pacific Research Center for Marine Biomedicine at the University of Hawaii

University of Miami

Harvard Medical School

Fisheries Research Agency of Japan, National Research Institute of Fisheries and Environment of Inland Sea

Woods Hole United States Geological Survey

Drs. Uwe John and Allan Cembella, Alfred Wegener Institute, Bremerhaven Germany

Dr. Satoshi Nagai, National Research Institute of Fisheries and Environment of the Inland Sea, Japan

Plum Island Sound Estuary Long Term Ecological Research (PIE-LTER) program in collaboration with Charles Hopkinson and Hap Garritt (MBL)

Dr. Wayne Wurtsbaugh, Utah State University

Dr. Philip Roberts, Georgia Tech

Dr. Sandra McLellan at the Great Lakes WATER Institute in Milwaukee,WI

Southern California Coastal Water Research Program

Activities and Findings

Research and Education Activities:

See attached file.

Findings:

See attached file.

Training and Development:

McGillicuddy - Research Training - Project 2

R/V Tioga voyage 383, July 2009
Bibiana Crespo, Postdoctoral fellow
Emily Brownlee, WHOI Summer Student Fellow

R/V Tioga voyage 386, July 2009
Shayla Farzan, WHOI Summer Student Fellow
Phil Wallhead, WHOI Postdoctoral Scholar

Training and development - Gast - Project 3

Elizabeth Halliday is a graduate student doing research as part of this project for her thesis.

Gast and Halliday are working with the Barnstable County Department of Health and the Environment to help introduce molecular methods into their water quality monitoring program.

Outreach Activities:

Outreach Activities - McGillicuddy - Project 2

3/09 UNOLS Fleet Operation in the Context of the Emergent Ocean Observing System. Committee on Evolution of the National Oceanographic Research Fleet, convened by the Ocean Studies Board of the National Research Council. Jonsson Center, Woods Hole, MA. (Invited)

09/09 Modeling Alexandrium fundyense Blooms in the Gulf of Maine: From Climatology to Forecasting. Ocean Science Journalism Fellows, WHOI.

4/10 Modeling Alexandrium fundyense Blooms in the Gulf of Maine: From Climatology to Forecasting. ODU Department of Ocean, Earth, and Atmospheric Sciences Seminar.

Outreach - Gast - Project 3

Gast and Halliday participated in a laboratory demonstration for Duxbury, MA middle school students who are involved in a local water quality monitoring and source tracking project.

Gast, Halliday and First presented talks on water quality and pathogens as part of the Columbia journalists training program that takes place at WHOI each year.

Gast and Halliday are collaborating with the WHOI Coastal Ocean Institute to design and implement a beach closure informational web site. (For more detailed information -please see attached file)

Journal Publications

Erdner, D.L. and D.M. Anderson, "Global transcriptional profiling of the toxic dinoflagellate Alexandrium fundyense using Massively Parallel Signature Sequencing.", BMC Genomics, p. 1, vol. 7:88, (2006). Published,

Nagai, S., L. McCauley, N. Yasuda, D.L. Erdner, D.M. Kulis, Y. Matsuyama, S. Itakura and D.M. Anderson., "Development of microsatellite markers in the toxic dinoflagellate Alexandrium minutum (Dinophyceae)", Molecular Ecology Notes, p. 756, vol. 6, (2006). Published, Anderson, D.M., Keafer, B.A., McGillicuddy, D.J., Mickelson, M.J., Keay, K.E., Libby, P.S., Manning, J.P., Mayo, C.A., Whittaker, D.K., Hickey, J.M., He, R., Lynch, D.R., Smith, K.W., "Initial observations of the 2005 Alexandrium fundyense bloom in southern New England: General patterns and mechanisms", Deep Sea Research II, p. 2856, vol. 52, (2005). Published,

Ralston D.K., McGillicuddy, D.J. and D.W. Townsend, "Asynchronous vertical migration and bimodal distribution of motile phytoplankton", Journal of Plankton Research, p. 80, vol. 29(9), (2007). Published,

Acinas, S.G, Sarma-Rupavtarm, R., Klepac-Ceraj, V., Polz, M.F., "PCR induced sequence artifacts and bias: insights from two 16S rRNA clone libraries constructed from the same sample. Appl. Environ. Microbiol.", Appl. Environ. Microbiol., p. 8966, vol. 71(12), (2005). Published,

Klepac-Ceraj, V., Ceraj, I., Polz, M.F., "CLUSTERER: extendable java application for sequence grouping and cluster analyses", Online Journal of Bioinformatics, p. 15, vol. 7(1), (2006). Published,

Hunt, D.E., Klepac-Ceraj, V., Acinas, S.G., Gauthier, C., Bertilsson, S., Polz, M.F., "Evaluation of 23S rRNA PCR Primers for use in Phylogenetic Studies of Bacterial Diversity.", Appl. Environ. Microbiol., p. 2221, vol. 72(3), (2006). Published,

Marcelino, L., Backman, V., Donaldson, A., Steadman, C., Thompson, J.R., Paccocha-Preheim, S., Lien, C., Lim, E., Veneziano, D., Polz, M.F., "Accurate identification of low abundant targets amidst similar sequences by revealing hidden correlations in oligonucleotide microarray data.", Proc. Natl. Acad. Sci. USA, p. 13629, vol. 103(37), (2006). Published,

Polz, M.F., Hunt, D.E., Preheim, S.P., Weinreich, D.M., "Patterns and mechanisms of genetic and phenotypic differentiation in marine microbes. Phil. Trans. R. Soc. Lond. B.", Phil. Trans. R. Soc. Lond. B., p. 2009, vol. 361, (2006). Published,

Veneziano, D., Klepac-Ceraj, V., Polz, M.F., "Likelihood estimation of richness and species abundance distribution in microbial communities.", Journal of Theoretical Biology, p. , vol. , ( ). Submitted,

Sogin, M.L., H.G. Morrison, J.A. Huber, D.Mark Welch, S.M. Huse, P.R. Neal, J.M. Arrieta, and G.J. Herndl., "Microbial diversity in the deep sea and the under-explored "rare biosphere.", Proc. Natl. Acad. Sci. USA, p. 12115, vol. 103(32), (2006). Published,

Messerli, S.M. and Greenberg, R.M., "Cnidarian toxins acting on voltage-gated ion channels.
", Marine Drugs, p. 70, vol. 4, (2006). Published,

Ehrenreich, I.M., J.B. Waterbury, and E.A. Webb, "The Distribution and Diversity of Natural Product Genes in Marine and Freshwater Cyanobacterial Cultures and Genomes.", Appl. Environ. Microbiol., p. 7401, vol. 71, (2005). Published,

Anderson, D.M., J.M. Burkholder, W.P. Cochlan, P.M. Glibert, C.J. Gobler, C.A. Heil, R. Kudela, M.L. Parsons, J.E. Rensel, D.W. Townsend, V.L. Trainer, and G.A. Vargo (in review)., "Harmful algal blooms and eutrophication: Examples of linkages from selected coastal regions of the United States.", Harmful Algae, p. 39, vol. 8, (2008). Published,

Erdner, D.L., J. Dyble, M.L. Parsons, P. Moeller, R.C. Stevens, K.A. Hubbard, M.L. Wrabel, S.K. Moore, K.A. Lefebvre, D.M. Anderson, P. Bienfang, R.R. Bidigare, M.S. Parker, P. Moeller, L.E. Brand, and V.L. Trainer, "Centers for Oceans and Human Health: A unified approach to the challenge of harmful algal blooms.", Environmental Health. Supplement, p. S2, vol. 7, (2007). Published,

Heisler, J., P. Glibert, J. Burkholder, D. Anderson, W. Cochlan, W. Dennison, C. Gobler, Q. Dortch, C. Heil, E.Humphries, A. Lewitus, R. Magnien, H. Marshall, K. Sellner, D. Stockwell, D. Stoecker, and M. Suddleson (in review)., "Eutrophication and harmful algal blooms: A scientific consensus.", Harmful Algae., p. , vol. , (2007). In press,

Ho, A.Y.T., J. Xu, X.C. Yuan, K. Yin, L. He, Y.L. Jiang, D.M. Anderson, and P.J. Harrison (in review)., "Seasonal and spatial dynamics of nutrients and phytoplankton biomass in Victoria Harbour and its vicinity before and after sewage abatement.", Mar. Poll. Bull., p. , vol. , (2007). Submitted,

Lilly, E.L., K. Halanych, and D.M. Anderson (in press)., "Species boundaries and global biogeography of the dinoflagellate "A. tamarense" complex of the dinoflagellate genus Alexandrium (Dinophyceae).", J. Phycol., p. 13, vol. 43, (2007). Published, McCauley, L.A.R., D.L. Erdner, S. Nagai, and D.M. Anderson, "Bioegeographic analysis of the globally distributed harmful algal bloom species Alexandrium minutum (Dinophyceae) based on LSU rDNA and ITS sequences, and microsatellite markers.", Journal of Phycology, Paris France, p. 599, vol. , (2009). in press,

Xu, Jie, A.Y.T. Ho, K. Yin, X. Yuan, D.M. Anderson, and P.J. Harrison (in review)., "Temporal and spatial variations in nutrient stoichiometry and regulation of phytoplankton biomass in Hong Kong waters: Influence of the Pearl River outflow and sewage inputs.", Mar. Poll. Bull., p. , vol. 57, (2008). Published,

Backer, L.C. and McGillicuddy, D.J.,, "Harmful Algal Blooms: At the interface between coastal oceanography and human health.", Oceanography, p. 94, vol. 19(2), (2006). Published,

Smith, K.W., McGillicuddy, D.J., and D.R. Lynch., "Parameter estimation using an ensemble smoother: the effect of the circulation in biological estimation.", Journal of Marine Systems, p. 162, vol. 76(1-2), (2009). Published,

Anderson, D.M., Libby, P.S., Mickelson, M.J., Borkman, D.G., He, R., McGillicuddy, D.J., "The 2005 New England red tide of Alexandrium fundyense: observations, causes, and potential outfall linkages.", Boston: MWRA Report 2007-10, p. , vol. , (2007). Published,

Aretxabaleta, A.L., McGillicuddy, D.J. , Smith, K.W., and D.R. Lynch, "Model Simulations of the Bay of Fundy Gyre: 1. Climatological Results", Journal of Geophysical Research, p. , vol. , (2007). Published, 10.1029

Dyble, J., Bienfang, P., Dusek, E., Griffiths, W., Hitchcock, G., Holland, F., Laws, E., Lerczak, J., McGillicuddy, D.J., Minnett, P., Moore, S., O'Kelly, C., Solo-Gabriel, H., and J. Wang., "Environmental controls, oceanography and population dynamics of pathogens and harmful algal blooms: Connecting sources to human exposure.", Environmental Health, p. , vol. , (2008). Published, 10.1186/1476-069x-7-s2-s5

Jill R. Stewart, Rebecca J. Gast, Roger S. Fujioka, Helena M. Solo-Gabriele, J. Scott Meschke, Linda A. Amaral-Zettler, Ericka Del Castillo, Martin F. Polz, Tracy K. Collier, Mark S. Strom, Christopher D. Sinigalliano, Peter D. R. Moeller, and A. Fredrick, "The coastal environment and human health: Microbial indicators, pathogens, sentinels and reservoirs", Environmental Health, p. , vol. 7(Suppl, (2008). Published,

Shimeta, J., R.J. Gast and J.M. Rose, "Community structure of marine sedimentary protists in relation to flow and grain size", Aquatic Microbial Ecology, p. 91, vol. 48, (2007). Published,

Sinigalliano, CD, Gidley, ML, Shibata, T, Whitman, D, Dixon, TH, Laws, E, Hou, A, Bachoon, D, Brand, L, Amaral-Zettler, L, Gast, R, Steward, GF, Nigro, OD, Fujioka, R, Betancourt, WQ, Vithanage, G, Mathews, J, Fleming, LE and HM Solo-Gabriele., "Impact of Hurricanes Katrina and Rita on the microbial landscape of the New Orleans area", PNAS, p. , vol. , (2007). Published,

Bogomolni A, Ellis J, Gast B, Harris R, Pokras M, Touhey K, Moore M, "Emerging Zoonoses in Marine Mammals and Seabirds of the Northeast U.S. Oceans '06", MTS/IEEE-Boston, Massachusetts September 18-21, 2006, p. , vol. , (2006). Published,

Sabehi, G. Kirkup, B. C., Rozenberg, M., Stambler, N., Polz, M.F., Beja, O., "Niche adaptation and spectral tuning in marine proteorhodopsins", ISME Journal, p. 48, vol. 1(1), (2007). Published,

Hunt, D. E., Gevers, D., Vahora, N. M., Polz, M. F., "Conservation of the chitin utilization pathway in the Vibrionaceae.", Appl. Environ. Microbiol., p. 4, vol. 74(1), (2008). Published,

Stocker, R, Seymour, J. R., Samadani, A., Hunt, D. E., Polz, M. F., "Rapid chemotactic response enables marine bacteria to exploit ephemeral microscale nutrient patches.", Proc. Natl. Acad. Sci., p. 420, vol. 105(11), (2008). Published,

Huse, S.M., J.A. Huber , H.G. Morrison, M.L. Sogin and D. Mark Welch, "Accuracy and quality of massively parallel DNA pyrosequencing.", Genome Biology, p. , vol. , (2007). Published,

Pope, W. H., Weigele, P. R., Chang, J., Pedulla, M. L., Ford, M. E., Houtz, J. M., Jiang, W., Chiu, W., Hatfull, G. F., Hendrix, R. W., and King, J., "Genome sequence, structural proteins, and capsid organization of the cyanophage Syn5: a "horned" bacteriophage of marine Synechococcus.", Journal of molecular biology, p. , vol. 368, (2007). Published, Weigele, P. R., Pope, W. H., Pedulla, M. L., Houtz, J. M., Smith, A. L., Conway, J. F., King, J., Hatfull, G. F., Lawrence, J. G., and Hendrix, R. W., "Genomic and structural analysis of Syn9, a cyanophage infecting marine Prochlorococcus and Synechococcus.", Environmental microbiology, p. 1675, vol. 9, (2007). Published,

H.L. Kite-Powell, L.E. Fleming, L.C. Backer, E. Faustman, P. Hoagland, A. Tsuchiya, L. Younglove, B.A. Wilcox, and R. Gast., "Linking the oceans to public health: current efforts and future directions.", Environmental Health, p. , vol. 7(Suppl, (2008). Published, 10.1186

Hunt, D. E., Lawrence, A. D., Gevers, D., Preheim, S., Alm, E. J., Polz, M. F., "Resource partitioning and sympatric differentiation among closely related bacterioplankton.", Science. 320:1081-1085., p. 1081, vol. 320, (2008). Published,

Fraser, C., Alm, E.J., Polz, M.F., Spratt, B., Hanage, W., "The bacterial species challenge: Making sense of genetic and ecological diversity.", Science. 323:741-746, p. , vol. 323, (2009). Published,

LeRoux, F., Zouine, M., Chakroun, N., Binesse, J., Saulnier, D., Bouchier, C., Zidane, N., Ma, L., Rusniok, C., Buchrieser, C., M??digue, C., Polz, M.F., Mazel, D., "Genome sequence of Vibrio splendidus: a dominant group of bacterioplankton presenting a large genotypic diversity.", Environ. Microbiol., p. , vol. , (2009). In Press,

Joss, M. J., Koenig, J., Labbate, M., Polz, M. F., Gillings, M. R., Stokes, H. W., W. Ford Doolittle, W. F., Boucher, Y., "ACID: Annotation of cassette and integron data.", Bioinformatics., p. , vol. , (2008). In Press.,

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Web/Internet Site

URL(s):

http://www.whoi.edu/science/cohh/whcohh/index.htm Anderson - The Northeast PSP site (http://www.whoi.edu/northeastpsp)

Description:

Additional Web Sites:
http://www.whoi.edu/sbl/liteSite.do?litesiteid=3230&articleId=13371
http://science.whoi.edu/users/mcgillic/cohh/oc412/data/
www.whoi.edu/people/rgast
www.whoi.edu/sites/zoonoses
http://amarallab.mbl.edu
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http://science.whoi.edu/users/ruoying/Redtide_05/movie.html
http://omgrhe.meas.ncsu.edu/Redtide/Redtide_06/
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Data from research cruises R/V Oceanus voyage 412, and R/V Endeavor cruises EN435 and EN437:
http://science.whoi.edu/users/mcgillic/cohh/oc412/data/
http://science.whoi.edu/users/mcgillic/oc445/
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http://science.whoi.edu/users/mcgillic/en451
Near-real-time nowcasting and Forecasting of the 2005, 2006, 2007, and 2008 blooms:
http://omglnx3.meas.ncsu.edu/yli/08forecast/dino_08.htm
http://www.whoi.edu/northeastpsp
http://vamps.mbl.edu

Other Specific Products

Product Type:

Poster presentation

Product Description:

04/06: Initial Observations of the 2005 Alexandrium fundyense Bloom in southern New England: General Patterns and Mechanisms. Symposium on Boston Harbor and adjacent coastal waters. New England Estuarine Research Society. Nantasket, MA.

11/06: D.M. Anderson, B.A. Keafer, D.J. McGillicuddy, and R. He. The 2005 and 2006 Alexandrium red tides: A tale of two blooms. Wellfleet Harbor Conference.

Sharing Information:

Presented at meetings.

Product Type:

Software (or netware)

Product Description:

We are currently collaborating with colleagues in Austria and Germany to develop widely applicable microarray software based on our paper Marcelino et al. (2006).

Sharing Information:

Will be available to interested researchers.

Product Type:

Software (or netware)

Product Description:

Env454 database schema; in-house scripts to assemble reads generated from the same PCR clone with different sequencing primers (?clonebyclone?) and to estimate the taxonomic distribution of clones amplified from a particular sample (?clone2taxbreak?).

Sharing Information:

Service using database will be available to interested researchers.

Product Type:

Software (or netware)

Product Description:

We are currently collaborating with colleagues in Austria and Germany to develop widely applicable microarray software based on our paper Marcelino et al. (2006).

Further, we have developed the AdaptML software, which can be used to detect ecologically cohesive bacterial populations among strains sampled from varied environmental samples.

Sharing Information:

See above.

Product Type:

Software (or netware)

Product Description:

Polz - We are currently collaborating with colleagues in Austria and Germany to develop widely applicable microarray software based on our Paper Marcelino et al. (2006).

Sharing Information:

Further, we have developed the AdaptML software, which can be used to detect ecologically cohesive bacterial populations among strains sampled from varied environmental samples.

Contributions

Contributions within Discipline:

Polz - Project 4:
We have finished sequencing of 75 genomes from our collection. This effort was funded by the Moore Foundation and the Broad Institute Sparc program. This is a significant step in providing marine microbiology with the necessary core dataset for future research. Annotation and correlation with data from the other ongoing sequencing efforts will provide additional value to the users of these genomes.

Contributions to Other Disciplines:

Contributions to Human Resource Development:

Polz - Project 4:
Undergraduate student research and training: The Polz lab has, over the past 6 years, hosted 17 undergraduate researchers who all stayed for more than one semester and have been working on their own projects. These included several students from other institutions, three underrepresented minorities and 14 women. This has resulted in 5 publications with 6 undergraduate co-authors.

Polz also participated in the INGEB Integrative Biology Workshop in P?tzcuaro, Mexico (October 2006), which trains students from Latin American countries.

High school student research and training: We are assisting students from the Thomas Jefferson High School for Science and Technology, Alexandria, in their project on detection and remediation of Vibrio contamination in seafood. Polz has met with a representative from the school and the lab is currently transferring protocols to the school for bacterial isolation and characterization. Moreover, the Polz lab has hosted high school students in research internships. Most recently, a student from the University School, Milwaukee who worked on characterization of antagonistic bacterial interactions.

Members of the Polz lab actively participated in setting up a high school student laboratory experience centered on bacteriophage characterization by purification, electron microscopy and protein analysis [http://web.mit.edu/pweigele/www/phiG01/Site/Welcome.html]. This activity will be continued and has also led to sequencing of 5 phages isolated by the Polz lab. These will serve to train the next batch of students in basic bioinformatics tools.

Popular science: The Museum of Science has a formal outreach activity with the MIT Earth Systems Initiative. The Polz lab actively participates in this activity, which involves: (1) Yearly PI visit to the Museum with podcast, New England Cable News spot, and presentation; (2) Quarterly researcher 'appearance' at the museum to be available for informal conversation with museum guests following a museum staff presentation in which their research is referenced; (3) Weekly staff presentation in which the ESI research efforts are highlighted as part of a general presentation on 'Global Warming,' 'Earth Dynamics' (or similar topics); (4) Daily availability of research highlights within a touchstory attached to the Earth Vitrine.

Special activity in response to hurricane Katrina: Polz took a group of undergraduate students to Lake Pontchartrain to study potential effects of Hurricane Katrina. In a week-long activity, the students carried out independent projects ranging from assessment of populations abundance of potential pathogens and indicators (vibrios and coliforms) to determination of heavy metal contamination in sediments. The group stayed at Southeastern Louisiana University in Hammond and interacted with local scientists, students and engineers involved in post-hurricane cleanup and lake studies.

Contributions to Resources for Research and Education:

Contributions Beyond Science and Engineering:

Polz - Project 4:

The creation and intense characterization of this strain collection will permit it to be used in testing technologies meant to identify and enumerate pathogens from among environmental isolates, allowing the precise cause of false positives and negatives to be discerned by associating them with well known environmental strains.

Conference Proceedings

Special Requirements

Special reporting requirements: None

Change in Objectives or Scope: None

Animal, Human Subjects, Biohazards: None

Categories for which nothing is reported:

Contributions: To Any Other Disciplines

Contributions: To Any Resources for Research and Education

Any Conference

<u>Research and Education Activities, Finding and Outreach</u>

Stegeman – Administrative Core

Research and Education Activities and Findings:

The Administrative Core continued to facilitate communication within the Center, with investigator meetings. The Administrative Core also organized a Center Retreat, March 5, 2010. The Director and Deputy Director also have arranged and participated in regular bi-monthly conference calls among the NSF/NIH Center Directors and with NOAA as well.

Anderson – <u>Project 1</u>

Activities:

During this project year, work focused on data analyses and interpretation related to Specific Aims 2, 4, and 5 of the project, which are to:

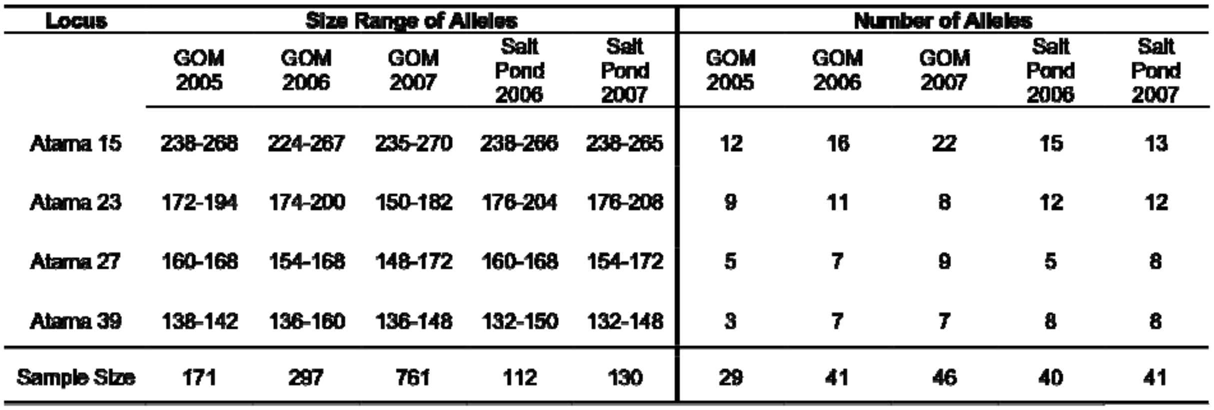
2. Determine the extent of natural genetic diversity of *Alexandrium* spp. in the Gulf of Maine;
4. Track changes in the relative abundance of *Alexandrium* genotypes in Bay of Fundy source population through time; and
5. Track changes in the genotypic diversity of *Alexandrium* populations through time throughout the Gulf of Maine.

Findings:

During this project year, we continued our studies of the spatial and temporal genotypic diversity of *Alexandrium* bloom populations in the Gulf of Maine (GOM), including the offshore Georges Bank region, the most northerly “upstream” population in the Bay of Fundy, Massachusetts Bay, Nantucket Shoals, and from Salt Pond, MA, an isolated embayment in the Nauset Marsh System (NMS) on Cape Cod. With all laboratory analyses completed, project activities focused on data analysis and interpretation of the hundreds of isolates genotyped in each project year.

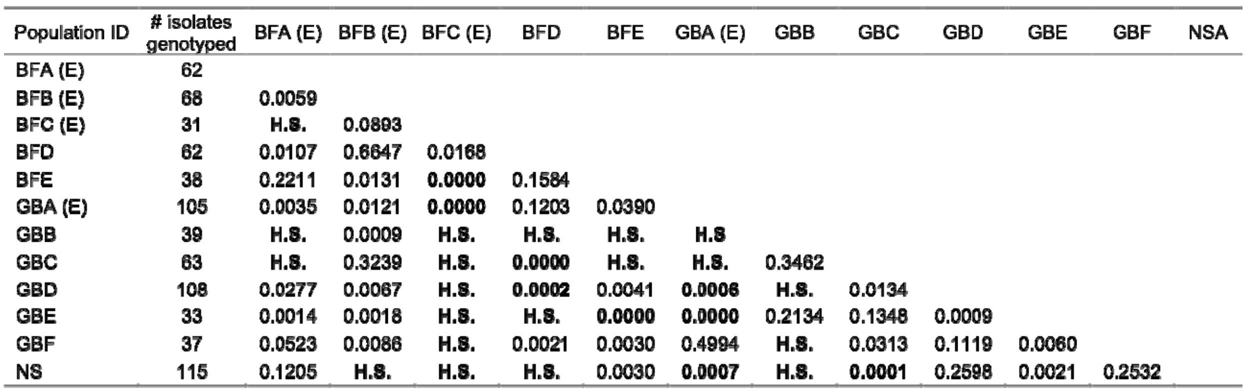
In total, ~1,500 isolates were genotyped at over the course of this project (Table 1). Our data sets include samples collected in 2005-2007 throughout the GOM, and populations sampled from Salt Pond in 2006-2007. Allele size ranges were comparable among sampling years and between the GOM and Salt Pond. In the GOM, the number of alleles was highest in 2007, likely reflecting the greater number of strains analyzed. Of the four microsatellite loci tested, Atama 15 produced the most alleles in all populations; interesting, the numbers of alleles observed at Atama 39 and Atama 23 were highest in the Salt Pond populations, despite the substantially lower numbers of strains analyzed. Clonal diversity (G:N) was also highest in populations sampled from Salt Pond, ranging from 81% to 97% genetically distinct cells.

Comparisons of genetic differentiation showed that *Alexandrium* blooms in the GOM and Salt Pond are not genetically homogenous and notably, populations present at the end of a bloom can be distinct from those at the start of a bloom. Among samples collected in 2005 from the GOM, late-bloom samples collected near Martha’s Vineyard, MA (MV) were genetically distinct from the early-bloom populations (Fisher’s combined test, $p<0.05$). Similarly, starting bloom populations in 2007 were largely homogenous, with greater heterogeneity observed among the later bloom populations. Comparisons



Locus	Size Range of Alleles					Number of Alleles				
	GOM 2005	GOM 2006	GOM 2007	Salt Pond 2006	Salt Pond 2007	GOM 2005	GOM 2006	GOM 2007	Salt Pond 2006	Salt Pond 2007
Atama 15	238-268	224-267	235-270	238-266	238-265	12	16	22	15	13
Atama 23	172-194	174-200	150-182	176-204	176-208	9	11	8	12	12
Atama 27	160-168	154-168	148-172	160-168	154-172	5	7	9	5	8
Atama 39	138-142	136-160	136-148	132-150	132-148	3	7	7	8	8
Sample Size	171	297	761	112	130	29	41	46	40	41

Table 1. Characteristics of microsatellite loci used in this study for samples collected from GOM (2005-2007) and Salt Pond (2006-2007).

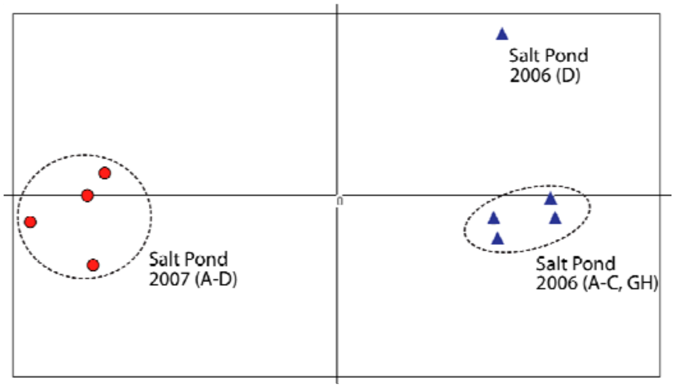


Population ID	# isolates genotyped	BFA (E)	BFB (E)	BFC (E)	BFD	BFE	GBA (E)	GBB	GBC	GBD	GBE	GBF	NSA
BFA (E)	62												
BFB (E)	68	0.0059											
BFC (E)	31	**H.S.**	0.0893										
BFD	62	0.0107	0.6647	0.0168									
BFE	38	0.2211	0.0131	**0.0000**	0.1584								
GBA (E)	105	0.0035	0.0121	**0.0000**	0.1203	0.0390							
GBB	39	**H.S.**	0.0009	**H.S.**	**H.S.**	**H.S.**	**H.S**						
GBC	63	**H.S.**	0.3239	**H.S.**	**0.0000**	**H.S.**	**H.S.**	0.3462					
GBD	108	0.0277	0.0067	**H.S.**	**0.0002**	0.0041	**0.0006**	**H.S.**	0.0134				
GBE	33	0.0014	0.0018	**H.S.**	**H.S.**	**0.0000**	**0.0000**	0.2134	0.1348	0.0009			
GBF	37	0.0523	0.0086	**H.S.**	0.0021	0.0030	0.4994	**H.S.**	0.0313	0.1119	0.0060		
NS	115	0.1205	**H.S.**	**H.S.**	**H.S.**	0.0030	**0.0007**	**H.S.**	**0.0001**	0.2598	0.0021	0.2532	

Table 2. Pair-wise comparisons (p-values) of extent of genetic differentiation among 2007 GOM *Alexandrium* populations sampled using Fisher's combined test. Bold numbers indicate statistically significant values ($p<0.05$) after sequential Bonferroni correction. (E) = starting bloom populations.

of starting bloom populations from the Bay of Fundy in 2005 and 2007 showed that these starting bloom populations were not significantly different from year to year (Fisher's combined test, $p < 0.05$). Similarly, comparisons of starting bloom populations sampled in 2005 and 2006 from Massachusetts Bay were not significantly different (Fisher's combined test, $p < 0.05$). Although these results indicate that starting bloom populations in all three sampling years were largely homogeneous, the genetic composition of *Alexandrium* populations change over the course of a bloom season, potentially reflecting the addition of genetically different populations that that germinate and form blooms at different times. Under this scenario, early blooming genotypes dominate starting bloom populations, and are subsequently admixed with later blooming genotypes, effectively representing genetically distinct "ecotypes" that comprise *Alexandrium* blooms in the GOM.

Fig 1. Principal components analysis of pairwise Fst values was used to determine how the populations from 2007 were clustered with populations from 2006. Three clusters were identified: the first comprising the Salt Pond samples from 2007, the second comprising Salt Pond 2006 samples A-C and Goose Hummock (GH), and the third comprising the late bloom sample from 2006.



This interpretation is supported by patterns of genetic diversity observed in Salt Pond bloom populations. In both 2006 and 2007, populations collected from Salt Pond were genetically distinct from those in the wider GOM. Furthermore, all 2007 Salt Pond bloom populations were genetically distinct from the 2006 bloom populations (Fisher's combined test, $p < 0.05$). A principal components analysis (PCA) of pairwise F_{ST} values suggested that *Alexandrium* blooms in Salt Pond are comprised of three or more distinct populations, which exhibit rapid turnover within and between bloom seasons. In addition to the genetic differentiation observed between sampling years, we found that in both 2006 and 2007, populations present earlier in the bloom in Salt Pond were genetically distinct from late bloom populations (Fisher's combined test, $p < 0.05$). Notably, the genetic composition of the bloom population in Salt Pond changed on the order of about three weeks. The observed change may be due to natural succession of the bloom community, potentially due to differences in the length of cyst dormancy among genetically distinct populations, or possibly driven by selection from environmental conditions, parasitism, and grazing by zooplankton and shellfish. Alternatively, temporal changes in genetic composition may reflect mixing of distinct genotypes from a separated population elsewhere in the NMS. These results highlight the need to investigate the genetic diversity *Alexandrium* populations from the other terminal endpoints within the NMS to assess the extent of inter-population mixing. Fortunately, we have leveraged our work carried out under the auspices of the COHH to obtain funding from NOAA Sea Grant to carry out such an investigation. Using the microsatellite markers employed in our COHH studies, we commenced an expansive study of *Alexandrium* bloom dynamics within the NMS, including the terminal endpoints of Salt Pond, Mill Pond, and Town Cove, which will help us understand the sources of toxic cells in the NMS and to identify mixing of populations.

Additionally, the results of our microsatellite studies also highlight the need to investigate selective forces during the course of the bloom as well as the genetic composition of the cyst seedbeds that inoculate the blooms in the GOM, which is the focus of current work under a supplement enhancement of Aim 2, supported by funding provided from the American Recovery and Reinvestment Act of 2009.

Outreach Activities:

Presentations by D.M. Anderson:

05/09 Invited talk, “The 2008 (and 2009) *Alexandrium* bloom”, Massachusetts Water Resources Authority Annual Science Meeting, Duxbury, MA (COHH, GOMTOX)

05/09 Invited talk, “Managing Toxic Algal Blooms in the Gulf of Maine”, Ecosystem Research and Coastal Management: Making the Connection at the Regional Scale, NOAA Science Center, Silver Spring, MD (GOMTOX, ECOHAB cyst project)

10/09 Invited talk, “New methods for counting HAB cells, Regional Symposium on Harmful Algal Blooms”, Regional Organization for the Protection of the Marine Environment, Kuwait (GOMTOX, EPA, ECOHAB Cyst I and II, COHH)

10/09 Invited talk, “The role of cysts in HAB population dynamics”, Regional Symposium on Harmful Algal Blooms, Regional Organization for the Protection of the Marine Environment, Kuwait (GOMTOX, ECOHAB Cyst I and II, COHH, SEED)

10/09 Anderson, D.M., D. McGillicuddy, R. He, S. Libby, D. Borkman, and M. Mickelson. “The historic 2005 New England red tide: potential linkages to the Massachusetts Bay sewage outfall”, GEOHAB Second Open Science Meeting on Harmful Algal Blooms and Eutrophication, Beijing, China. (GOMTOX, COHH).

10/09 Invited talk, Anderson, D.M., B. Keafer, K. Norton, D.J. McGillicuddy, R. He, C.H. Pilskaln, D. Couture, and J.L. Martin. “Toxic blooms of *Alexandrium fundyense* in the Gulf of Maine: the role of cysts in population dynamics and long-term patterns of shellfish toxicity”. PICES 2009 Annual Meeting, Understanding ecosystem dynamics and pursuing ecosystem approaches to management, Jeju, Korea. (ECOHAB Cysts I and II, GOMTOX, SEED, COHH)

10/09 “Suppression and control of harmful algal blooms: the slow pace of progress in an important area of HAB science”. Understanding ecosystem dynamics and pursuing ecosystem approaches to management, Jeju, Korea. (ECOHAB Cysts I and GOMTOX), COHH, SEED)

04/10 Forecasting the New England red tide: present status and future enhancements. Oceans and Human Health Symposium and Workshop, Washington, DC

Presentations by others:

11/09 Moustafa, A., D.L. Erdner, D.M. Kulis, D.M. Anderson, D. Bhattacharya, “Deep transcriptomics of toxic red tide dinoflagellate *Alexandrium tamarense*”. Presentation at the Fifth Symposium on Harmful Algae in the U.S., Ocean Shores, WA.

11/09 Erdner, D.L., L. Percy, L.A.R. McCauley, K. Libera, R. Withall, B.A. Keafer, J. Lewis, and D.M. Anderson. “A quantitative real-time PCR assay for the identification and enumeration of planktonic cells and resting cysts of *Alexandrium fundyense*”. Presentation at the Fifth Symposium on Harmful Algae in the U.S., Ocean Shores, WA.

11/09 Evans, A.N., A. Moustafa, D.L. Erdner, D.M. Anderson, D. Bhattacharya, D.M. Kulis, and J.D. Hackett. “Transcriptome analysis of bacteria-phytoplankton interactions in *Alexandrium tamarense*. Poster presentation at the Fifth Symposium on Harmful Algae in the U.S., Ocean Shores, WA.

McGillicuddy – Project 2

Research and Education Activities

Our originally proposed specific aims are to:

1) Formulate a suite of population dynamics models for the various genotypes of *A. fundyense*. Model formulation will be guided by existing observations, as well as laboratory experiments to be conducted in Project 1 (Anderson).

2) Incorporate the ensemble of population models into existing models of Gulf of Maine coastal hydrodynamics.

3) Use the coupled physical-biological models to construct hindcast simulations of *A. fundyense* survey observations to be collected jointly with Project 1 (Anderson).

4) Diagnose the simulations to determine the processes regulating the space/time expression of the different genotypes in terms of *A. fundyense* abundance.

5) Utilize toxigenicity data for the various genotypes (provided by Project 1 (Anderson)) together with the coupled physical-biological models (Aim 3) to make predictions of shellfish toxicity along the coast. Toxicity predictions will be tested with observations from ongoing shellfish monitoring programs.

Findings

WHCOHH funding allowed for opportunistic sampling of a severe red tide event in the Gulf of Maine in July 2009. Severe PSP outbreaks along the Maine coast prompted an unscheduled turnaround of the GOMTOX MacLane sampler near GoMOOS mooring B in order to maintain continuity of that time-series. Visual observations of discolored water prompted surface sampling to and from the mooring site, revealing *A. fundyense* concentrations ranging from 10^4 cells l^{-1} to in excess of 10^5 cells l^{-1} (Figure 1).

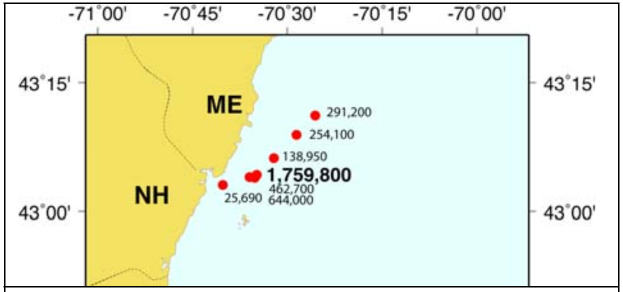


Figure 1. Surface *A. fundyense* concentrations observed on July 10, 2009 (whole cell counts).

A survey cruise on R/V *Tioga* (voyage # 383) was undertaken on July 12. Sampling consisted of (1) underway surface counts on a south-to-north line in transit to the Cape Ann line, (2) full hydrographic stations in along the Cape Ann line, and (3) full hydrographic stations on the eastern half of the Boston line (Figure 2). Cell counts were low in Massachusetts and Cape Cod Bays. The western part of the Cape Ann line was devoid of cells, but offshore the numbers were high, peaking at over 7000 cells l^{-1}. Due to time constraints we were unable to delimit the offshore edge of the population, as the easternmost station was near 2000 cells l^{-1}. Given the southward flow characteristic of this area, it seems logical to infer that this offshore population is connected with the extreme bloom conditions along the coast to the north. These data suggest the southern extent of that population has not gone much further south than the Cape Ann line, at least in surface waters. Whether or not deeper populations extend further to the south will be determined when the deeper samples (10, 20, and 30m) are analyzed.

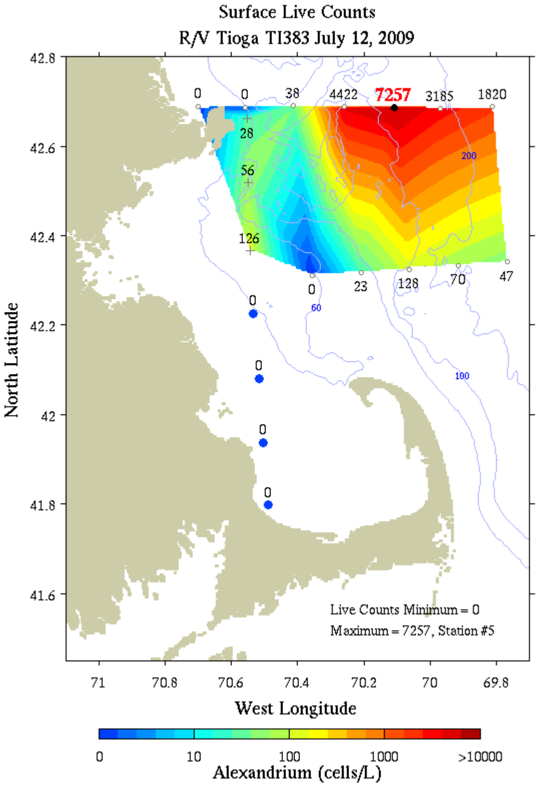


Figure 2. Surface *A. fundyense* concentrations observed on R/V *Tioga* 383 July 12, 2009 (live counts).

A regional scale mapping effort was conducted on voyage 386 of R/V *Tioga* July 19-23. Cell counts were very low overall, with the 100 cells l^{-1} threshold broken only in a few places along transects off Casco Bay, Isle au Haut, and Southwest Harbor (Figure 3).

The first day of sampling (Saco Bay and Casco Bay lines) was accompanied by an aerial survey executed by spotter pilot Norman St. Pierre and observer Michael Brosnahan. No discolored water was observed in the survey area from Cape Cod Bay to Boothbay Harbor. However, another pilot (George) reported seeing red water two weeks earlier near Portsmouth, NH. Mr. St. Pierre reported that on July 15 another pilot noted discolored water in the general vicinity of where it had been seen during the mooring cruise on July 10.

On July 22 a near-shore underway survey was conducted in coastal waters of Southwest Harbor, Frenchman Bay, Winter Harbor / Mosquito Harbor, Schoodic Point, and Prospect Harbor (Figure 4). Cell concentrations less than 200 cells l^{-1} confirmed the bloom was over in the near-shore region as well.

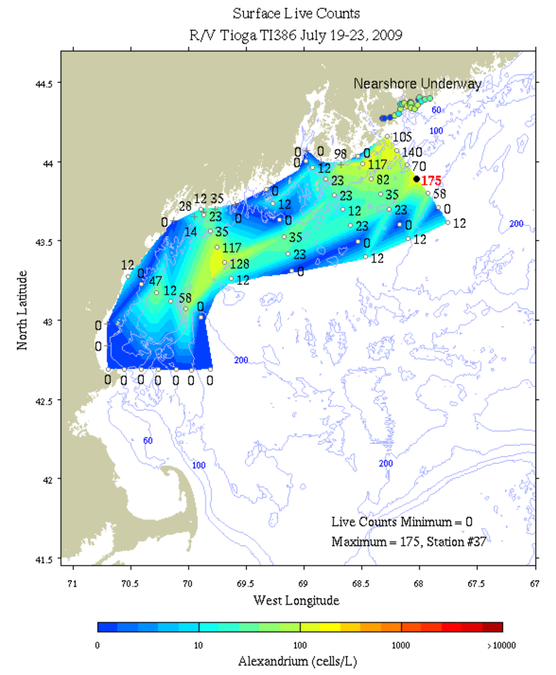


Figure 3. Surface *A. fundyense* concentrations observed on R/V *Tioga* 386 July 19-23, 2009 (live counts).

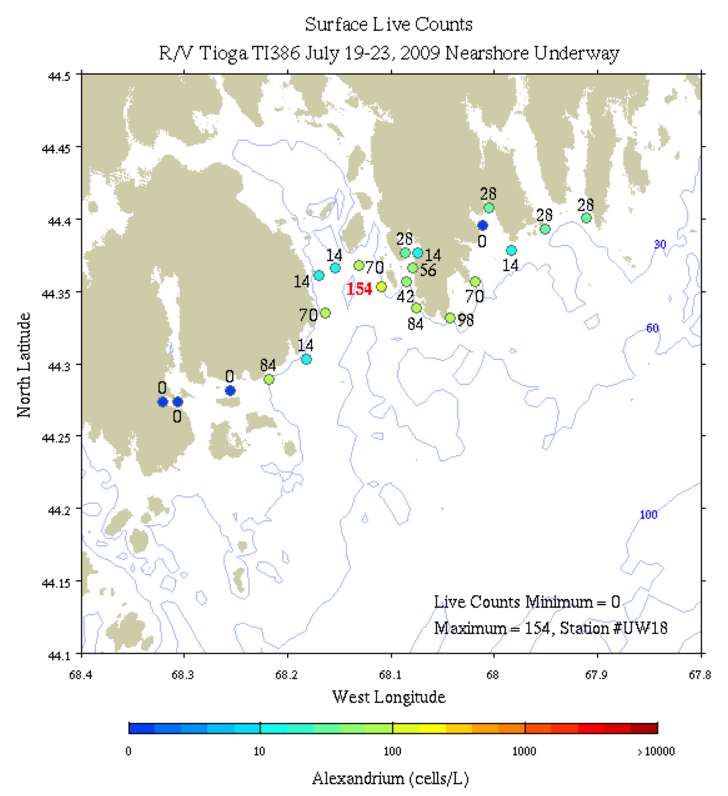


Figure 4. Surface *A. fundyense* concentrations observed on R/V *Tioga* 386 July 22, 2009 (live counts).

Research and Education Activities – **Gast** - **Project 3**

Gast has developed and taught a graduate class on Oceans and Human Health. Center investigators Anderson and Kite-Powell gave lectures for the course.

Findings

The technician working on the project in Gast's lab resigned. It took several months to identify a suitable replacement, and that person has only been working half time. The remaining funds have been used to support this technician to complete work on the project during the no-cost extension.

We have completed the checking and submission of the *Legionella* sequence data. One manuscript has been submitted and is in review, another is being prepared for submission.

The graduate student (Halliday) supported by the project has been applying the qPCR method that she developed for beach sand to samples collected in the summer of 2009 as part of her thesis. Samples were collected at beaches in Maine and Massachusetts during the summer, and will be collected in the summer of 2010 in Massachusetts. The student has also accomplished the analysis of pyrosequencing data from beach sand samples, and is preparing a manuscript for submission.

Activities and Findings – Polz - Project 4

1. Describe major research and education activities of the project

For the period covered by this no cost extension, we continued the work on *Vibrio* population characterization. Importantly, we were able to address the previous problems with our constant denaturant capillary electrophoresis (CDCE) technique. We made repairs to the machine and it is now running in 96-well format so that we are able to carry out massively parallel quantitative PCR using this machine. We favor this QPCR technique over conventional ones because it allows simultaneously discovery of populations and their quantification. In the following months, we will quantify vibrios in environmental samples we have taken over the past 6 years. This includes several time series and spatially explicit sampling along environmental gradients. For example, we have monthly samples stretching over 3 years from the coastal ocean, seasonal transects along the Plum Island estuary (our model site), and hourly samples during a 24-hour period. The combined analysis will allow unprecedented resolution of population dynamics on different spatial and temporal scales. Combined with our previous characterization of population properties, we expect important insights into the ecological dynamics of coastal *Vibrio* populations.

Other continuing efforts include the characterization of genomic diversity among *Vibrio* populations and the sequencing of plasmids found in over 1,000 strains. The latter is expected to contribute ~400 plasmid sequences to the database, thus expanding available data by roughly one third. Moreover, we expect important insights into the dynamics and diversity of plasmids within environmental bacterial populations. Finally, we have completed the methods development for isolation of vibriophages so that we will be able to take advantage of our large strain collection to characterize the diversity and interaction patterns of bacterial hosts and their viral predators.

Significance

The last few years have seen rising concern about the emergence of new variants of pathogens and spread of existing pathogens due to local or global environmental change. This has focused attention on the ecological context of pathogens in both the human body and the environment. Advances in population biology, aided by genomics, have demonstrated that many closely related (genomic) variants of microbial species exist in the environment. Furthermore, it has been shown that virulent bacteria frequently emerge from non-virulent strains via lateral gene transfer and it has been suggested that bacterial genomes are capable of extensive recombination. This raises the fundamental question to what extent observed genomic variants represent ecological and evolutionary units that can be seen as the bacterial equivalent to the eukaryotic sexual species. Do observed genomic variants occupy different environmental niches or do they represent a common gene pool capable of rapid ‘assembly’ of new variants in response to environmental challenges? These questions are crucial for interpretation of pathogen biology, risk assessment of emergence, and insights into how representative currently extensively studied strains (e.g., of *E. coli* or of pathogenic species) are for the ‘species’ they represent.