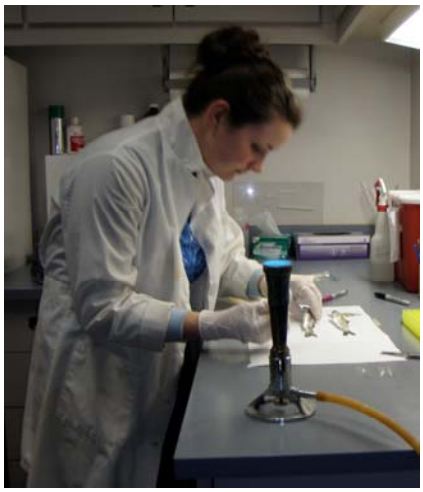
DEPARTMENT OF MICROBIOLOGY

December 2011

OBSERVE



WONDER

DISCOVER


# Research and Higher Education

Oregon State University OSU

# FROM THE CHAIR

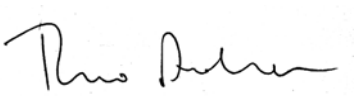
Greetings to all our friends of OSU Microbiology as we again reach the time of year that invites reflection on what the year has brought. It is wonderful to be able to report that 2012 at OSU has been a year filled with optimism and busy building. For Microbiology, we've added two new faculty through national searches in Environmental Microbiology and Prokaryotic Systems Biology: **Rebecca Vega Thurber** and **Kimberly Halsey**, who are introduced on the following pages. They are part of a cohort of almost 100 faculty joining OSU. As I mentioned last year, this rebuilding of faculty ranks has been made possible by enrolment increases to about 24,000 students, among whom are increasing numbers paying out-of-state tuition. This has buffered us against the continuing decline of state funds. This disinvestment is a nation-wide trend, but OSU is unusual in having sufficient alternative revenue sources to drive growth. As you can imagine, it feels great to be in this situation! Senior Instructor Linda Bruslind and myself have had the honor of serving on the Faculty Senate Executive Committee over the last two years, helping to advise the OSU administration on the most appropriate ways to manage the opportunities we find ourselves with.

There has also been busy building of the bricks and mortar type. Nash Hall has a new neighbor, the Linus Pauling Science Center, which houses part of the Chemistry Department, the Linus Pauling Institute and a new large auditorium. Renovation of the Nash Hall utilities is now complete, with new lighting, ventilation and paint throughout, and installation of a limited power back-up system. Cindy Fisher was a great help throughout the complicated sequence of moves necessitated by the floor-by-floor work that required vacation of each floor for 2-3 months (see her report on page 10). We were able to remodel Prof. Steve Giovannoni's lab on the second floor in concert with this general renovation of Nash Hall. A challenge for the coming years will be to obtain the funds to extend such remodeling to our other labs, which retain the original, 40-year-old benches and layout.

This year brought the departure of two faculty, Prof. Dennis Hruby and Instructor Stephanie Yarwood. Dr. Hruby, who had been half time at OSU for the last few years, is Chief Scientific Officer of SIGA Technologies at their research labs in Corvallis. He was an undergraduate in Microbiology at OSU and joined our faculty in 1983. For most of his 28 years in the department, Dr Hruby was continually funded by NIH for his work on Vaccinia virus, resulting in over 100 journal articles. He taught Virology. Dr. Yarwood served as Instructor/Advisor for the last 4 years, teaching mainly MB230 Introduction to Microbiology. She established a great rapport with the students in her class and with the students she supervised as teaching assistants in her lab classes. Dr. Yarwood has taken an Assistant Professor position at the University of Maryland.

I'm especially delighted to relay the news that two of our faculty were awarded special honors this year, while another was promoted with tenure. Prof. **Steve Giovannoni** was awarded the College of Science FA Gilfillan Memorial Award for Distinguished Scholarship in Science and the ASM Procter & Gamble Award in Applied and Environmental Microbiology for 2011. He presented a lecture on his work at the ASM meeting in New Orleans. In March, Prof. **Luiz Bermudez** was named OSU Distinguished Professor in recognition of his prolific studies on *Mycobacterium* and his general leadership at OSU. In May, Prof. **Martin Schuster** heard the good news from the Provost's office: promotion to Associate Professor with tenure. You can read about Dr. Schuster's research on page 5. He teaches Bacterial Pathogenesis, Biology of the Prokaryotes, and in the Molecular and Cellular Graduate Program. On the following pages, you will also find short reports of other activities in the Department, which I think you will find interesting.

***With best wishes for a happy, healthy and peaceful Holiday Season and 2012,***



Theo W. Dreher, Ph.D.

## BECKY VEGA THURBER LAB:

My lab's research uses interdisciplinary and high technology approaches to address questions about how viruses and microbes function in and affect the environment. Using a combination of empirical experimentation, field work, metagenomics, microscopy and molecular biology, my research provides important insight into a variety of fields including: virology, microbiology, coral reef ecology, animal physiology, and the evolution of symbioses.

**Viral Disease Ecology of Tropical Reefs.** Using microscopy and metagenomic techniques, we study how viruses are important in regulating many aspects of marine biology and oceanography. A majority of our studies focus on the isolation, identification, and evaluation of eukaryotic viruses associated with important marine species. Coral reefs are hotspots of biodiversity but are increasingly threatened by factors such as climate change, pollution, and overfishing. One effect of these combined stressors is that corals are more frequently suffering from diseases of unknown origin. By isolating the viruses from healthy and sick corals, we can begin to understand which viruses may contribute to disease and decline of these precious habitats. Currently we have several projects on the types of viruses associated with Caribbean, Hawaiian, and Indo-Pacific coral diseases and bleaching events. We also are evaluating the types and effects of viruses on the development, fecundity, and health state of several species corals from across the globe.

**Marine Phage Dynamics and Genomics.** In addition to eukaryotic viruses, we study the ecology of marine phages, the viruses that infect bacteria and archaea. Our lab investigates the types, roles, and abundances of phages in the sea. To do this we use next generation sequencing and bioinformatics to sequence, assemble, and annotate phage genomes that we have isolated from a habitat. Once annotated, we can infer various things about the phages, including their potential hosts and the effects on their host's physiology and ecology. Currently we are focusing our work on the phages associated with methane seeps off the Coast of Oregon and California.

**Roles of Marine Bacteria on the Degradation of Coastal Habitats.** Microscopic marine Bacteria, Archaea and Eukaryotes play pivotal roles in the oceans. On coral reefs microbes are responsible for continued remineralization of important nutrients and are also symbiotic members of corals themselves. As temperatures, nutrient concentrations, and top down pressures change, so does the structure and function of the microbial component of those environments. Such alterations maybe have negative effects on the community of benthic or aquatic animals and plants. A major focus in my lab is to understand how shifts in environmental parameters drive changes (structural and functional) in the microbial community and how these changes then cascade down to the function of that habitat. To do this, we perform on site (in the Florida Keys) experimental manipulations (herbivore abundance and inorganic nutrient concentrations) of reef habitats and then monitor the communities of microbes associated with corals and macroalgae.

**Influence of Predatory Bacteria on Marine Microbial Ecology.** The top down regulation of marine microbial communities is thought to be driven mostly by either phage lysis or consumption by eukaryotic predators. Bacteriovorax species are a unique group of predatory bacteria whose role in marine food web dynamics is often overlooked or ignored. We monitor the natural dynamics of these organisms in marine systems to better understand their biology and ecology. However we also use them as a model system to ask questions about predator-prey dynamics on surfaces in the ocean. To do this we cultivate several strains of Bacteriovorax and prey marine bacteria to conduct in lab experiments that mimic natural conditions in the environment.

# KIMBERLY HALSEY LAB:

## Environmental Microbiology, Phytoplankton Ecophysiology

**Research goal:**

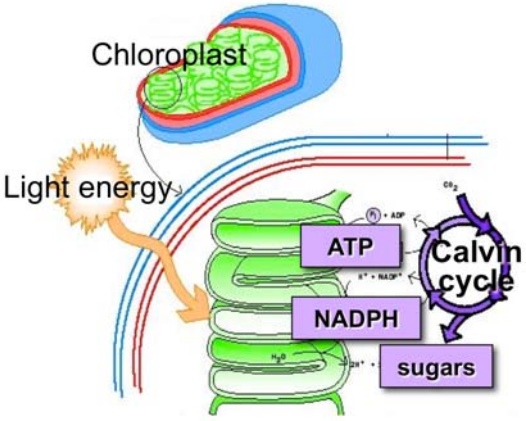
My research goal is to understand the processes that control the flow of carbon and energy through the marine carbon cycle. Phytoplankton are the primary conduit through which atmospheric $CO_2$ is converted to organic carbon in aquatic systems. Research in my lab will focus on how phytoplankton metabolism leading to net carbon accumulation changes in response to different environmental variables (i.e., nutrients and light). These metabolic strategies can then be used to improve global models of primary production.

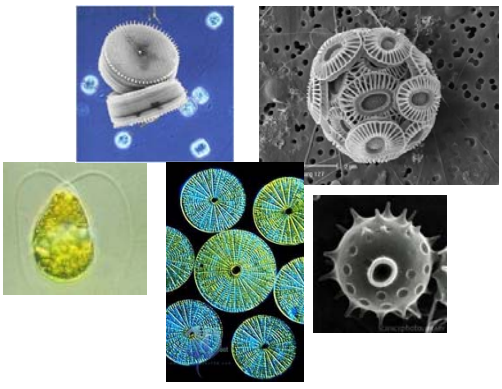
**Phytoplankton metabolism**

Phytoplankton are single celled microbes in the ocean that utilize light energy to fix atmospheric carbon dioxide into organic carbon and to produce energy for cellular growth. My recent research has demonstrated that that the energy derived from photosynthesis is allocated into metabolic sinks that vary between phytoplankton groups and with environmental conditions. However, phytoplankton growth efficiencies are remarkably conserved across phytoplankton groups, suggesting that models based on underlying principles of cellular energy economy may emerge.

**Growth optimization**

An NSF-funded project is underway to expand our understanding of photosynthate utilization to a range of taxonomic groups representing important representatives of marine phytoplankton communities: cyanobacteria, picoeukaryotes, diatoms, and larger chlorophytes. These studies generally utilize chemostat-grown cells to conduct a wide range of whole cell and biochemical analyses. We are also working to link our understanding of nutrient-driven metabolism to phases of the cell cycle and diel growth. These studies are guided by our recent findings that showed that shifts in photosynthate utilization function to balance cellular energetic availability with biosynthetic requirements.



## MICROBIOLOGY STUDENT ASSOCIATION (MSA)

There are a lot of wonderful things about being a microbiology student at Oregon State University: the people in the department, the fun upper-division classes, the close-knit community – but one of the best things about majoring in microbiology is the Microbiology Student Association (MSA), which brings all of these aspects together.

It's hard to imagine for me now, but fall term of freshman year I knew virtually no one in microbiology. Because there is a lot of lead-up to the good stuff (good stuff meaning, of course, the microbiology courses), most microbiology majors don't take any major-related classes until spring term of sophomore year. MSA is a way to get around that problem. By attending events, manning the microbiology booth at science nights and discovery days, and going on field trips, you can be included in the microbiology community at Oregon State even without taking classes. By the time I got to take all the classes I'd been looking forward to, I already knew a lot of the people in them and many of the professors who taught them.

That being said, the very best experience I had in MSA was going to New Orleans for the 111th American Society for Microbiology General Meeting. Our group was made up of five students and our advisor, Linda. Who got to go was decided by our involvement in MSA over the past years and our work in research labs. I couldn't believe my luck when I was one of the people who got picked – it would be my first time at a conference, and my first time in the south (a trip to Disney World when I was six notwithstanding). All of us were excited, and not just because we were sick of the Oregon weather.

If you've never been at a conference before it's hard to explain how overwhelming they are. I was a little stunned the entire time. Everywhere I went there were people who knew *a lot* about microbiology, whether they were in academia or the industry. I found I could ask anyone, "What work do you do?" and end up with a lesson's worth of information on their specialty. One woman working for a chemical company was trying to find alternatives to kill *Cryptosporidium*, a parasite I had been learning about in my parasitology class earlier that term. The conversation I had with her transformed *Cryptosporidium* from a case study in a class to a real problem plaguing people with pools in Florida. Furthermore, the talks I went to ranged from the up-close-and-personal stories of gut microbiota to the types of bacteria living in the open ocean. To say I learned a lot is an understatement. I was preaching to my roommates about the importance of eating yoghurt and non-greasy foods for months afterward.

All in all, being in MSA has livened up my experience as a microbiology major, both on campus and off campus. And it's not just us college kids who love it. One fond memory of a Science Night is of a young girl making a science bracelet and loudly proclaiming, "This is the best booth *ever*!" I heartily agree.

***-Valerie Mullen, Microbiology Undergraduate***

***Our group in New Orleans***
***Lacey Schultz, Alyssa Carey,***
***Elise Grellman, Linda Bruslind,***
***Valerie Mullen, Claire Glasgow***

**MSA trips to ASM conferences are in part funded by the generous donations of Sheila van Zandt, Class of 1959.**

# MARTIN SCHUSTER LAB:

## Many strains, one infection.

We work in the area of bacterial sociology. We are trying to understand how and why bacteria communicate to perform important cooperative behaviors such as infection and biofilm formation. This process of cell-cell communication is generally referred to as "quorum sensing". In one project, we characterized differences in the quorum-sensing ability of pathogenic *Pseudomonas aeruginosa* bacteria isolated from individual patients suffering from the genetic disorder cystic fibrosis. This study was performed by Cara Wilder, a former PhD student in my lab who graduated in April 2011 and is now a postdoctoral fellow at the University of Maryland. Her work, published in the professional journal *Infection and Immunity* barely two years ago, has already found its way into the classroom: It has been used by the authors of the new 2011 edition of our *MB430* textbook "*Bacterial Pathogenesis: a Molecular Approach*" to illustrate the heterogeneity of strain phenotypes in an infection .

***Cara Wilder***

**BOX 19–3 The Broader View—*P. aeruginosa* Variation**

Most accounts of infections read as if a single strain with a given repertoire of characteristics is responsible for the infection. A recent study of the diversity of strain phenotypes of *P. aeruginosa* in an actual infection produced a surprising finding that challenges the one strain-one phenotype paradigm. The study looked at the phenotypes of 9 to 12 isolates each from the lungs of eight different adult cystic fibrosis patients. The characterization of the isolates focused on quorum-sensing regulators, which have been thought to play a key role in biofilm formation in the cystic fibrosis lung and thus in the pathogenesis of *P. aeruginosa* infections in cystic fibrosis patients. The investigators found a wide range of quorum-sensing phenotypes, from completely inactive alleles of some regulatory genes to completely active ones. This type of variation was seen not only between different patients, but also within the same patient.

The authors stated, "Conclusions about the properties of *P. aeruginosa* QS [quorum-sensing] populations in individual CF [cystic fibrosis] infections cannot be drawn from the characterization of one or a few selected isolates." Perhaps more striking was the implication that there was not a strong selection for maintenance of the functions of regulatory proteins responsible for the control of different quorum-sensing response systems. These results suggest that a broader view of the complexity of different phenotypes that can be sustained in the same lung environment is needed. It will be interesting to see if the same type of functional variation is found in other "essential" virulence factors, such as adhesins, exotoxins, and proteases.

*Source:* C. N. Wilder, G. Allada, and M. Schuster. 2009. Instantaneous within-patient diversity of *Pseudomonas aeruginosa* quorum-sensing populations from cystic fibrosis lung infections. *Infect. Immun.* 77:5631–5639.

***Brett Mellbye***

## Bacterial resistance to novel drugs: it matters to be social.

In this work, conducted by third-year Graduate student Brett Mellbye, we applied concepts from microbial social evolution to antivirulence drug resistance. Antivirulence drugs have taken center stage in the search for novel antimicrobials. They differ from traditional antibiotics in that they target bacterial virulence rather than growth *per se*. This property is thought to alleviate the considerable problem of drug resistance, although there is currently no evidence to support this notion. We investigated how bacterial social interactions would influence the resistance of pathogens to antivirulence drugs that target cooperative behaviors such as the production of shared extracellular enzymes and toxins. We predicted that social cheating by a drug-sensitive majority would delay population growth and prevent enrichment of drug-resistant cells. In the bacterial world, cheaters are individual cells that do not contribute but reap the benefits of the production of extracellular factors by others, thereby gaining a competitive advantage. We supported our hypothesis by proof-of-principle co-culturing experiments, using *Pseudomonas aeruginosa* as a model. This work challenges our current thinking about the efficacy of antivirulence strategies and highlights the potential of cooperative behaviors as novel drug targets. To read more: Mellbye, B.L. and Schuster, M. (2011) The sociomicrobiology of antivirulence drug resistance: a proof of concept. *MBio*, in press.

## BRUCE GELLER LAB:

As we all have heard, resistance to antibiotics is increasing at an alarming rate. Every week there is an article in a newspaper or magazine about super-bacteria that can't be cured with antibiotics anymore. The problem is that genes for resistance to antibiotics are being shared among bacteria. This sharing is not limited to inheritance of genes, where one bacterial cell passes its genes to its offspring. Genes are being passed from one species of bacteria to another. Compounding the problem is the fact that pharmaceutical companies are not discovering new antibiotics fast enough to keep ahead of the spreading resistance.

I've taken a different approach to solving the problem. Instead of the traditional strategy of screening thousands of samples or chemicals to find one new antibiotic, I have designed synthetic DNA-like molecules that kill bacteria by interfering with specific genes that are essential for growth of bacteria. I'm working closely with a small pharmaceutical company in Corvallis, AVI BioPharma, which developed the chemistry required to synthesize the DNA-like molecules that I use.

Ten years ago when I first tested the DNA-like compounds, which are called PMOs, they were ineffective. The reason for this is that they don't cross the outer membrane of Gram-negative bacteria such as *E. coli* and *Salmonella*. Fortunately, we were able to attach a membrane-penetrating peptide to the end of the PMO. After years of experimentation, we now have peptide-PMOs (PPMOs) that are as potent as most standard antibiotics, such as tetracycline and ampicillin.

We are now in the animal testing stage of developing PPMOs against two highly antibiotic-resistant respiratory pathogens: *Burkholderia cepacia* complex and *Acinetobacter baumannii*. *B. cepacia* complex infects the lungs of immune-suppressed patients and those with cystic fibrosis. *A. baumannii* is one of the leading causes of hospital-acquired, respiratory-associated pneumonia.

We recently reported that one of our PPMOs is highly effective in reducing infection of a highly antibiotic-resistant strain of *B. cepacia* complex in mice (Greenberg et al., 2010. J. Infect. Dis. 201:1822). In addition, we have found that a single, daily dose of 5 micrograms of PPMO can significantly increase survival of mice with acinetobacter pneumonia (see survival graph below). This low dose would translate to about 25 milligrams for a human, which is about 10 times less than what is typically given for a standard antibiotic. Because the dose is low, side effects should be minimal. Our goal is to file a new drug application with the Food and Drug Administration by 2013, which would then allow us to test the PPMOs in humans.

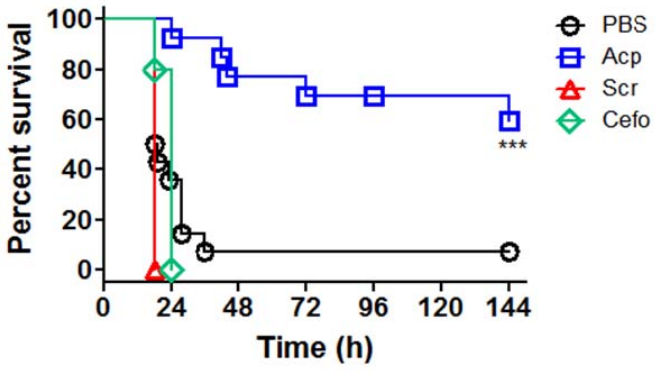



Figure 1. Mice were infected intranasally with *A. baumannii* 17976 and treated intranasally once daily with 5 μg (RXR)4-AcpP, (RXR)4-Scrambled control, or saline, or intraperitoneally with 2 mg

## MAHFUZ SARKER LAB:

### *Clostridium* spores are infectious morphotype

*Clostridium* species are important anaerobic, Gram-positive, spore-forming, enteric bacterial pathogens. *Clostridium* dormant spores are highly resistant to heat and other environmental insults, and can survive for long periods in the environment. Once conditions are favorable, these spores undergo germination, an irreversible process by which a dormant spore is transformed into a metabolically active cell. These *Clostridium* cells then produce toxins and cause disease in humans and animals. One approach to develop efficient therapies against clostridial diseases is to block or induce spore germination. Blocking spore germination would block the resumption of growing vegetative cells, while inducing germination would yield spores that have lost their resistance properties and thus becoming more sensitive to inactivation by milder treatments.

Sarker lab has been working on many important research avenues such as, i) molecular mechanisms of spore germination; ii) developing spore inactivation strategies; and iii) molecular mechanism of spore-host interactions.

Besides nutrient germinants, host-specific factors also play important roles in spore germination. Indeed, in a recent study with *Bacillus anthracis*, it has been shown that anthrax spores lacking all spore cortex lytic enzymes (CLEs) are able to germinate *in vitro* with whole blood and serum despite their lack of germination in nutrient-rich media, suggesting that host-specific enzymes with peptidoglycan (PG) hydrolyzing activity might be involved in spore germination *in vivo*. Consequently, in our study we have found that the main germinant receptors are not required for *C. perfringens* spore germination in blood due to the presence of a host serum germination factor with PG hydrolyzing activity (most likely lysozyme) that triggers significant germination by directly degrading the spore's PG cortex.

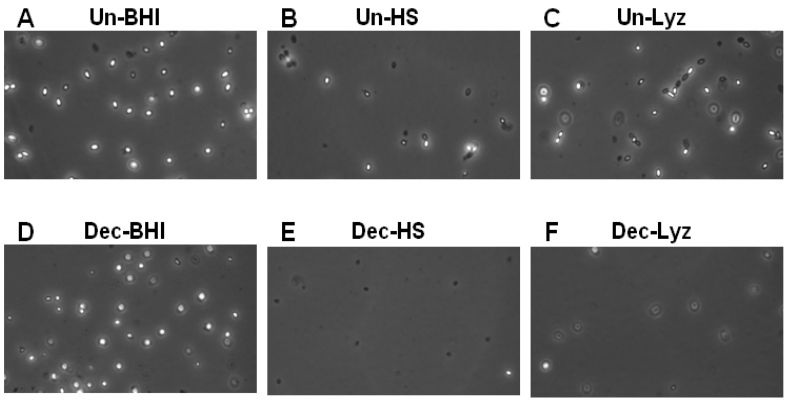



**Fig. 1. Human serum increases germination of decoated *C. perfringens* spores lacking CLEs.** Untreated (A, B, and C) and decoated (D, E, and F) spores of strain DPS117 (Δ*cspB*) were heat-activated and incubated at 37ºC for 5 h in BHI broth (A and D), human serum (B and E) and 1 µg/ml lysozyme (C and F) and then photographed under phase-contrast microscope.

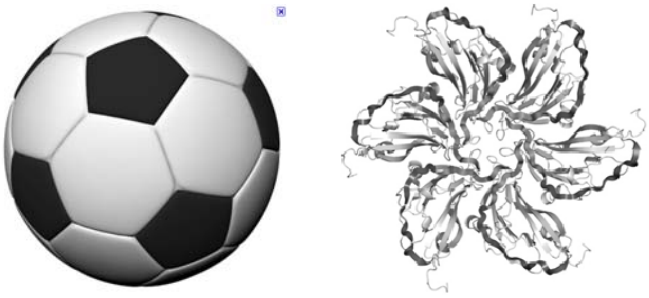
Also, host factors derived from intestinal epithelial cells can trigger germination of bacterial spores, as germination of *Bacillus cereus* spores induced in cultured enterocytes through the *gerA*-type germination receptors. Consequently, we have investigated the germination response of *C. perfringens* and *C. difficile* spores upon incubation with three different (CaCo-2, HeLa and HT-19) cultured human epithelial cell lines. Our results show that spore germination response is induced by epithelial cells and varies between spores of surveyed *Clostridium* species and strains.

Collectively, our recent findings might well have implications in understanding the mechanism of clostridial spore germination *in vivo*.

To read more: 1) Paredes-Sabja D, and M. R. Sarker. 2011. Host serum factor triggers germination of *Clostridium perfringens* spores lacking the cortex hydrolysis machinery. J. Med. Microbiol. 2011 Jul 28. [Epub ahead of print]. 2) Paredes-Sabja, D. and M. R. Sarker. 2011. Germination response of spores of the pathogenic bacterium *Clostridium perfringens* and *Clostridium difficile* to cultured human epithelial cells. Anaerobe. 17: 78-84.

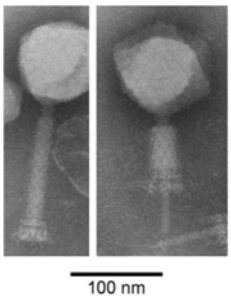
## THEO DREHER LAB:

Research in the Dreher lab for much of the last two decades has focused on the plant-infecting positive strand RNA virus Turnip yellow mosaic virus (TYMV). Our most recent paper describing the work of grad student Josh Powell assesses the role of the first few amino acids of the viral coat protein (CP). The spherical TYMV virions are formed by 180 copies of the CP encasing the genomic RNA; as in a soccer ball, the CP molecules in the virion are arranged in subgroups that form pentamers and hexamers. Crystal structures have shown that the first few amino acids link to form a circular chain to stabilize the hexamer (see middle of figure). It has been hypothesized that these amino acids constitute a conformational switch that can form the circle (leading to hexamers) or not (leading to pentamers), and would thus be essential in the formation of virions. Josh showed that amino acids could be removed from the N-terminus of the CP and still allow infection in Chinese cabbage plants, producing virions with normal morphology. Thus, the switch hypothesis is not correct, but this part of the CP is important because the mutant virions were less stable and more porous, providing poorer protection for the genome between infections. We are using X-ray crystallography with mutant CPs to learn more about the role of this part of the CP. To read more: *Turnip yellow mosaic virus forms infectious particles without the native beta-annulus structure and flexible coat protein N-terminus.* JD Powell, E Babar and TW Dreher, 2011, Virology, in press.



These days it has become well recognized that bacteriophages are the most abundant life form present throughout the environment at a count of more than 10 times higher than that of bacterial cells. Phages are killers of their hosts, and as such are important in nutrient recycling and in shaping microbial communities. Dick Morita from this department was one of the first to recognize the prevalence and importance of phage with his 1979 paper: *Evidence by electron micrographs for a high incidence of bacteriophage particles in the waters of Yaquina Bay, Oregon: ecological and taxonomical implications.*Torrella F, Morita RY, *Appl Environ Microbiol.* 37:774-8.

To date, phages in marine systems have been quite intensively studied, whereas there has been little work in freshwater systems. The Dreher lab recently isolated a phage from the middle and upper reaches of the Klamath River that infects a freshwater strain of *Synechococcus*. The phage, S-CRM01, is a member of the myovirus family of phages related to the well-studied T4 phage that infects *E. coli*. Myophages are widespread and abundant, and have among the most architecturally complex virions (see picture). We determined the sequence of the 179,000 bp double-stranded DNA genome and performed a detailed annotation of its gene content. This phage is a close relative of a group of over a dozen marine cyanomyophages that infect *Synechococcus* and/or *Prochlorococcus*, two abundant planktonic marine cyanobacteria. However, it is also the most distinct of this group of phages. These relationships indicate that freshwater and marine phage populations share a common gene pool but that there is also significant isolation between the two environments. Amazingly, the genome includes 33 transfer RNA genes, including one for each of the 20 amino acids that ribosomes assemble into proteins (although no initiator tRNA gene). This number of tRNA genes is greater than in some bacterial genomes!




To read more: *A freshwater cyanophage whose genome indicates close relationships to photosynthetic marine cyanomyophages.* TW Dreher et al., 2011, Environ. Microbiol. 13:1858-74.

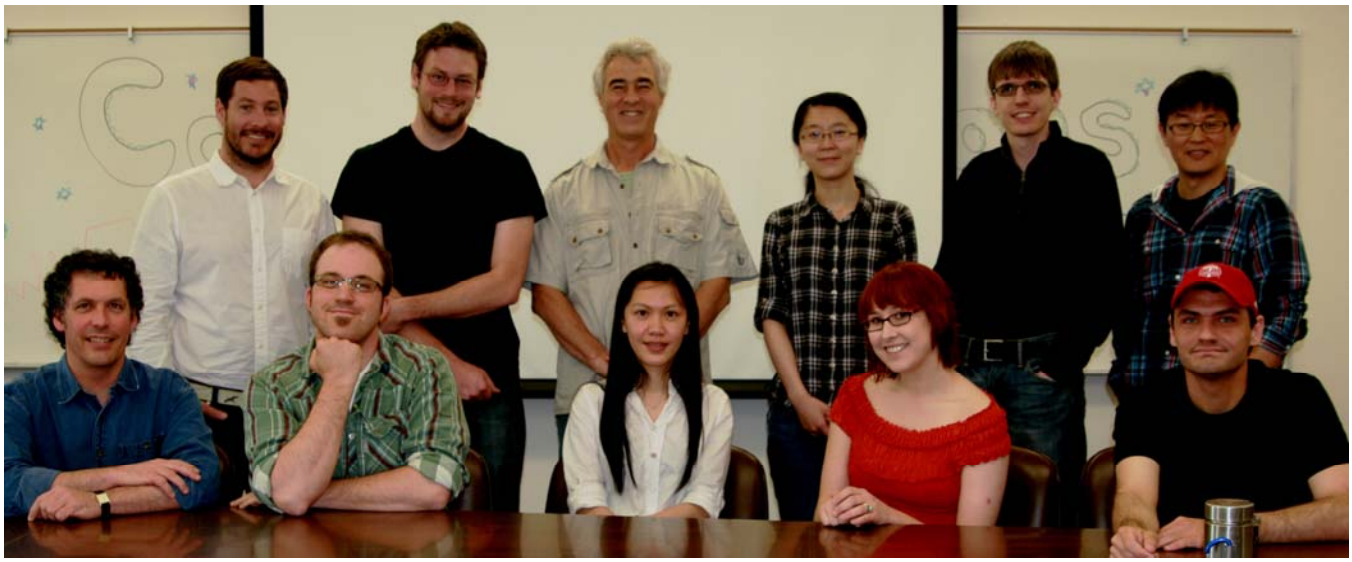
## STEPHEN GIOVANNONI LAB:

My research group happily returned in June to remodeled labs thanks to the combined efforts of Theo Dreher, Cindy Fisher, and Sherman Bloomer, Dean of the College of Science and Sonny Ramaswamy, Dean of the College of Agricultural Sciences. Among the many benefits are reduced equipment noise in rooms where students have their desks, and a reduction of contamination in environmental rooms, which now have HEPA filtered air. Many of our oligotrophic bacterial cultures, like SAR11, divide only once a day and plateau at low final cell densities, requiring large volumes. These factors made contamination a big issue. The renovated lab will house a microfluidic workstation now being constructed by Microbiology graduate student Zack Landry. In collaboration with Stephen Quake's group at Stanford, Zack is developing single genome amplification procedures to obtain genome sequences from bacterioplankton we can't culture.

We've been particularly pleased this year to have distinguished Korean Professor Jang Cheon Cho from Inha University visiting us on sabbatical. Dr. Cho, a former postdoc of the lab, is one of the world's leading scientists culturing marine bacteria. Also joining us this year are postdocs Yanlin Zhao, from the People's Republic of China, and Ben Temperton, from Plymouth Marine Labs, U.K. Prominent scientists have suggested that SAR11 cells attained their extraordinary successes by becoming generally resistant to phage predation. They'll find little support from Yanlin, who is now studying three SAR11 phages in culture. One of them efficiently inserts as a prophage at an integration site located in conserved residues of leucine tRNA genes.

One of the most interesting stories to emerge from our research group this year was a phylogenomic study by Cameron Thrash that examined the origins of mitochondria. Parasitic bacteria in the Rickettsiales had long been suspected as the origin of mitochondria, but Cameron found that new data provide more support for a SAR11 origin of mitochondria. The debate is not over and we can expect a flurry of papers on this controversial subject.

To read the paper: J. Cameron Thrash, Alex Boyd, Megan J. Huggett, Jana Grote, Paul Carini, Ryan J. Yoder, Barbara Robbertse, Joseph W. Spatafora, Michael S. Rappé, & Stephen J. Giovannoni. Phylogenomic evidence for a common ancestor of mitochondria and the SAR11 clade. 2011. Scientific Reports 1:doi:10.1038/srep00013



**GIOVANNONI LAB**

Back row, l to r, Dr. Cameron Thrash, Zachary Landry, Dr. Stephen Giovannoni, Jing Sun, Dan Smith, Dr. Jang-Cheon Cho,

Front row, l to r, Kevin Vergin, Paul Carini, Dr. Yanlin Zhao, Amy Carter, Tony Bertagnolli

# NASH HALL CONSTRUCTION COMPLETED

2012 will usher in a new era for Nash Hall; one without major construction. Over the past six years, the building infrastructure has been brought into the 21st century. The extensive list of improvements include a new energy efficient HVAC, (heating, ventilation, air conditioning) system, new chemical fume hoods in each major lab, updated constant temperature systems for the walk-in incubator rooms, coolers and freezers of the building, an emergency generator, three new sterilizers and a new reverse osmosis water system. In addition to the infrastructure upgrades to the building, safety has also been enhanced with the addition of a building wide fire sprinkler system and a seismic upgrade. Lastly, architectural and functionality improvements were made to the interior and exterior of the building with fresh paint and an updated color scheme; new lighting, windows and blinds; exterior landscaping and a covered bike area on the north side of the building.

## Giovannoni Lab Renovation

While most research groups were only displaced from their laboratory and office space for three months during the recent HVAC construction, the Giovannoni lab group spent ten months in temporary lab space so their two laboratories and incubator rooms on the second floor could be renovated.

The wish list included more bench space within their laboratories, separate noisy equipment from the main labs and reduce the mold contamination problems in their incubator rooms. The renovated spaces feature new standard height cabinets and countertops that replaced the low bench space in the middle of each lab. New upper cabinets with glass doors replaced open shelving over the new and original base cabinetry. The remaining original cabinets were refinished to match the new cabinets in both labs. Glassware preparation activities and ultra cold freezers are now housed in a separate room within one of the main laboratories. Low temperature incubator rooms are equipped with new HEPA filters, washable walls and ceilings, new compressors to control the temperature and programmable digital controls.

The group moved back into their labs in August and is now settled into their new space.

***Before***

***After***

# MICHAEL KENT LAB:

## Research on Diseases of Zebrafish in the Department of Microbiology

The zebrafish (*Danio rerio*) has long been a popular aquarium fish. The use of aquatic animals as models in biomedical research has dramatically increased in the last decade, largely led by the exploitation of the zebrafish (*Danio rerio*) model. The ZFIN web site (**http://zfin.org**) lists about 5,000 researchers and over 700 laboratories that use the zebrafish. As with any laboratory animal, it is important that research subjects be free of diseases and pathogens. Of course virulent pathogens that cause high mortality are a concern, but pathogens in research animals that may not cause overt disease are also important. These subclinical infections are often associated with non protocol induced variation, and thus may compromise research. This is a major focus of Dr. Michael Kent's research in the Department of Microbiology.

The National Center for Research Resources (NCRR) at the NIH has funded Dr. Kent since he arrived at OSU in 1999 to study diseases of zebrafish, and they fund an R24 grant to Dr. Kent to study the two most common diseases in zebrafish, mycobacteriosis and microsporidiosis (Figure 1). Drs. Luiz Bermudez (Microbiology and Biomedical Sciences) and Robert Tanguay (Environmental and Molecular Biology) here at OSU are co-investigators with Dr. Kent on this grant. These two chronic diseases are extremely prevalent in zebrafish research facilities, and Dr. Kent and colleagues are investigating their pathogenesis and modes of transmission. The same species of *Mycobacterium* that cause mycobacteriosis in zebrafish infect humans, and the zebrafish has already proven to be a useful surrogate model to study tuberculosis. Research with live fish with *Mycobacterium* infections is conducted in our BSL-2 (Biosafety Level 2) laboratory on the 5th floor in Nash Hall, as all of these bacteria are potential human pathogens (Figure 2). Dr. Kerry McPhail (College of Pharmacy) will soon use this lab to conduct drug screening for novel agents against *Mycobacterium* infections using the zebrafish model.

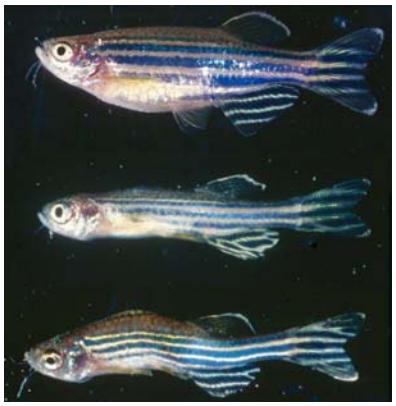


Figure 1. Healthy zebrafish (top) with two fish infected with the microsporidium *Pseudoloma neurophilia*. These fish show emaciation and skeletal deformities, two changes frequently seen in infected fish.

The NCRR also funds a unique training grant, overseen by Drs. Tanguay and Kent, to train veterinarians in research using aquatic species (**http://ehsc.oregonstate.edu/ncrr**). Several faculty in the Department and other units at OSU are involved, and presently two veterinarian post-doctoral fellows in this program are pursuing graduate degrees in the Microbiology Graduate Program. Dr. Trace Peterson is working with Dr. Kent on transmission of *Mycobacterium* spp., and Dr. Aimee Reed is working with Dr. Ling Jin (Biomedical Sciences) on fish viruses.

Drs. Tanguay and Kent and their laboratories staff have recently developed the only SPF (Specific Pathogen Free) zebrafish laboratory in the country, housed at the Sinhubber Aquatic Resource Laboratory (SARL) (**http://ehsc.oregonstate.edu/SARL**). Fish are SPF for the microsporidium parasite *Pseudoloma neurophilia*, the most common pathogen of zebrafish, which has been observed in more than 50% of research facilities. We discovered that the parasite is maternally transmitted, and we often see the parasite within fish eggs. Therefore, we developed this SPF lab by screening broodfish and their progeny with molecular diagnostic tests developed in the Kent lab. Thousands of these fish have been provided to OSU researchers. We are now selling these fish to the research community, and have distributed SPF fish to 12 other universities (**http://ehsc.oregonstate.edu/orderzebrafish**). Working with Dr. Kent, the OSU Veterinary Diagnostic Service (VDL) (**http://oregonstate.edu/vetmed/diagnostic**) now provides a molecular diagnostic test for *P. neurophilia* to the research community. Dr. Kent also works closely with VDL staff on diagnostics of other diseases in zebrafish and other fish species.

Dr. Kent also a Co-Principal Investigator with the NIH Zebrafish International Resource Center (ZIRC), University of Oregon (**http://zebrafish.org/zirc/home/guide.php**). This large center provides mutant lines of zebrafish around the world, and also provides a diagnostic service to the research community. Here he works closely with the ZIRC veterinarian, Dr. Katy Murray (a graduate from OSU College of Veterinary Medicine), where he provides assistance with diagnostic evaluations and consolations on other fish health issues.

***Our BSL-2 zebrafish facility in the Department of Microbiology. From left to right: Dr. Michael Kent, Justin Sanders (PhD student), Dr. Trace Peterson (DVM), and Benjaporn Somridhivej (PhD student).***

## Microbiology Faculty Member Awarded $4.4 million for Bioenergy Education and Scholarships

**Kate Field,** Associate Professor of Microbiology, heads a new OSU program in Bioenergy Education. OSU has been awarded $4.4 million for a Bioenergy education program, funded by the Agriculture and Food Research Initiative (AFRI) of the USDA. Field's experience directing BioResource Research, OSU's biosciences research major, gave her the ideas for the grant proposal. She reports that the education grant is part of a $40 million dollar Regional Coordinated Agricultural Project involving collaboration between Bioenergy industries, regional universities, and extension services. "The goal of the entire project is to prepare the Pacific Northwest to meet regional bioenergy goals using regionally-appropriate woody energy crops. OSU will use the money for scholarships and interdisciplinary courses and programs at the pre-college, bachelor's and master's levels."

Field will establish research-based undergraduate, master's, and high school enrichment programs at OSU. Microbiology undergraduates, for example, will be able to earn a Minor in Bioenergy while majoring in Microbiology or another major in the colleges of Agricultural Science, Forestry, Engineering, Business, Science, or Education. Bioenergy Minor students will participate in Bioenergy research projects, working with regional Bioenergy research, extension and industry partners. Generous scholarships include $1000 (per year) awards as well as full-tuition scholarships, and additional funding is available to support undergraduate research and internships.

Field anticipates that OSU will start admitting students to the new Bioenergy minor, and awarding scholarships, next winter, to start in fall term 2012.

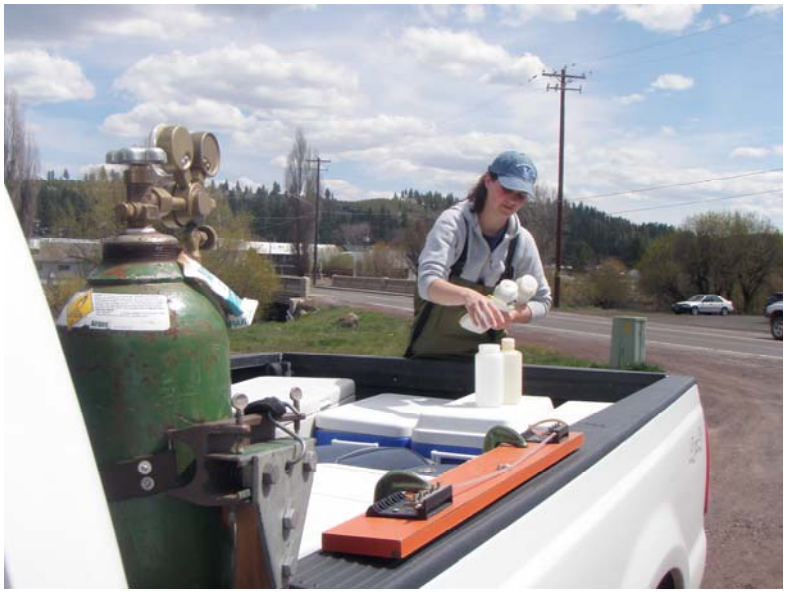
## JERRI BARTHOLOMEW LAB:

Research in my laboratory continues to focus on myxozoan disease in salmon and host-parasite interactions using that model; however, we recently entered into collaboration with Dr. Oriol Sunyer, University of Pennsylvania, whose research uses rainbow trout as a model for understanding the human immune system. Initial studies in our laboratory were conducted by Sarah Bjork, a former graduate student. By using trout that survived infections with the intestinal myxozoan parasite, *Ceratomyxa shasta*, Sarah aided in the discovery that a novel antibody in fish, IgT, plays a role in mucosal immunity and may be used as a parallel model for human mucosal antibodies (Zhang et al., 2010). Sarah received her PhD in 2010 and now works for the Oregon Department of Fish and Wildlife as a microbiologist.

***Charlene Hurst, Ph.D. student***

Recently, PhD student Charlene Hurst, began working with the U. Penn. group and incorporated some of her own research interests into the project. The focus of her research is in understanding the host-parasite interaction dynamics between *C. shasta* and the rainbow trout host. One goal of her research is to further knowledge about the functional role of IgT; specifically whether this antibody can protect fish from future infections with *C. shasta*. Charlene is also interested in understanding how the host responds to different infection scenarios. In the wild, fish become infected with multiple parasite strains, but typically only one strain causes mortality. We are interested in whether the order and number of strains infecting a host can alter disease progression. If infection with an avirulent parasite strain protects the fish from disease caused by a more virulent parasite strain, this could be the basis for a natural vaccination strategy.

Zhang, Y., I. Salinas, J. Li, D. Parra, S. Bjork, Z. Xu, S. E. Lapatra, J. Bartholomew and O. Sunyer. 2010. IgT, a primitive immunoglobulin class specialized in mucosal immunity. *Nature Immunology* 11: 827-835.



**Department of Microbiology**
**Oregon State University**
**220 Nash Hall**
**Corvallis, OR 97331-3804**

# PETER BOTTOMLEY LAB:

## After >100y a major paradigm shift occurs even in soil microbiology!

As many of you will recall, microbiology emerged as an experimental science in the late 19th century, driven by the perils of infectious agents, microbial contamination of water supplies, and food and beverage spoilage. At the same time, agricultural scientists were worried that food production would be outstripped by the rapid expansion of the human population. During this period, microbiologists began to explore the role of microbes in enhancing soil fertility by releasing essential plant nutrients from composts and manures. Some of you might remember the name of the Russian microbiologist, Sergei Winogradskyi, who isolated the soil bacteria that we refer to as "nitrifiers". These bacteria are classified as *chemolithoautotrophic* because they extract energy from the oxidation of either ammonium or nitrite salts to nitrate salts, and obtain all of their carbon requirements for growth from carbon dioxide. They are the "gate keepers" of the nitrogen cycle and influence the efficiency with which N fertilizer is converted to nitrates and consumed by agricultural crops.

For over 100 years we were convinced that the process of ammonia oxidation was carried out by a few well-characterized species of bacteria. However, about 6y ago, the world of environmental microbiology was shaken by the discovery of ammonia oxidizing archaea (AOA), which are radically different microorganisms from the ammonia oxidizing bacteria (AOB). However, we had no idea when and where the AOA contributed to soil nitrification, or if their contribution was influenced by the soil type, plant community, or specific environmental conditions. My colleagues and I have developed an assay that allows us to measure the relative contributions of these two distinct types of microorganisms to soil nitrification. We have investigated a number of different soils throughout Oregon and shown that AOA dominate ammonia oxidizing activity in pasture soils, and in some coastal forest soils of very low pH <4. In cropped soils, however, we have found that whereas both AOA and AOB contribute to ammonia oxidation throughout the year, AOA are dominant during the fall and winter months, and AOB increase their contributions as the soils warm during the spring and especially after the addition of N fertilizer. From our research we hope to get a better understanding of what regulates the contributions of AOB and AOA to soil nitrification, and determine if these shifts affect the efficiency of N fertilizer use during crop production.

**Suggested reading.**

Taylor, A.E., L.H. Zeglin, S. Dooley, D.D. Myrold, and P.J. Bottomley. (2010) Applied and Environmental Microbiology, 76: 7691-7698.