BacPath 11, Molecular Analysis of Bacterial Pathogens Conference Wyong, NSW, 25–28 September 2011

The 11th biennial Molecular Analysis of Bacterial Pathogens Conference (BacPath 11) was held 25–28 September 2011 at the Mercure Kooindah Waters Resort in Wyong, NSW. The meeting attracted 121 attendees, 100 of whom were ASM members, coming from all states.

As is traditional for BacPath Meetings, speakers were selected from amongst abstracts submitted by PhD students and early career researchers. The standard of talks was again notably high and very diverse, covering topics within the fields of virulence, persistence and resistance. The poster sessions were held in the evenings and this allowed everyone to peruse a total of 69 posters on a very broad variety of topics. Thanks to the generosity of sponsors, a number of seminar and poster prizes were on offer to research students and early career researchers. The judges had a particularly tough job adjudicating these due to the large number of high-quality presentations. Kate Mackin (Monash University) and Kathryn Holt (University of Melbourne) took out the student and postdoc seminar awards, respectively, and Min Yan Teh (University of Adelaide) and Tim Barnett (University of Queensland) won the corresponding poster prizes.

Invited speaker presentations were a highlight.

Andrew Camilli from Tufts University School of Medicine and Howard Hughes Medical Institute, Boston, USA, spoke on the transition of *Vibrio cholerae* into and out of the host. He

described fascinating hierarchical gene expression patterns over the course of infection of the small intestine, including early changes that are modulated by the second messenger cyclic diguanylate, and late changes that prepare *V. cholerae* for dissemination and transmission. The success of *V. cholerae* as a pathogen in causing devastating epidemic and pandemic cholera seems to lie in the successful transition between the aquatic environment where it normally resides and the accidental human host. His talk also covered vaccine development. Using naturally produced outer membrane vesicles as a mucosal vaccine, he showed that an effective LPS-based vaccine appears to work by inhibiting bacterial motility through mucosal antibodies.

Richard Brennan from Duke University School of Medicine, Durham, USA outlined the structural basis for regulation of the MtrCDE multidrug efflux system of *Neisseria gonorrhoeae*. This pump affords the pathogen resistance to both innate host defences and externally administered antimicrobial agents. He described how MtrR, the transcriptional regulator of the *mtrCDE* operon, is able to bind to distinct classes of inducing agents, with subtle differences in binding mechanism evident between particular ligands.

Maria Schumacher also from Duke University School of Medicine, Durham, USA, described her studies on the molecular mechanisms of *hipA*-mediated drug tolerance and its regulation in *E. coli*. The expression and activity of the HipA protein is tightly controlled by the HipB protein to promote transient dormancy in small sub-populations of bacterial cells. Antibiotics can fail to completely eradicate infections because of these "persister" cells, which are impervious to bactericidal effects of the agent and are able to revert to active growth after the treatment. She outlined the structural transitions that occur in the HipA protein as a consequence of HipB binding, and how these modulate HipA activity.

Gordon Dougan from the Wellcome Trust Sanger Institute, Cambridge, UK, talked about an *in vivo* murine screen for the identification of host infection susceptibility genes. In an exciting development for the research community, the Sanger Institute has embarked on a project to make mutants in individual genes in both the mouse and in cell lines, and then make them freely available.

Mark Walker from the University of Queensland presented an overview of his work on the evolution of and selection for the pandemic hyperinvasive group A Streptococcal M1T1 clone. M1T1, first detected in the mid-1980s, causing severe invasive disease in humans, has disseminated worldwide. The precise molecular evolutionary events selecting for its emergence were tracked using next-generation sequencing and phylogenetic analysis of a WHO strain collection of M1 GAS. Acquisition of a bacteriophage-encoded DNase increased virulence of the M1T1 precursor and then the phage-encoded superantigen SpeA probably provided selection advantage for the global dissemination. The study highlighted emergence of virulent clones from commensal populations or ones causing only benign infection, and provided an excellent example of how bulk genome sequencing can enhance our understanding of how pathogenic clones emerge.

The welcome mixer held on the first evening, free periods in the afternoons, including a coastal walk, and the poster sessions in the evenings provided ample opportunity for people to catch up and for students and postdocs to meet one another and begin to form useful networks. We are already looking forward to BacPath 12 (2013) in Queensland.

The organisers wish to especially thank all of the speakers and poster presenters for making the scientific program such a success, and the research students and staff from UTS, UNSW, Sydney and Macquarie universities who contributed greatly to the smooth running of the conference by helping with the website, the abstract book, bag packing, transport, registration, roving microphone and so on

BacPath 11 Organising and Scientific Program Committee

Ruth Hall (Chair), Neville Firth (Deputy Chair), Ruiting Lan, Ian Paulsen, Lynne Turnbull, Cynthia Whitchurch

ASM – NZMS Postgraduate Research Travel Award

Stephen Marsh

Firstly, I would like to thank the ASM for the opportunity to travel to New Zealand to visit my co-supervisor and group collaborator in Dunedin, Dr Joel Tyndall, and to present at the New Zealand Microbiological Society annual conference. I gained a lot from the experience and returned to Australia inspired, stimulated, and equipped with new knowledge and skills that I was eager to apply to my PhD project.

Dr Tyndall is an expert in molecular modelling and simulation and I spent eight days with him in Dunedin at the University of Otago, focusing on the *in silico* aspect of my project. Specifically, I was interested in creating a simulated model system of my protein of interest (*Chlamydia trachomatis* HtrA/DegP) to allow the identification of structural regions and residues that may be important for the regulation of HtrA activity in *C. trachomatis*. As a result, the outcomes of this visit included:

- An in-depth understanding of the PyMOL molecular visualisation program and its ability to view and manipulate protein structures.
- The computational representation of our inhibitor compounds predicting specific interactions with the protein.
- An ability to predict the effects of amino acid mutagenesis on protein structure and function, to better inform my mutagenesis experiments.
- An understanding of protein crystal structures: their creation, use, adjustment and manipulation.

Most significantly, I returned from my visit with Dr Tyndall with three elegant molecular models of *C. trachomatis* HtrA/DegP, representing each of its oligomeric states. In the absence of a published crystal structure (a future aim of my project), these models will be indispensable in informing the experimental aims of my project.

Following my time in Dunedin, I travelled to Palmerston North to attend the New Zealand Microbiological Society annual conference. My presentation went well and I received some nice feedback afterwards. I attended several sessions each day and found it fascinating to see the diverse areas of research students are pursuing in New Zealand and to listen to some very compelling and engaging speakers.

Overall, it was a successful trip that allowed me to gain valuable skills and data that will greatly benefit my PhD, while providing necessary experience in presenting scientific research at an international conference. I thank ASM once again for this extraordinary opportunity.

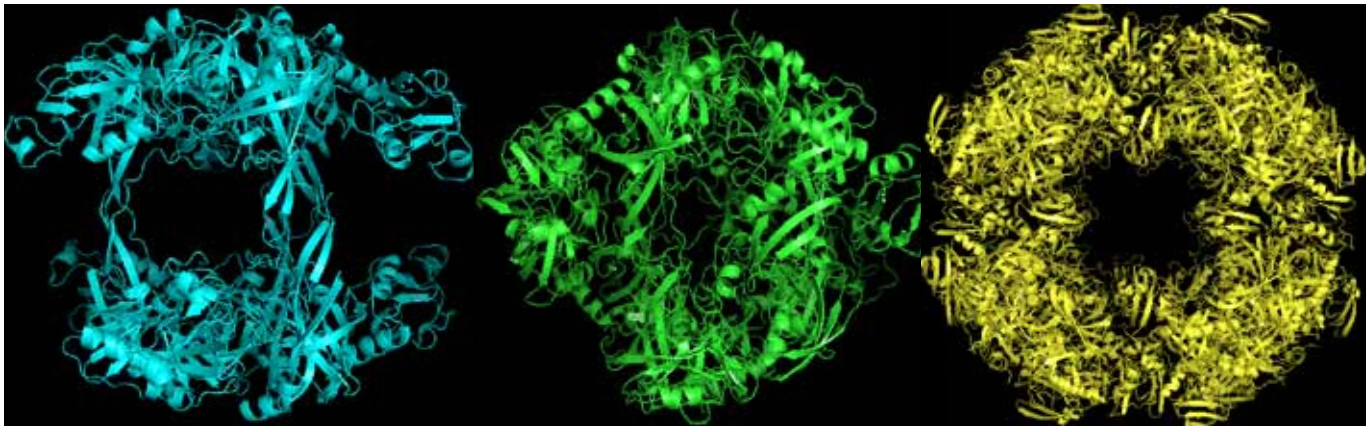


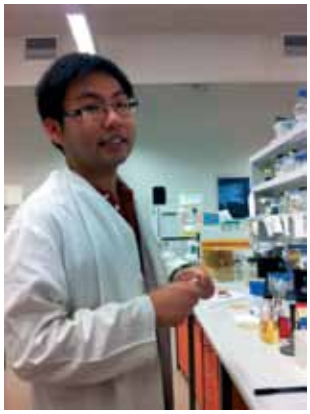
Figure 1. Chlamydia trachomatis HtrA/DegP structural models. Open hexamer (cyan), closed hexamer (green), isocosatetramer (yellow).

Microbiology Australia issues for 2012 include

May:	**Viral Gastroenteritis – Ruth Bishop and Carl Kirkwood**
July:	**ASM 2012 Conference issue**
September:	**Beneficial Microbes - Ipek Kurtböke and Ian Macreadie**
November:	**One Health – Martyn Jeggo and John Mackenzie**

Burnet Hayes Postgraduate Award

Andrew Liew



I am currently a second year PhD student in the laboratory of Professor Liz Harry at the University of Technology Sydney. My project involves elucidating the protein–protein interactions and protein dynamics of the protein, FtsZ, in the pathogenic organism *Staphylococcus aureus*. FtsZ is a bacterial protein that forms a ring at the future division site, marking the region for cytokinesis. FtsZ is currently an intensely investigated antibacterial target. However, in contrast to the relatively well-studied process of cell division in *Bacillus subtilis*, very little is known about how the cell division process is orchestrated in *S. aureus*. *S. aureus* cells not only differ in size and shape to *B. subtilis* cells but also divide in three consecutive, perpendicular planes, unlike *B. subtilis* which only divides in a single division plane. These differences suggest that the regulation of cell division is different between these organisms and although many cell division proteins are conserved, novel cell division proteins are probably present in *S. aureus*.

As a first approach to identifying novel cell division proteins in *S. aureus*, a plasmid-based system was developed for the production of FtsZ fused to GFP (green fluorescent protein) and the subsequent isolation of cell division protein complexes containing this protein in *S. aureus*. The GFP fusion was successfully used to affinity-purify several cell division proteins known to interact with FtsZ in model organisms, but these interactions have never been observed *in vivo* in *S. aureus*. Furthermore, several novel FtsZ-interacting proteins involved in cellular metabolism and stress responses were co-purified with FtsZ-GFP. Interestingly, one of the candidate proteins co-purified with FtsZ in that screen was a stress response protein which has been shown to be important for proper cell division in *E. coli*. We wanted to further characterise the stress protein and elucidate its role in *S. aureus*. Specifically, we wanted to determine which cell division protein would interact with the candidate protein.

To continue with this project and as part of my ongoing research training as a PhD student, I have been given a fantastic opportunity, through the Australian Society for Microbiology Burnet Hayes award to work in a world-leading laboratory specialising in *S. aureus* at the University of Sheffield. This laboratory had recently published a landmark paper describing a system for detecting *S. aureus* protein–protein interactions utilising a bacterial two-hybrid assay in *E. coli*[1]. I was able to utilise this assay to screen for interactions between the candidate stress protein and other *S. aureus* cell division proteins. We determined novel interactions between this protein and the proteins that were isolated in a protein complex in my earlier work, as well as with DivIVA. DivIVA is a cytoplasmic protein that is involved in ensuring proper positioning of the cell division apparatus in *B. subtilis*. Utilising the same two-hybrid system, I also determined the interactions of DivIVA with other *S. aureus* cell division proteins and uncovered multiple protein–protein interactions involving almost all the division proteins. In *S. aureus*, deletion of *divIVA* surprisingly shows no obvious phenotype when grown in rich media[2]. However, based on the multiple interactions exhibited by DivIVA, it would now be important to determine the exact role of DivIVA in *S. aureus*. Currently, we are characterising the *divIVA* deletion in combination with other gene deletions for any observable phenotypic effects. This might provide a novel link between cell division and stress pathways in the *S. aureus* cell.

The usefulness of the two-hybrid system also extends beyond determining protein–protein interactions as the system is currently being established in our laboratory as a drug screening assay. This assay involves screening compound libraries to identify candidate compounds that disrupt specific protein–protein interactions in *S. aureus* with promising candidate compounds potentially being further developed into antimicrobial compounds.

In addition to the laboratory stay in Sheffield, my attendance at the SGM conference in York, as part of the award, was also very enlightening. The conference provided valuable insight into the latest unpublished progress and results from prominent researchers in the field of bacterial cell division. The conference also allowed me to establish networking opportunities with other PhD students using similar protein interaction assays and fluorescence microscopy techniques. Additionally, I also received very constructive ideas and comments regarding the data that I presented at the conference.

In summary, the award has allowed me to gain valuable experience in conducting laboratory research overseas and also provided new avenues to pursue for my PhD project as well as giving me networking opportunities with other researchers in the United Kingdom.

References

1. Steele, V.R. *et al*. (2011) Multiple essential roles for EzrA in cell division of *Staphylococcus aureus*. *Mol. Microbiol.* 80, 542–555.
2. Pinho, M.G. and Errington, J.A. (2004) A divIVA null mutant of *Staphylococcus aureus* undergoes normal cell division. *FEMS Microbiol. Lett.* 240, 145–149.

ABSANZ 2011 Inaugural Annual Conference Report

The Association of Biosafety for Australia & New Zealand (ABSANZ) was registered as a not-for-profit organisation in November 2010, and started our first membership year in February 2011. In line with ABSANZ Objectives, we held our inaugural conference at The Sebel Citigate, Albert Park, Melbourne from 10-14 October 2011.

ABSANZ Inaugural Conference.

We are pleased to report that we had 135 participants at our inaugural conference, which was really a fantastic attendance; and wonderful support from our Sponsors and Exhibitors.

Workshops were held prior to the commencement of our first conference, including Gaseous Decontamination and Safe Handling of Biologically Hazardous Materials.

Cocktail Function.

The official meeting got off to a great start on Tuesday evening with Jim Walsh from the Elizabeth R Griffin Research Foundation sharing the story of the death of Elizabeth Griffin from ocular exposure to the *Macacine herpesvirus 1*, and how that had lead to the establishment of the Foundation, which is now recognized as a principal advocate of responsible research that serves to improve human and animal health. This was then followed by cocktails, hosted by our Exhibitors.

The President's Address by Dr Tony Della-Porta, entitled "How did we get here: the principles of biocontainment and biosafety?" was an informative presentation on how investigations of laboratory-acquired infections have contributed to the general principles of biocontainment and biosafety.

Annual Gala Dinner.

The first day covered sessions on Designing for Compliance, Liquid Waste Treatment, Ethics and Dangerous Discoveries and the operation of the SSBA System. Our first Annual General Meeting was held, during which three Standing Committees were formed:

Professional Development Standing Committee

Political Liaison Standing Committee

ABSANZ Conference Standing Committee

We concluded the first day with our Annual Gala Dinner, with Dr Andi Horvath, the Senior Curator of Science Communication of Museum Victoria, providing informative entertainment.

The second day included sessions on Hendra Virus, Understanding and Interpreting the New Biosafety Cabinet Standard, and Maintenance and Upkeep of Facilities. The afternoon included sessions on Dealing with Non-Compliance, the Quality Assurance Program, the New Auckland PC3 Laboratory and New Advances in Biocontainment Steam Sterilisers, concluding with a session on Commissioning Facilities. Copies of these presentations are available to ABSANZ Members on our website.

IFBA Members

As a new member of the International Federation of Biosafety Associations (IFBA), we were fortunate enough to have IFBA join our inaugural conference, and the final day of conference included the 24th Meeting of IFBA and an IFBA/APBA Asia Pacific Strategic Planning Meeting.

We would like to express our immense gratitude to our Sponsors, including the Australian Society of Microbiology, Exhibitors, Members, IFBA and Attendees. We look forward to our 2012 Conference to be held in Brisbane from 29 October to 2 November being an even greater success!

If you are interested in becoming a Member or finding out more about 2nd Conference, please visit www.absanz.org.au or email admin@absanz.org.au.

ABSANZ Objectives

1. Promote the field of biosafety and biorisk management in Australia & New Zealand
2. Facilitate the networking and collaboration between biosafety and biosecurity professionals
3. Facilitate access to biosafety and biorisk management expertise
4. Provide a forum for consensus development in biosafety and biorisk management
5. Facilitate training and professional development in biosafety and biorisk management
6. Be a peak body for representation on matters of biosafety and biosecurity

ASM 2012 Annual Scientific Meeting and Exhibition

1 – 4 July 2012
Brisbane Convention and Exhibition Centre

www.asm2012.org

Abstract submission extended

submissions close Friday, 23 March 2012

The **Australian Society for Microbiology** is pleased to invite you to its Annual Scientific Meeting, to be held at the Brisbane Convention and Exhibition Centre from 1 – 4 July 2012. The meeting is Australia's largest and most prestigious microbiological conference, attracting researchers, clinicians, professionals and supporters from all microbiological disciplines.

The conference program will include plenary lectures delivered by world leaders in Medical and Veterinary Microbiology, Applied and Environmental Microbiology, Virology and Molecular Microbiology. Symposia, other oral and poster presentations, and workshops round out a stimulating scientific program.

The format of the meeting for 2012 has been redesigned. In today's busy world it is increasingly difficult to attend a five day conference. ASM has responded by removing one day from the program, and changing the program scheduling. Our goal is to provide delegates with a richer, more concentrated experience, which also provides the time and opportunity for networking.

The Australian Society for Microbiology
bringing Microbiologists together