Annual Report for Period: 05/2010 - 04/2011
Submitted on: 05/05/2011
Principal Investigator: Stegeman, John J.
Award ID: 0430724
Organization: Woods Hole Ocean Inst
Submitted By:

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: Lerczak, 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: Ralston, David

Worked for more than 160 Hours: Yes

Contribution to Project:

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

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: Brosnahan, Michael

Worked for more than 160 Hours: Yes

Contribution to Project:

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

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: 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: 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

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

Dr. Deanna Erdner, University of Texas at Austin

Activities and Findings

Research and Education Activities:
See attached file.

Findings:
See attached file.

Training and Development:
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:

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.,

Man-Aharonovich, D., Tzahor, S., Kirkup, B.C., Yogev, T., Berman-Frank, I., Polz, M.F., Oded B??j??, O., Mandel-Gutfreund, Y., "Studying core-photosystem-II psbA genes and transcripts in the marine environment using machine learning classification.", Genome Biol., p. , vol. , (2008). Submitted,

Halliday, E., "Knowledge is Power? In a world shaped by science, are scientists responsible for keeping the public informed of their research and discoveries?", Ethics in Environmental Science and Politics, p. , vol. , (2009). Published, 10.3354/esep00101

Rose JM, Gast RJ, Bogomolni A, Ellis J, Lentell B, Touhey K and M Moore., "Occurrence and patterns of antibiotic resistance in vertebrates off the Northeastern United States coast.", FEMS Microbiology Ecology, p. 421, vol. 67, (2009). Published,

Amaral-Zettler LA, Rocca JD, Lamotagne MC, Dennett MR and RJ Gast., "Changes in microbial community structure in the wake of Hurricanes Katrina and Rita.", Environmental Science and Technology., p. , vol. , (2008). Published, 42: 9072-9078.

Halliday, E., "Testing the waters and closing the beaches.", Oceanus 47, p. , vol. , (2008). Published, Bogomolni A, Gast RJ, Ellis J, Dennett M, Pugliares K and M Moore., "Vectors or Victims? Marine vertebrate zoonoses from coastal waters of the Northwest Atlantic.", Diseases of Aquatic Organisms, p. , vol. , (2008). Published, 81(1):13-38

Lasek-Nesselquist E, Bogomolni A, Gast RJ, Mark Welch D, Ellis J, Sogin ML and M Moore., "Molecular characterization of Giardia intestinalis haplotypes in marine animals: variation and zoonotic potential.", Diseases of Aquatic Organisms, p. 39, vol. 81(1), (2008). Published,

Aretxabaleta, A.L., McGillicuddy, D.J., Smith, K.W., Manning, J.P. and D.R. Lynch., "Model Simulations of the Bay of Fundy Gyre: 2. Hindcasts for 2005-2007 Reveal Interannual Variability in retentiveness.", Journal of Geophysical Research, p. , vol. , (2007). Submitted,

He, R. and D.J. McGillicuddy, "Historic 2005 toxic bloom of Alexandrium fundyense in the west Gulf of Maine: 1. In situ Observations of Coastal Hydrography and Circulation.", Journal of Geophysical Research-Oceans, 113, C07039, p. , vol. , (2008). Published, 10.1029/2007JC004601

He, R., McGillicuddy, D.J.,Keafer, B.A. and D.M. Anderson, "Historic 2005 toxic bloom of Alexandrium fundyense in the western Gulf of Maine: 2. Coupled Biophysical Numerical Modeling.", Journal of Geophysical Research-Oceans, 113, C07040, p. , vol. , (2008). Published, 10.1029/2007JC004602

Manning, J.P., McGillicuddy, D.J., Pettigrew, N.R., Churchill, J.H. and L.S. Incze, "Drifter Observations of the Gulf of Maine Coastal Current.", Continental Shelf Research, p. 835, vol. 29 (7), (2009). Published,

Stock, C.A., McGillicuddy, D.J., Anderson, D.M., Solow, A.M. and R.P. Signell, "Blooms of the toxic dinoflagellate Alexandrium fundyense in the western Gulf of Maine in 1993 and 1994: A comparative modeling study.", Continental Shelf Research, p. 2486, vol. (27), (2007). Published,

Juhl, A.R., C.A. Martins, and D.M. Anderson., "Toxicity of Alexandrium lusitanicum to gastropod larvae is not caused by paralytic-shellfish-poisoning toxins.", Harmful Algae, p. 567, vol. 7, (2008). Published,

Anderson, D.M., "Harmful algal blooms and ocean observing systems: needs, present status and future potential.", Fisheries for Global Welfare and Environment, K. Tsukamoto, T. Kawamura, T. Takeuchi, T.D. Beard, Jr., and M.J. Kaiser (Eds.), p. 317, vol. , (2008). Published,

Anderson, D.M., "Approaches to monitoring, control, and management of harmful algal blooms (HABs).", Proceedings of the International Conference on Coastal and Ocean Governance, East Asian Seas Congress, Ocean & Coastal Management, p. , vol. , (2009). In Press,

Tobe, K., D. Kulis, D.M. Anderson, M. Gladstone, and L.K. Medlin., "Detecting intact algal cells with whole cell hybridisation assays. In: Methods for quantitative phytoplankton analysis - estimating cell numbers", Karlson, B., Bresnan, E., and Cusack, E., eds., IOC Manuals and Guides, UNESCO, Paris), p. , vol. , (2009). In Press,

Antonopoulos, D. A., S. M. Huse, H. G. Morrison, T. M. Schmidt, M. L. Sogin, and V. B. Young., "Reproducible Community Dynamics of the Gastrointestinal Microbiota Following Antibiotic Perturbation.", Infect Immun, p. , vol. , (2009). In Press,

Dethlefsen, L., S. Huse, M. L. Sogin, and D. A. Relman., "The pervasive effects of an antibiotic on the human gut microbiota, as revealed by deep 16S rRNA sequencing.", PLoS Biology, p. e280, vol. 6(11), (2008). Published,

Huber, J. A., H. G. Morrison, S. M. Huse, P. R. Neal, M. L. Sogin, and D. B. Mark Welch., "Effect of PCR amplicon size on assessments of clone library microbial diversity and community structure.", Environ Microbiol, p. , vol. , (2009). Published,

Huse, S. M., L. Dethlefsen, J. A. Huber, D. M. Welch, D. A. Relman, and M. L. Sogin., "Exploring microbial diversity and taxonomy using SSU rRNA hypervariable tag sequencing.", PLoS Genet, p. , vol. 4, (2008). Published, 4:e1000255.

Turnbaugh, P. J., M. Hamady, T. Yatsunenko, B. L. Cantarel, A. Duncan, R. E. Ley, M. L. Sogin, W. J. Jones, B. A. Roe, J. P. Affourtit, M. Egholm, B. Henrissat, A. C. Heath, R. Knight, and J. I. Gordon., "A core gut microbiome in obese and lean twins.", Nature, p. 480, vol. 457, (2009). Published, Glibert, P.M., Azanza, R., Burford, M., Furuya, K., Abal, E., Al-Azri, A., Al-Yamani, F., Andersen, P., Anderson, D.M., "Ocean urea fertilization for carbon credits poses high ecological risks.", Marine Pollution Bulletin, p. 1049, vol. 56, (2008). Published,

Ho, A.Y.T., J. Xu, K. Yin, Y. Jiang, X. Yuan, L. He, D.M. Anderson, J.H.w. Lee, P.J. Harrison, "Seasonal variation in size-fractionated phytoplankton biomass and production along a eutrophic gradient in Hong Kong waters.", Marine Ecology Progress Series, p. , vol. , (2008). Submitted,

Huber, J.A., Mark Welch D.B., Morrison H.G., Huse S.M., Neal P.R., Butterfield D.A., Sogin M.L., "Microbial population structures in the deep marine biosphere", Science, p. 97, vol. , (2007). Published,

Keijser, B.J.F., E. Zaura, S.M. Huse, J.M.B.M. van der Vossen, F.H.J. Schuren, R.C. Montijn, J.M. ten Cate, W. Crielaard, "Pyrosequencing Analysis of the Oral Microflora of Healthy Adults.", Journal of Dental Research, p. 1016, vol. 87(11), (2008). Published,

Laws, E.A., Fleming, L.E. and Stegeman, J.J., "Centers for Oceans and Human Health: Contributions to an emerging discipline.", Environmental Health, p. , vol. 7 (S2), (2008). Published,

Lerczak, J.A., Geyer, W.R. and Ralston, D.K., "The Temporal Response of the Length of a Partially-Stratified Estuary to Changes in River Flow and Tidal Amplitude.", Journal of Physical Oceanography., p. , vol. , (2009). Accepted,

Pukatzki, S. et al., "Identification of a conserved bacterial protein secretion system in Vibrio cholerae using the Dictyostelium host model system.", Proc Natl Acad Sci U S A, p. 1528, vol. 103(5), (2006). Published,

Sinigalliano, C.D., M.L. Gidley, T. Shibata, D Whitman, T.H. Dixon, E. Laws, A. Hou, D. Bachoon, L. Brand, L. Amaral-Zettler, R.J. Gast, G.F. Steward. O.D. Nigro, R. Fujioka, W.Q. Betancourt, G. Vithanage, J. Mathews, L.E. Fleming, and H.M. Solo-Gabriele., "Impacts of Hurricane Katrina on the Microbial Landscape of the New Orleans Area.", Proceedings of the National Academy of Sciences of the United States of America, p. 9029, vol. 104(21), (2007). Published,

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

McCauley, L.A.R., D.L. Erdner, S. Nagai, M.L. Richlen, and D.M. Anderson, "Biogeographic analysis of the globally distributed harmful algal bloom species Alexandrium minutum (Dinophyceae) based on rRNA gene sequences and microsatellite markers.", J. Phycol., p. , vol. 45: 454, (2009). Published,

Li, Y., R. He, D.J. McGillicuddy, Jr., D.M. Anderson, and B.A. Keafer., "Investigation of the 2006 Alexandrium fundyense bloom in the Gulf of Maine: In situ observations and numerical modeling.", Cont. Shelf Res., p. 2069-2082, vol. 29(17), (2009). Published,

T??be, K., D. Kulis, D.M. Anderson, M. Gladstone, and L.K. Medlin., "Detecting intact algal cells with whole cell hybridisation assays. In: Methods for quantitative phytoplankton analysis ??? estimating cell numbers", IOC Manuals and Guides, UNESCO, Paris), Karlson, B., Bresnan, E., and Cusack, E., eds., p. , vol. , (2009). In press,

He, R., D. J. McGillicuddy, D. Anderson and B. Keafer, "Gulf of Maine Circulation and Harmful Algal Bloom in Summer 2005- Part 2: Coupled Biophysical Modeling, J. Geophys.", Res., p. C07040,, vol. 113, (2008). Published, 10.1029/2007JC004602

Lynch, D.R., McGillicuddy, D.J., and F.E. Werner,, "Skill assessment for coupled biological/physical models of marine systems.", Journal of Marine Systems,, p. 1-3, vol. 76(1-2), (2009). Published,

Stow, C.A., Jolliff, J., McGillicuddy, D.J., Doney, S.C., Allen, J.I., Friedrichs, M.A.M., Rose, K.A., and P. Wallhead, "Skill Assessment for Coupled Biological/Physical Models of Marine Systems.", Journal of Marine Systems, p. 4-15., vol. 76(1-2), (2009). 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. 162-170, vol. 76(1-2), (2009). Published, Manning, J.P., McGillicuddy, D.J., Pettigrew, N.R., Churchill, J.H. and L.S. Incze,, "Drifter Observations of the Gulf of Maine Coastal Current.", Continental Shelf Research, p. 835-845, vol. 29(7), (2009). Published,

Aretxabaleta, A.L., McGillicuddy, D.J., Smith, K.W., Manning J.P. and D.R. Lynch, "Model Simulations of the Bay of Fundy Gyre: 2. Hindcasts for 2005-2007 Reveal Interannual Variability in Retentiveness", ournal of Geophysical Researc, p. C09005, vol. Jh 114, (2009). Published, 10.1029/2008JC004948

Li, Y., He, R., McGillicuddy, D.J., Anderson, D.M. and B.A. Keafer, " Investigation of 2006 Alexandrium fundyense bloom in the Gulf of Maine: In-situ observations and numerical modeling", Continental Shelf Research, p. 2069-2082, vol. 29, (2009). Published,

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.", BMC Bioinformatics, p. 118, vol. 10, (2008). Published,

Kirkup, B.C. , Chang, L.A., Chang, S., Gevers, D., Polz, M.F., "Vibrio chromosomes share common history", BMC Microbiol, p. , vol. , (2010). In press,

Preheim, S.P., Boucher, Y., Wildschutte, H., David, L.A., Veneziano, D., Alm, E.J., Polz, M.F, "Generalists dominate Vibrio populations in the microbiome of marine animals. Environ.", Microbiol, p. , vol. , (2010). In press,

Man-Aharonovich, D., Philosof, A., Kirkup, B.C., Le Gall, F., Yogev, T., Berman-Frank, I., Polz, M.F., Vaulot, D., B??j??, O., "Diversity of active marine picoeukaryotes in the eastern Mediterranean Sea unveiled using photosystem-II psbA transcripts.", ISME J, p. , vol. , (2010). In press,

Wildschutte, H., Preheim, S.P., Hernandez, Y., Polz, M.F., "-Antigen Hyper-Variability and Lateral Gene Transfer of the wbe Region Among Vibrio splendidus.", Enviornmental Biology, p. , vol. , (2010). In press,

Anderson, D.M., A.D. Cembella, and G.M. Hallegraefff, "Progress in understanding harmful algal blooms (HABs): Paradigm shifts and new technologies for research, monitoring and management", Annual Reviews in Marine Science, p. , vol. , (2011). Submitted,

Aretxabaleta, A. L., K. W. Smith, D. J. McGillicuddy Jr and J. Ballabrera-Poy, "Model initialization in a tidally energetic regime: A dynamically adjusted objective analysis", Ocean Modelling, p. 219, vol. 36, (2011). Published,

Bienfang, P. K., S. V. Defelice, E. A. Laws, L. E. Brand, R. R. Bidigare, S. Christensen, H. Trapido-Rosenthal, T. K. Hemscheidt, D. J. McGillicuddy, D. M. Anderson, H. M. Solo-Gabriele, A. B. Boehm and L. C. Backer, "Prominent human health impacts from several marine microbes: history, ecology, and public health implications", Int J Microbiol, p. , vol. , (2011). Published, doi:10.1155/2011/152815

Boucher, Y., O. X. Cordero, A. Takemura, D. E. Hunt, K. Schliep, E. Bapteste, P. Lopez, C. L. Tarr and M. F. Polz, "Local Mobile Gene Pools Rapidly Cross Species Boundaries To Create Endemicity within Global Vibrio cholerae Populations", MBio, p. , vol. 12, (2011). Published, doi: 10.1128/mBio.00335-10

Bowen, J. L., B. B. Ward, H. G. Morrison, J. E. Hobbie, I. Valiela, L. A. Deegan and M. L. Sogin, "Microbial community composition in sediments resists perturbation by nutrient enrichment", ISME J., p. , vol. , (2011). Epub ahead of print,

Chan, C.X., M.B. Soares, M.F. Bonaldo, J.H. Wisecaver, J.D. Hackett, D.M. Anderson, D.L. Erdner, and D. Bhattacharya, "Analysis of dinoflagellate genes reveals complex evolutionary history of a free-living microbial eukaryote", Natu, p. , vol. , (2011). Submitted,

Erdner, D.L., Richlen, M.L., McCauley, L.A.R., Anderson, D.M., "Intrapopulation Diversity and Dynamics of a Widespread Bloom of the Toxic Dinoflagellate Alexandrium fundyense", PLoS ONE, p. , vol. , (2011). Submitted,

Gast, R., D. Moran, M. Dennett, W. Wurtsbaugh and L. Amaral-Zettler, "Amoebae and Legionella pneumophila in saline environments", Journal of Water and Health, p. 37, vol. 9, (2011). Published,

Gast, R. J., L. Gorrell, B. Raubenheimer and S. Elgar, "Redistribution of enterococci in beach sands owing to erosion and accretion", Applied and Environmental Microbiology, p. , vol. , (2011). Submitted, Hackett, J.D., J.H. Wisecaver, M.L. Brosnahan, D.M. Kulis, D.M. Anderson, D. Bhattacharya, and F.G. Plumley, "ndependent evolution of saxitoxin synthesis in cyanobacteria and dinoflagellates", Mol. Biol. and Evol., p. , vol. , (2011). Accepted,

Halliday, E. and R. J. Gast, "Bacteria in Beach Sands: An Emerging Challenge in Protecting Coastal Water Quality and Bather Health", Environ Sci Technol., p. 370, vol. 45, (2011). Published,

Harrison, P.J., K. Furuya, P. Glibert, J. Xu, H.B. Liu, K. Yin, J.H.W. Lee, and D.M. Anderson, "Geographical distribution of red and green Noctiluca scintillans.", Chinese J. Oceanology & Limnology, p. , vol. , (2011). Accepted,

Jiang, M., M. Zhou, S.P. Libby, and D.M. Anderson, "Dynamics of a mesoscale eddy off Cape Ann, Massachusetts in May 2005", Deep Sea Research-I, p. , vol. , (2011). Submitted,

John, S. G., C. B. Mendez, L. Deng, B. Poulos, A. K. M. Kauffman, S. Kern, J. Brum, M. F. Polz, E. A. Boyle and M. B. Sullivan, "A simple and efficient method for concentration of ocean viruses by chemical flocculation", Environmental Microbiology Reports, p. 195, vol. 3, (2011). Published,

Kirkup, B. C., Jr., L. Chang, S. Chang, D. Gevers and M. F. Polz, "Vibrio chromosomes share common history", BMC Microbiol, p. 137, vol. 10, (2010). Published,

Levinton, J., M. Doall, D. Ralston, A. Starke and B. Allam, "Climate Change, Precipitation and Impacts on an Estuarine Refuge from Disease", PLoS One, p. , vol. 6, (2011). Published, doi:10.1371/journal.pone.0018849

Materna, A., F. Friedman, C. Bauer, C. Cruz, S. Chen, I. Huang, A. Gillens, S. Clarke, M. Polz and E. Alm, "Shape and evolution of the fundamental niche in marine bacteria", Proc. Natl. Acad. Sci. USA, p. , vol. , (2011). Submitted,

McGillicuddy, D. J., "Models of harmful algal blooms: Conceptual, empirical, and numerical approaches", Journal of Marine Systems, p. 105, vol. 83, (2010). Published,

McGillicuddy, D. J., B. deYoung, S. C. Doney, P. M. Glibert, D. Stammer and F. E. Werner, "Models: Tools for Synthesis in International Oceanographic Research Programs", Oceanography, p. 126, vol. 3, (2010). Published,

McGillicuddy, Jr., D.J., D.W. Towsend, R. He, B.A. Keafer, J.L. Kleindinst, Y. Li, J.P. Manning, D.G. Mountain, M.A. Thomas, and D.M. Anderson, "Suppression of the 2010 Alexandrium fundyense bloom by changes in physical, biological, and chemical properties of the Gulf of Maine", Limnol. & Oceanogr, p. , vol. , (2011). Submitted,

Pan, G., J. Chen, and D.M. Anderson, "Modified local sands for the mitigation of harmful algal blooms", Harmful Algae, p. 381, vol. 10, (2011). Published,

Preheim, S. P., Y. Boucher, H. Wildschutte, L. A. David, D. Veneziano, E. J. Alm and M. F. Polz, "Metapopulation structure of Vibrionaceae among coastal marine invertebrates", Environmental Microbiology, p. 265, vol. 13, (2011). Published,

Preheim, S. P., S. Timberlake and M. F. Polz, "Merging taxonomy with ecological population prediction: a case study of Vibrionaceae", Appl. Environ. Microbiol., p. , vol. , (2011). Submitted,

Ralston, E. P., H. L. Kite-Powell and A. Beet, "An estimate of the cost of acute health effects from marine pathogens and toxins in the United States", Water and Health, p. , vol. , (2011). Accepted,

Richlen, M.L., Erdner, D.L., McCauley, L.A.R., Anderson, D.M., "Genetic variability and rapid population succession during blooms of Alexandriumfundyense (Dinophyceae) in the Nauset Marsh System, Cape Cod, MA", Molecular Ecology, p. , vol. , (2011). Submitted,

Shapiro, B. J., J. Friedman, O. X. Cordero, S. P. Preheim, S. C. Timberlake, G. Szabo, M. F. Polz and E. J. Alm, "Mechanisms of speciation among sympatric ocean bacteria", Science, p. , vol. , (2011). Submitted, Tong, M., D.M. Kulis, E. Fux, J.L Smith, P. Hess, Q. Zhou, and D.M. Anderson, "The effects of growth phase and light intensity on toxin production by Dinophysis acuminata from the northeastern United States", Harmful Algae, p. 254, vol. 10, (2011). Published,

Wang, L., S. Chen, K. L. Vergin, S. J. Giovannoni, W. Chan, M. S. Demott, K. Taghzadeh, M. Cutler, S. Timberlake, E. J. Alm, M. F. Polz, J. Pinhassi, Z. Deng and P. C. Dedon, "DNA phosphorothioation is ubiquitous feature of bacterial genomes", Proc. Natl. Acad. Sci. USA, p. 2963, vol. 108, (2011). Published,

Wildschutte, H., S. P. Preheim, Y. Hernandez and M. F. Polz, "O-antigen diversity and lateral transfer of the wbe region among Vibrio splendidus isolates", Environmental Microbiology, p. 2977, vol. 12, (2010). Published,

Books or Other One-time Publications

Thompson, J.T., Marcelino, L., Polz, M.F., "Diversity and sources of human bacterial pathogens and overview of methods of their detection and quantification.", (2006). Book, Published
Editor(s): Shimshon Belkin and Rita Colwell
Bibliography: Ocean and Health: Pathogens in the Marine Environment. Springer. p. 464.

Martins, C.A., "Functional genomics of a non-toxic culture of Alexandrium lusitanicum.", (2006). Thesis, Published
Collection: MIT/WHOI Joint Program in Oceanography
Bibliography: N/A

Hunt, D.E., "Aquatic microenvironments in bacterial ecology and diversity.", (2008). Thesis, Published
Editor(s): MIT Cambridge
Collection: MIT doctoral thesis
Bibliography: n/a

Reddy, C.M., Stegeman, J.J. and Hahn, M.E., "Chapter 7: Organic Pollutants: Presence and Effects in Humans and Marine Animals.", (2008). Chapter of a book, Published
Editor(s): In: P. Walsh, S. Smith, L. Fleming, H. Solo-Gabriele and W. Gerwick (Editors)
Collection: Oceans and Human Health: Risks and Remedies from the Seas. Elsevier B.V., pp. 121-144.
Bibliography: Oceans and Human Health: Risks and Remedies from the Seas. Elsevier B.V., pp. 121-144.

Thompson, J.R., "Emergent Patterns of Diversity and Dynamics in Natural Populations of Planktonic Vibrio Bacteri", (2005). Thesis, Published
Editor(s): MIT/WHOI Joint Program, Cambridge, MA.
Collection: Postdoctoral thesis
Bibliography: MIT/WHOI Joint Program

Thompson, J.R., Marcelino, L.A. and Polz, M.F., "Diversity, sources, and detection of human bacterial pathogens in the marine environment.", (2005). research paper, Published
Editor(s): S. Belkin (Editor)
Collection: Oceans and Health: Pathogens in the Marine Environment.
Bibliography: Oceans and Health: Pathogens in the Marine Environment.Springer, New York, pp. 29-68.

Thompson, J.R. and Polz, M.F., "Dynamics of Vibrio populations and their role in environmental nutrient cycling.", (2006). Chapter of a book, Published
Editor(s): F.L. Thompson, B. Austin and J. Swings (Editors)
Collection: The Biology of Vibrios. ASM Press, pp. 190-203.
Bibliography: The Biology of Vibrios. ASM Press, pp. 190-203.

Harrison, P.J., J. Xu, K. Yin, J.H.W. Lee, D. M. Anderson, H.B. Liu, and A.Y.T. Ho., "Algal Blooms and red tides in Hong Kong: Which, when, where and why.", (2009). proceedings, Published
Collection: Proceedings of the 13th International Conference on Harmful Algae (in press).
Bibliography: N/A

Anderson, D.M., "Approaches to monitoring, control, and management of harmful algal blooms (HABs).", (2009). C onference Proceeding, Published
Bibliography: Proceedings of the International Conference on Coastal and Ocean Governance, East Asian Seas Congress 2006, Ocean & Coastal Management Journal 52: 342-347.

arrison, P.J., J. Xu, K. Yin, J.H.W. Lee, D. M. Anderson, H.B. Liu, and A.Y.T. Ho, H, "Algal Blooms and red tides in Hong Kong: Which, when, where and why.", ( ). Conference Proceeding, In press
Bibliography: Proceedings of the 13th International Conference on Harmful Algae

Thompson, J.T., Marcelino, L., Polz, M.F., " Diversity and sources of human bacterial pathogens and overview of methods of their detection and quantification.", (2009). Chapter in book, Published
Editor(s): Shimshon Belkin and Rita Colwell (Eds.)
Bibliography: Ocean and Health: Pathogens in the Marine Environment. Springer. p. 464.

Amaral-Zettler, L., L. F. Artigas, J. Baross, L. Bharathi, A. Boetius, D. Chandramohan, G. Herndl, K. Kogure, P. Neal, C. Pedros-Alio, A. Ramette, S. Schouten, L. Stal, A. Thessen, J. de Leeuw and M. Sogin, "Life in the World's Oceans: Diversity, Distribution and Abundance", (2010). Book, Published
Editor(s): A. McIntyre
Bibliography: Blackwell Publishing Ltd.: pp 223-245

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
http://science.whoi.edu/users/mcgillic/en435/
http://science.whoi.edu/users/mcgillic/en437/
http://science.whoi.edu/users/ruoying/Redtide_05/movie.html
http://omgrhe.meas.ncsu.edu/Redtide/Redtide_06/
http://omgrhe.meas.ncsu.edu/Redtide/Redtide_07/
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/
http://science.whoi.edu/users/mcgillic/oc447
http://science.whoi.edu/users/mcgillic/en448
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:

Contributions to Other Disciplines:

Contributions to Human Resource Development:

Undergraduate and Graduate trainees have been involved in all aspects of the program.

Contributions to Resources for Research and Education:

Contributions Beyond Science and Engineering:

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 within Discipline
Contributions: To Any Other Disciplines
Contributions: To Any Resources for Research and Education
Contributions: To Any Beyond Science and Engineering
Any Conference

NSF OCE-0430724: Research and Education Activities, Findings and Outreach

Stegeman – Administrative Core

Research and Education Activities and Findings:

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

Center Leadership and Investigators participated in the Oceans and Human Health Symposium and Workshop in Washington, D.C. in April 2010. This meeting included presentations for Congressional members and Staff on OHH issues.

Center Director John Stegeman presented a perspective on the U.S. program on Oceans and Human Health at the EurOCEAN 2010 conference in Ostende, Belgium in October. The talk, available online (http://www.eurocean2010.eu/gallery?album=1944&pic=34617), was requested by the organizers to help the European marine science community in planning for initiatives to propose to the EU for the next decade.

Center Member Mitch Sogin (MBL) participated in research on microbial populations in the Gulf of Mexico, in the aftermath of the Deep Horizon oil blowout. Studies to assess microbial assemblages are important to understanding the fate of hydrocarbons in the Gulf.

Center Investigators also made presentations at OHH sessions at several Society meetings, including the Gordon Research Conference on Oceans and Human Health.

Productivity: Center Investigators have **30** papers published, submitted or in press this year.

Anderson – Project 1

Research and Education Activities:

During this project year, work focused on completing 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. \

During this past year, project activities focused on data analysis and interpretation of microsatellite studies in Salt Pond in 2009; we also prepared and submitted manuscripts describing microsatellite studies completed in the GOM (2005) and Salt Pond (2006-2007).

Our 2006-2007 studies conducted in Salt Pond and the GOM showed that blooms in each 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. In both 2006 and 2007, populations collected from Salt Pond were genetically distinct from those in the wider GOM. 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. A manuscript describing these results was recently submitted to Molecular Ecology for publication. Additionally, we leveraged our work carried out under the auspices of the COHH to obtain funding from NOAA Sea Grant to investigate the genetic diversity *Alexandrium* populations from the other terminal endpoints within the NMS, and to assess the extent of inter-population mixing.

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. These studies showed that *A. fundyense* populations from Town Cove, Mill Pond, and Salt Pond were all significantly different from each other (Fisher's exact test, $p<0.05$; Table 1), indicating that population mixing among the terminal endpoints of the system is restricted. These results were supported by F_{ST} values, which indicated low but significant genetic differentiation. Samples collected from the Nauset Inlet were significantly different from Mill Pond, but not from Salt Pond or Town Cove, indicated that mixing may occur between the central marsh and the latter two endpoints of the system. All samples collected from the NMS, including those collected from the Inlet, were significantly different from the GOM, indicating restricted genetic exchange between the *A. fundyense* populations in the NMS and those responsible for coastal blooms.

Table 1. Extent of genetic differentiation among *A. fundyense* populations from the Nauset Marsh System, and the Gulf of Maine (GOM) sampled in 2009. Differentiation estimators F_{ST} are shown in the upper half of the matrix and Fisher's combined test (p values) are shown in the lower half of the matrix. Bold numbers indicate significant values ($p<0.05$) after sequential Bonferroni correction. H.S. = highly significant.

	Nauset Inlet	**Town Cove**	**Mill Pond**	**Salt Pond**	**GOM**
Nauset Inlet		**0.02870**	**0.06452**	**0.02109**	**0.08112**
Town Cove	0.042860		**0.00899**	**0.01806**	**0.03322**
Mill Pond	**0.002489**	0.006190		**0.02929**	**0.04238**
Salt Pond	0.006039	**H.S.**	**H.S.**		**0.04684**
GOM	**H.S.**	**H.S.**	**H.S.**	**H.S.**	

One interesting result of this study was the detection of rapid and significant temporal differentiation among the temporal samples collected at each location. Within Salt Pond, Mill Pond, and Town Cove, the genetic composition of populations changed during bloom progression (Table 2); notably, the succession of genetically distinct populations at each location occurred very rapidly, on the order of seven days. These data contributed to the development of new hypotheses regarding the impact of the selective forces on the genetic composition of blooms, which comprised the basis of a proposal to NSF that is currently under review. This proposed research will investigate the impact of selective forces on bloom dynamics within the unique experimental system of the salt ponds and will provide an in-depth analysis of the way that *A. fundyense* populations evolve over time, contributing to understanding bloom regulation.

Table 2. Temporal genetic differentiation among *A. fundyense* samples from (A) Salt Pond (SP); (B) Mill Pond (MP); and (C) Town Cove (TC) in 2009. Sampling dates are shown after sample names. Differentiation estimators F_{ST} are shown in the upper half of the matrix and Fisher's combined test (p values) are shown in the lower half of the matrix. Bold numbers indicate significant values ($p<0.05$) after sequential Bonferroni correction. H.S. = highly significant.

(A)	**SP N2 (4/6)**	**SP N3 (4/13)**	**SP N5 (4/27)**	**SP N6 (5/4)**	**SP N2 (4/6)**
SP N2 (4/6)		-0.06106	-0.00471	-0.02420	
SP N3 (4/13)	**H.S.**		**0.08500**	**0.04742**	**H.S.**
SP N5 (4/27)	**0.000018**	**H.S.**		0.00426	**0.000018**
SP N6 (5/4)	0.035376	**H.S.**	**H.S.**		0.035376

(B)	**MP N2 (4/6)**	**MP N3 (4/13)**	**MP N5 (4/27)**	**MP N7 (5/11)**
MP N2 (4/6)		0.02993	-0.04658	-0.00364
MP N3 (4/13)	0.012748		-0.04843	**0.06125**
MP N5 (4/27)	**0.005092**	**0.000384**		-0.06146
MP N7 (5/11)	0.054430	**0.000000**	0.072902	

(C)	**TC N4 (4/20)**	**TC N5 (4/27)**	**TC N7 (5/11)**
TC N4 (4/20)		0.01148	0.00566
TC N5 (4/27)	**0.002481**		-0.00971
TC N7 (5/11)	**0.000269**	**H.S.**	

Outreach Activities: Presentations by D.M. Anderson:

06/10 Anderson, D.M., S. Libby, D. Borkman, R. He, M. Mickelson, and D.J. McGillicuddy. "The historic 2005 red tide of *Alexandrium fundyense*: potential linkages to the

Massachusetts bay sewage outfall", 6th International Conference on Marine Pollution and Ecotoxicology, Hong Kong.

08/10 Anderson, D.M., "Modeling and forecasting *Alexandrium* blooms and shellfish toxicity in the Gulf of Maine", Stakeholder workshop on modeling climate and toxic blooms of *Alexandrium* catenella in Puget Sound, University of Washington, Seattle, WA

10/10 Anderson, D.M., D.J. McGillicuddy, Jr., .A. Keafer, and R. He. "Bloom dynamics of the red tide dinoflagellate *Alexandrium fundyense* in the Gulf of Maine: A synthesis and progress towards a forecasting capability", PICES 2010 Annual Science Meeting, Portland, OR

11/10 Invited plenary, "Population dynamics of *Alexandrium fundyense* of the Gulf of Maine: A synthesis and outlook for improved management and forecasting", 14th International Conference on Harmful Algae, Hersonissos-Crete, Greece

11/10 Invited talk, "Forecasting the New England Red Tide", Nankai University, Tianjin China

12/10 Invited talk, "The expanding problem of red tides and harmful algal blooms globally and in the Arabian Gulf region: impacts, trends and management issues, Abu Dhabi"

01/11 Invited talk, "Population dynamics of *Alexandrium fundyense* of the Gulf of Maine: A synthesis and outlook for improved management and forecasting", Jinan University, Guangzhou, China

01/11 Plenary, "Changing Oceans and Human Health", 11th National Conference on Science, Policy, and the Environment, Washington, DC

02/11 Invited talk, "Bloom dynamics of the red tide dinoflagellate *Alexandrium fundyense* in the Gulf of Maine: A synthesis and progress towards a forecasting capability", ASLO 2011 Aquatic Sciences Meeting, Puerto Rico

03/11 Invited talk, "Bloom dynamics of the red tide dinoflagellate *Alexandrium fundyense* in the Gulf of Maine: a synthesis and progress towards a forecasting capability", Northeast Shellfish Sanitation Association, Rye, NH

03/11 Invited talk, "Forecasts of toxic red tides and shellfish toxicity in the Gulf of Maine: Modeling and ocean observations applied to a significant societal problem", NOAA CSCOR, Silver Spring, MD

03/11 Invited talk, "Forecasts of toxic red tides and shellfish toxicity in the Gulf of Maine: Modeling and ocean observations applied to a significant societal problem", Stony Brook University, Stony Brook, NY

04/11 Invited talk, "Bloom dynamics of the red tide dinoflagellate *Alexandrium fundyense* in the Gulf of Maine: A synthesis and progress towards a forecasting capability", Northeast Algal Society 50th Anniversary Symposium, Woods Hole, MA

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

For the period 2005-2009, the abundance of resting cysts in bottom sediments from the preceding fall was a first-order predictor of the overall severity of spring/summer blooms of *Alexandrium fundyense* in the western Gulf of Maine and southern New England. Observations in the fall of 2009 indicate cyst abundance off mid-coast Maine was significantly higher than it was preceding a major regional bloom in 2005. A seasonal ensemble forecast was computed using the fall 2009 cyst abundance and the range of forcing conditions for the period 2004-2009, suggesting a large bloom was likely in the western Gulf of Maine in 2010. Real-time forecasts of *A. fundyense* abundance made during the bloom season were generally within the range of variation predicted by the seasonal ensemble forecast. However, a major bloom did not materialize in 2010 (Figure 1).

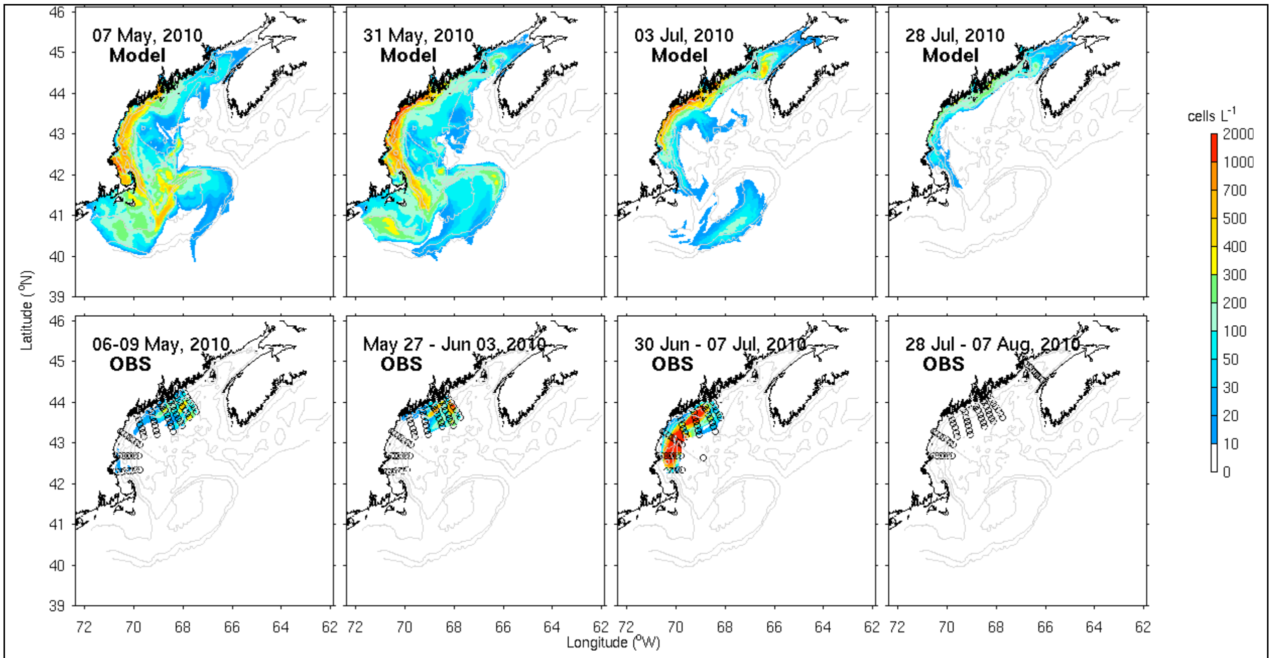

Figure 1. *A. fundyense* model predictions (top row) and observations (bottom row) for early May, late May / early June, late June / early July, and late July / early August. For a complete description of the forecast system and 2010 results, see http://omglnx3.meas.ncsu.edu/GOMTOX/2010forecast/. Note that the cell count maps in the bottom row include all available stations (open circles).

Hydrographic survey data indicate that conditions in spring/summer 2010 were outside the envelope of prior observations used to construct the ensemble forecast. Water mass anomalies indicate a regional-scale change in circulation with direct influence on *A. fundyense*'s niche (near-surface waters were warmer, fresher, more stratified, and had lower nutrients than prior years). Moreover, a weaker-than-normal coastal current lessened *A. fundyense* transport into the western Gulf of Maine and Massachusetts Bay. Satellite ocean color observations indicate the 2010 spring phytoplankton bloom was more intense and crashed earlier than usual. Thus it appears that early-season nutrient depletion caused a temporal mismatch with *A. fundyense*'s endogenous clock that regulates the timing of cyst germination. These findings highlight the difficulties of ecological forecasting in a changing oceanographic environment, and underscore the need for a sustained observational network to drive such forecasts.

Highlights

- Fall cyst abundance was a first-order predictor of spring/summer HABs 2005-2009
- Forecast models predicted a large HAB event in 2010 based on high cyst abundance
- The predicted bloom did not materialize due to anomalous hydrographic conditions
- The advective nature of these changes suggests they can be forecast months in advance

Gast and Amaral-Zettler - <u>Project 3</u>

Research and Education Activities:

Findings

Gast again taught a graduate class she developed on Oceans and Human Health. Center investigators Anderson and Kite-Powell again gave lectures for the course. Gast and the graduate student Halliday both interact with the Provincetown Water Quality Working Group, which was established by the town to explore the source of water quality exceedance events at local beaches, and to develop a remediation strategy. Gast and Halliday provided a draft document recommending several options for the microbial source tracking. Halliday also used molecular methods to test water samples collected in 2010 at one beach for the presence of human fecal material as a proof of concept. Gast and Halliday have also sequenced portions the 16S genes from atypical putative *Enterococcus* isolates from the Town of Barnstable Health Department in order to help improve their ability to conduct accurate plate counts. Most of the atypical isolates were actually *Staphylococcus* species.

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. Most of 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 published on the presence of *Legionella pneumophila* in amoebae in saline environments (Gast, Moran, Dennett, Wurstbaugh, Amaral-Zettler & Gast, 2011); another describing the diversity of *Legionella* species in saline environments is near submission.

The graduate student (Halliday) supported by the project has developed and applied a qPCR for beach sand to samples collected in the summers of 2009 and 2010 as part of her thesis. Based upon the data, she has successfully developed a correlation-based model that accurately mimics the fecal indicator plate counts for the water column during the summer of 2010, which was a dry year. She is now working on completing assays for To date, she has published two manuscripts; one describing the qPCR method (Halliday, Griffith & Gast, 2010) and a review article on indicators and pathogens in beach sand (Halliday & Gast, 2010). The student has also accomplished the analysis of pyrosequencing data from beach sand samples, and is preparing a manuscript for submission. The remaining supply funds are being used to help support the student's laboratory work, and allowed us to accomplish human source tracking for the Provincetown Water Quality Working group at the beach where we have been working.

As part of the original grant, we were funded for two pilot projects. The first was a collaboration with Elgar and Raubenheimer in AOPE, and examined whether the reworking of beach sands by waves could redistribute enterococci within the beach. The manuscript reporting this data is currently being revised for publication in Continental Shelf Research. The second was a collaboration with Ralston in AOPE and placed two Accoustic Doppler Current Profilers in the harbor of the Provincetown beach where we were sampling in the summer of 2010. The information has been used to help establish water residence time, and current strength and direction relative to the beach area.

Vibrionales Populations in Mt. Hope Bay:

To examine the effects of thermal pollution on potentially pathogenic species and those known to be associated with increased water temperature, we conducted a separate pyrotag experiment to focus on the vibrio community structure within Mt. Hope Bay. Our experiment employed a combination of a universal forward primer and vibrio-specific reverse primer and as such amplified more than just the vibrio but also several other gammaproteobacterial tags. The overall trend in the data show that Vibrionales communities are well represented in the summer both in the surface and at depth (5-7 m) while populations are relatively less abundant in the winter at the surface and even less so at depth. Noteworthy is that the relative abundances of Vibrionales at our sampled stations in the winter is highest at Station 1 (the station closest to the thermal outfall) and negligible at the remaining stations. We hypothesize that warming has allowed sub-populations of vibrios to "overwinter" at depth in the bay thereby increasing their overall year-round presence in the estuary. Analyses of the overall dataset is ongoing with an emphasis on examining vibrio diversity and membership of potential pathogenic species.

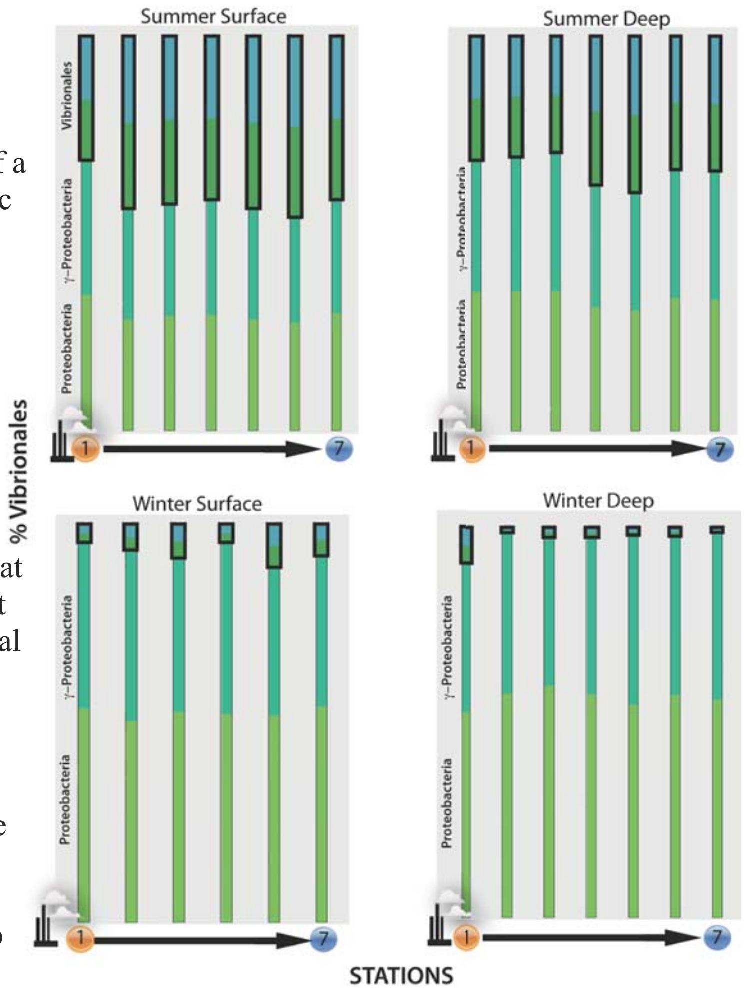

Figure 2. Comparisons of Vibrionales communities (in black boxes) in Mt. Hope Bay, MA along a transect of 7 stations extending away from the Brayton Point Power Plant and the thermal outfall from the once-through-cooled system. Vibrionales are shown as a percentage of the larger gramma-proteobacterial targeted community. Seasonal (August and February) and depth data are shown. Data based on taxonomic assignments of V4 hypervariable rRNA gene pyrotags.

WH-COHH Publications during the past year

Amaral-Zettler, L., L. F. Artigas, J. Baross, L. Bharathi, A. Boetius, D. Chandramohan, G. Herndl, K. Kogure, P. Neal, C. Pedros-Alio, A. Ramette, S. Schouten, L. Stal, A. Thessen, J. de Leeuw and M. Sogin (2010). A global census of marine microbes. Life in the World's Oceans: Diversity, Distribution and Abundance. A. McIntyre, Blackwell Publishing Ltd.**:** pp 223-245.

Anderson, D.M., A.D. Cembella, and G.M. Hallegraefff. "Progress in understanding harmful algal blooms (HABs): Paradigm shifts and new technologies for research, monitoring and management." Annual Reviews in Marine Science (Submitted.)

Aretxabaleta, A. L., K. W. Smith, D. J. McGillicuddy Jr and J. Ballabrera-Poy (2011). "Model initialization in a tidally energetic regime: A dynamically adjusted objective analysis." Ocean Modelling **36**(3-4): 219-227.

Bienfang, P. K., S. V. Defelice, E. A. Laws, L. E. Brand, R. R. Bidigare, S. Christensen, H. Trapido-Rosenthal, T. K. Hemscheidt, D. J. McGillicuddy, D. M. Anderson, H. M. Solo-Gabriele, A. B. Boehm and L. C. Backer (2011). "Prominent human health impacts from several marine microbes: history, ecology, and public health implications." International J. of Microbiology **2011**: doi:10.1155/2011/152815.

Boucher, Y., O. X. Cordero, A. Takemura, D. E. Hunt, K. Schliep, E. Bapteste, P. Lopez, C. L. Tarr and M. F. Polz (2011). "Local Mobile Gene Pools Rapidly Cross Species Boundaries To Create Endemicity within Global Vibrio cholerae Populations." MBio. 2011 Apr 12(2). pii: e00335-10. doi: 10.1128/mBio.00335-10

Bowen, J. L., B. B. Ward, H. G. Morrison, J. E. Hobbie, I. Valiela, L. A. Deegan and M. L. Sogin (2011). "Microbial community composition in sediments resists perturbation by nutrient enrichment." ISME Journal (Epub ahead of print)

Chan, C.X., M.B. Soares, M.F. Bonaldo, J.H. Wisecaver, J.D. Hackett, D.M. Anderson, D.L. Erdner, and D. Bhattacharya. "Analysis of dinoflagellate genes reveals complex evolutionary history of a free-living microbial eukaryote." Nature (Submitted.)

Erdner, D.L., Richlen, M.L., McCauley, L.A.R., Anderson, D.M. " Intrapopulation Diversity and Dynamics of a Widespread Bloom of the Toxic Dinoflagellate Alexandrium fundyense." PLoS ONE (Submitted.)

Gast, R., D. Moran, M. Dennett, W. Wurtsbaugh and L. Amaral-Zettler (2011). "Amoebae and Legionella pneumophila in saline environments." Journal of Water and Health **9**(1): 37.

Gast, R. J., L. Gorrell, B. Raubenheimer and S. Elgar "Redistribution of enterococci in beach sands owing to erosion and accretion." Applied and Environmental Microbiology. (In Revision).

Hackett, J.D., J.H. Wisecaver, M.L. Brosnahan, D.M. Kulis, D.M. Anderson, D. Bhattacharya, and F.G. Plumley. Independent evolution of saxitoxin synthesis in cyanobacteria and dinoflagellates. Molecular Biology and Evolution (In Press).

Halliday, E. and R. J. Gast (2010). "Bacteria in Beach Sands: An Emerging Challenge in Protecting Coastal Water Quality and Bather Health." Environ Sci Technol. **45**(2):370-379

Harrison, P.J., K. Furuya, P. Glibert, J. Xu, H.B. Liu, K. Yin, J.H.W. Lee, and D.M. Anderson. "Geographical distribution of red and green *Noctiluca scintillans*." Chinese J. Oceanology & Limnology. (In Press).

Jiang, M., M. Zhou, S.P. Libby, and D.M. Anderson. "Dynamics of a mesoscale eddy off Cape Ann, Massachusetts in May 2005." Deep Sea Research-I (Submitted.)

John, S. G., C. B. Mendez, L. Deng, B. Poulos, A. K. M. Kauffman, S. Kern, J. Brum, M. F. Polz, E. A. Boyle and M. B. Sullivan (2011). "A simple and efficient method for concentration of ocean viruses by chemical flocculation." Environmental Microbiology Reports **3**(2): 195-202.

Kirkup, B. C., Jr., L. Chang, S. Chang, D. Gevers and M. F. Polz (2010). "Vibrio chromosomes share common history." BMC Microbiology **10**(1): 137.

Levinton, J., M. Doall, D. Ralston, A. Starke and B. Allam (2011). "Climate Change, Precipitation and Impacts on an Estuarine Refuge from Disease." PLoS One **6**(4):doi:10.1371/journal.pone.0018849.

Materna, A., F. Friedman, C. Bauer, C. Cruz, S. Chen, I. Huang, A. Gillens, S. Clarke, M. Polz and E. Alm "Shape and evolution of the fundamental niche in marine bacteria." Proc. Natl. Acad. Sci. USA (In Review).

McGillicuddy, D. J. (2010). "Models of harmful algal blooms: Conceptual, empirical, and numerical approaches." Journal of Marine Systems **83**(3-4): 105-107.

McGillicuddy, D. J., B. deYoung, S. C. Doney, P. M. Glibert, D. Stammer and F. E. Werner (2010). "Models: Tools for Synthesis in International Oceanographic Research Programs." Oceanography **23**(3): 126-139.

McGillicuddy, Jr., D.J., D.W. Towsend, R. He, B.A. Keafer, J.L. Kleindinst, Y. Li, J.P. Manning, D.G. Mountain, M.A. Thomas, and D.M. Anderson. "Suppression of the 2010 *Alexandrium fundyense* bloom by changes in physical, biological, and chemical properties of the Gulf of Maine." Limnology & Oceanography. (Submitted.)

Pan, G., J. Chen, and D.M. Anderson. 2011. Modified local sands for the mitigation of harmful algal blooms. Harmful Algae **10**: 381-387.

Preheim, S. P., Y. Boucher, H. Wildschutte, L. A. David, D. Veneziano, E. J. Alm and M. F. Polz (2011). "Metapopulation structure of Vibrionaceae among coastal marine invertebrates." Environmental Microbiology **13**(1): 265-275.

Preheim, S. P., S. Timberlake and M. F. Polz (2011). "Merging taxonomy with ecological population prediction: a case study of Vibrionaceae." Applied and Environmental Microbiology. (Submitted)

Ralston, E. P., H. L. Kite-Powell and A. Beet (2011). "An estimate of the cost of acute health effects from marine pathogens and toxins in the United States." Water and Health. (In Press).

Richlen, M.L., Erdner, D.L., McCauley, L.A.R., Anderson, D.M. "Genetic variability and rapid population succession during blooms of Alexandriumfundyense (Dinophyceae) in the Nauset Marsh System, Cape Cod, MA." Molecular Ecology. (Submitted.)

Shapiro, B. J., J. Friedman, O. X. Cordero, S. P. Preheim, S. C. Timberlake, G. Szabo, M. F. Polz and E. J. Alm "Mechanisms of speciation among sympatric ocean bacteria." Science. (Submitted.)

Tong, M., D.M. Kulis, E. Fux, J.L Smith, P. Hess, Q. Zhou, and D.M. Anderson. 2011. "The effects of growth phase and light intensity on toxin production by *Dinophysis acuminata* from the northeastern United States." Harmful Algae **10**(3) 254-264

Wang, L., S. Chen, K. L. Vergin, S. J. Giovannoni, W. Chan, M. S. Demott, K. Taghzadeh, M. Cutler, S. Timberlake, E. J. Alm, M. F. Polz, J. Pinhassi, Z. Deng and P. C. Dedon (2011). "DNA phosphorothioation is ubiquitous feature of bacterial genomes." Proc. Natl. Acad. Sci. USA **108**(7): 2963-2968.

Wildschutte, H., S. P. Preheim, Y. Hernandez and M. F. Polz (2010). "O-antigen diversity and lateral transfer of the wbe region among Vibrio splendidus isolates." Environmental Microbiology **12**(11): 2977-2987.