

*A Centre for Infectious Diseases and Microbiology - Public Health (CIDM-PH), and
Marie Bashir Institute for Infectious Diseases & Biosecurity (MBI) publication*

The Broad Street Pump

Foodborne Diseases: Changing Epidemiology and Disease Control

A/Prof Vitali Sintchenko

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Marie Bashir Institute for Infectious Diseases and Biosecurity, University of Sydney*

This issue of Broad Street Pump is devoted to foodborne diseases. The laboratory diagnosis of foodborne infections, their epidemiology and surveillance has been one of major interests and responsibilities of our laboratory and our team. We are delighted to present to you abstracts of a recent research Symposium organised by the CIDM-Public Health and held at Westmead and hope you find their content useful and informative. Please feel free to visit CIDM-Public Health website for details of speakers and their presentations.

The Symposium has been especially relevant for CIDM-PH because of the recent announcement of NSW Health Translational Research Grants. Our team has been awarded the grant "Translating pathogen genomics into improved public health outcomes: Prospective evaluation of the effectiveness of genome sequencing-guided investigation of outbreaks". As many of you would know, we have reached the level of precision when we can estimate contacts between people by the similarity of genomes of bacteria that people carry. If genomes of two strains of *Salmonella* recovered from two separate patients, who may not know each other at all, are very similar, it is very likely that these two patients have acquired their infection from the same source. Our project aims to translate these innovative approaches of bacterial genome analysis into the practice of public health. We argue that genomics guided surveillance can detect foodborne pathogens with higher accuracy and timeliness than current systems.



Inside this issue

Foodborne Diseases: Changing Epidemiology and Disease Control Introduction (p1-2)

Abstracts: Foodborne Diseases: Changing Epidemiology and Disease Control Symposium (p3-5)

NSW Health Translational Research Grant (p6)

Staff Profile: Dr Michael Walsh (p7)

Upcoming Events (p8-9)

- * *Facing the public health challenges of bacterial sexually transmitted infections*
- * *MBI Zoonoses Node Workshop*
- * *The Open Source Outbreak: Battling Communicable Diseases with Data*
- * *MBI Colloquium*
- * *CIDM-PH Colloquium*

Foodborne Diseases: Changing Epidemiology and Disease Control Research *(continued from page 1)*

We will target two major foodborne diseases (salmonellosis and listeriosis), which are high-burden and life-threatening diseases worldwide and in Australia, but have significant potential for prevention. *Salmonella enterica* is a leading cause of severe foodborne infections and associated community outbreaks in Australia. Timely identification of disease clusters is of paramount importance to effective outbreak control; however, no timely reliable subtyping schemes are available for serovars other than *Salmonella* Typhimurium to guide public health interventions. *Listeria* is a relatively uncommon pathogen of public health importance although has a case fatality rate of 30%. Current methods for characterisation are often unreliable to identify clusters and implement control interventions. Whole genome sequencing (WGS)-based technology, with its superior resolution power, can significantly improve tracking of bacterial pathogens. However, current efforts have been limited to the analytical aspects of WGS and bioinformatics applications. While recent retrospective studies of outbreaks from overseas and Australia have convinced early adopters about the feasibility of WGS-guided biosurveillance, critical questions about routine implementation of this technology into disease control systems remain unanswered. This project will address these key questions by measuring the effectiveness of WGS-based characterisation of the above pathogens in NSW, and by identifying real-life enablers and barriers to WGS adoption in a before-after state-wide trial. The project's aims are closely aligned with Strategic Plans of the NSW Health Pillars and the Strategic Plan for NSW Health Pathology.

But the leap forward that genomics guided surveillance offers to us requires a lot of coordination and, not surprisingly, our project will be conducted by a team representing laboratory scientists, clinicians and epidemiologists from ICPMR-Pathology West reference laboratories working together with academics from Marie Bashir Institute, The University of Sydney and our partners from Health Protection of the NSW Health. The Project is led by Vitali Sintchenko and Jon Iredell and associate investigators Sharon Chen (ICPMR-Pathology West), Chris Lowbridge, Kirsty Hope (NSW Health), Grant Hill-Cawthorne (The University of Sydney) and Ruiting Lan (University of New South Wales).



Dr Vicky Sheppeard, NSW Health Protection, presenting at the 'Foodborne Diseases' Symposium at Westmead



A/Prof Martyn Kirk, Australian National University, presenting at the 'Foodborne Diseases' Symposium at Westmead

Foodborne Diseases: Changing Epidemiology and Disease Control Research

Foodborne Disease – NSW Epidemiology, Challenges and Strategies

Vicky Sheppeard, Kirsty Hope, Neil Franklin & Brett Archer, NSW Health Protection

This presentation covered the epidemiology of notifiable enteric diseases in NSW from 2011 – 2016, with a focus on foodborne enteric conditions.

The challenges for surveillance and control vary by pathogen and include changing laboratory methods, antimicrobial resistance, global food production and distribution, and possibly climate change.

Public health strategies to address these challenges need to be tailored to the condition, and include emerging laboratory methods, clinician and community education, and incorporation of new technology into surveillance. Simultaneously a skilled workforce of surveillance officers, epidemiologists and food inspectors must be maintained.

Impact of Culture-Independent Testing on Public Health Laboratory Surveillance

John Bates, Public Health Microbiology, Queensland Health

Queensland saw the introduction of CIDT testing for faecal pathogens in late 2013. The public health lab had been trying to raise awareness of the likely implications of this for some time. Whilst there are significant advantages for clinical labs testing for enteric pathogens and parasites, there are also a number of disadvantages for public health surveillance. In Queensland, we have been fortunate that the clinical labs have all agreed to do reflex culture on PCR positive specimens. In addition, the public health lab has offered a service in providing culture for PCR +ve/Culture negative specimens. Data will be presented on the outcomes of this initiative. Whilst we receive some samples for *Salmonella* culture, this testing has concentrated on the recovery of *Shigella* and *Yersinia enterocolitica* from these specimens. Although this has bolstered the recovery of these enteric pathogens, it has also presented major challenges to the laboratory in terms of workload. The PHLN formed a working group in 2014 to facilitate discussion on the impacts of CIDT and provide recommendations on how best to ensure the continued supply of public health surveillance data. In addition, there have been a number of reviews on the impact of the introduction of this testing, and these will be discussed briefly.

Sequencing of *Salmonella* for Identification and Analysis in Local and Global Contexts

Vitali Sintchenko, Centre for Infectious Diseases and Microbiology-Public Health and Sydney Medical School, The University of Sydney

Whole-genome sequencing (WGS) of *Salmonella* has become an increasingly valuable source of evidence in the investigation of food-borne outbreaks. The effectiveness of WGS depends on the robustness and completeness of jurisdictional laboratory surveillance systems. The emerging evidence suggests that WGS-enhanced detection and analysis of outbreaks can be delivered in an actionable timeframe and can assist in (a) clarifying epidemiological curves of outbreaks and uncovering hidden links and associated risk factors, (b) discrimination of outbreak-linked and sporadic cases, and (c) distinguishing recrudescence from re-infection. This presentation will focus attention on the role of genomic surveillance in tracing the origins of the strains causing community outbreaks. WGS-guided case-control studies of community outbreaks of salmonellosis (i.e. a laboratory-confirmed infection with the *Salmonella* genome within 5 SNPs difference of the outbreak WGS profile) serve as a powerful example of the added value of sequencing to public health investigations. The utility and resolution of core genome MLST in reconstruction of transmission pathways will be examined using examples of the recent outbreak of *Salmonella* Bareilly and the genomic surveillance of *S. Enteritidis* in New South Wales. Our experience demonstrates that combining WGS and geographic metadata improves source tracking and surveillance. The exponential growth of sequencing data from national reference laboratories which has been deposited to international databases further strengthens the utility of WGS technology in tracing global food contamination events back to their source. The growing recognition of security of international trade as the priority for Global Health has made tracking of foodborne diseases especially important.

Foodborne Diseases: Changing Epidemiology and Disease Control Research

A BERRY BAD SIGN: Public Health Perspectives of a Hepatitis A Outbreak

Shopna K Bag, Communicable diseases, Western Sydney Public Health Unit, WSLHD

In February 2015, a nationwide food recall was instituted for Nanna's Frozen Berries due to Hepatitis A Virus (HAV) contamination concerns. Multiple locally acquired cases of Hepatitis A virus (HAV) infection had been identified in people who consumed frozen berries across Australia. While the source of the Hepatitis A virus was unconfirmed, the berries were the only common exposure for all cases. In recent years, frozen berries have caused a number of outbreaks overseas. Hepatitis A is endemic in many parts of the world, with nearly half of all cases of HAV reported in Australia being acquired overseas. This outbreak raises issues in the identification and testing of Hepatitis A in food, as well as the need for timely detection of outbreak cases by newer laboratory methods.

The Added Value of Whole Genome Sequencing in the Investigation of *Salmonella* Outbreaks

Qinning Wang¹, Cristina Sotomayor¹, Rajat Dhakal¹, Ranjeeta Menon¹, Peter Howard², Craig Shadbolt³, Kirsty Hope⁴, Vitali Sintchenko^{1,5}

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³ NSW Food Authority

⁴ Communicable Diseases Branch, Health Protection, NSW Ministry of Health

⁵ Sydney Medical School, The University of Sydney

Salmonellosis is the most common foodborne gastrointestinal disease caused by *Salmonella enteric* pathogens. There are currently more than 2,500 serotypes (serovars) in *Salmonella* according to the Kauffmann-White scheme on the basis of the serologic identification of somatic and flagella antigens. Most of them are human pathogens in which *Salmonella* Typhimurium (STM) is the predominant serotype identified in Australia, accounting for more than half of all *Salmonella* serotypes and causing severe gastroenteritis and major food borne outbreaks. Other salmonella serotypes have been also responsible for community outbreaks, although they were less frequent. In NSW several outbreaks due to salmonella serovars other than STM were reported between January 2015 and August 2016. These included local food-borne outbreaks of *S. Agona*, *S. Bareilly*, and *S. Mbandaka* and multi-jurisdictional outbreaks of *S. Saintpaul* and *S. Hvittingfoss*, with more than 40 cases on average involved in each of the outbreaks.

To investigate the link between clinical cases and food sources, whole genome sequencing (WGS) based on Illumina technology was implemented at ICPMR-CIDM-Public Health. Multiple approaches to the comparison of bacterial genomes were applied to validate analytic pipelines. In general, all raw sequencing data was subjected to QC checks before the analysis. The SNP calling and core genome MLST typing have been employed as two principle approaches. Several genomic analysis packages and pipelines including CLC Workbench, web-based servers and the MDU pipeline Nullarbor were used. WGS-based typing results and classification results from different pipelines were compared and validated. For each outbreak investigation, the outbreak clusters containing closely and possibly related isolates were identified. A report containing both SNP calling and core genome MLST results were sent to the OzFoodNet and Public Health for the integrated epidemiological analysis.

Our experience with the application of WGS to the investigation of *Salmonella* outbreaks demonstrated the added value of high-resolution and high-throughput capacity of this technology. Genomic surveillance becomes more accessible and acceptable in communicable disease control as the cost of WGS decreases and the turnaround time improves not just only for the sequencing step but also by means of the well-designed and validated analytic pipelines. WGS is expected to be of utmost benefit to communicable disease surveillance and outbreak investigations and will play an increasingly important role in public health laboratory surveillance.

Foodborne Diseases: Changing Epidemiology and Disease Control Research

Salmonellosis in New South Wales: From Controlling Outbreaks to a 30% Disease Reduction Strategy

Craig Shadbolt, NSW Food Authority

In recent years, Australia has recorded some of the highest salmonellosis rates in the developed world. Outbreaks and sporadic illness linked to a variety of food commodities, and changing climatic conditions are contributing to these elevated rates. In 2015, the NSW Food Authority announced a strategic approach to risk management of pathogens, including a 30% reduction target of foodborne salmonellosis by 2021. Using a combination of risk analysis, information on foodborne disease trends, better attribution data, and greater collaboration of industry and government stakeholders it is anticipated that salmonellosis rates will be reduced from the current elevated level.

Exploring surveillance requirements for certain public health threats in intensively farmed animals

Robyn Alders^{1,2} and Peter Daniels²

¹*Faculty of Veterinary Science and School of Life and Environmental Sciences, University of Sydney*

²*Charles Perkins Centre / Marie Bashir Institute Healthy Food Systems: Nutrition* Diversity* Safety, University of Sydney*

Society might expect that animals farmed to meet the food security needs of people globally will not pose a serious public health threat. Experience indicates the situation is otherwise. The Nipah virus outbreak in Malaysia was incomprehensible at the time. Farm workers became sick and died with a case fatality rate of 50% from a disease caught from the pigs on farms; a risk unheard of previously. Fortunately Nipah was not contagious among people. Analyses of pandemic H1N1 2009 influenza in people indicate that it too arose in intensively farmed animals, and it did spread quickly among people globally. Mercifully infections were not usually lethal. The avian influenza strains H5N1 and H7N9, have high human case fatality rates but are not contagious. None-the-less, intensively farmed animals are building up quite a record as a source of undesirable human diseases while at the same time seeing a degradation of the nutritional profile of the resulting carcase. The emergence of the next outbreak is unpredictable, as are its essential characteristics: pathogenicity and transmissibility. The animal health sector should deliver systems of diagnosis, surveillance and control of infections in animal populations. Farming businesses should recognise and understand responsibilities to monitor and know the infection status of their animal populations with respect to disease threats to food security, farming profitability and human health. This would be good risk management. However routine surveillance of intensively farmed animal populations for any such infections does not occur. Usually investigations start in response to outbreaks. Real time monitoring is not part of the production business model partly due to the cost implications. The technical capacity exists and is getting cheaper but there is perceived to be an unwillingness to undertake comprehensive surveillance. A better understanding throughout the whole of society – political, scientific and popular – is needed. Farmers, traders, industry managers, regulators, consumers all have to want to manage the threat of infections on intensive farming units, to value it and to pay for it.

NSW Health Translational Research Grant recipients - A/Prof Vitali Sintchenko & Prof Jon Iredell



\$10.2 million for life-changing research

04 Oct 2016

The NSW Government has announced \$10.2 million in Translational Research Grants to ensure innovative ideas advance from the laboratory to the frontline of patient care.

Health Minister Jillian Skinner and Minister for Medical Research Pru Goward visited Westmead Hospital on October 4 to announce the 24 recipients in the inaugural round.

The grants range from \$50,000 to \$1 million for projects of one to two years' duration.

Mrs Skinner said she was proud to deliver funding for the projects.

"The 24 recipients of the inaugural grants are innovative, scientifically rigorous and demonstrate strong cross-sector partnerships, which have the potential to translate rapidly into treatments and better health services."

Ms Goward added: "some of our brightest minds are dedicated to unlocking the secrets of ill health, disease and cure. The cutting-edge research projects we recognise today have the potential to make lives better and to ease suffering."

Among the recipients announced were \$550,000 to Westmead Hospital researchers Associate Professor Vitali Sintchenko and Professor Jon Iredell, who will use whole genome sequencing of pathogens for rapid identification, tracking and assessment of antibiotic resistance of tuberculosis and for control of salmonellosis and listeriosis.



NSW Minister for Medical Research Pru Goward, NSW Health Minister Jillian Skinner MP, Geoff Lee MP, Seat of Parramatta, Dr Rajat Dhakal, A/Prof Vitali Sintchenko

Staff Profile

Name: Dr Michael Walsh

Position: Senior Lecturer in Infectious Diseases Epidemiology, MBI, University of Sydney

Email: michael.walsh1@sydney.edu.au

Dr Michael Walsh is an infectious disease epidemiologist with the Marie Bashir Institute for Infectious Diseases and Biosecurity. He is interested in the complex ecologies of human and animal pathogens and their interaction with hosts, vectors, and environments to delineate landscapes of infection risk. As such, he explores complex etiologies using methods from traditional spatial epidemiology, as well as more modern applications of biogeography, ecology and data science to inform infectious disease inference and prediction. Michael is particularly interested in endemic and emerging zoonotic infections, and the ways in which interactions among wild and domesticated animals in anthropogenically altered landscapes enhance the potential for pathogen spillover from primary reservoir hosts to novel hosts. Michael has 17 years' experience as an epidemiologist and is currently investigating the landscape epidemiology of both Hendra virus and Ross River virus. Michael has taught infectious disease epidemiology and epidemiologic methods for over 12 years on the faculty of New York University and the State University of New York, Downstate. Michael has recently joined the faculty at the University of Sydney and the Westmead Institute for Medical Research as Senior Lecturer in Infectious Disease Epidemiology.



CONTACT US

For more information on any articles or CIDM-PH & MBI events, or to join the e-lists and receive regular updates, please contact us at:

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Upcoming Events....



Facing the public health challenges of bacterial sexually transmitted infections



Confirmed presenters:

- Overview of STIs and the local public health response | A/Prof Bradley Forssman
- Antimicrobial resistance among bacterial STIs | Prof David Lewis
- Gonococcal antimicrobial resistance surveillance in Australia | Prof Monica Lahra
- Molecular approaches to containing and managing antimicrobial resistant gonorrhoea | A/Prof David Whiley
- What can whole genome sequencing tell us about chlamydial infection? | Dr Rebecca Rockett
- Determination of *Treponema pallidum* strain variability and macrolide resistance using molecular assays | Ms Kaitlin Tagg
- Detecting antimicrobial resistance in *M. genitalium* – the key to best therapy | Dr Neisha Jeoffreys
- STIs in the new PrEP era – what to expect and how to respond | Dr Shailendra Sawleshwarkar

Event Details

Friday, 28 October 2016
8.30am – 1.30pm

Lecture Theatre 2, Westmead Education and Conference Centre, Westmead Hospital

Registration:

https://sydney.onestopsecure.com/onestopweb/VWW/tran?UDS_ACTION=DEFAULT&UDS_ACTION_DATA=1245

Cost: \$75 (includes morning tea and light lunch)

This event is co-hosted by Centre for Infectious Diseases & Microbiology- Public Health, the Western Sydney Sexual Health Service and the Marie Bashir Institute.
For more information visit sydney.edu.au/mbi



Advances in Microbial Genomics for Public Health and Clinical Microbiology

Tue 15 November 2016, 8:00 AM – 6:30 PM

The Peter Doherty Institute for Infection and Immunity, Melbourne

Registration & Program: <https://www.eventbrite.com.au/e/advances-in-microbial-genomics-for-public-health-and-clinical-microbiology-tickets-25691942291?aff=ehomecard>

Doherty Applied Microbial Genomics at the University of Melbourne and the **Centre for Infectious Diseases and Microbiology-Public Health/Marie Bashir Institute for Emerging Infectious Diseases** of the University of Sydney will be co-hosting a one-day symposium at the Peter Doherty Institute for Infection & Immunity, entitled “Advances in Microbial Genomics for Public Health and Clinical Microbiology” that will critically examine the impact of microbial genomics on public health and clinical microbiology practice overseas and in Australia, and show how this cutting edge technology is helping protect the public from the threat of infectious diseases.

Confirmed speakers include international experts Prof Jennifer Gardy from the British Columbia Centre for Disease Control and Dr Phil Ashton from Public Health England, as well as national experts in the fields of applied microbial genomics, epidemiology and antimicrobial resistance that includes Prof Eddie Holmes from the University of Sydney, Prof Darren Trott from the University of Adelaide and Prof Jodie McVernon from the University of Melbourne.

Congratulations...

Whitley Awards 2016

The Best of Australasian Zoological Literature in 2016.

Each year, the Royal Zoological Society of New South Wales (rzsnsw.org.au) conduct the Whitley Awards to seek out and acclaim the best publications published in the previous 12 months relating to Australasian zoology and the unique fauna of the region. The Whitley Medal and Special Commendation are the most sought after prizes in Australian zoological publishing.

Certificate of Commendation

Category: Natural History Guide

Title: A Guide to Mosquitoes of Australia

*Authors: Cameron Webb, Stephen Doggett
and Richard Russell*

Publisher: CSIRO



Upcoming Events....



The Open-Source Outbreak: Battling Communicable Diseases with Data

Professor Jennifer Gardy, Centre for Disease Control,
Vancouver, British Columbia, Canada

Co-hosted by CIDM-PH and MBI

Event Details

Date: Friday, 18 November 2016

Time: 3 – 4pm

Location: Level 2 Conference Room,
Westmead Institute for Medical Research



Changing climates, evolving patterns of land use, and increased travel mean that more and more infectious diseases are emerging. From old foes in new forms, like the antibiotic-resistant “superbugs”, to newer threats like Ebola and Zika virus, public health is constantly dealing with outbreaks and epidemics. As part of this battle, public health researchers are exploring how new data streams can influence our response to emerging pathogens. This new, data-driven epidemiology is full of innovative stories, from genome sequencing to reconstruct who infected who in an outbreak, to scraping online resources like Twitter for surveillance, to crowd-sourcing analysis of a novel pathogen through open, online lab notebooks.

The Speaker – Professor Jennifer Gardy, Centre for Disease Control, Vancouver, British Columbia, Canada

Professor Jennifer Gardy is a Senior Scientist at the British Columbia Centre for Disease Control, Assistant Professor at the School of Population and Public Health, University of British Columbia (UBC), and Associate Member at the Microbiology & Immunology, UBC. She received her PhD in molecular biology and biochemistry from Simon Fraser University, and began working for the BC Centre for Disease Control in 2009. Her main research interests are in genomic epidemiology and surveillance. In 2014, she was appointed the Canada Research Chair in Public Health Genomics.

This seminar is co-hosted by Centre for Infectious Diseases & Microbiology- Public Health and the Marie Bashir Institute. Afternoon tea will be provided.

Registration is FREE.

To **REGISTER** please email: <https://www.eventbrite.com.au/e/the-open-source-outbreak-battling-communicable-diseases-with-data-seminar-tickets-27803926292>

Enquiries: jou.Orszulak@health.nsw.gov.au

For more information visit: www.wslhd.health.nsw.gov.au/CIDM-PH or www.sydney.edu.au/mbi

CRICOS 00026A

Dates for your diary...

2 November 2016

**MBI Zoonoses Node
Workshop**

Abercrombie Business School
University of Sydney

Registration is free, but all attendees must
[register online](#)

3 November 2016

MBI Colloquium

New Law School

University of Sydney

Registration is free, but all attendees must
[register online](#)

25 November 2016

CIDM-PH Colloquium

Westmead Education & Conference
Centre

Registration is free

[https://](https://cidmphcolloquium2016.eventbrite.com.au)

cidmphcolloquium2016.eventbrite.com.au

Thank you....

The Department of Entomology at Westmead recently ran a charity auction at the '12th Mosquito Control Association of Australia and Arbovirus Research in Australia' Symposium at the Gold Coast, Queensland. The auction was in honour of a former mosquito monitor who worked with the Arbovirus Surveillance Program for over 25 years. Sadly he suffered from ill health after his retirement and took his own life. The team managed to raise approx. \$3,600, which was donated to 'Beyond Blue' with the receipt presented to his widow at the meeting.