DEPARTMENT OF MICROBIOLOGY

December 2012

OBSERVE

WONDER

DISCOVER

RESEARCH AND HIGHER EDUCATION

Oregon State UNIVERSITY OSU

FROM THE CHAIR

I am delighted to extend warm greetings once again to our extended OSU Microbiology family as we approach the end of 2012. I write this note on 12/12/12, and doing so on such an auspiciously labeled date surely portends well for the coming year. Based on recent successes at OSU and in the department, my mood is indeed buoyant in anticipating 2013.

Many of you will have been aware that OSU student numbers have been steadily increasing over the last few years, and now stand at about 26,000. The Microbiology major count is now over 300, far above the 140 or so that was stable over much of the previous decade. Student growth is expected to taper off for the next several years, as we have now reached the point where room scheduling for lectures has become very difficult, with consequences such as for the coming winter term forcing the delivery of back-to-back MB310 lectures because a large enough room for all students was not available. We're also not always able to keep up with seat availability for labs, forcing a few students to rearrange their schedules. These problems are being addressed with new building plans, and students are increasingly signing up for online courses, not always because of unavailability of seats (convenience, preferred learning style, are other reasons). Along with some challenges, higher student numbers have benefitted OSU. Tuition revenue, particularly from out-of-state students, has fueled the most dynamic growth the university has seen for over 20 years, in the face of a generally struggling economy and public sector. Over 100 faculty positions have been added over the last two or so years, including three new research faculty in this department, and there have been some new funds for infrastructure support.

Two of our new faces, Assistant Professors **Becky Vega Thurber** and **Kim Halsey**, have now been with us for a little over a year, and they have brought their fresh energy to the classroom and their lab research. The third new Assistant Professor, **Ryan Mueller**, started on the job this past September. As he describes on the next page, he is already playing a leading part in a large new project funded by the Gordon and Betty Moore Foundation. A fourth new face this year, though not filling a new position, is Instructor/Advisor **Tasha Biesinger** (see page 11), who began in the summer, replacing Stephanie Yarwood (now at University of Maryland). The contributions of these new colleagues open up new possibilities. For instance, with the addition of a new Microbial Systems graduate course this year, we will for the first time have a short core course component taken by all incoming Microbiology graduate students. We think this will help the new students form mutually supportive friendships, while introducing them to the remarkably broad impact of microbiology across many branches of science. Their future careers may involve close interactions with engineers, mathematicians and meteorologists, in addition to the more traditional interactions with clinicians, ecologists or biochemists. We want to prepare students for careers that will likely include some unexpected twists.

I mentioned last year that Prof. **Steve Giovannoni** was the recipient of university and professional awards. That was true again during 2012 as Steve's group continues to produce prominent advances in understanding marine bacteria. He was awarded a second major American Society for Microbiology award, the USFCC/J. Roger Porter Award in recognition of sustained contributions to establishing a culture collection invaluable for studying marine microbial diversity. Steve was presented with the Tiedje Award at the 14th International Society for Microbial Ecology conference in Copenhagen in August, and this year was also named 2012 OSU Distinguished Professor. These awards recognize the many impactful contributions Steve's group has made since he arrived at OSU about 25 years ago.

Two other causes for celebration this year: first, the promotion to Full Professor of **Jerri Bartholomew**. Jerri leads a large and well-funded group conducting a complex set of projects centered around infectious disease challenges to wild fish in the Pacific Northwest. Her work carries on the OSU Microbiology tradition in fish health microbiology established in the days of past department head **John Fryer**. Second, **Linda Bruslind**, Head Advisor and Senior Instructor, received the ***Frederick Horne Award for Excellence in Teaching Science*** from the College of Science. This award recognizes sustained excellence in teaching science, and rewards Linda for making microbiology come to life for students through classroom and experiential activities (see page 9).

I hope you enjoy reading about the activities in the Department on the following pages.

With best wishes for a happy, healthy and peaceful Holiday Season and 2013,

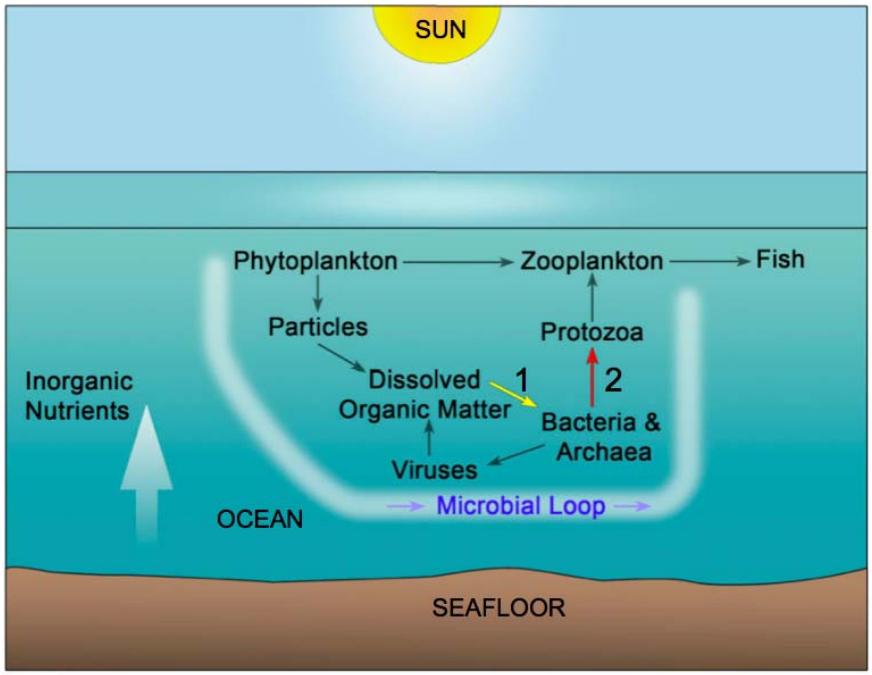
Theo W. Dreher, Pernot Professor and Chair

RYAN MUELLER LAB:

I began as an Assistant Professor at OSU in September this year. The focus of my lab's research will be on **Microbial Food Web Interactions** in aquatic habitats. It has been almost 30 years since a group of prominent aquatic ecologists published a seminal manuscript discussing and questioning the role of microbes in aquatic food webs (Azam, et al. 1983). Revisiting this excellent commentary today we find that, although the field of microbial ecology has made important strides in addressing some of these ideas, there is still significant and interesting work to be done. Namely, technological innovations and an ever-expanding wealth of DNA sequence information are allowing contemporary studies to better characterize the "microbial loop" (see figure below), by identifying key populations involved in biogeochemical cycles and describing interactions between these microbes at the molecular level.

We have recently received funding from the Moore Foundation to begin work examining an important step of the microbial loop: microbial heterotrophic consumption of fixed carbon produced by phytoplankton (arrow #1 in figure). Second-year grad student Sam Bryson will head this project and is beginning experiments to quantify the utilization and preferences of common forms of dissolved organic carbon by microbial populations. Sam will be working closely with collaborators at Lawrence Livermore and Oak Ridge National Labs to develop and refine mass spectrometry techniques that will quantify stable isotope incorporation into newly synthesized proteins, as a measure of a given population's activity. The goal of this work will be to answer the general question of "Who is doing what in these communities?", helping to define functional guilds and redundancy in these ecosystems.

Another aspect of my research will be exploring the opposite side of the microbial loop, the consumption of these bacterial consumers by eukaryotic grazers (arrow #2 in figure). This will expand on previous work of mine by examining molecular mechanisms for survival of *Vibrio cholerae* strains (an important aquatic pathogen responsible for cholera pandemics) under defined experimental conditions with these grazers. Using newly developed molecular biology techniques (i.e., "-omics") alongside traditional bacterial genetic approaches, I would like to better define the adaptations of this pathogen to environmental stresses and chemical signals involved in this interaction.



Adapted by permission from Macmillan Publishers Ltd: Nature Reviews Microbiology 5, 782-791 (October 2007)

Finally, I'd like to give a sincere thank you to all in the OSU community who have created such a supportive and welcoming environment for me as I enter into the next phase of my career. I'm really looking forward to working with everyone in the years to come!

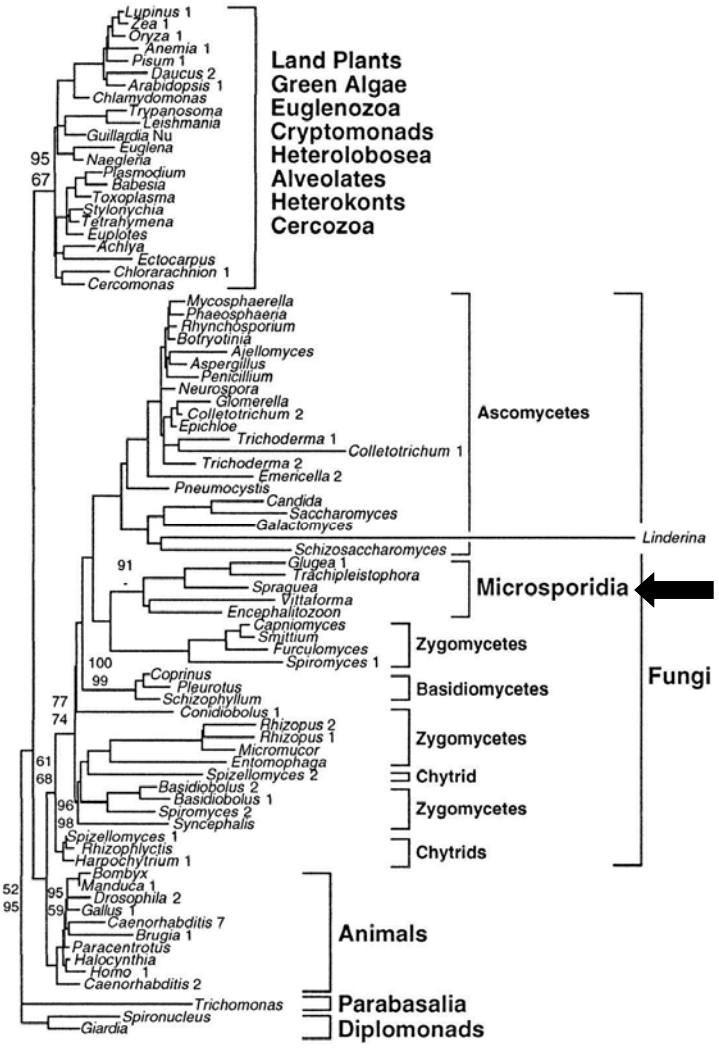
Cover Page includes picture of Microbiology grad student, Rory Welch. Rory and College of Earth, Ocean & Atmospheric Sciences Postdoctoral Fellow, Andrew Thurber, spent this fall researching in Antarctica. Their blog can be read on the Microbiology Department web site: http://microbiology.science.oregonstate.edu/home

MICHAEL KENT LAB:

Vertical transmission of *Pseudoloma neurophilia*:

A microsporidian parasite infecting the zebrafish, *Danio rerio*

The Microsporidia are a diverse group of eukaryotic, unicellular, obligate intracellular parasites. The true phylogeny of the Microsporidia has been difficult to establish. They were originally included in the Archezoa, a group of eukaryotes which branched prior to the acquisition of the mitochondrial symbiont. However, they have more recently been shown to possess a relict mitochondrion called a mitosome and genomic analyses place the Microsporidia as either early-branching fungi or sister to the Zygomycetes (see phylogenetic tree at right). With over 1,200 described species infecting hosts in virtually all animal phyla including several which infect humans, the success of the Microsporidia is demonstrated by their diversity. They are especially important pathogens of insects and fish and generally cause disease in immunocompromised hosts. With the pandemic of AIDS, they have become important pathogens in humans.



The ubiquity of the Microsporidia also makes them important natural pathogens of laboratory animals. Three microsporidia occur as common underlying infections in important laboratory animals: *Pseudoloma neurophilia* in zebrafish, *Encephalitozoon cuniculi* in rabbits and rodents, and *Nematocida parisii* in the nematode *Caenorhabditis elegans*. In addition to the direct impacts of infectious disease on laboratory animals (e.g., on population and overall health of the animals), animals chronically infected with a pathogen such as a microsporidian parasite can cause significant non-protocol induced variation in experiments. For example, subtle changes in host-physiology such as immune modulation in response to microsporidian infection can confound results obtained from experiments examining immune development and function. Also, experimental immunosuppression of laboratory animals that harbor chronic microsporidian infections can lead to the unexpected death of these animals. These problems are compounded when these infections produce little to no clinical signs, resulting in occult infections in a laboratory population. In spite of the difficulties faced by researchers using animals harboring chronic infections, this situation does provide some benefits in terms of the ability to study pathogenesis and transmission of microsporidian parasites in a well-described animal model.

Microsporidia have been shown to employ a diverse range of transmission strategies. Several microsporidian species are transmitted horizontally, generally through ingestion of spores from either fecally contaminated water or tissue from dead infected hosts. Vertical transmission of numerous species of Microsporidia has been reported in insects, and has been indicated for a few species that infect fish. Vertical transmission, especially transovarial transmission, of pathogens has important implications in the control of these diseases in insect and fish populations. Thus, the question of transmission method is important not only to further our understanding of the biology of this cryptic group of pathogens but from a management perspective.

The zebrafish, *Danio rerio,* is a very important model in biomedical research, and the microsporidium, *Pseudoloma neurophilia,* is prevalent in these fish in laboratory facilities. This host-parasite system provides an excellent vertebrate model for investigating transmission and development of microsporidia. We frequently observe *Pseudoloma neurophilia* in developing oocytes and ovaries of adult zebrafish and we consistently detect parasite DNA by PCR in eggs and water collected at spawning. Recently, we also detected large numbers of spores in developing embryos within eggs spawned by infected adults. We also observed infections in post-hatch fry and juveniles from infected parents that were reared under controlled laboratory conditions. Together, these experiments and observations are the first to verify the intra-ovum transmission of a microsporidian parasite in a vertebrate.

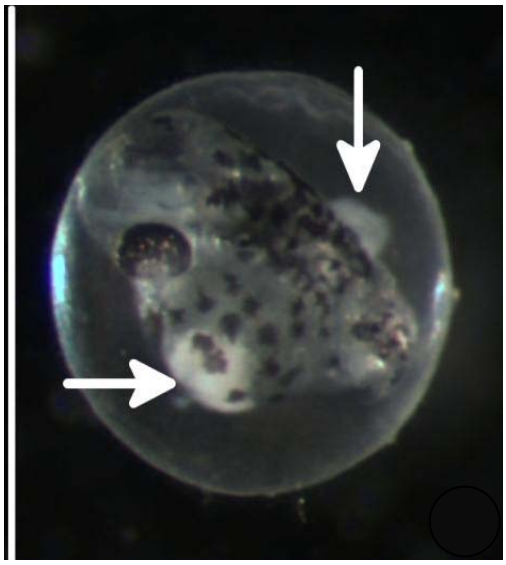
The high prevalence of a microsporidian parasite with different modes of transmission: horizontal via cohabitation and consumption of infected tissue, and vertical via transovarial transmission in a well-described vertebrate animal model provides the basis for further study of the evolution of virulence. The genome of the zebrafish has been extensively sequenced and annotated. We are also currently in the process of sequencing the genome of *P. neurophilia* with our collaborator, Nicolas Corradi, at the University of Ottawa. This will be the first sequenced genome of a microsporidium from a fish, and will allow for further study of host-pathogen interactions and the genomic basis for virulence in the context of different transmission strategies.

For more information, see:

Sanders JL, Watral V, Kent ML. (2012) Microsporidiosis in zebrafish research facilities. In Press. ILAR Journal 53:106-113.

Kent M, Buchner C, Watral V, Sanders J, LaDu J, Peterson T, Tanguay R (2011) Development and maintenance of a specific pathogen free (SPF) zebrafish research facility for *Pseudoloma neurophilia*. Dis. Aquat. Org. 95:73-79.

Sanders JL, Kent ML (2011) Development of a sensitive assay for the detection of *Pseudoloma neurophilia* in laboratory populations of the zebrafish *Danio rerio*. Dis Aquat Org 96:145-156.



Pseudoloma neurophilia in a developing zebrafish embryo (arrows).
See cover for image of spores with characteristic posterior vacuoles.

BECKY VEGA THURBER LAB:

Viruses of the algal symbiont of corals

Virtually all animals and plants form symbioses with microorganisms, and these associations are often essential to the ecological and evolutionary success of their hosts. Endosymbiotic dinoflagellate algae in the genus *Symbiodinium* form mutualistic associations with many invertebrate species and are vitally important to the construction and persistence of coral reefs, as they supply more than 90% of the coral's energy requirements and enhance their host's rates of calcification. Coral reefs are increasingly destroyed by natural and anthropogenic threats such as elevations in sea water temperatures due to climate change. One major mechanism of coral reef loss is thermal induced "bleaching" or the loss of the *Symbiodinium* algae and/or chlorophyll from coral tissues that results in the pale or white appearance of coral colonies.

Bleaching most commonly results from oxidative stress within the algal symbiont's chloroplasts, which triggers the expulsion of the algae from coral tissues via unresolved mechanisms. Bleaching induced by bacteria (*Vibrio* spp.), although controversial, has been reported, and viral infections also have been hypothesized to be an unrecognized cause of some bleaching and involvement in some of the >18 coral diseases. However, until now no viruses of these coral algal symbionts have been identified.

We recently published a manuscript on the first discovery of viruses that infect the coral symbiont. In this work we presented genomic evidence that at least two types of viruses infect *Symbiodinium*. These novel viruses are related to +RNA and dsDNA viruses. We found evidence for these viral genomes through viral metagenomics and next-generation sequencing of viral transcripts collected from coral hosts and isolated *Symbiodinium* cultures. The one virus is related to a *Heterocapsa circularisquama*-infecting positive strand RNA virus (HcRNAV), a virus that infects free-living dinoflagellates closely related to our *Symbiodinium*. Our data indicate the presence of a highly novel dinornavirus of the coral algal symbiont.

We also obtained evidence for the presence of a novel group of viruses that appear to be undescribed and distinct members of the nucleocytoplasmic large DNA virus (NCLDV) family. These viruses infect the algal symbiont while it resides in the host and while it is in isolated culture. Now our immediate research priority is to isolate these viruses from *Symbiodinium* cultures, analyze the viral life cycle and annotate its genome, and ultimately conduct infection studies to determine how these viruses impact the flexibility and/or stability of coral-algal symbioses, and thus long term reef health and resilience.

For more information, see:

Correa, A.S., Welsh, R.M., and Vega Thurber, R. (2012) Unique Nucleocytoplasmic dsDNA and +ssRNA Viruses are Associated with the Dinoflagellate Endosymbionts of Corals. *International Society of Micro bial Ecolgy Journal* doi:10.1038/ismej.2012.75

Grad Student, Stephanie Rosales / Vega Thurber Lab

WALT REAM LAB:

Streptococcus, *Prevotella*, and *Veillonella* species predominate in the gastric microbiota of patients with inflammatory bowel disease and in control patients

This year the Ream laboratory completed a study of gastric microbiota in patients with inflammatory bowel disease (IBD). Dr. Amnon Sonnenberg, a gastroenterologist at the Portland VA Medical Center, conceived the project and supplied gastric biopsies from patients who volunteered to participate. Larry Hodges did the bench work, and undergraduates Chris Brown, Scott Belozer, E. J. Chesnutis, and Sarah Layoun did DNA sequence searches. Chis and E. J. are in medical school, and Sarah is working in Brian Druker's lab at OHSU as she applies to PhD programs. Scott is a senior this year and plans to enter medical school next year. Chris and Scott received Howard Hughes Medical Institute Summer Research Fellowships, and Sarah received a Jaworski Fellowship. A brief description of the study follows.

Helicobacter-negative gastritis (HNG) is common in Crohn's disease (CD, a common form of IBD) patients but rare in IBD-free controls. Infiltrates of neutrophils, lymphocytes, and histiocytes suggest an infectious agent may cause HNG. The high correlation between Crohn's disease and HNG and their similar epidemiology suggest that the same infectious agent may cause both diseases. We compared bacterial populations in gastric biopsies from IBD patients and controls to investigate the intriguing correlation between HNG and IBD, particularly Crohn's disease. Gastric bacterial populations are simpler than those in the colon, so we extracted DNA from gastric biopsies and used DNA sequencing and terminal restriction fragment length polymorphisms to identify bacterial 16S ribosomal RNA (rRNA) genes amplified by polymerase chain reaction (PCR). Quantitative PCR indicated the amount of bacterial DNA associated with each biopsy.

We studied 19 CD, 5 ulcerative colitis, and 22 IBD-free control patients. Biopsies from >90% of the patients contained *Streptococcus*, *Prevotella*, and *Veillonella* species, which comprised 13% of the gastric microbiota in CD patients and 5.5% in IBD-free controls (Fig 1). Five patients with active or severe CD and HNG (gastric inflammation) had the largest populations of *Veillonella*, which ranged from 19-36% of the gastric microbiota. If *Helicobacter*-negative gastritis and Crohn's disease are caused by a single, widespread organism able to establish large populations in the stomach, our study limits the candidates to three genera: *Streptococcus*, *Prevotella*, and *Veillonella*. Among these genera, only *Veillonella* species established larger populations, on average, in CD patients than in IBD-free controls. This trend was more pronounced among CD patients with the most severe IBD and gastritis.

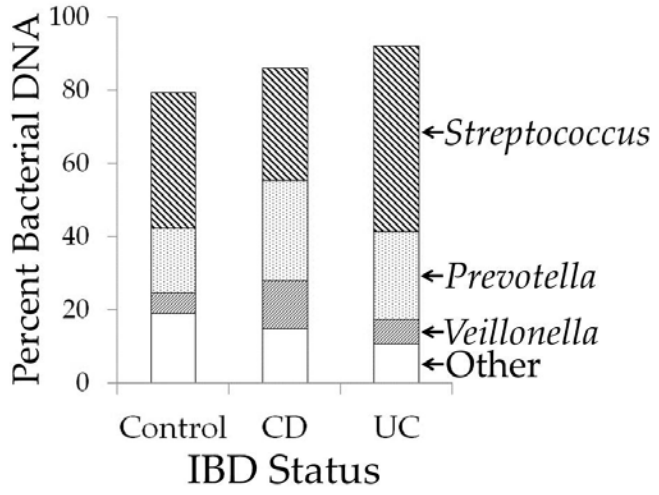


Figure 1. Relative abundance of bacterial 16S rDNA from the most common genera in gastric biopsies.

Patients with IBD had larger gastric bacterial populations, on average, than IBD-free controls (Fig. 2). This trend was more pronounced among IBD patients with chronic gastric inflammation. IBD-free patients with no gastric inflammation had the smallest gastric bacterial populations (with two exceptions). Inflammation in the stomach and colon frequently coincided with large gastric bacterial populations, which suggests that host factors may render CD patients susceptible to excessive bacterial growth in the stomach. Future studies should address the cause of this gastric bacterial overgrowth. The increased proportion of *Veillonella* species in the gastric microbiota of CD patients suggests that future studies should investigate the role of these species in *Helicobacter*-negative gastritis and Crohn's disease.

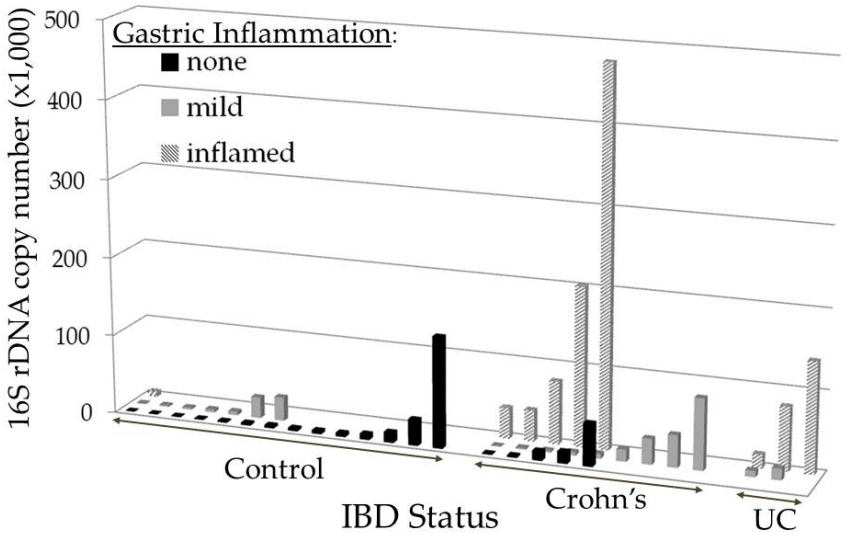


Figure 2. Gastric bacterial DNA copy number in IBD patients and controls with and without gastric inflammation. Numbers indicate copies (in thousands) of bacterial 16S rDNA contained in nucleic acids extracted from a single biopsy. Each bar represents an individual patient with chronic (hatched gray), mild (solid gray), or no (black) gastric inflammation. Patients are grouped by IBD status.

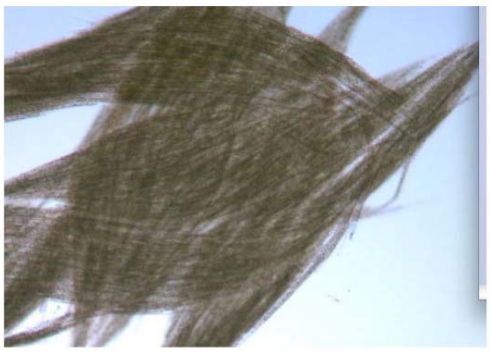
THEO DREHER LAB:

The Dreher lab is currently close to completing a two-year project investigating the toxigenic status of cyanobacterial blooms that occur in reservoirs in the Cascade foothills of the Willamette Valley. These blooms consist of genera that are potentially toxic, and occur in reservoirs that are either used as the direct source of drinking water (Dexter Reservoir/City of Lowell) or are upstream of municipal water intake sites (Dexter Reservoir/Springfield, Dorena Reservoir/Cottage Grove, Detroit Reservoir/Salem). The blooms are typically dominated by *Anabaena* and *Aphanizomenon,* which have been associated in the literature with the potential for accumulation of microcystin, anatoxin-a, saxitoxin and cylindrospermopsin cyanotoxins. Consequently, blooms containing more than 15,000 cells per ml of these genera trigger a requirement for weekly raw and finished water testing for the above four toxins (*Aphanizomenon flos-aquae* was recently exempted from this requirement). In view of the costs of such testing and the lack of evidence on the actual presence or absence of the toxins in Dexter Reservoir, the City of Lowell spearheaded an effort to determine the toxicity of Willamette Valley blooms, culminating in the grant funded by the State of Oregon.

After the first year of study, we have observed no measurable amounts of microcystin and anatoxin-a in water samples from the 2011 blooms in Dexter and Dorena Reservoirs, although there is some indication from genetic analyses that toxin genes are present at very low levels in the system. Initial indications are that the 2012 blooms have also not been associated with measurable toxin. If the results do indeed show no or very low toxin levels associated with blooms, a case can be made for considering the cyanobacteria causing these blooms as being non-toxigenic. Oregon Health Authority may then release the affected drinking water utilities from the full frequency of mandated toxin testing in view of the specific information on local bloom characteristics (a basal level of testing will always be advisable). This will rely on being able to identify the cyanobacteria that are considered locally as non-toxigenic. We are using polymerase chain reaction (PCR) and high-throughput next-generation sequencing of DNA sequences to identify the cyanobacterial bloom components.

For more information see:

Dreher, T.W. and Bozarth, C.S., Harmful Algal Blooms: What can genetic techniques reveal? Lakeline (North American Lake Management Society), Fall 2012, 12-16.



Anabaena (left) and *Aphanizomenon* (right) cyanobacterial colonies.

Cyanobacterial bloom sampling at Dexter Reservoir with portable field microscope.

MICROBIOLOGY STUDENT ASSOCIATION (MSA)

On Nov. 9-10, 2012, Dr. Linda Bruslind and Dr. Tasha Biesinger accompanied 27 undergraduate microbiology majors up to the University of Washington in Seattle, to attend the Northwest branch meeting of the American Society for Microbiology. The meeting started with a keynote speaker on Friday evening, Dr. Nancy Freitag, talking about the bacterium *Listeria monocytogenes*, followed by an opening reception. On Saturday there were talks all day from 8:30-5 pm, with one room for presentations about research and one room for presentations about clinical microbiology. Participants were allowed to move freely from one room to the other, based on interest. Linda and Tasha attended a lunch time gathering of undergraduate educators, with presentations on funding undergraduates projects using the internet ("Crowd Funding") and implementing research in the classroom. The group returned home to OSU around 11 pm on Saturday.

Here are impressions of the trip from two students:

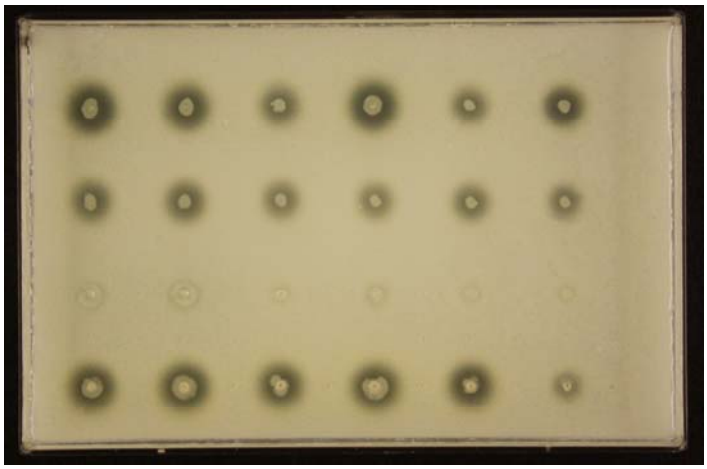
In November I was able to attend the American Society for Microbiology Northwest Conference in Seattle along with other Microbiology Student Association (MSA) members. During the two day conference, we were able to attend talks about the latest research being conducted in microbiology from around the country. The talks were split up into research and clinical microbiology sessions. Since both sessions were happening at the same time, we had the option to pick and choose the topics we wanted to attend. One of the graduate student presenters was Brett Mellbye, a fellow Beaver, who presented his ongoing work on quorum sensing in *Pseudomonas aeruginosa*. This was my favorite lecture because he explained his research with exceptional enthusiasm and clarity. This trip was more than just presentations on microbiology, as we were able to walk around the city of Seattle, spend time with fellow MSA members, and meet great people in this field. We were all very fortunate to have our advisors organize this trip; OSU had the most undergrad students attend this great experience! — Mukhdip Singh

On the weekend of November 9, 2012, the students of OSU's Microbiology Student Association traveled over 500 miles (both ways) to attend the American Society of Microbiology Northwest conference in Seattle, Washington. I truly enjoyed the conference because I felt that I gained so much from it. The research oral presentations reminded me why research is so exciting, while the clinical presentations showed me the type of person I want to become in my career. Out of all the talks, the one that stood out to me was the presentation of a forensic microbiologist. I enjoyed his talk because he ensured his audience understood what he was discussing without being condescending and he clearly illustrated how microbiology played a role in his work. I will never forget the awe I felt when he showed a picture of a heart infected with bacteria. Walking away from that presentation, I realized that when I graduate from Oregon State and enter into my career path, I want to be able to give a fun filled talk that captures the audience's attention - I want to give a presentation that is not only easy to understand, but ignites passion and excitement about the future. Overall, the trip was a great experience because whether it was bonding with other students, learning about the cutting edge research occurring in various areas of microbiology, or just enjoying the breathtaking view of Seattle, every student had something they took away from the trip. — Jessica Tran

MARTIN SCHUSTER LAB:

Powered by orange, talented graduate students, and NSF.

We work in the area of bacterial sociology. This young field of study explores how and why bacteria communicate and cooperate to perform important group behaviors such as infection and biofilm formation. We have been fortunate to expand our research in this field with a new three-year grant from the National Science Foundation awarded earlier this year. These funds also allowed me to take on two new, very talented graduate students, Kyle Asfahl and Joe Sexton, who joined our Microbiology program from Arkansas and Georgia, respectively. One of the senior Graduate students, Rashmi Gupta, in turn graduated in June and left the lab for a postdoctoral position with fellow department member Luiz Bermudez. Rashmi was the first Graduate student to join the lab since my arrival at OSU in 2006, and her contributions were instrumental in getting the lab up and running. Her productive work resulted in three first-author papers in respected scientific journals. Rashmi's commencement in Reser Stadium with Michelle Obama's inspirational keynote address was one of the highlights of the year.



Strains of the bacterium *Pseudomonas aeruginosa* displaying different levels of cooperation. The cooperative secretion of proteolytic enzymes breaks down skim milk in the growth medium, resulting in a zone of clearance around the bacterial colony. These enzymes are important virulence factors as they degrade human proteins during infection.

Forr more information, see:

Gupta R, Schuster M. (2012) Quorum sensing modulates colony morphology through alkyl quinolones in *Pseudomonas aeruginosa. BMC Microbiology* **12:**30**.**

KIMBERLY HALSEY LAB:

K. Halsey, M. Graus, and C. Thrash aboard the R/V Ronald H. Brown. Photo taken at the end of the ten day cruise that began at Boston Harbor and ended in Bermuda.

Kimberly Halsey (Assistant Professor, environmental microbiology) and Cameron Thrash (post-doctoral research, Steve Giovannoni Lab) participated in a research cruise during August, 2012, as part of a new NSF-sponsored program to study metabolism of volatile organic carbon compounds (VOCs) in the oceans. This new project is a collaboration between the Halsey and Giovannoni laboratories in the Microbiology Department and atmospheric physicists Joost DeGouw and Martin Graus at University of Colorado. The data collected during the cruise is still being analyzed, but using a proton transfer reaction mass spectrometer (PTRMS) and a newly designed experimental system, we have been able to measure the production of certain VOCs by phytoplankton and consumption by marine bacteria. Small volatile compounds (e.g., methanol, acetone, formaldehyde, and methyl chloride) are difficult to study using traditional methods and because of this, their importance in overall carbon cycling may be overlooked. The tip-off that these compounds might be rapidly cycled in the oceans was the unexpected predicted genomic capacity in abundant marine bacteria to utilize VOCs.

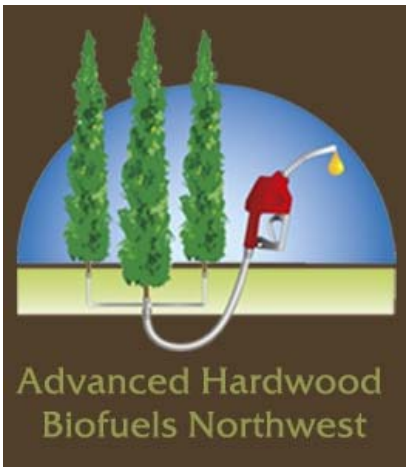
Dynamic stripping cells linked to the PTRMS for measurement of VOC metabolism in the oceans.

TASHA BIESINGER

Tasha Biesinger joined the department at the beginning of summer 2012 as our Instructor and Advisor responsible for teaching the MB 230 Introductory Microbiology lecture and lab, and MB 435/535 Pathogenic Microbes Lab. She hails from Salt Lake City, Utah, although she has also lived in Houston, TX, Heidelberg and Berlin, Germany, and in various parts of Russia. Virology has been the mainstay of her research throughout the years, with her graduate work focusing on pathogenicity factor of HIV. Some minor research done as undergraduate and post-graduate work included the cattle pathogen, Blue Tongue Virus and a (relatively) recently discovered ubiquitous human virus, Torque Teno Virus. While viruses will always hold the position of 'most amazing microbial group' in her heart, she will freely admit that bacteria are pretty darn amazing too, especially the pathogens. Tasha started working in June of this year and has very comfortably settled in to the community and looks forward to years of growth and improvement of curriculum delivery and supporting and advising our Microbiology students!

KATE FIELD LAB:

New Bioenergy Minor at OSU led by Microbiology Faculty Member



Dr. Kate Field, who usually does research on microbial water quality, can recently be found leading a new endeavor: the Bioenergy Minor. Field is a Co-PI on a grant funded by the National Institute of Food and Agriculture (NIFA) of the U.S. Department of Agriculture (USDA). The grant is titled "System For Advanced Biofuels Production From Woody Biomass In The Pacific Northwest" and, at $40 million, is the largest grant ever funded by the USDA. The project team comprises educators, researchers, and industries from throughout the Northwest, California and Colorado. The purpose of this very large grant (and others like it in different parts of the US) is to prepare the US to meet its biofuels goals (currently set at 36 billion gallons per year by 2022) and develop bioenergy into a viable industry capable of providing usable amounts of energy and employment. Meeting these goals could produce new jobs in a revitalized rural and agricultural economy, increase energy independence, and reduce global warming.

University and industry research partners on this project are concentrating on developing a sustainable biofuels industry using hybrid poplar as a feedstock. The goal is to generate liquid biofuels, including gasoline, diesel, and jet fuel, that are fully compatible with existing infrastructure. The target is to produce 400 million gallons of biofuel per year from 400,000 acres of hybrid poplar plantations around the Pacific Northwest. Hybrid poplar grows rapidly and sustainably and can be harvested on a 3-year rotation; it can be intercropped with other biomass crops. Using a conversion process based on microbial fermentation, facilities in Boardman, Oregon, can already convert biomass from poplar, alder, crop residues, and other sources to ethanol, acetone, and other products.

However, for the bioenergy industry to succeed, people in the region must be prepared for it. The goal of the education partners on this project is therefore to prepare an educated workforce capable of meeting bioenergy needs of the region well into the future. Dr. Field's team is developing high school, four-year college, and master's level Bioenergy curricula and programs. A team at the Agricultural Center of Excellence in Washington State is developing community college programs.

As a result of this project, OSU undergraduates can now minor in Bioenergy. The new Bioenergy Minor began in fall 2012 and is open to students in any major. The minor has already attracted students from majors as diverse as Chemical Engineering, Biological Engineering, Agricultural Business Management, Business, and Forestry. Coursework in the minor introduces core bioenergy concepts, regional bioenergy and regional issues, research and policy. Students undertake a research project of their choice with a research mentor. The minor provides competitive scholarships, internships, and funds to support student research in faculty or industry laboratories. Because of the very diverse team collaborating in the project, internship and research opportunities include such diverse areas as engineering, microbiology, business development, sociology, education, plant molecular genetics, and wildlife biology.

It is envisioned that the future will see diverse and decentralized implementation of microbial fermentation-based biofuel processes to produce energy products and help keep biowastes out of landfills. **More information on the USDA program and OSU's participation can be found at:**

http://agsci.oregonstate.edu/bioenergy/
http://ahb-nw.com/

JERRI BARTHOLOMEW LAB:

Research in the Bartholomew lab is centered around myxozoan parasites of salmon. We utilize long-term monitoring, and inter-disciplinary approaches to ask questions about disease dynamics and host-parasite interactions. Sascha Hallett is a scientist in the lab and this year published a 5-year monitoring study of *Ceratomyxa shasta* effects on salmon in the Klamath River, OR/CA. Seven lab members contributed to the manuscript, which tracked parasite density in water samples, and salmon mortality after exposure in the river. They found a difference in mortality-density thresholds for two salmon species: when exposed to ten *C. shasta spores,* Chinook reached a 40% mortality threshold, but coho salmon reached this threshold when exposed to only five spores.

In December, graduate student Michelle Jordan successfully defended her Master's thesis. Michelle obtained a dual M.S. in Microbiology and Water Resources Science. Her project focused on defining habitat for *Manayunkia speciosa* (the invertebrate host of *C. shasta*) in terms of variables that could be predicted by hydraulic models. A collaboration was forged with the U.S. Fish & Wildlife office in Arcata, CA, to develop the hydraulic models. The goal of the modeling is to determine whether manipulating river discharge could lessen the disease burden to fish by decreasing *Manayunkia speciosa* density. Post doctoral researcher Julie Alexander will continue this collaboration, completing additional sampling and data analysis.

Michelle sampling for Manayunkia speciosa in the Klamath River, CA.

Julie Alexander and USFWS-Arcata researchers sampling on the Klamath River, CA.

For more information, see:

Sascha L. Hallett, R. Adam Ray, Charlene N. Hurst, Richard A. Holt,Gerri R. Buckles, Stephen D. Atkinson, and Jerri L. Bartholomew. (2012). Appl. Environ. Microbiol. 78:3724-3731

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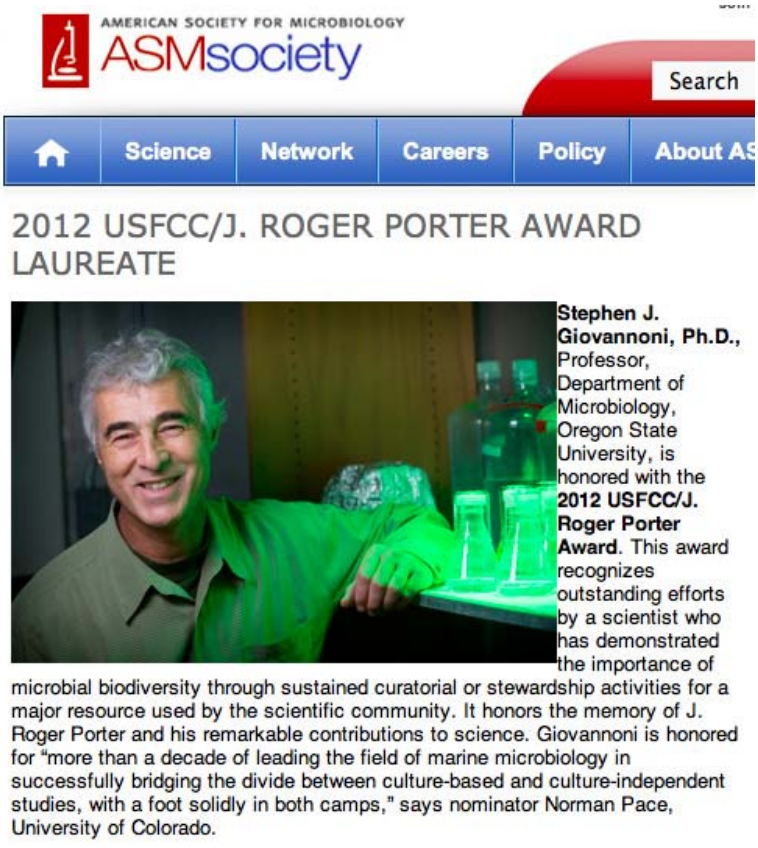

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2012 USFCC/J. ROGER PORTER AWARD LAUREATE

Stephen J. Giovannoni, Ph.D., Professor, Department of Microbiology, Oregon State University, is honored with the **2012 USFCC/J. Roger Porter Award**. This award recognizes outstanding efforts by a scientist who has demonstrated the importance of microbial biodiversity through sustained curatorial or stewardship activities for a major resource used by the scientific community. It honors the memory of J. Roger Porter and his remarkable contributions to science. Giovannoni is honored for "more than a decade of leading the field of marine microbiology in successfully bridging the divide between culture-based and culture-independent studies, with a foot solidly in both camps," says nominator Norman Pace, University of Colorado.