The Australian Society for Microbiology
bringing Microbiologists together

NSW-ACT Branch

Syntrophy

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From the editor

By Maurizio Labbate

Dear Branch Members,

Welcome to this edition of Syntrophy. Following our AGM, I'm excited to become the Chair of the ASM NSW/ACT Branch Committee for the next 2 years.

I wanted to thank all those for attending the AGM and participating in our virtual event. I'll start by thanking Jim Manos for being our Chair for the last 2 years. Although Jim is stepping down from his role as Chair, he will remain a valuable member of the committee. I also wanted to wish Mohammad Hamidian all the best as he steps down from the committee and thank him for all his work especially with organising the Nancy Millis Award event.

I would like to warmly welcome new members to our committee (Amy, Evan, Laurence, Jo, Heema). The committee looks forward to their fresh input and we hope they enjoy being involved. An introduction to our new members can be found inside this issue.

In this Syntrophy, we bring you an Event Report of our AGM speaker, Prof. David Tscharke. We also have a Focus Article from UTS PhD Student Mozammel Hoque and an article on bioluminescent bacteria from undergraduate UTS student Quincy Hayward.

As vaccination rates go up, we see a flicker of hope that we will begin to open up by the end of the year. We hope that we can bring our members the full breadth of our events next year including the Annual ASM Symposium in Sydney!

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Submissions and enquiries can be directed to the Syntrophy Coordinator via the ASM NSW-ACT Branch Secretary.

Organisations with research opportunities, or companies seeking to fill positions are welcome to place an advertisement in an upcoming issue of Syntrophy. Please contact the Secretary with your details for inclusion.

For information on the NSW-ACT branch committee, events and awards, please see:
https://asm-nswact.org.au/

Branch News: New committee members

Amy Cain

Dr Amy Cain has a BSc (Hons I) in Biochemistry and PhD from the University of Sydney, where she investigated movement of antibiotic resistance genes in *Salmonella enterica* with Prof. Ruth Hall. Next Amy moved to Cambridge, UK, to work as a research fellow at the Wellcome Sanger Institute with Prof. Julian Parkhill - developing genomics techniques like TraDIS to examine resistance gene networks. Then she moved to the Liverpool School of Tropical Medicine in Malawi, tracking and sequencing hospital-acquired resistant infections.Amy established her own research group in 2019 at Macquarie University, where she is currently an ARC DECRA fellow in the Department of Molecular Sciences and the Centre of Excellence in Synthetic Biology and Applied Biosciences. She focuses on developing new antibiotics using functional genomic techniques, novel single-cell microfluidics-based methodology, adaptive evolutionary approaches and the Galleria high-throughput *in vivo* model. She also uses synthetic biology to create microbes that degrade plastics. See google scholar and lab website.

Evan Gibbs

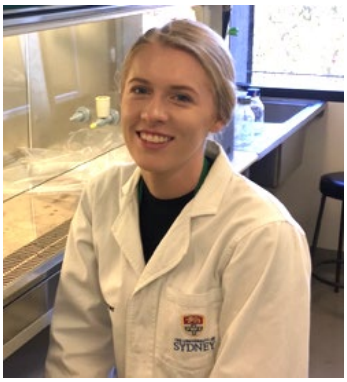
Evan Gibbs is currently a PhD candidate in the Bacterial Regulation and Transport Laboratory (BRaT Lab) at the University of Newcastle (UoN) under Dr Karl Hassan. His PhD candidature focuses on antimicrobial resistance and alternative sources to fossil fuel-based products. He also collaborates with a team of innovative PhD candidates and postdocs on autonomously forming, polymicrobial synthetic scaffolds. Currently he is the Postgraduate Representative for Research on the UoN Academic Senate, Research Committee, IBC and Student Representative Council. Together with two other PhD candidates he advises the inaugural iGEM Team and Australasian SynBio Team, The DeNovocastrians. He also led a prize-winning team in the UON Ideas Spark Competition that aims to use 3D printed devices incorporating synthetic microbial communities to knockdown mosquito populations in a target area. Twitter @EvoGibbs

Laurence Don Wai Luu

Laurence Luu is a Postdoctoral Research Associate in Dr. Natalia Castaño Rodríguez's and A/Prof. Nadeem Kaakoush's research group at the University of New South Wales. He is researching how interactions between host immunogenetics and microbiome lead to gastrointestinal cancers and inflammatory bowel diseases. Laurence completed his PhD in 2018 under the supervision of Prof. Ruiting Lan and Dr. Sophie Octavia where he investigated the evolution of *Bordetella pertussis* to vaccines. During his PhD, he discovered new adaptations that were associated with increased fitness in the Australian *B. pertussis* population. This discovery garnered widespread media attention and led to a national call to improve vaccines for whooping cough. website Twitter: @LaurenceLuu

Branch News: New committee members

Joanna Rothwell



Joanna is a PhD candidate under the supervision of Professor Dee Carter at the University of Sydney as part of the ARC Training Centre for Food Safety in the Fresh Produce Industry. Her current project involves investigating the efficacy of current and novel post-harvest chemical treatments in fresh produce processing. The goal of her project is to lessen food waste and to reduce the survival of food borne pathogens in fresh food. Currently, Jo is investigating the application of cold atmospheric plasma activated water to fresh produce processing which is an up-and-coming technology with lower health and environmental impacts compared to existing sanitisers. Prior to this, Joanna completed her Bachelor of Science with an honours project testing a novel anti-fungal drug against invasive mould species. Twitter: @joannarothwell

Heema Vyas

Heema K N Vyas is a Post-Doctoral Research Associate with Dr Anne Mai-Prochnow at the University of Sydney, where she is researching the effect of cold atmospheric plasma on bacterial biofilms. Heema's PhD was at the University of Wollongong, focussed on designing and optimising a Group A Streptococcus (GAS) host pharyngeal cell biofilm model and utilising this model to assess the role of pharyngeal cell surface glycans in mediating GAS biofilm formation. Heema's interests in microbiology have led to a position on the Joint Academic Microbiology Seminars (JAMS) committee. In addition to her research interests, Heema advocates for mental health and wellbeing in academia, and as a woman of colour in STEMM, Heema is passionate about ensuring parity for all in STEMM. Heema has been involved in several blog posts and interviews exploring wellbeing in the life sciences, and as a panellist and active committee member for equity, diversity, and inclusivity initiatives in STEMM/academia. Follow her on Twitter @HKNVee

Event Report: Post-AGM talk

Prof. David Tscharke

Australian National University

"A CRISPR way to engineer large DNA viruses"

Report by Nick Coleman

After our AGM, the Zoom audience of 27 attendees was treated to a fantastically engaging talk by Prof. David Tscharke from ANU, who led us through his lab's adventures using CRISPR-Cas9 methods to genetically modify herpesviruses and poxviruses.

David spun a great tale describing the ups and downs of attempting to apply new molecular tools in uncharted waters (in this case, large DNA viruses). The talk was notable for its clarity in addition to its strong scientific content, enabling even a card-carrying bacteriologist (yours truly) to not only understand the material but also to get excited about it.

The talk was in fact a masterclass in how to effectively communicate specific scientific facts while simultaneously weaving in deeper themes about how the scientific process works; e.g. the idea that in some cases (e.g. herpesviruses), new tools like CRISPR behave exactly as advertised, while in others (e.g. poxviruses), much trial and error is needed to optimise and troubleshoot the procedures. A case-by-case approach appears to be the rule in molecular virology, just as in many other areas of microbiology research.

David made a strong case for the value of creating new genetic tools in microbiology, as a way of not only accelerating research, but also for building collaborations. I am guessing that I wasn't the only one in the audience who was reconsidering how we make knockouts in each of our favourite microbes. The committee thanks David for giving up his Wednesday evening to share his research with us and wishes him and his lab all the best with their ongoing research on large DNA viruses.

Focus Article

Experimental evolution of Vibrio cholerae during protozoan predation

Md Mozammel Hoque

The iThree Institute, Faculty of Science, University of Technology Sydney

Mutations are the primary means of genetic variation leading to pathogen evolution (Lee et al., 2012), and often result from alteration of genomic composition caused by single-base substitutions, insertions and deletions (INDELs) and duplications. The assessment of the timing and types of these mutations that arise is crucial for advancing our understanding of population genetics and how pathogens adapt to specific environments. The rate of mutations varies considerably among different organisms and also depends on the environments where they survive and multiply (Sung et al., 2012).

Most opportunistic pathogens spend considerable amounts of time in the environment where they interact with numerous biotic and abiotic factors. Heterotrophic protozoa, for example, control bacterial population structure and composition (Sherr, 2002). Protozoa also serve as hosts for many opportunistic pathogens in the environment and play crucial roles in modulating pathogenic traits. To date, a growing number of reports highlight mechanisms of patho-adaptation of opportunistic pathogens in response to protozoan predation, and often these adaptation strategies are associated with genetic mutations. But the understanding of genetic diversity in response to long-term protozoan predation pressure is generally lacking.

To address this knowledge gap, my PhD project was designed to identify the long-term effects of protozoan predation on an opportunistic pathogen using the model protozoan predator, *Acanthamoeba castellanii,* and the prey *Vibrio cholerae*. The free-living amoeba, *A. castellanii,* is a heterotrophic protozoan frequently found in aquatic environments. The waterborne bacterium, *V. cholerae,* is the etiological agent of cholera, and capable of resisting predation and surviving inside *A. castellanii*. This pair of microbes are therefore ideal for the study of predator-prey interactions (Espinoza-Vergara et al., 2020).

In my PhD project, a clinical strain of *V. cholerae* was adapted with and without the presence of *A. castellanii* over 500 generations using an experimental evolution approach. The genetic variation that resulted from the long-term experiment were identified by sequencing the evolved isolates at different time points. Overall, we observed an increased rate of mutations in amoeba-adapted *V. cholerae* compared to the non-adapted control (Figure 1A). On average, the amoeba-adapted *V. cholerae* showed approximately 1.3-fold increase mutation rate (4.72×10^{-8} per nucleotide per generation) compared to non-adapted *V. cholerae* (3.71×10^{-8} per nucleotide per generation).

The rate of mutations observed in this experiment was higher in the earlier stages and then showed a significant decrease by the end in both amoeba-adapted and non-adapted *V. cholerae* (Figure 1A). These data are consistent with previous observations that bacteria decrease mutation rates to adapt in a specific environment (Sprouffske et al., 2018). The mean base pair substitution (BPS) mutational spectra analysis revealed that A:T → G:C and G:C → A:T transition mutations and A:T → C:G and G:C → C:G transversions largely contribute to the observed increased mutational rate in adapted *V. cholerae* (Figure 1B).

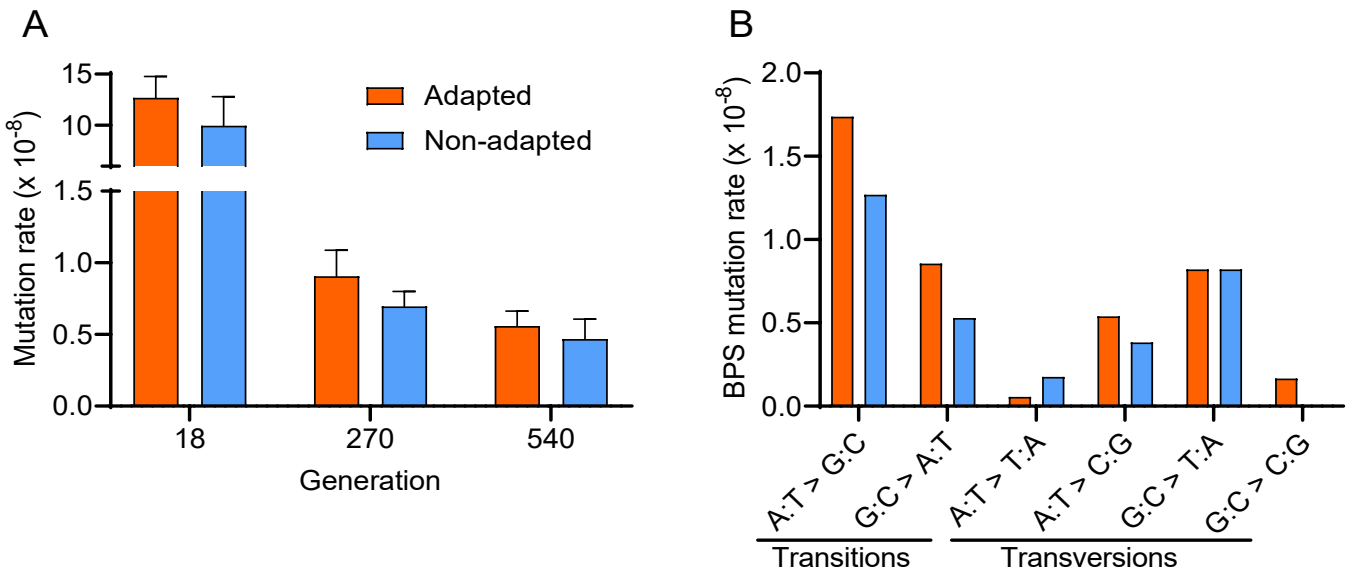


Figure 1. Mutation rate and base pair substitutions of amoeba-adapted and non-adapted *V. cholerae*. (A) Mean mutation rate per nucleotide per generation are shown for amoeba adapted and non-adapted *V. cholerae* isolates from different generations. Error bars are standard errors of the mean. (B) Mean BPS mutation rate per nucleotide per generation of each transition and transversion are shown for amoeba adapted and non-adapted *V. cholerae.*

Overall, the findings presented here suggest that protozoan predation accelerates the accumulation of DNA mutations in opportunistic pathogens. This provides a new insight into the mutagenic pressures associated with protozoan predation and how predation may fuel the evolution of pathogens in the environment.

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About the author

Md Mozammel Hoque is a PhD candidate under the supervision of A/Prof. Diane McDougald at the iThree Institute, Faculty of Science, University of Technology Sydney. His current research focuses on finding the effects of protozoan predation on opportunistic bacterial pathogens.

Upcoming Events

JAMS

Joint Academic Microbiology Seminars

MINIMA MAXIMA SUNT

28th September

6:00pm: Fraser Macleod, PhD student, UNSW
"Asgardians of the Galaxy – Bringing the Legends to the Lab"

6:30pm: Dr Carol Pong, Postdoctoral Researcher, USYD
"The DNA-binding domain of Tnp26, the transposase of insertion sequence IS26"

Online via zoom:
Meeting ID: 813 1098 7970 , password: 531337
Hosts: Nathan Williams and Jo Rothwell
When: 6pm Tuesday 28th September 2021

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