Communicable Diseases Control Conference 2017

Infectious diseases: a global challenge

2017 ABSTRACT BOOK

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Tuesday 27 June 2017

Concurrent Session 1A – Foodborne
Grand 1&2, 11:30am - 1:00pm

A multi-state outbreak of Salmonella Hvittingfoss associated with melons in Australia, 2016

Presenter: Katherine Todd

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Abstract:

Introduction: Whole genome sequencing (WGS) is an evolving pathogen subtyping technology increasingly used in outbreak investigation. An outbreak of Salmonella Hvittingfoss occurred between 14 June and 2 August 2016 across six states and territories of Australia. A multi-jurisdictional investigation, including WGS, was launched to determine the source and control the outbreak.

Methods: We interviewed cases from four states and territories using a Salmonella hypothesis-generating questionnaire. We compared fresh fruit and vegetable consumption frequencies for cases with community participants, and conducted a case-control analytic study including 27 cases of S. Hvittingfoss and 48 age-matched controls. Concurrently, food-traceback activities were conducted in multiple states and territories and a selection of case isolates further characterised using WGS.

Results: During the outbreak period 144 cases were notified. The majority of cases (51%) were aged under 5 years. Binomial comparison of cases and community participants implicated watermelon and rockmelon as potential sources. Univariate analysis of the case-case study indicated consumption of rockmelon (OR 7.2, 95% CI 1.87-27.93), fresh fruit salad (OR 5.4, 95% CI 1.2-27.1), and strawberries (OR 3.3, 95% CI 1.1-10.7) were significantly associated with increased risk of infection. On 2 August 2016 rockmelons from the implicated grower were recalled. WGS identified two separate strains of S. Hvittingfoss amongst outbreak cases.

Conclusion: This outbreak was likely caused by rockmelons. WGS was a useful adjunct to the epidemiological investigation but should be considered alongside the epidemiological evidence. The co-ordinated approach between jurisdictions was essential for timely control of this outbreak.

Multi-state outbreak of Salmonella Saintpaul attributed to bean sprouts

Presenter: Megge Miller

Authors: Dr Megge Miller1, Ms Jacque Stephens1, Ms Alessia Centofanti1, Dr Kirsty Hope2, Dr Katherine Todd2, Mr Craig Shadbolt3, Associate Professor Vitali Sintchenko4, Mr Anthony Draper5, Dr Ben Polkinghorne6, Mr James Flint7, Ms Laura Ford5, Ms Marion Easton8, Dr Deborah Williamson10

Affiliations: 1SA Health, Adelaide, Australia, 2NSW Health, Sydney, Australia, 3NSW Food Authority, Sydney, Australia, 4Centre for Infectious Diseases and Microbiology, University of Sydney, Sydney, Australia, 5Northern Territory Department of Health, Darwin, Australia, 6Office of Health Protection, Australian Government Department of Health, Canberra, Australia, 7Hunter New England Population Health, NSW Health, Newcastle, Australia, 8Australian Capital Territory Health, Canberra, Australia, 9Department of Health and Human Services, Victoria, Melbourne, Australia, 10Peter Doherty Institute for Infection and Immunity, Melbourne, Australia

Abstract:

Introduction: In December 2015, an increase in Salmonella Saintpaul was detected through routine surveillance in South Australia and, later, New South Wales, Australian Capital Territory, and Northern Territory. This investigation aimed to determine whether the concurrent increases in S. Saintpaul notifications across multiple jurisdictions were linked, and to identify and control the source.
Methods: Food frequencies from hypothesis generating interviews were compared against Victorian food consumption data. A case-case study was conducted in SA and NSW. Trace back was conducted on fresh produce supplied to SA restaurants where cases reported eating. A selection of human isolates from the outbreak were further characterised using whole genome sequencing (WGS) and were compared with food and environmental isolates.

Results: Hypothesis generating interviews suggested a fresh produce source. The case-case study found mung bean sprouts were associated with illness (adjusted OR 18; 95% CI 5.3-60.5; p<0.0001). WGS results produced by laboratories in Victoria and NSW indicated that human cases from multiple jurisdictions were related. The trace back investigation in SA led to one mung bean sprout producer. An environmental swab and retail samples of mung bean sprouts tested positive for S. Saintpaul indistinguishable from the clinical isolates by WGS.

Conclusions & recommendations: WGS linked cases between jurisdictions and a fresh produce food item. This outbreak validated the capacity for WGS supported multi-jurisdictional investigations, highlighting the importance of investment in resources to aid in data sharing and collaboration across jurisdictions and sectors to identify difficult to trace food sources, such as fresh produce.


Presenter: Cameron Moffatt

Authors: Mr Cameron Moffatt1, Professor Cate D’Este1, Dr Karina Kennedy2,3, Associate Professor Martyn Kirk1

Affiliations: 1National Centre For Epidemiology and Population Health, Canberra, Australia, 2Canberra Hospital and Health Services, Canberra, Australia, 3The Medical School, Australian National University, Canberra, Australia

Abstract:

Introduction: Campylobacter infections commonly cause self-limiting enterocolitis but evidence describing incidence trends and hospitalisation within Australia is limited. We provide a detailed review of notifications and hospitalisations in the Australian Capital Territory (ACT).

Methods: Using routine notification data, public hospital discharge data (morbidity coding and chart review) and hospital-generated microbiology data, we examined gender, age, seasonality and hospitalisation status of cases between 2004-2013. Crude incidence was calculated using mid-year population estimates, with negative binomial regression used to estimate incidence rate ratios (IRR). Associations between hospitalisation status and gender, age and season were assessed via logistic regression.

Results: We identified 4376 Campylobacter notifications, including 2397 males (54.8%). Crude incidence across the study period was 124.1 per 100,000 population but did vary over time. Male incidence was significantly higher (IRR 1.21, 95% CI 1.14-1.28, p<0.001), while a high summer incidence was evident (IRR 1.15, 95% CI 1.06-1.25, p=0.001). Hospital morbidity data showed 307 incident admissions, with microbiology data and medical record review adding a further 285 admissions (hospitalisation rate 13.5%). Hospitalisation was strongly associated with specific age groups, notably those aged over 80 (OR 2.80, 95% CI 1.53-5.14 p=0.001) and between 20-29 years (OR 2.45, 95% CI 1.42-4.23, p=0.001).

Conclusion & Recommendations: The ACT has elevated disease incidence with typically higher rates among males. The characteristic spring rise in incidence was less evident with incidence highest during summer. Substantial underreporting of Campylobacter-associated hospital admissions exists, revealing a high rate of hospitalisation. More detailed understanding of factors associated with hospitalisation is required.

Evaluation of whole genome sequencing for surveillance of Salmonella Typhimurium in NSW

Presenter: Daneeta Hennessy

Authors: Ms Daneeta Hennessy1,2, Kirsty Hope2, Paula Spokes2, Qinning Wang1, Chayanika Biswas1, Peter Howard1, Alicia Arnott1, Vitali Sintchenko1

Affiliations: 1Centre For Infectious Diseases and Microbiology - Public Health, ICPMR, Pathology West, Westmead Hospital, Westmead, Australia, 2Communicable Diseases Branch, Health Protection NSW, North Sydney, Australia

Abstract:

Introduction: Whole genome sequencing (WGS) of Salmonella has demonstrated higher cluster discrimination than other typing methods in retrospective studies, but few evaluations of prospective use of WGS in surveillance have been reported. We describe our experience of implementing routine WGS for Salmonella Typhimurium as part of an ongoing study evaluating the effectiveness of WGS in control of foodborne infections in NSW.

Methods: All isolates of Salmonella Typhimurium submitted to the NSW Enteric Reference Laboratory from 1st October 2016 were subjected to whole genome sequencing in addition to the MLVA typing. Comparison of WGS and MLVA results is reported elsewhere. Clusters of highly-related isolates identified by WGS were investigated by interviewing cases about their exposure history, in order to identify epidemiological links to other cases and source. The timeliness of WGS data and ease of integration into existing data collection systems and public health workflows were evaluated prospectively.
Results: We will present preliminary findings of the concordance between WGS-identified clusters and epidemiological information. Challenges to optimal integration of routine WGS into Salmonella Typhimurium surveillance will be discussed, including: development of a reporting method that was easy to interpret without losing critical detail, compatibility of reporting with other states, public health staff training, timeliness of results, and the effect of culture-independent testing on the number of isolates available for sequencing.

Conclusion & Recommendation: Whole genome sequencing supports high resolution of Salmonella Typhimurium laboratory surveillance, but the practical challenges to implementation must be overcome for this to translate into improved public health outcomes.

Salmonellosis in Queensland 2000-2011: source attribution modelling and patterns of disease

Presenter: Emily Fearnley

Authors: Dr Emily Fearnley, Dr Aparna Lal, Dr Kathryn Glass, Dr Russell Stafford, John Bates, Associate Professor Martyn Kirk

Affiliations: 1Australian National University, 2Department of Health, Queensland Government

Abstract:

Queensland consistently reports higher rates of salmonellosis compared to the national average. We describe epidemiology of salmonellosis in Queensland, focussing on differences between Typhimurium and non-Typhimurium subtypes, and conducted source attribution modelling to improve understanding of transmission.

We obtained data on Salmonella serotypes in humans and non-humans, 2000–2011 from the Department of Health, Queensland. Human disease rates were compared by age groups and seasonality assessed. Data from non-human sources was categorised into reservoir sources: bovine, chicken, egg, nuts, ovine and porcine. We used WinBugs to apply Bayesian source attribution modelling to human and non-human data, reporting 95% Credible Intervals (CrI) to assess uncertainty

Human infection with non-Typhimurium salmonellae were consistently higher than Typhimurium rates, at 39/100 000 compared to 11/100 000 in 2011. Rates of non-Typhimurium were highest in children 0-4 years. Non-Typhimurium infections demonstrated seasonal patterns increasing in warmer, wetter periods. The source attribution model attributed the largest proportion of cases to chicken (43.7%, 95%CrI 27 - 59.5), followed by nuts (17.5%, 95%CrI 12.6 - 22.2), eggs (17%, 95%CrI 1.3 – 33.6) and bovine (2.4%, 95% CrI 0.4-7.5), with ovine and porcine <1 %. S. Typhimurium infections were largely attributed to chicken and egg reservoirs, and non-Typhimurium to all reservoirs.

High rates of non-Typhimurium salmonellae in children and seasonality indicate potential environmental sources. Attribution of nuts as a reservoir suggests environmental sources of infection with probable contamination on the tree and during harvesting. Whole genome sequencing and systematic environmental sampling would improve understanding of transmission of non-Typhimurium infections.

Diversity, invasiveness and antimicrobial resistance in human non-typhoidal Salmonella in Australia

Presenter: Mary Valcanis

Authors: Dr. Deborah Williamson, Ms Courtney Lane, Ms Mary Valcanis, Ms Janet Strachan, Ms Marion Easton, Dr. Anders Gonçalves da Silva, Dr. Glen Carter, Professor Timothy Stinear, Associate Professor Martyn Kirk, Professor Benjamin Howden

Affiliations: 1Microbiological Diagnostic Unit Public Health Laboratory, Doherty Institute, Melbourne, Australia, 2Doherty Applied Microbial Genomics, Department of Microbiology and Immunology, Doherty Institute, Melbourne, Australia, 3Australian National University, Canberra, Australia

Abstract:

Introduction: Australia has one of the highest reported rates of salmonellosis in the world. To date however, the serovar distribution and associated antimicrobial resistance (AMR) patterns of non-typhoidal Salmonella enterica (NTS) in Australia have not been systematically assessed. Such information provides critical knowledge about AMR in the food chain, in addition to informing decisions about public health. We assessed longitudinal data on NTS over a thirty-five-year period, obtained through a national surveillance system.

Methods: We analysed data on NTS from the National Enteric Pathogen Surveillance System (NEPSS) between 1979 and 2015 (n=130,990 isolates). We assessed trends in serotype distribution and AMR, with a focus on resistance to clinically relevant antimicrobials. We examined associations between specific serovars and invasive disease. Whole genome sequencing was used to characterise resistance mechanisms in 334 isolates that were phenotypically resistant to third-generation cephalosporins.

Results: S. Typhimurium predominated across the study period, followed by S. Virchow. Overall, 17.0% of isolates were resistant to at least one antimicrobial. Multi-drug resistance and fluoroquinolone resistance were predominantly associated with recent overseas travel, particularly to South East Asia. Unusually, the most common CTX-M type identified was CTX-M-55, which was found predominantly in S. Typhimurium monophasic variant 4,[5],12:i-.
Conclusion: Our findings provide valuable public health knowledge about the serovar trends and AMR profiles of NTS in Australia. Clinically relevant AMR, particularly to fluoroquinolones, is driven largely by patients returning from areas with high levels of AMR. Ongoing surveillance is critical to identify potential local sources of resistant isolates.

Concurrent Session 1B – Vaccines
Grand 3, 11:30am - 1:00pm

Higher zoster hospitalisations in Indigenous Australians: is vaccination at younger age warranted?

Presenter: Meru Sheel

Authors: Dr Meru Sheel1,2, Dr Frank Beard1,3, Dr Aditi Dey1,3, Associate Professor Kristine Macartney1,3, Professor Peter McIntyre1,3

Affiliations: 1National Centre for Immunisation Research and Surveillance, Westmead, 2National Centre for Epidemiology and Population Health, Australian National University, Acton,, , 3University of Sydney, Sydney,

Abstract:

Background: In November 2016, a vaccine for herpes zoster (HZ) was introduced onto Australia’s National Immunisation Program (NIP) for all individuals aged 70 years, including a 5-year catch-up program for those aged 71-79 years. Aboriginal and Torres Strait Islander (Indigenous) people are eligible to receive funded pneumococcal and influenza vaccines at 50 years of age due to higher risk. As limited published data on incidence of HZ among Indigenous Australians are available, no Indigenous-specific recommendations currently exist for HZ vaccine.

Methods: We used data from the Australian Institute of Health and Welfare National Hospital Morbidity Database to compare rates of HZ-related hospitalisation in Indigenous and non-Indigenous populations for the years 2007-2011. Negative binomial regressions were used to estimate age-specific hospitalisation rates, incidence rate ratios (IRR) and 95% confidence intervals (CI).

Results: We identified 214 Indigenous and 11,670 non-Indigenous hospitalisations. IRR for hospitalisation of Indigenous people aged 50-59 years and 60-69 years compared with their non-Indigenous counterparts was 1.80 (95% CI: 1.24–2.60) and 1.70 (95% CI: 1.21–2.37), respectively. Notably, 95% CI around hospitalisation rates per 100,000 in Indigenous people aged 60-69 years (31.9; 95% CI: 21.2–48.0) overlapped those for non-Indigenous people aged 70-79 years (44.6; 95% CI: 43.0–46.3).

Conclusions: The incidence of severe HZ in Indigenous Australians aged 50-69 years is high in comparison to non-Indigenous Australians. In the absence of more complete data on incidence, this warrants consideration of whether HZ vaccine should be recommended and funded for Indigenous Australians from 50 years of age.

Assessing the potential impact of a maternal RSV vaccine with mathematical models

Presenter: Kathryn Glass

Authors: Dr Kathryn Glass1, Alexandra Hogan1, Dr Patricia Campbell3, Dr Christopher Blyth2, Janice Lim2, Parveen Fathima2, Dr Stephanie Davis1, Dr Hannah Moore2

Affiliations: 1Australian National University, Canberra, Australia, 2Telethon Kids Institute, Perth, Australia, 3University of Melbourne, Melbourne, Australia

Abstract:

Introduction: Respiratory Syncytial Virus (RSV) is a leading cause of respiratory infections in young children. A maternal vaccine for RSV is now in phase 3 trials, and mathematical models are needed to assess the likely benefit of this vaccine and its optimal delivery.

Methods: We fitted a mathematical model of RSV to linked data from Western Australia and used it to estimate the impact of a maternal RSV vaccine for different levels of vaccine effectiveness, coverage and duration of protection.

Results: Our baseline model (50% coverage, 80% effectiveness) results in a 26% reduction in hospitalisations in children aged 0-2 months, and a 40% reduction in hospitalisations in children aged 3-5 months. The effect in 0-2 month children is most sensitive to the effectiveness of the vaccine, while the effect in 3-5 month children is most sensitive to the duration of protection.

Conclusion and Recommendation: A maternal vaccine for RSV could reduce hospitalisations in young children by up to 40%, provided the vaccine has high effectiveness and 50% coverage of pregnant women could be achieved.
Can GP data be used to monitor vaccination coverage in targeted programs?

Presenter: Rob Menzies

Authors: Dr Rob Menzies1, Mr Dauda Badmus1

Affiliations: 1School of Public Health and Community Medicine, UNSW, Sydney, Australia

Abstract:

Background: Vaccination coverage is difficult to measure in people with medical risk factors aged ≥6 months (eligible for free influenza vaccine since 2010), and this may be a challenge for the new National Immunisation Register. We investigated a potential alternative source.

Method: MedicineInsight is a general practice network that extracts de-identified data on 3.8 million patients in 550 Australian general practices. We identified patients eligible for free influenza vaccine based on diagnosed medical risk factors or age (≥65 years), and calculated the proportions with a recorded influenza vaccination, annually from 2008 to 2014. We compared these with the 2009 Adult Vaccination Survey (AVS), a national random telephone survey based on self-reported risk factor and vaccination status.

Results: The recorded influenza vaccination coverage for MedicineInsight patients was lower than for AVS participants, at 50.0% (95%CI: 47.4-52.7) and 74.6% (95%CI: 73.1-76.0) respectively in all patients aged ≥65 years, and 16.5% (15.4-17.7) and 36.2% (95% CI N/A) respectively for those aged 18-64 years with medical risk factors. There was no evidence of an increase in coverage amongst those aged 18-64 years with medical risk factors following vaccine funding in 2010.

Conclusions and recommendations: MedicineInsight data will not capture vaccinations given to patients at a second clinic, or at other settings such as school or work. However it may be useful in monitoring vaccination coverage trends in people with medical risk factors, as long as the level of under-recording of vaccination is taken into consideration, and remains constant over time.

The epidemiology of a large mumps outbreak in Western Australia 2015-2016

Presenter: Darren Westphal

Authors: Darren Westphal1,2,3, Clare Huppatz4, Ashley Eastwood5, Jane Davies6, Heather Lyttle4, Marisa Gilles4, Avram Levy3, Gary Dowse1

Affiliations: 1Communicable Disease Control Directorate, Department Of Health (WA), Perth, Australia, 2Wesfarmers’ Centre for Vaccines and Infectious Diseases, Telethon Kids Institute, Perth, Australia, 3National Centre for Epidemiology & Population Health, Australian National University, Canberra, Australia, 4Western Australia Country Health Service, Perth, Australia, 5PathWest Laboratory Medicine, Perth, Australia

Abstract:

Background: Between 2009 and 2014, an average number of 23 cases of mumps were notified annually in Western Australia (WA). This primarily reflected overseas acquisition with limited local transmission. We describe a genotype G mumps outbreak that commenced in the east Kimberley region in March 2015 before spreading to other remote parts of the state and metropolitan boarding schools.

Methods: Mumps is notifiable in WA. Cases were either laboratory confirmed or epidemiologically linked to a laboratory-confirmed case. Laboratory diagnosis was by polymerase chain reaction and/or serology. Case information was ascertained through follow-up by Public Health Nurses/Practitioners. We described demographic characteristics, vaccination status and outbreak control activities.

Results: Between 3 March 2015 and 30 September 2016, 884 outbreak-related mumps cases were notified. Of these, 89.1% were Aboriginal and 51.7% were male. The median age was 21 years (range 8 months to 64 years). The highest proportion of cases was among Aboriginal Australians aged between 10-19 years. Of cases <20 years, 6% were partially and 86% fully vaccinated against mumps. Overall, 4% of cases were hospitalised and 6% of males reported symptoms of orchitis.

Discussion: This is another example of a growing number of mumps outbreaks reported in recent years among highly vaccinated populations. That this outbreak disproportionately affected Aboriginal Western Australians living in remote WA is exceptional. Further studies that help to explain the apparent higher susceptibility of Aboriginal people in WA to mumps are needed.

Assessing influenza vaccine effectiveness in Indigenous and other special risk populations

Presenter: Monique Chilver

Authors: Ms Monique Chilver1, Professor Nigel Stocks1, Dr James Fielding2, Dr Sheena Sullivan3

Affiliations: 1The Australian Sentinel Practices Research Network, The University Of Adelaide, Australia, 2The Victorian Infectious Diseases Reference Laboratory, Melbourne, Australia, 3The World Health Organisation Collaborating Centre on the Reference and Research on Influenza, Melbourne, Australia
Abstract:

Introduction: The National Immunisation Program funds free seasonal influenza vaccination for groups at risk of severe influenza. This includes persons over 65 years of age, pregnant women, people with medical conditions that can result in complications from influenza, and Aboriginal and Torres Strait Islander (ATSI) people.

The Australian Sentinel Practices Research Network (ASPREN) is funded by the Commonwealth’s Department of Health to undertake national sentinel surveillance of influenza in a primary care setting. ASPREN data are utilised to provide vaccine effectiveness (VE) estimates for the seasonal influenza vaccine. To date, no VE estimates have been published for special risk populations from national primary care data.

Methods: From 2014-16 patients presenting to an ASPREN sentinel site with an influenza-like illness were systematically selected for influenza detection by real-time polymerase chain reaction (RT-PCR). A case test-negative design was used to calculate the odds ratio of vaccination in cases compared to controls.

Results: A total of 174 ATSI persons presented, of whom 102 were swabbed for PCR detection of a respiratory virus. The odds ratio of having influenza was 0.14 (95% CI: 0.04-0.50) among ATSI persons, compared to only 0.6 (95% CI: 0.51-0.71) among non-indigenous persons.

Conclusion and recommendations: Protection from vaccination was higher in the ATSI population. VE for other special risk groups, including pregnant women and the elderly will be presented. Higher numbers are required to produce robust, adjusted estimates, highlighting the need for enhanced surveillance in special risk populations.

Burden and risk factors for influenza-coded hospitalisation in NSW and WA children

Presenter: Hannah C Moore

Authors: Dr Chris C Blyth1,2, Dr Parveen Fathima1, Dr Lisa McCallum3, Dr Heather F Gidding5, Dr Hannah C Moore1, on behalf of the ACIR Linkage Investigator Team

Affiliations: 1Telethon Kids Institute, The University of Western Australia, West Perth, Australia, 2Princess Margaret Hospital for Children, Australia, 3University of New South Wales, Sydney, Australia

Abstract:

Introduction: Influenza is one of the most common vaccine preventable diseases. Australian data on the incidence of severe influenza in children and impact of comorbidities are required to inform national vaccine policy.

Methods: A retrospective population-based cohort study was undertaken using de-identified, individually-linked records from state and Commonwealth administrative datasets. Perinatal records for 1.4 million children born 2001-2012 in NSW and WA were linked to deaths and hospitalisation records (2001-2014). Incidence rates and incidence rate ratios for ICD10-coded hospitalisations were estimated using person-years at risk (py) in the cohort <13 years of age. The association between pre-existing comorbidities and influenza-coded hospitalisation in the first 2 years of life was measured by Cox regression.

Results: Overall in children less than 13 years of age the rate of influenza-coded hospitalisation was 64/100,000py (95%CI:63-66) and highest in the young (<6months: 197/100,000; 6-11months: 165/100,000; 12-23months 109/100,000). Overall influenza-coded hospitalisation rates were higher in boys than girls (IRR: 1.20 [1.14-1.26]), Indigenous compared with non-Indigenous children (IRR: 2.14 [1.97-2.34] and WA-born compared with NSW-born children (IRR: 1.15 [1.09-1.22]). Children with pre-existing conditions were at significantly greater risk of influenza hospitalisation, especially immunosuppressed children (aHR 7.50; 5.57-10.09) and children with metabolic (aHR 7.03; 4.99-9.90) or cardiac conditions (aHR 6.16; 5.43-6.99) adjusting for gender, Indigenous status and state of birth.

Conclusion & Recommendation: Influenza-associated hospitalisation remains significant, particularly in the young, among Indigenous children, and those with medical comorbidities. It is expected that a substantial proportion of these admissions could be prevented through seasonal influenza vaccination.
The value of data linkage for evaluating Australia’s childhood immunisation program

Presenter: Heather Gidding

Authors: Associate Professor Heather Gidding1,2, Dr Lisa McCallum1, Ms Parveen Fathima3, Associate Professor Tom Snelling4,5, Associate Professor Bette Liu3, Professor Nick de Klerk3, Associate Professor Christopher Blyth5,6,7, Dr Vicky Shepperd4, Professor Ross Andrews5, Professor Louisa Jorm9, Professor Peter McIntyre2, Dr Hannah Moore3, on behalf of the ACIR linkage investigator team

Affiliations: 1School of Public Health and Community Medicine, UNSW Medicine, UNSW Sydney, Sydney, Australia, 2National Centre for Immunisation Research and Surveillance, Westmead, Australia, 3Wesfarmers Centre for Vaccines and Infectious Diseases, Telethon Kids Institute, The University of Western Australia, Perth, Australia, 4Department of Infectious Diseases, Princess Margaret Hospital, Perth, Australia, 5Menzies School of Health Research, Charles Darwin University, Darwin, Australia, 6School of Medicine, University of Western Australia, Perth, Australia, 7Department of Microbiology, PathWest Laboratory Medicine WA, Princess Margaret Hospital, Perth, Australia, 8Communicable Diseases, Health Protection NSW, NSW Ministry of Health, Sydney, Australia, 9Centre for Big Data Research in Health, UNSW Medicine, UNSW Sydney, Sydney, Australia

Abstract:

Introduction: Australia’s Childhood Immunisation Register (ACIR) contains insufficient information to comprehensively evaluate our immunisation program. We describe linkage of ACIR to state health databases and initial evaluations of the pneumococcal conjugate vaccine (PCV) program.

Methods: State health, national death and ACIR databases were linked for children born in Western Australia and New South Wales in 1996-2012. We restricted the cohort to children born from 2001 for the PCV analysis. Dose-3 coverage was calculated at age 12 months. Invasive pneumococcal disease (IPD) rates were compared using Cox proportional hazards models, with vaccine effectiveness (VE) = (1- adjusted hazard ratio) x 100%.

Results: The cohort includes 1.95 million children (97,789 Indigenous) with 18.0 million person years of follow-up to 2013. The linked data provide the first estimates of:

-PCV coverage and relative burden of IPD in extremely pre-term children (<28 weeks gestation): during the targeted program (2001-04) rates were 5.4 times higher (95% CI: 2.2-13.0) compared with full-term children but PCV coverage was only 24% (compared with ≥90% in 2005-13).

-VE for Aboriginal children: VE for ≥3 PCV doses against IPD caused by the 7 serotypes in PCV7 was 95.1% (95% CI: 58.0%-99.4%) compared with 92.3% (95% CI: 86.5%-95.7%) for non-Aboriginal children.

Conclusion & Recommendation: Linkage of ACIR to other health data has provided the first robust estimates of coverage, disease burden and VE in specific risk groups. Given only Nordic countries have similarly comprehensive linked data and expansion to a whole-of-life immunisation register, ongoing linkage is vital to optimise immunisation policies in Australia and internationally.

Characterising disease patterns in remote Indigenous communities to inform transmission models

Presenter: Patricia Campbell

Authors: Dr Patricia Campbell1, Mr Will Cunningham1, Professor Ross Andrews2, Dr Therese Kearns2, Ms Roslyn Gundjirryirr Dhurrkay2, Professor Jonathan Carapetis3, Associate Professor Steven Tong1, Professor Jodie McVernon1

Affiliations: 1The Peter Doherty Institute for Infection and Immunity, The University of Melbourne, Melbourne, Australia, 2Menzies School of Health Research, Darwin., Australia, 3Telethon Kids Institute, Subiaco, Australia

Abstract:

Introduction: Severe diseases arising as sequelae of superficial skin and throat infections with group A streptococcus (GAS) are important causes of morbidity and mortality in remote Indigenous communities. Sustained control of GAS infection is hampered by an incomplete understanding of the mechanisms of GAS transmission. As GAS is known to be the main contributor to skin sores in these populations, data on skin sore presentations may be used to estimate trends in GAS infections.

Methods: We re-analysed retrospectively collected clinic presentation data for children from five remote communities enrolled in the East Arnhem Healthy Skin Project. We calculated monthly prevalence of skin sores and throat infections and scabies. Prevalence was compared across years to determine temporal trends, and within years to assess seasonality.
**Results:** Clinic data on 417 children aged from birth to five years were analysed. Skin sore and scabies prevalence fluctuated between 10–20% and 5–15%, respectively. Throat infections were less common, with prevalence ranging from 0–12%. Stratification revealed one community to be different to the others, with skin sore and scabies prevalence up to 60% and 50%, respectively. We found no evidence of seasonality in skin sore or scabies prevalence.

**Conclusion and Recommendations:** These findings are informing development of a compartmental model of GAS transmission. While seasonality appears unnecessary in such a model, drivers of differences in prevalence between communities need further investigation. Our analyses will provide estimates of determinants of GAS epidemiology to support model-informed design of sustainable interventions against GAS infection and sequelae.

Our work is a re-analysis of data that has been previously published, and was collected with individual and community consent. The data collection as well as this subsequent analysis was approved by HREC, including its Aboriginal Ethics Subcommittee.

### Pathogen-specific incidence of viral respiratory infections: record linkage study of 470,000 children

**Presenter:** Hannah Moore

**Authors:** Ms Faye Janice Lim1, Dr Christopher Blyth1,2,3,4, Dr Parveen Fathima2, Professor Nicholas de Klerk1, Dr Hannah Moore1

**Affiliations:** 1Telethon Kids Institute, Subiaco, Australia, 2School of Paediatrics and Child Health, The University of Western Australia, Crawley, Australia, 3Department of Infectious Diseases, Princess Margaret Hospital for Children, Perth, Australia, 4PathWest Laboratory Medicine WA, Princess Margaret Hospital for Children, Perth, Australia

**Abstract:**

**Introduction:** Hospital discharge diagnosis codes are often used when estimating the burden of respiratory infections. However, reliance on diagnosis codes alone may underestimate the true burden. Using linked laboratory data, we describe the pathogen-specific incidence rates of respiratory viruses among 469,589 children born in Western Australia 1996-2012 and hospitalised 2000-2012.

**Methods:** We analysed linked hospital admission, infectious disease notification and laboratory testing data from respiratory specimens collected within 48 hours of admission. We calculated the frequency and rates of virus detection for children in the cohort aged up to 16 years. To identify groups where under-ascertainment for respiratory viruses was greatest, we used logistic regression to determine factors associated with failure to test.

**Results:** 9% of 484,992 all-cause hospital admissions linked to a laboratory record for respiratory virus testing. While 62% (n=26,893) of linked admissions were coded for a respiratory infection, 38% (n=16,734) recorded other diagnoses, notably viral infection of unspecified sites. Of those tested, incidence rates were highest for respiratory syncytial virus (247 per 100,000 child-years) followed by parainfluenza (63 per 100,000 child-years). Admissions among older children and those without a respiratory diagnosis were associated with failure to test for respiratory viruses.

**Conclusion and recommendation:** Linked data can enhance diagnostic codes when estimating the true burden of disease. In contrast to current emphasis on influenza, respiratory syncytial virus and parainfluenza were the most common viral pathogens among hospitalised children in this cohort. By characterising those failing to be tested, we can begin to quantify the under-ascertainment of respiratory viruses.

### Burden of acute respiratory infections across Western Australian emergency departments

**Presenter:** Rosanne Barnes

**Authors:** Dr Rosanne Barnes1, Dr Christopher C. Blyth2,3,4, Professor Peter Richmond1,4, Professor Nick de Klerk5, Dr Meredith Borland6, Dr Parveen Fathima2, Ms Faye J. Lim1, Dr Hannah C. Moore1

**Affiliations:** 1Wesfarmers Centre for Vaccines and Infectious Diseases, Telethon Kids Institute, The University of Western Australia, Subiaco, Australia, 2School of Paediatrics and Child Health, The University of Western Australia, Crawley, Australia, 3PathWest Laboratory Medicine WA, Princess Margaret Hospital for Children, Subiaco, Australia, 4Princess Margaret Hospital for Children, Subiaco, Australia, 5Telethon Kids Institute, The University of Western Australia, Subiaco, Australia

**Abstract:**

**Introduction:** Most burden studies investigating acute respiratory infections (ARIs) in Western Australia (WA) are limited to hospitalisation data. Further, studies examining Emergency Department (ED) presentations in rural and remote EDs across Australia are particularly rare. This study examines ED presentation records with the aim of assessing the overall and age-specific burden of ARIs among Aboriginal and non-Aboriginal children presenting to WA EDs from 2002 to 2012.

**Method:** In a retrospective population-based cohort study linking ED presentations to birth and perinatal records, we examined presentation rates for metropolitan, rural and remote Aboriginal and non-Aboriginal children from 469,589 births. We used ED diagnosis information to categorise presentations into ARI groups and calculated age-specific rates across geographical regions using the mother’s postcode at the time of her child’s birth.
Results: Of the 1,862,283 linkable ED records, 1,606,257 had complete WA postcode information. Overall 26% of ED presentations across WA were for ARIs. For Aboriginal children the highest presentation rates were for those aged 1-5 months in the Great Southern and Pilbara regions with rates of 1,479 and 1,299 per 1000 child-years respectively. For non-Aboriginal children, rates were highest for children 6-11 months, particularly in the Southwest (475/1000 child-years). Broad ‘respiratory disease’ diagnoses accounted for the highest Aboriginal rates.

Conclusion & Recommendation: One in four ED presentations in WA children are for ARIs, representing a significant out-of-hospital burden with some evidence of geographical disparity. Planned linkages with hospital discharge diagnosis data will aid in assessing the sensitivity and specificity of ARI diagnoses in ED.

Respiratory virus associated community- acquired pneumonia in Western Australian Children: case-control study

Presenter: Mejba Bhiuian

Authors: Mr Mejba Bhiuian1,2, Dr Thomas Snelling2, Dr Peter Richmond1,2,3, Ms Rachel West2, Dr Meredith Borland3, Ms Joanne Montgomery4, Dr David Smith1,4, Dr Lea-Ann Kirkham1,2, Dr Ruth Thorton1,2, Dr Christopher Blyth1,2,3

Affiliations: 1The University of Western Australia, Perth, Western Australia, 2Telethon Kids Institute, The University of Western Australia, Perth, Australia, 3Princess Margaret Hospital for Children, Perth, Western Australia, 4PathWest Laboratories, Perth, Western Australia

Abstract:

Introduction: Globally, community-acquired pneumonia (CAP) is the leading cause of hospitalisation and death in children. Respiratory viruses (RV) are reported to account for 13-81% of CAP in children globally, however, data from Western Australia is limited. This study aimed to determine the contribution of RV to childhood CAP to help inform the development of effective diagnosis, treatment and preventive strategies.

Methods: A case-control study among children aged <18years was conducted in Perth, Western Australia. Cases were children with radiologically-confirmed pneumonia admitted at Princess Margaret Hospital (PMH) and controls were healthy children identified either from PMH outpatient clinic or from a local immunisation clinic. Case-control ratio was 1:1. Nasopharyngeal swabs (NPS) were collected from both cases and controls to determine RV using polymerase chain reaction.

Results: From May’15 to July’16, 132 cases and 132 controls were enrolled. The median age was 3.4 years (IQR= 1.8–6.2) for cases and 2.1 years (IQR= 1.5–4.5) for controls. The presence of any RV was identified in 60% (n=79) of cases compared to 21% of controls (n=28) (p<0.001). Respiratory syncytial virus (RSV) was the most common, being identified in 23% of cases compared to 2% of controls (p<0.001). Rhinovirus presence was similar in both cases (15%) and controls (14%). Other viruses identified were influenza (8% versus 1%), parainfluenza (6% versus 0%) and metapneumovirus (6% versus 1%).

Conclusion & Recommendation: Respiratory viruses, particularly RSV, contribute significantly to childhood pneumonia in Western Australian children. This study underscores the importance of vaccines against respiratory viruses to prevent childhood pneumonia. Enhanced pertussis management protocol in response to an infected HCW in a high risk setting.

Presenter: Kerryn Lodo

Authors: Ms Kerryn Lodo1, F Howes1, S McKeown1, M Veitch1

Affiliations: 1Department of Health and Human Services, Australia

Abstract:

Introduction: The Tasmanian Communicable Disease Unit (CDPU) was notified in January 2017 of a healthcare worker (HCW) with a positive pertussis test. The HCW worked with neonates across three institutions. CDPU initiated healthcare setting contact tracing prioritising prevention in exposed neonates. Initiation of the CDPU response was delayed as pertussis was not suspected due to vaccination, the delay in the HCW receiving their result and CDPU protocol to limit active follow up of pertussis cases to <5 years.

Method: CDPU identified 63 exposed neonates. Neonates were classified as eligible or not-eligible for post-exposure prophylaxis (PEP), based on time since exposure. PEP-eligible contacts were provided access to paediatric clinics. Ineligible contacts were given advice and medical assessment if symptomatic. Approximately 20 social contacts were identified. Information was provided to all.

Results: Of the 63 neonatal contacts, 50 were eligible and 13 were ineligible. Of the 50 eligible, 47 received PEP. Of these, three were symptomatic on assessment, however all tested negative. Of the 13 contacts that were ineligible for PEP, ten were symptomatic. Of these, six were tested and all were negative. One symptomatic social contact tested positive for pertussis.

Conclusions and recommendations: The secondary case in a social contact demonstrated the infectiousness of the HCW. The delay in diagnosis and response and overconfidence in the effectiveness of pertussis vaccination contributed to avoidable exposures in high-risk neonates. Protocols to respond to pertussis notifications need mechanisms to identify cases who may have high risk contacts. Education of HCWs is also required to help prevent future outbreaks.
Concurrent Session 1D – Vaccine Safety
Element Room, 11:30am - 1:00pm

AusVaxSafety: a new active vaccine safety surveillance system in Australia

Presenter: Anastasia Phillips
Authors: Dr Anastasia Phillips1,2, Ms Alexis Pillsbury1,2, Dr Helen Quinn1,2, A/Prof Kristine Macartney1,2, AusVaxSafety Team2
Affiliations: 1National Centre for Immunisation Research and Surveillance (NCIRS), Sydney, Australia, 2AusVaxSafety Consortium, Australia

Abstract:

Background: Australia’s vaccine safety surveillance system was reviewed following unexpected serious adverse events following immunisation (AEFI) with influenza vaccine in 2010. Harnessing novel safety surveillance tools that utilise consumer feedback, we formed the national AusVaxSafety network in 2014 to conduct real-time active surveillance of vaccine safety.

Methods: AusVaxSafety continuously compiles vaccine safety data following routine immunisation encounters in hospital- and community-based clinics, general practices and Aboriginal Medical Services. Parents or patients provide feedback via SMS or email on reactions following vaccination; reports of medical attendance are followed up. Cumulative results are analysed and reported regularly to providers and the public.

Results: By September 2016, data from ~10,000 children (response rate >70%) demonstrated that influenza vaccines had a safe profile, with <1% of reactions involving medical attendance. In the first 9 months of surveillance of pertussis-containing booster vaccines, data from more than 7,400 children receiving an 18 month dose and 6,600 receiving a 4 year dose was obtained. Medical attendance was reported for <2% of reactions following either dose. Recently implemented zoster vaccine safety surveillance of over 3700 patients shows with a very low rate of medically attended events with no safety signals identified to date.

Conclusions and recommendation: AusVaxSafety surveillance effectively engages providers and the public, has high participation rates and has confirmed the reassuring safety profile of vaccines under surveillance. Active safety surveillance should continue for nationally funded vaccines in Australia.

Flexible active, real-time vaccine safety surveillance: customising AusVaxSafety to monitor new vaccines

Presenter: Alexis Pillsbury
Authors: Ms Alexis Pillsbury1,5, Dr Helen Quinn1,2,5, Dr Anastasia Phillips1,3,5, Associate Professor Kristine Macartney1,2,4,5, AusVaxSafety team
Affiliations: 1National Centre For Immunisation Research & Surveillance (NCIRS), Westmead, Australia, 2Discipline of Child & Adolescent Health, University of Sydney, Australia, 3School of Public Health, University of Sydney, Australia, 4Department of Microbiology & Infectious Diseases, Children’s Hospital Westmead, Australia, 5AusVaxSafety Consortium

Abstract:

Background: AusVaxSafety has monitored the safety of influenza and pertussis-containing vaccines in children. From November 2016, the surveillance system began monitoring the new zoster vaccine which was funded for those aged 70-79 years.

Methods: AusVaxSafety Zostavax surveillance relies on 2 computer-based reporting mechanisms: SmartVax and Vaxtracker. Both utilise patients’ self-report (SMS/email) of reactions experienced post-vaccination. SmartVax reports reactions occurring within 3 days of vaccination and Vaxtracker within 16 days. De-identified data are aggregated for analysis and reported to the Department of Health and the public. Individual medical attendances for reactions are flagged for follow-up, and cumulative attendances are monitored for potential safety signals.

Results: By January 2017, data from ~2700 participants demonstrated this new vaccine’s safety, with <1% of reactions requiring a medical attendance. More than 97% of participants thus far participated via SmartVax; 8% reported reactions. For SmartVax participants, injection site reactions were most commonly reported (2.7%), followed by ‘other’ reactions (2.1%) including fatigue, tiredness, or headache. To date, reaction rates reported in Vaxtracker have been higher. Sixteen total rashes have been reported (14 SmartVax; 2 Vaxtracker).

Conclusions: AusVaxSafety Zostavax surveillance has demonstrated this new vaccine’s safety. It has revealed a number of rash cases which may merit follow-up to ensure that these are not occurring in immunocompromised individuals incorrectly receiving the vaccine. The ability of our real-time, active surveillance system to be customised to monitor issues specific to a new vaccine is advantageous, particularly as AusVaxSafety prepares to expand to monitor all National Immunisation Program vaccines.
Text messaging to monitor for adverse events following Bexsero® vaccination

Presenter: Alan Leeb

Authors: Dr Alan Leeb1, Ian Peters1,2, Dr Annette Regan3, A/Prof Kristine Macartney4,5,6, Dr Robyn Gibbs7, Chloe Thomson7,8, Prof Paul Effler7,8

Affiliations: 1Smartvax, Ballajura, Australia, 2Datavation, Perth, Australia, 3School of Public Health, Curtin University, Bentley, Australia, 4University of Sydney, Sydney, Australia, 5National Centre for Immunisation Research & Surveillance of Vaccine Preventable Diseases, Westmead, Australia, 6Paediatrics & Child Health, Children’s Hospital, Westmead, Australia, 7Communicable Disease Control Directorate, Department of Health Western Australia, Shenton Park, Australia, 8School of Pathology and Laboratory Medicine, University of Western Australia, Crawley, Australia

Abstract:

Introduction: Bexsero® meningococcal B vaccine was introduced to the Australian market in 2014. During pre-market evaluations of Bexsero®, fever was identified as a common adverse event in young children. Because fever following immunisation can be a risk factor for febrile convulsion, active monitoring for adverse events following immunisation (AEFI) with Bexsero® in children is needed.

Methods: Smartvax® is a short message service (SMS) tool used by general practitioners (GPs) in Australia to monitor patients for AEFI. Patients (or parents of patients) are invited to respond to a SMS three days post-vaccination to report any AEFI experienced. Potentially serious AEFI are flagged for follow-up. Data are provided to the GP and centrally collated for AEFI monitoring. We reviewed AEFI information for 806 patients who received Bexsero® in 2016.

Results: The majority of patients were children <5 years of age (n=679; 84.2%): 274 (34.0%) were <12 months and 189 (23.4%) were <24 months of age. In total, 30.1% of patients experienced any reaction; 13.0% experienced fever and 16.5% experienced pain or swelling at the injection site. A total of 2.2% of patients sought medical care for the reaction. No febrile seizures were identified. There were no differences identified by age or dose number.

Conclusions: Our data show that nearly one-in-three patients experience an AEFI with Bexsero®. Although fever was common, no febrile convulsions were identified. These data support the safety of meningococcal B vaccination in Australia and could be used to communicate to parents regarding anticipated AEFI with Bexsero®.

AusVaxSafety: Active, real-time surveillance to monitor seasonal influenza vaccine safety in children

Presenter: Alexis Pillsbury

Authors: Ms Alexis Pillsbury1,4, Dr Helen Quinn1,2,4, Associate Professor Kristine Macartney1,2,3,4, AusVaxSafety team4

Affiliations: 1National Centre For Immunisation Research & Surveillance (NCIRS), Westmead, Australia, 2Discipline of Child and Adolescent Health, University of Sydney, Australia, 3Department of Microbiology & Infectious Diseases, Children’s Hospital Westmead, Australia, 4AusVaxSafety Consortium

Abstract:

Background: AusVaxSafety national, active vaccine safety surveillance was established to monitor reactions of young children receiving seasonal influenza vaccination following a 2010 safety concern. As the composition of influenza vaccines changes annually, yearly monitoring is important.

Methods: Surveillance relies on computer-based reporting mechanisms which capture SMS/email reports of reactions. Aggregated, de-identified data including descriptive details like vaccine brand and details regarding reactions are reported weekly to the Department of Health and the public. Individual medical attendances for reactions are followed up, and cumulative attendances monitored for potential safety signals.

Results: From 2015-16, >9,500 children were enrolled and >7,000 provided data. Ten percent reported reactions, including fever (3.7%), injection site reaction (2.5%) or rash (0.9%); 48% received concomitant vaccines. There was no difference between those who received concomitant vaccines and had a fever and those who did not receive a concomitant vaccine (4.1% vs. 3.6%; p=0.308). There was, however, a significant difference between those who had a fever and sought medical attention for their reaction and those who did not have a fever (24.1% vs. 0.9%; 0.000). There was a higher reaction rate associated with trivalent vaccine, predominantly given in 2015, than with quadrivalent vaccine, predominantly given in 2016: 10.8% compared with 9.2%; p=0.023.

Conclusions: Two years of AusVaxSafety data provides reassurance of the safety of seasonal trivalent and quadrivalent influenza vaccines in young children. Having a robust, real-time vaccine safety surveillance system in place will be beneficial should the live attenuated influenza vaccine (LAIV) become approved for use in Australia.
Real-time vaccine safety surveillance for delayed AEFIs with serial SMS: STARSS RCT

Presenter: Gabriella Lincoln

Authors: Professor Michael Gold1, Dr Gabriella Lincoln1, Professor Nigel Stocks1, Professor Annette Braunack-Mayer1

Affiliations: 1University of Adelaide, Australia

Abstract:

The Stimulated Telephone-Assisted Rapid Safety Surveillance (STARSS) RCT involves soliciting parent and vaccinee reports of medical events following immunization [MEFI] by sending SMS reminders at day 2, 7 and 14 post-immunisation. The purpose of using multiple reminders is to ensure that any delayed-onset reactions to vaccines, such as febrile seizures triggered by live attenuated vaccines, are also captured because they occur several days after immunization.

In this presentation we describe results of the STARSS study with regard to the frequency of response at the different time points of the surveillance for the different vaccines, the lag time between the confirmed MEFI and the report by SMS to the STARSS surveillance portal thereafter for the various time-points, as well as the typologies of reported symptoms.

Preliminary results, from 1895 enrolled participants (SMS group only), showed that the multiple SMS reminders yielded a consistent overall responder rate across the three time points of 92%, with an overall MEFI rate of around 6%, of which 10% were assessed as being due to an adverse events following immunization (AEFI).

Finally we will corroborate the above findings with those of a parallel post-surveillance survey carried out with the same participants and attempt to elucidate the potential mechanisms accountable for non-response to the surveillance SMS reminders.

Searching for swollen little limbs: AusVaxSafety expands to monitor pertussis booster vaccines

Presenter: Helen Quinn

Authors: Dr Helen Quinn1,2, Ms Alexis Pillsbury1, Dr Anastasia Phillips1, Dr Kristine Macartney1,2

Affiliations: 1National Centre for Immunisation Research and Surveillance, Westmead, Australia, 2Discipline of Child and Adolescent Health, University of Sydney, Sydney, Australia

Abstract:

Background: Since 2014 AusVaxSafety has monitored the safety of influenza vaccines in children. In conjunction with the reintroduction of the 18 month pertussis booster in March 2016, this system was expanded to conduct active surveillance for adverse events following immunisation with pertussis booster vaccines in children aged 12 months to <7 years.

Methods: AusVaxSafety pertussis surveillance utilises data sourced from 3 computer-based reporting tools; SmartVax, Vaxtracker and STARSS, which capture parent reports (SMS/email) of reactions experienced by their child within 3 days of vaccination. De-identified data are aggregated for analysis and reported to the Department of Health and the public. Individual medical attendances for reactions are flagged for follow-up, and cumulative attendances are monitored for potential safety signals.

Results: By January 2017, data from 11573 participants receiving a booster vaccine, demonstrated the safety of pertussis boosters. Injection site reactions (ISRs) and fever were the most frequently reported reactions at both schedule points. Less than 1% of the ISRs required a medical attendance. Among these, one third were classified as extensive limb swelling (ELS) following the 18 month dose, compared with two thirds classified as ELS following the 4 year dose.

Conclusions: AusVaxSafety pertussis surveillance did not identify any unexpected reactions. ELS was more common in those receiving a 4 year booster dose, but occurred rarely among all participants. As children who have received the 18 month dose reach the 4 year schedule point, AusVaxSafety will be able to monitor for any increase in ISRs/ELS following this second pertussis booster.
Poster Presentations – P1
Grand 7 & Lobby, 1:30pm – 1:45pm

P1.001 - Acute disseminated encephalomyelitis (ADEM) and routine childhood immunisations

Presenter: Timothy Martin

Authors: Dr Timothy Martin\textsuperscript{1}, Dr Nigel Crawford\textsuperscript{1}, Ms Hazel Clothier\textsuperscript{3}, Ms Mee Lee Easton\textsuperscript{3}, Associate Professor Michael Fahey\textsuperscript{2}, Associate Professor Jim Buttery\textsuperscript{2}

Affiliations: \textsuperscript{1}Royal Children's Hospital, Parkville, Australia, \textsuperscript{2}Monash Children's Hospital, Clayton, Australia, \textsuperscript{3}Murdoch Children's Research Institute, Parkville, Australia

Abstract:

Introduction: Vaccinations are an important defence against communicable diseases, however immunisation program effectiveness is linked to safety perceptions. Acute disseminated encephalomyelitis (ADEM) is an autoimmune, demyelinating disorder that has been described following almost every vaccination. However neural-tissue containing rabies vaccines are the only vaccines proven to cause ADEM.

Aim: To investigate the potential association between routine childhood immunisations and ADEM.

Methods: Clinical information was linked to vaccination records in all children aged 0–6 years admitted with ADEM to the two tertiary paediatric hospitals in Victoria, Australia from 2000–2015. Diagnostic consistency was ascertained utilising the Brighton Collaboration criteria. The self-controlled case-series methodology was employed to determine the relative incidences of ADEM in 5–28 and 2–42 days risk intervals (RI) post-vaccination.

Results: 49 cases were eligible for analysis, 51% were male. The median age at ADEM diagnosis was 3.32 years (range 0.3–6.7 years), with three vaccine-proximate cases who received vaccinations 23, 25 and 28 days prior to ADEM onset. Two patients had received the 4 year old scheduled vaccinations and one patient the 1 year old vaccinations: all comprised the measles, mumps and rubella (MMR) vaccine. The relative incidence for the 5–28 day RI was 0.9667 (95%CI 0.3007–3.1081, p-value=0.9546) and 0.5428 (95%CI 0.1688–1.7453, p-value=0.3052) for the 2–42 day RI.

Conclusion and recommendation: These results do not support an association between ADEM occurrence and routine childhood immunisation. This is reassuring, however further investigation using an appropriately powered study is warranted, particularly to explore any possible association between ADEM and MMR vaccine.

P1.002 - Does telephone health data correlate with more traditional data sources?

Presenter: Mica Hartley

Authors: Ms. Mica Hartley\textsuperscript{1}, Dr Janice Biggs\textsuperscript{2}, Mr. Carlo Leonessa\textsuperscript{3}, Dr Kathryn Glass\textsuperscript{1}

Affiliations: \textsuperscript{1}Australian National University, Canberra, Australia, \textsuperscript{2}Healthdirect Australia, Sydney, Australia

Abstract:

Introduction: Telephone health services have the potential to greatly increase scope and timeliness of disease surveillance but are not as trusted as traditional forms of surveillance. However, research in the US, Canada and the UK has shown that telephone data correlates very well with other surveillance systems and often leads these by up to two weeks.

Methods: The Healthdirect nurse triage telephone helpline (HNTTH), which receives over 700,000 calls per year captures demographic details and characteristics of symptoms from participants. We identify cases of influenza like illness in this data, and compare them to emergency department (ED), laboratory, Flutracker and general practice (GP) data using cross-correlation functions.

Results: Correlation for the HNTTH was best with EDs (correlation of 0.82-0.99), good with GPs (0.68 – 0.91), and Flutracker (0.61-0.89), and worst with labs (0.42-0.97). In all data sources, the highest correlation occurred when comparing weekly aggregate data rather than daily; when comparing percent positive rather than counts; and when the HNTTH led the other data set by zero or one weeks.

Conclusion and Recommendation: We demonstrate the contribution of using HNTTH data sources to public health surveillance, through showing that an increase in calls to the HNTTH is very likely to occur simultaneously or one week in advance of an increase in visits to EDs, meaning we could provide advance warning.

We propose building a surveillance system using this data so that stakeholders can receive trustworthy, timely and accurate estimates of the level of influenza-like illness in the community.
P1.003 - Household sharing practices and transmission of Staphylococcus aureus in the community

Presenter: Catherine Bennett

Authors: Ms Selina Cook, Dr Elyse Dunn, Ms Ekaterina Bogatyreva, Ms Christine Parrott, Professor Catherine Bennett

Affiliations: Centre for Population Health Research, Deakin University, Burwood, Country

Abstract:

Introduction: The emergence and spread of antibiotic resistance in Staphylococcus aureus (S. aureus) in the community, especially multi-resistant strains (MRSA) is of concern, but surprisingly little is known about transmission mechanisms within households.

Methods: Detailed information on sharing of common household items (handtowels, bath towels, liquid soap, bar of soap, lotion, toothbrush, razors/shaver, comb/hairbrush, nail clippers, clothing, bedroom, bed, computer, deodorant) was collected in the Community-Onset Staphylococcus aureus Cohort (COSAHC) study that investigated 291 households in Melbourne (2008-2012) with a laboratory confirmed community-onset S. aureus infection. S. aureus colonisation was assessed with nasal and axilla swabs for 737 participants. Sharing data were analysed by pairs with colonisation proportions calculated as at least 1 person in a pair colonized in the nose, axilla or both sites.

Results: Sharing was most common for handtowels (82% of pairs), liquid soap (80%), nail clippers (73%) and computers (72%), but relationship dependent. We found a strong dose effect where S. aureus colonization increased in pairs sharing more often, with 0% S. aureus colonisation in the 10th percentile rising rapidly to 100% colonisation of S. aureus for those in the top 50th percentiles. This was also true for the strains responsible for the initial clinical infection, with colonisation only appearing in the top 50th percentiles for sharing, rising between 10% and 20% per decile, reaching 100% by the 90th percentile.

Conclusions: Understanding patterns of household sharing and the association with S. aureus transmission will help determine appropriate interventions to control the spread in the community.

P1.004 - Involving Aboriginal health workers when supporting Aboriginal people affected by Meningococcal Disease

Presenter: Cassia Lindsay

Authors: Ms Cassia Lindsay, Associate Professo Peter Massey, Fakhrul Islam, Professor David Durrheim

Affiliations: Hunter New England Population Health Service, Hunter Medical Research Institute

Abstract:

Introduction: Invasive Meningococcal Disease (IMD) is a serious bacterial infection, caused by Neisseria meningitidis, which may cause serious disease and fatality. Notification rates are four times higher for Aboriginal and Torres Strait Islander people than non-Indigenous Australians. Despite this disparity in disease occurrence there is little known about specific attention paid to supporting Aboriginal and Torres Strait Islander peoples affected by IMD.

Methods: To better understand how Aboriginal and Torres Strait Islander families affected by IMD were being supported in NSW, a Hunter New England Aboriginal Population Health Trainee, contacted a CD team member from each NSW PHU office (15 in total), and undertook a phone interview survey which took 5-10 minutes. The responses were then de-identified, and collated for review by the NSW Infectious Disease Network.

Results: The responses indicated that most PHUs do not routinely offer a differentiated service for Aboriginal patients and their families. Involving an Aboriginal Health Worker (AHW) and/or Aboriginal Health Liaison Officer (AHLO) could enhance culturally sensitive support and service delivery for Aboriginal and Torres Strait Islander peoples and families.

Conclusion and Recommendation: Information about the potential role of AHW and AHLO, and an offer of their involvement should be routinely included in the care of all Aboriginal cases of IMD. The development of a set of principles, expectations, and supporting resources, would assist this to occur.

P1.005 - Recurrent Invasive Pneumococcal Disease, Victoria 2006-2015: Serotypes and Implications for Immunisation

Presenter: Janet Strachan

Authors: Janet Strachan, Ms Lucinda Franklin, Dr Deborah Williamson

Affiliations: Microbiological Diagnostic Unit Public Health Laboratory, University Of Melbourne, Australia, Communicable Disease Epidemiology and Surveillance, Department of Health and Human Services, Melbourne, Australia

Abstract:

Introduction: Understanding the causative serotypes of invasive pneumococcal disease (IPD) is important to determine theoretical coverage of multivalent pneumococcal vaccines recommended for those at risk of infection.
Communicable Diseases Control Conference 2017 – Monday 26 to Wednesday 28 June 2017

Method: We analysed pneumococcal serotyping data from Victorian patients with recurrent IPD to determine whether targeted immunisation with either 13-valent pneumococcal conjugate (PCV13) or 23-valent polysaccharide vaccines (PPV23) would be beneficial.

Results: We identified 54 patients from Victoria with recurrent culture-positive IPD from 2006-2015 (second infection > one month after initial isolation of Streptococcus pneumoniae from a sterile site).

Forty-five percent of patients were < 65 years old. Serotypes cultured from both initial and recurrent infections generally reflected those causing IPD in the Victorian population. No single serotype was associated with increased likelihood of recurrence. Only 9/54 (17%) patients had initial and recurrent infections with the same serotype. Non-vaccine serotypes were more likely in the period after the addition of PCV13 to the childhood immunisation schedule in 2011. Where the initial IPD infection occurred from 2006-2010, 15/34 (44%) recurrent infections were due to PCV13 serotypes while 23/34 (62%) were PPV23 serotypes. From 2011-2015, 7/23 (30%) recurrent infections were with PCV13 serotypes and 10/23 (44%) PPV23 serotypes. Since 2011, 3/8 (38%) patients with recurrent IPD aged <65 years had a second/third infection caused by a PPV23 serotype.

Conclusion: Current serotyping data suggest targeted immunisation programs with PCV13 or PPV23 for IPD cases aged <65 years would only prevent a small number of recurrent IPD cases in Victoria.

P1.006 - Transmission of antibiotic-resistant clones: key driver of antimicrobial resistance in Neisseria gonorrhoeae

Presenter: Kerrie Stevens

Authors: Dr Jason C Kwong1,2,3,4, Dr Eric Chow5,6, Ms Kerrie Stevens3, Professor Timothy P Stinear1,2, Assoc. Prof. Torsten Seeman1,2, Professor Christopher K Fairley5,6, Associate Clinical Professor Marcus Chen5,6, Professor Benjamin P Howden1,2,3,4

Affiliations: 1Doherty Applied Microbial Genomics, Peter Doherty Institute for Infection & Immunity, University of Melbourne, Melbourne, Australia, 2Department of Microbiology and Immunology, University of Melbourne, Melbourne, Australia, 3Microbiological Diagnostic Unit Public Health Laboratory, University of Melbourne, Melbourne, Australia, 4Department of Infectious Diseases, Austin Health, Heidelberg, Australia, 5Melbourne Sexual Health Centre, Alfred Health, Carlton, Australia, 6Central Clinical School, Monash University, Clayton, Australia, 7Victorian Life Sciences Computation Initiative, Carlton, Australia

Abstract:

Background: Antimicrobial resistance in Neisseria gonorrhoeae (NG) is an urgent public health problem, with few remaining therapeutic options. It is assumed that transmission of antibiotic-resistant strains between individuals plays a key role in the dissemination of antimicrobial resistance; however direct evidence to support this is limited. To evaluate further we applied whole-genome sequencing (WGS) and compared NG isolates from men who have sex with men (MSM) partner couples.

Methods: Of 1723 MSM couples who attended the Melbourne Sexual Health Centre between September 2005 and September 2014, 33 couples were identified where both partners had a positive NG culture from ≥1 clinical site (urethral/pharyngeal/rectal). Whole genome sequencing of all NG isolates (n=92) was performed on the Illumina MiSeq/NextSeq. Multi-antigen (NG-MAST), multi-locus (MLST) sequence types and putative antibiotic resistance determinants for each isolate were derived from the sequence data. Similarity was determined from whole-genome core-single nucleotide polymorphisms (SNPs) and accessory gene content comparisons.

Results: NG isolates from MSM infected at multiple sites displayed identical NG-MAST and MLST and were clonal based on SNP analysis. Isolates from couples were also clonal for 32/33 couples. Where resistance determinants were present, isolates from couples carried identical resistance determinants.

Conclusion: This study provides evidence that MSM sexual partners are infected with the same strain of NG, including resistance determinants, which provides evidence that transmission of antibiotic-resistant clones between sexual partners plays a key role in the dissemination of gonococcal antimicrobial resistance

P1.007 - Influenza and non-influenza respiratory viruses are equally important in adult respiratory hospitalisations

Presenter: Cara Minney-Smith

Authors: Ms Cara Minney-Smith1,2, A/Prof Linda Selvey2, Dr Avram Levy1,3, Clin/Prof David W Smith1,3

Affiliations: 1Pathwest Laboratory Medicine WA, Nedlands, Australia, 2School of Public Health, Curtin University, Bentley, Australia, 3School of Pathology and Laboratory Medicine, University of Western Australia, Nedlands, Australia

Abstract:

Introduction: Influenza viruses are known to be a significant cause of adult hospitalisations, but less is known about the contribution of other respiratory viruses. This study compared the contributions of different respiratory viruses to admissions and clinical outcomes of patients admitted to SCGH with a respiratory illness.
Methods: Data from adults admitted to SCGH with a respiratory illness were linked with PathWest RT-PCR results for respiratory viruses including influenza A (INF-A), influenza B (INF-B), respiratory syncytial virus (RSV), human metapneumoviruses (hMPV), and parainfluenzaviruses (PIV). Proportions of patients with each virus were calculated, and multiple regression analyses conducted to assess their associations with hospital admission and clinical outcomes including ICU admission, ventilation, pneumonia, length of stay and death.

Results: INF-A was the most commonly detected virus, being found in 13.9% of patients. This was followed by RSV (5.8%), hMPV (4.8%), INF-B (4.4%) and PIV (3.9%). In multivariable analyses, patients admitted to ICU and patients requiring ventilation had significantly lower odds of having hMPV than INF-A (OR 0.289, p=0.026 and OR 0.115, p=0.037 respectively). No significant differences between INF-A and RSV, PIV or INF-B were seen for any of the clinical outcomes investigated.

Conclusion and Recommendation: INF-A was detected more than twice as often as the next most frequent virus, however the combined non-influenza respiratory viruses were more common in hospitalised patients. Therefore, both influenza and non-influenza viruses are capable of producing severe illness, requiring high level hospital care. Research into reducing impact of non-influenza viruses through prevention and treatment is important.

P1.008 - Use of enhanced surveillance to monitor appropriate treatment for gonorrhoea

Presenter: Bradley Forssman

Authors: Associate Professor Bradley Forssman, Ms Lisa Allchin, Ms Jane Thomas

Affiliations: 1Public Health Unit, Nepean Blue Mountains Local Health District, Penrith, Australia

Abstract:

Introduction: The incidence of gonorrhoea infection and antimicrobial resistance is increasing in Australia. Inappropriate antibiotic use contributes to resistance, but there is no monitoring of gonorrhoea treatment in the community. We piloted a system of enhanced surveillance to monitor adherence to national management guidelines.

Methods: For two years from September 2014, GPs diagnosing newly notified cases of gonorrhoea were sent a letter and questionnaire. The questionnaire obtained information on patient characteristics and treatment. If treatment was inconsistent with guidelines, the Public Health Medical Officer telephoned the treating doctor by to discuss appropriate management and ensure re-testing was undertaken. Univariate analyses were undertaken using X2 tests to assess associations between patient characteristics and treatment.

Results: 186 enhanced surveillance questionnaires were sent, and 171 returned (response rate 91.9%). 14% (24/171) of doctors indicated that they did not provide the recommended treatment. There were no statistically significant associations between any patient characteristics and provision of appropriate treatment. Various reasons were given for not following recommendations, including: allergic reactions; use of old guidelines; needle phobia; and, patient was asymptomatic therefore did not require treatment. Treatment failure or re-infection was not indicated by repeat notifications. Overall, doctors were appreciative of the personal contact and updated information regarding management of gonorrhoea.

Conclusion: The majority (86%) of doctors in this population provided appropriate management of gonorrhoea according to current national guidelines. This study has demonstrated that enhanced surveillance could be used to provide targeted education to GPs, as well as monitor appropriate use of antibiotics.

P1.009 - Rubella serosurveillance 2012-2013: Are we on track for elimination in Australia?

Presenter: Chathura Edirisuriya

Authors: Dr Chathura Edirisuriya, Dr Alexandra Hendry, Dr Helen Quinn, Dr Frank Beard

Affiliations: 1National Centre For Immunisation Research and Surveillance, Westmead, Australia, 2Epidemiology Unit, Ministry of Health, Colombo, Sri Lanka, 3University of Sydney, Sydney, Australia

Abstract:

Introduction: Vaccination is the mainstay of prevention of rubella and congenital rubella syndrome. There is a global push to eliminate rubella. A national rubella immunisation program has been in place in Australia since 1971. We aimed to analyse 2012-2013 national serosurvey data for rubella to compare immunity by age and with previous serosurveys.

Method: We randomly selected 2729 serum specimens (of individuals aged 1-49 years) from a bank of 12,411 specimens collected opportunistically from 32 laboratories around Australia in 2012 and 2013. Anti-rubella IgG enzyme immunoassay assay was used to determine antibody levels in the selected samples.
Communicable Diseases Control Conference 2017 – Monday 26 to Wednesday 28 June 2017

Results: The overall positive, equivocal and negative seroprevalence against rubella was 91.8%, 1.0% and 7.2%, respectively. The lowest age-specific proportion seropositive was in the 1-<2 year age group (79.6%). The proportion seropositive was significantly lower in males than in females in the 30-34 (80.0% versus 96.5%), 35-39 (85.9 versus 96.8%) and 40-44 (86.0% versus 95.9%) year age groups. No significant differences were seen between the 2012-2013 and previous serosurveys, with the exception of an increase of 13.6% (p=0.045) in immunity in the 1-<2 year age group between 1996-1999 and 2012-2013.

Conclusions: There is generally high seroprevalence of antibody against rubella in the Australian population with no evidence of waning immunity. These findings, in conjunction with high measles-mumps-rubella vaccine coverage and low disease incidence, suggest that Australia is close to elimination of rubella.

Recommendations: Rubella seroprevalence should be periodically monitored. Greater genotyping of rubella samples is required to determine if Australia has achieved elimination.

P1.010 - Psittacosis- an emerging infectious disease in rural veterinary schools?

Presenter: Rebecca Stow

Authors: Miss Natasha Larter1, Mrs Rebecca Stow1

Affiliations: 1Murrumbidgee Local Health District, Albury

Abstract:

This paper reports on the investigation into the possible second zoonotic transmission of Chlamydia Psittaci from horses at a rural veterinary school resulting in illness in a cluster of staff and students. In 2014 a similar cluster of illness was reported, investigated by the Murrumbidgee Local Health District surveillance team and presented at the Communicable Disease Conference in 2015. Ten of 30 people who worked with 3 unwell foals, reported symptoms of; but not limited to, malaise, cough, myalgia and headaches; three were hospitalised and all 10 cases reported to a local general practitioner where serology and pharyngeal swabs were collected. The 3 foals all tested PCR+ to C.psittaci. One human case was also PCR+ on a respiratory specimen. Further pathology testing on human cases is pending. The public health surveillance team conducted interviews on the 10 suspected cases and 5 exposed cases who remained well. As a result it was hypothesised that through exposure to Foal 3, aerosolised infected particles containing Chlamydia Psittaci had infected staff and students who were in attendance at the veterinary clinic. The investigation, to date, is still ongoing as the surveillance team wait for return of convalescent serology.

While there is limited investigation into the transmission of Chlamydia psittaci from horses to humans, this paper aims to explore the new modes of transmission of zoonotic diseases. We aim to present findings of new host reservoirs emphasising the need for enhanced surveillance and control measures within veterinary clinics to minimise the risk of zoonotic diseases.

P1.011 - A genomics-based workflow for antimicrobial resistance surveillance in Victoria

Presenter: Susan Ballard

Authors: Dr Susan Ballard1, Dr Mark Schultz2,2, Dr Norelle Sherry2,2, Kerrie Stevens2, Dr Michelle Sait1, Dr Takehiro Tomita1, Dr Anders Gonçalves da Silva1,1, Dr Jason Kwong2,3, Dr Torsten Seemann2, Dr Deborah Williamson1,2, Professor Ben Howden1,2,3

Affiliations: 1Microbiological Diagnostic Unit Public Health Laboratory (MDU PHL), Department of Microbiology & Immunology, The University of Melbourne at the Peter Doherty Institute for Infection and Immunity, Melbourne, Australia, 2Department of Microbiology & Immunology, The University of Melbourne at the Peter Doherty Institute for Infection and Immunity, Melbourne, Australia, 3Department of Infectious Diseases, Austin Health, Heidelberg, Australia, 4Victorian Life Sciences Computation Initiative, University of Melbourne, Melbourne, Australia

Abstract:

The introduction of the National Alert System for Critical Antimicrobial Resistances (CARAlert) has altered the process by which laboratories are required to identify and confirm critical antimicrobial resistances. Confirmation of resistance may include the identification of molecular resistance determinants, necessitating the confirming laboratory to provide and maintain a large suite of molecular assays. Moreover, the recent Victorian carbapenemase-producing Enterobacteriaceae (CPE) guidelines extends the requirement of MDU PHL, as the state public health reference laboratory and a CARAlert confirmatory laboratory, to provide genomics-based analysis of CPE isolates to determine clonality.

To meet these requirements MDU PHL has developed and implemented an iterative workflow incorporating genomics for rapid detection of critical antimicrobial resistance mechanisms. This includes a real-time PCR on suspected CPE isolates for a pre-defined range of carbapenemase genes, followed by whole genome sequencing to determine the allelic variant and identify rarer gene targets. Additionally the sequence data of isolates is used to assist in predicting putative transmission networks to facilitate epidemiological investigation. Using our genomics-based workflow as an exemplar, this presentation will describe the key bioinformatics pipelines along with the challenges posed to achieve workflow accreditation in public health laboratories in Australia.
P1.012 - A snapshot of Chlamydia trachomatis genetic diversity using MLST in metropolitan Australia

Presenter: Jen Danielewski

Authors: Dr Jen Danielewski1,2, Samuel Phillips1,2, Fabian Y. S. Kong3, Kirsty S Smith4, Jane S Hocking3, Rebecca Guy4, Christopher K Fairley5,6, Suzanne M Garland1,2,7, Sepehr N Tabrizi1,2,7

Affiliations: 1Department of Microbiology and Infectious Diseases, The Royal Women’s Hospital, Victoria, Australia, 2Murdoch Childrens Research Institute, Victoria, Australia, 3Melbourne School of Population and Global Health, University of Melbourne, Melbourne, Australia, 4The Kirby Institute, University of New South Wales, NSW, Australia, 5Melbourne Sexual Health Centre, Alfred Health, Victoria, Australia, 6Central Clinical School, Monash University, Victoria, Australia, 7Department of Obstetrics and Gynaecology, University of Melbourne, Victoria, Australia

Abstract:

Introduction: A detailed snapshot of anogenital Chlamydia trachomatis genetic variation using high resolution multilocus sequence typing (MLST) is presented. From clinical samples, we examine circulating C. trachomatis genetic variation, predominantly within the MSM population, and a small heterosexual population, and compare these to strains circulating globally.

Methods: From a pool of 880 C. trachomatis positive samples derived from two clinical studies, 76 pre- and post-treatment samples (n=152) with the same genovar were sequenced for 5 variable allele regions of the C. trachomatis genome. The C. trachomatis MLSTDB Index was queried to identify known and new allele variants. Sequence tags (STs) denoting the 5 alleles were subsequently analysed to create a minimum spanning tree (MST).

Results: MLST analysis revealed 25 STs in total, 6 new allele variants and 7 new STs not described elsewhere in the world. Of the 8 most common global STs, 7 were found in Australia (4 from MSM, 3 from heterosexuals). Newly identified STs were predominantly found in MSM samples. MST analysis demonstrated two main branches; ST clusters on one branch contained all heterosexual samples and some MSM, while clusters on the other branch contained STs identified in MSM only.

Conclusions: Although the genovar distribution in the Australian population is similar to that globally, MLST provided a diverse C. trachomatis strain profile, with novel circulating STs creating distinct local population signatures. The discriminatory power of MLST could be used to identify local sexual networks to focus on interventions such as testing and partner notification to prevent reinfection.

P1.013 - Recurrent Invasive Meningococcal Disease with two different Serogroups: A Case Report

Presenter: Fiona Vosti

Authors: Ms Fiona Vosti1, Ms Kim Bannan1, Dr Lana Sundac2, Dr Satyamurthy Anuradha1,3

Affiliations: 1Gold Coast Public Health Unit, Southport, Australia, 2Gold Coast University Hospital, Southport, Australia, 3The University of Queensland, Southport, Australia

Abstract:

Introduction: Recurrences of invasive meningococcal disease (IMD) have been observed in patients with terminal complement component defects due to inefficient formation of the lytic membrane attack complex (MAC).

Methods and Results: A 24-year old male presented to the Emergency Department with a 4-day history of headache and vomiting, and noted to have a rash and decreased consciousness on admission. He was PCR positive for N meningitidis and subsequently notified as Serogroup Y. He was treated in the Intensive Care Unit (ICU) with Ceftriaxone and was given a conjugate ACWY vaccine at discharge.

Three months later, he experienced some vomiting followed 12-hours later by headache and neck stiffness. He was noted to have a recurrent IMD notified this time as Serogroup B and received two doses of Meningococcal B vaccine post-discharge. He recovered completely with no residual complications after both episodes. A thorough investigation revealed deficiency of both C5 and C7 components of complement.

Conclusion and Recommendation: The serogroup most commonly reported as responsible for recurrent N meningitidis infections is serogroup Y. However, we report recurrent severe IMD due to two different serogroups of N meningitidis in a patient with complement deficiency.

Complement deficiencies should be considered in any patient with recurrent infections caused by N meningitidis.
P1.014 - Increase of invasive meningococcal disease in NSW

Presenter: Nathan Saul

Authors: Dr Nathan Saul¹, Ms Paula Spokes¹, Dr Vicky Sheppeard¹

Affiliations: ¹NSW Health, Sydney, Australia

Abstract:

Background: Invasive meningococcal disease (IMD) is a serious, potentially fatal, disease caused by the bacterium Neisseria meningitidis. There are multiple serogroups of the causative organism with serogroup B, C, W, and Y endemic in Australia. Vaccination against IMD is serogroup dependent with only serogroup C currently on the national schedule. Recently an increase in IMD cases was observed in NSW, this study presents the descriptive epidemiology of IMD in NSW.

Methods: Cases of IMD were notified if they fit the national case definition. Information on these cases was collected as part of routine public health follow up as per the NSW and national control guidelines. This information was entered into the state notifiable disease database as per reporting requirements. Molecular epidemiology utilising whole genome sequencing and descriptive epidemiological analysis were conducted.

Results: Since 2014 there has been an increase in invasive meningococcal disease in NSW. This follows a seventeen year period of decline in notifications. The increase has been associated with a change in serogroup frequencies with an increase of W and Y.

Conclusion: An increase in serogroup W IMD has been observed in NSW, this has also been reflected in national data with serogroup W increasing in most States and Territories. This increase is likely to be linked to a hyper-virulent strain of N. meningitidis serogroup W which has also been observed in South America and the UK. Ongoing state and national monitoring of IMD notifications is necessary to inform public health interventions for this pathogen.

P1.015 - Genome-wide comparison of Corynebacterium diphtheriae identifies differences between respiratory and cutaneous strains

Presenter: Verlaine Timms

Authors: Dr Verlaine Timms¹, Ms Trang Nguyen², Ms Marion Yuen², Ms Taryn Crighton², Dr Rebecca Rockett¹, A/Prof Vitali Sintchenko¹,³

Affiliations: ¹Centre For Infectious Diseases And Microbiology - Public Health, Westmead Hospital, Sydney, Australia, ²Centre for Infectious Disease and Microbiology - Laboratory Services, ICPMR-Pathology West, Westmead, Sydney, Australia, ³Marie Bashir Institute for Infectious Diseases and Biosecurity, Sydney Medical School, The University of Sydney, Sydney, Australia

Abstract:

Introduction: Corynebacterium diphtheriae is the main etiological agent of diphtheria which remains a global disease and can cause life-threatening infections, particularly in infants and children. Vaccination with diphtheria toxoid protects against infection with toxin producing strains. However, a growing number of apparently non-toxigenic but potentially invasive C. diphtheriae strains are identified in countries with low prevalence of diphtheria, raising concerns about other virulence factors and the population dynamics of the species.

Methods: This study examined genomic variation among 47 C. diphtheriae isolates collected in Australia over a 10-year period using whole genome sequencing (WGS). Phylogeny was determined using SNP-based mapping and genome-wide analysis. Standard multi-locus sequence typing (MLST) was determine from WGS data using public databases.

Results: C. diphtheriae sequence type (ST) 32, a non-toxigenic ST with evidence of enhanced virulence that is also circulating in Europe, appears to be endemic in Australia. Isolates from temporospatially related patients displayed the same ST and similarity in their core genomes. The genome-wide analysis highlighted a role of pilins, adhesion factors and iron utilization in infections caused by toxigenic as well as non-toxigenic strains.

Conclusion and Recommendation: The genomic diversity of toxigenic and non-toxigenic strains of C. diphtheriae in Australia suggests multiple local and overseas sources of infection and colonisation. Our findings suggest that molecular surveillance of co-circulating toxigenic and non-toxigenic C. diphtheriae is important in order to inform targeted public health actions and policy for this highly successful pathogen.
P1.016 - Crusted Scabies Notifiable Disease NT. Improving Detection and Management Using Clinical Information Systems

**Presenter:** Michelle Dowden  
**Authors:** Ms Michelle Dowden

**Affiliations:** 1One Disease, Darwin

**Abstract:**

**Introduction:** In January 2016 Crusted Scabies was made a Notifiable Disease in the Northern Territory (NT) under the Notifiable Diseases Act NT. Crusted Scabies is notifiable by laboratory on detection of scabies mites and an IFD physician or Dermatologist review of the patient in order to meet the case definition.

An essential component of the public health response for Crusted Scabies is CDC informing local health service staff who the clients are with Crusted Scabies and what is required for management including household contacts. Most importantly people who have had Crusted Scabies must have lifelong follow-up which includes regular skin checks and live in a ‘scabies free zone’ to prevent reinfection.

**Method:** An audit of 488 flies within Clinical Information Systems (CIS) was undertaken. The purpose of the clinical audit was to determine the number of clients with a definite diagnosis of Crusted Scabies (CS) according the CDC case definition. The audit also determined if Crusted Scabies clients had flags and reminders in place for long term follow up and care.

**Results:** The findings of the audit revealed 85 clients had a definitive diagnosis of Crusted Scabies.

**Recommendations:** More education is needed around detection, diagnosis and long-term management of Crusted Scabies. The inclusion of electronic prompts within Clinical Information Systems will assist health service staff to provide appropriate, comprehensive and timely of care. In the same way a disease register is able to maintain records of a specific disease or condition for a population.

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P1.017 - Salmonella Sequelae: Post-Infectious Irritable Bowel Syndrome and Reactive Arthritis Following an Outbreak

**Presenter:** Siobhan St George  
**Authors:** Ms Siobhan St George1,2,3, Ms Joy Gregory2, Dr Katherine Gibney2,4, Dr Katrina Roper1

**Affiliations:** 1NCEPH - Australian National University, Canberra, Australia, 2Victorian Department of Health and Human Services (DHHS), Melbourne, Australia, 3Microbiological Diagnostic Unit Public Health Laboratory (MDU-PHL), University of Melbourne, Australia, 4Peter Doherty Institute for Infection and Immunity, Melbourne, Australia

**Abstract:**

**Introduction:** Despite the considerable estimated disease burden of sequelae due to Salmonella infection, a review of published literature found no publications on the incidence of post-infectious irritable bowel syndrome (PI-IBS), and a limited number on reactive arthritis (ReA) following Salmonella infection in Australia. The primary aim of this study was to determine the proportion of Victorian Salmonella cases associated with a recent outbreak that developed symptoms indicative of PI-IBS and/or ReA following their infection.

**Methods:** Eligible subjects were sent a questionnaire which asked whether they had experienced symptoms consistent with PI-IBS and/or ReA in the six month period since their Salmonella illness/infection. Descriptive statistics were used to analyse responses.

**Results:** 195 subjects with a median age of 45 years (62% female) were mailed the questionnaire. 87 subjects (44%) with a median age of 51 (69% female) responded. 24 respondents (28%) reported abdominal pain and gastrointestinal symptoms indicative of PI-IBS, and 11 (13%) reported experiencing new joint symptoms consistent with ReA.

**Conclusion:** Representing the first investigation into PI-IBS following Salmonella infection in Australia, this study found 28% of participants reported symptoms indicative of PI-IBS. This percentage is high compared to other studies, perhaps due in part to selection bias and/or the nature of self-reporting. The proportion of participants who reported symptoms indicative of ReA is comparable to other studies. This study contributes important local information that can be used to inform more complete estimates of the burden of Salmonella in Australia, allowing for global comparison and informed policy development and prioritisation.
P1.018 - Pneumococcal conjugate vaccine evaluation method for resource-limited settings: the LAO PDR example

Presenter: Fiona Russell

Authors: Fiona Russell1, Ruth Lim1, Eileen Dunne1, Keo Vilivong1, Jana Lai2, Molina Choummannivong4, Vanphanom Sychareun4, Jocelyn Chan2, S Phommachanh3, Malisa Vongsakdi3, Chanthphone Siladeth3, Melinda Morpeth3, Amy Gray3, R Phetsouvanh3, Jason Hinds4, Siddhattha Datta4, Kim Fox4, Paul Newton4, Cattram Nguyen4, David Dance3, Kim Mulholland2, Anohn Xeuatvongsa2

Affiliations: 1The University of Melbourne, Parkville, Australia, 2Murdoch Childrens Research Institute, Parkville, Australia, 3Lao-Oxford-Mahosot Hospital- Welcome Trust Research Unit, Vientiane, Lao PDR, 4University of Health Sciences, Vientiane, Lao PDR, 5St George’s, University of London, London, UK, 6World Health Organization, Vientiane, Lao PDR, 7Center for Disease Control, Atlanta, USA, 8Ministry of Health, Vientiane, Lao PDR

Abstract:

Introduction: The World Health Organization has pneumococcal conjugate vaccine (PCV) impact evaluation guidelines, yet few low-income countries (LICs) can employ the methodologies outlined. In Lao PDR, the 13-valent PCV (PCV13) was introduced in 2013. We describe PCV13 impact methods to augment existing guidelines and describe preliminary findings.

Methods: Hospital-based acute respiratory infection (ARI) and carriage surveillance: In a 3y prospective study of 2-59m old children admitted with ARI, clinical features and PCV13 status are recorded, and a nasopharyngeal (NP) swab is taken. Vaccine effectiveness (VE) against hypoxic ARI was calculated using odds ratios, which were estimated using logistic regression models, adjusted for age, season and time since PCV13 introduction. PCV13 carriage rates were calculated by month.

Community pneumococcal NP carriage surveys: Pre- and two years post-PCV13 carriage surveys of healthy infants too young to be vaccinated and toddlers 12-23m old were undertaken. NP swabs are examined by lytA qPCR, with molecular serotyping performed by microarray.

Results: There were 438 children with ARI and 13.5% were hypoxic. Hypoxic ARI was less common in PCV13 vaccinated than unvaccinated children (10.8% vs 19.9%, p=0.01). The unadjusted and adjusted PCV13 VE against hypoxic ARI were 0.52 (95%CI 0.14-0.73, p=0.012) and 0.35 (95%CI 0.23-0.65, p=0.185), respectively. PCV13 carriage rates are declining in vaccinated children with ARI. Pre-PCV13 carriage rates of PCV13 types were 6.3% and 32.8% in the infants and toddlers, respectively. Post-PCV13 results are pending.

Conclusion: We expect evidence of PCV impact in Laos PDR using this feasible approach for LICs.

P1.019 - Influenza Antiviral Prophylaxis for Outbreaks in NSW Residential Aged Care Facilities

Presenter: Robin Gilmour

Authors: Ms Robin Gilmour1, Miss Wedyan Meshreky2, Miss Daneeta Hennessy2, Dr Sean Tobin1, Dr Vicky Sheppeard1

Affiliations: 1Health Protection Nsw, North Sydney, Australia, 2NSW Health Department, North Sydney, Australia

Abstract:

Background: Influenza outbreaks are common in residential aged care facilities (RACF) and place vulnerable residents at a greater risk of hospitalisation and death. National control guidelines recommend that influenza antivirals (IA) be considered for prophylaxis as well as treatment during RACF influenza outbreaks. A 2014 Cochrane review questioned the value of IA for both treatment and prophylaxis. This study explored the impact of IA prophylaxis on RACF influenza outbreaks reported to NSW public health units (PHU) during the 2015 winter influenza season.

Methods: We conducted a retrospective cohort study of influenza outbreaks reported to NSW PHUs from 1 June 2015 to 31 October 2015. Outcome measures were influenza attack rate and outbreak duration.

Results: Influenza outbreaks in 86 RACFs were included. A total of 145 (1.6%) residents were hospitalised and 54 (0.6%) residents died. 52 RACFs used IA prophylaxis and 34 did not. Shorter mean outbreak duration and lower attack rates were observed in the prophylaxis group. However, there were no statistically significant differences observed between the two groups.

Conclusion: Variations in the implementation of outbreak response measures within and between groups made it difficult to draw conclusion about the value, if any, of IA prophylaxis. The study provided valuable insights into the challenges faced by RACFs when implementing IA prophylaxis along with challenges in the collection of data in the RACF setting. Suggestions are made for improving the management of influenza outbreaks in RACFs according to national control guidelines.
**P1.020 - Harm, risk, benefit balance: patient notification and the utilitarianism of public health**

**Presenter:** Meredith Wickens  
**Authors:** Ms Meredith Wickens\(^1\), Dr Christine Selvey\(^1\), Dr Vicky Sheppeard\(^1\), Dr Jeremy McAnulty\(^1\)  
**Affiliations:** \(^1\)Health Protection NSW, North Sydney, Australia  
**Abstract:**
Notifying patients following potential risk exposure can facilitate early diagnosis and treatment, as well as avert ongoing public health risk by avoiding further transmission.  
In 2015 and 2016 four large patient notification activities were carried out in Sydney, NSW following identification of potential infection risk from breaches of infection control in private dental practices. Patients who had had invasive procedures were advised to attend their general practitioner to seek testing for hepatitis B (HBV), hepatitis C (HCV) and HIV.  
An evaluation of blood borne virus (BBV) notifications received by NSW Health following the largest activity was conducted. While four patients with HBV infection and four with HCV infection reported no risk factors for infection other than their invasive dental procedure, it was not possible to identify definitive evidence of transmission of infection at the clinics.  
Patient notification activities are resource intensive, and will varyingly impact individual patients, practitioners, health systems and the community at large. Assessment of factors including financial costs, physical and mental health outcomes and public confidence in healthcare, and to whom these accrue, must be considered to balance the harms, risks, and benefits.  
While separate incidents will continue to require individualised assessment, a streamlined approach facilitated by agreed parameters may provide guidance, consistency and transparency for future decision making by public health agencies.

**P1.021 - Suspected Outbreak of Lassa Fever in Plateau State, Nigeria: Retrospective Data Assessment**

**Presenter:** Stephen Akar  
**Authors:** Mr Stephen Akar\(^1\), Mr Celestine Ameh\(^1\), Dr Patrick Nguku\(^1\)  
**Affiliations:** \(^1\)Nigerian Field Epidemiology and Laboratory Training Programme/African Field Epidemiology Network, Abuja, Nigeria  
**Abstract:**
**Background:** Nigeria remains endemic for Lassa fever, a viral haemorrhagic disease caused by the Lassa fever virus. Bauchi State has consistently reported cases annually since 2012. On 22nd August, 2016, a 27-year old woman from Tafawa Balewa LGA died of Lassa fever. The objective of this study was to determine the socio-demographic characteristics of health workers in Tafawa Balewa LGA of Bauchi State.  
**Methods:** A cross-section study involving the use of pre-tested semi-structured questionnaires was used to obtain data from health workers in Tafawa Balewa LGA of Bauchi State. Data obtained include: age, sex, marital status, occupation/profession, years of experience, Lassa fever training. Descriptive statistics was done on the variables with categories expressed in frequencies and proportions.  
**Results:** A total of 73 health workers were interviewed across nine health facilities. Males constituted 43.8% (32) of health workers. The average age was 28.3 years. Medical doctors constituted 5.5%(4) of health workers, nurses 13.7(10), laboratory professionals 13.7%(10), CHEW 21.9%(16), EHO 5.9%(5), student trainees 32.9%(24) and others 5.5%(4). While 54.8% (40) of health workers were married 43.8% (32) and 1.4% (1) were single and widowed respectively. Equal proportions of health workers (49.3%) belong to the Islamic and Christendom faith. The average years of practice was 6.03 years. The proportion of health workers who had no Lassa fever training was 83.6% (61).  
**Conclusion:** The proportion of health workers with Lassa fever training is grossly inadequate to combat nosocomial transmission of the virus as the disease continue to occur annually in the LGA and neighboring States.
P1.022 - Hepatitis E virus infection in a cohort of patients with acute hepatitis

Presenter: Helen Faddy

Authors: Dr Helen Faddy1, Dr Ashish Shrestha1, Mr Oliver McGrath2, Prof. Graeme Nimmo3, Mr Robert Gibb3, Prof. Robert Flower1

Affiliations: 1Research and Development, Australian Red Cross Blood Service, Brisbane, Australia, 2School of Biomedical Sciences, Queensland University of Technology, Brisbane, Australia, 3Central Laboratory, Pathology Queensland, Brisbane, Australia

Abstract:

Introduction: Viral hepatitis is caused by a number of different viruses, including hepatitis E virus (HEV). Indeed, HEV has emerged globally as one of the causative agents of acute hepatitis. In non-endemic countries, HEV infection is mainly considered in acute hepatitis patients with recent overseas travel history. However, autochthonous HEV infections in many countries traditionally considered non-endemic are increasingly being reported, thus HEV cases may be missed in non-travellers. This study measured the frequency of HEV infection in a cohort of patients with non-A, non-B, non-C hepatitis.

Methods: Samples (n=981) from Queensland patients with non-A, non-B, non-C hepatitis were tested for the presence of HEV IgG, IgM and antigen.

Results: Overall 55 samples (5.61%; 95% CI: 4.17-7.05%) were positive for HEV IgG. Age, sex, ALT levels and ethnicity were not associated with HEV IgG sero-positivity. HEV IgM, or HEV antigen, were detected in 3, or 4 samples, respectively.

Conclusion & Recommendation: Markers of HEV infection were detected in a cohort of Queensland patients with acute hepatitis. The rate of prior infection was similar to the Australian blood donor population. Markers of current infection were detected, but at a lower rate than expected; additional studies are required to identify other causes of hepatitis. These results, together with our previous work showing HEV IgG in ~6% Australian blood donors, including detectable HEV IgG in donors with no overseas travel, suggest autochthonous HEV infection in Australia occurs, which necessitates increased Australian public health awareness with respect to HEV.

P1.023 - Does Queensland chew into more than it’s fair share of rabies immunoglobulin?

Presenter: Penny Hutchinson

Authors: Dr Penny Hutchinson1, Dr Margaret Young2, Dr Kari Jarvinen1, Dr Bhakti Vasant3, Dr James Smith4

Affiliations: 1Darling Downs Hospital and Health Service, Toowoomba, Australia, 2Wide Bay Hospital and Health Service, Hervey Bay, Australia, 3Metro South Hospital and Health Service, Brisbane, Australia, 4Metro North Hospital and Health Service, Brisbane, Australia

Abstract:

Australia is free of terrestrial lyssavirus. Post exposure prophylaxis (PEP) is provided for potential Australian Bat Lyssavirus exposures and potential lyssavirus exposures overseas. Human Rabies Immunoglobulin (HRIG) use is escalating for monkey bites and scratches, although transmission risk is minimal. We examined PEP use in Queensland to inform a search for alternative approaches that promote sustainable HRIG use and potentially promote equitable HRIG distribution globally.

Case report data for all potential lyssavirus exposures in Queensland were extracted for the period 1/1/2015 to 31/8/2016. Data analysis included volume of HRIG that could potentially be saved was calculated based on recent Public Health England recommendations for more streamlined PEP.

6,224 mLs HRIG was used in the 20-month period. Most lyssavirus exposures (493/885) occurred outside Australia, of which 62 percent occurred in Indonesia, predominantly Bali. Two-thirds of overseas exposures involved monkey interactions. A saving of 1,565 mLs HRIG would have been made if contemporary UK guidelines were followed.

Disproportionate HRIG use by wealthy countries is an issue of global distributive justice. Increasing obesity and travel to rabies-endemic countries, will increase HRIG use. Current PEP guidelines to prevent human rabies in Australia and other industrialised nations raise ethical dilemmas. HRIG sparing PEP options, exposure avoidance and support for canine rabies control in resource poor countries should be considered.

Australia needs to work more closely with relevant international animal and human health authorities, to better understand the risk profile of contact with non-human primates.

P1.024 - An outbreak of staphylococcal gastroenteritis associated with Asian market food, Northern Territory.

Presenter: Anthony Draper

Authors: Mr Anthony Draper1, Mr Michael Spry2, Ms Claire Morton2, Mr Sean Bourke2, Mr Joshua Heath3, Ms Sheree Scott4, Mr Justin Lim2, Ms Elva Gela2, Mr Christian James3, Dr Peter Markey3
Abstract:

**Introduction:** We investigated 2 outbreaks of acute gastroenteritis after people consumed laksa. Both outbreaks triggered an alert from the Emergency Department Syndromic Surveillance System at Royal Darwin Hospital.

**Methods:** We conducted a case series and environmental investigation of implicated sites and collected food samples. A case was anyone who experienced vomiting and/or diarrhoea after eating Asian food in Darwin, from 8 August 2016. We used a standard questionnaire to collect clinical information and record food consumption. Additional cases self-reported following media reports.

**Results:** There were 24 cases; 100% reported vomiting; 23/24 (96%) reported diarrhoea. The median incubation period was 3 hours (range 0.7 – 20 hours) and median illness duration was 6 hours (range 1-24 hours). Staphylococcal enterotoxin was detected in 2/3 stool samples and 3 samples of cooked laksa. Uncooked noodles from 5 Asian restaurants in Darwin were sampled but staphylococcal enterotoxin wasn’t detected. However, unacceptable levels of Bacillus cereus and Staphylococcus aureus were detected in uncooked noodles originating from one local supplier. These noodles were stored at ambient temperature by a market stall trader prior to serving which facilitated bacterial growth. Environmental health observations resulted in this market stall trader and the noodle supplier being issued prohibition notices for breaches of the Food Act.

**Conclusion and recommendations:** A safe environment is required for production of market food. Storing noodles at ambient temperature prior to serving facilitates the growth of organisms if the noodles are contaminated during or soon after production. Noodles should be refrigerated to prevent gastroenteritis outbreaks.

**P1.025 - SMS for post-licensure vaccine surveillance – Acceptable to participants? STARSS RCT**

**Presenter:** Gabriella Lincoln

**Authors:** Professor Michael Gold1, Dr Gabriella Lincoln1, Professor Nigel Stocks1, Professor Annette Braunack-Mayer1

**Affiliations:** 1University of Adelaide, Australia

**Abstract:**

In Australia there is increasing use of active SMS based surveillance for post-licensure surveillance of vaccines. However, few studies have evaluated public attitudes, acceptability (including the requirement for consent) and evaluated the impact of SMS based surveillance on perceptions of vaccine safety.

The Stimulated Telephone Assisted Rapid Safety Surveillance (STARSS) study is an NHMRC funded RCT whose primary aim is to evaluate the detection of Adverse Events Following Immunisation (AEFI) by using two SMS intervention groups utilising nurse-assisted and self-reported follow-up as compared to a control group. Four weeks following enrolment a random sample of participants is contacted in-order to administer a comprehensive telephone survey. The survey covers questions on attitudes to public health safety surveillance and vaccine safety, trust in the sources of health information including the internet, data privacy and issues around opt-in and opt-out consent. In addition, the survey aims to capture information about medical events experienced but not reported to the STARSS system and the reason for non-response to the surveillance SMS reminders.

To date over 2,800 participants (SMS intervention and control groups) have been enrolled in STARSS (covering all ages and all vaccines) from 30 GP, local council and hospital sites in South Australia and New South Wales. 937 participants have completed the survey. In this presentation we will present the preliminary findings of this survey.

**Concurrent Session 2A – One Health**

Grand 1&2, 2:00pm – 3:30pm

**Psittacosis from horses, what’s the risk? Applying OneHealth surveillance to emerging zoonoses**

**Presenter:** Kat Taylor

**Authors:** Dr Kat Taylor1, Dr Peter Massey1, Dr James Branley, Dr Catherine Chicken, Dr Joan Carrick, Dr Jane Heller2, Paul Freeman3, Brendon O'Rourke4, Dr Kirsty Hope4, Dr Rod Givney, Professor David Durrheim1

**Affiliations:** 1Hunter New England Local Health District, Newcastle, 2Charles Sturt University, 3NSW Department of Primary Industries, 4NSW Health Protection, Ministry of Health
Abstract:

Introduction: Recent case reports of undiagnosed human illness clusters associated with Chlamydia psittaci-affected equine reproductive events identified the need for a systematic approach to investigating this emerging risk. We developed a OneHealth surveillance platform in a sentinel horse breeding district, which was piloted during the 2016 foaling season.

Methods: A multidisciplinary team was formed with representation from State animal and human health agencies, reference laboratories, Infectious Diseases, the local equine veterinary practice and medical practice and academic institutions. Surveillance protocols detailing cross-notification of equine cases of Chlamydia psittaci and public health follow-up of human contacts were developed consultatively. Contacts of PCR-confirmed equine cases were interviewed using a structured questionnaire. Regular surveillance updates were provided to participating agencies.

Results: Between June and November 2016, 184 equine reproductive losses occurred, of which 37 (20%) tested positive for C. psittaci PCR. A total of 58 human contacts were identified, of which 42 were successfully interviewed. 12 people were investigated for psittacosis (8 symptomatic, 4 asymptomatic). C. psittaci PCR was negative for all tested, while respiratory PCR testing yielded alternate diagnoses in two people. Two people had serological evidence of previous Chlamydia species exposure and two demonstrated seroconversion on screening enzyme-linked immunosorbent assay (ELISA), but none met the standard case definition for acute psittacosis on subsequent confirmatory microimmunofluorescence testing.

Conclusions and recommendations: We successfully applied OneHealth principles to explore an emerging equine pathogen. Despite intensive follow-up, no confirmed cases of psittacosis were identified, suggesting the risk of zoonotic transmission, if any, is low.

Paediatric invasive Group a Streptococcus… an underrated disease in the developed world

Presenter: Natasha Ching

Authors: Dr Natasha Ching1,2, Dr Nigel Crawford3,4,5, Mrs Alissa McMinn3, Mrs Ciara Baker2,4, Ms Kate Brownlee3, Mrs Margaret Gibson3, Mrs Donna Lee3, Dr Pierre Smeesters2, Mrs Gena Gonis6, Dr Samar Ojaimi1,7, Associate Professor Jim Buttery1,3,7, Associate Professor Andrew Steer2,4,5

Affiliations: 1Department of Paediatrics, Monash University, Clayton, Australia, 2Group A Streptococcus Research Group, Murdoch Children’s Research Institute, Parkville, Australia, 3SAEFVIC, Murdoch Children’s Research Institute, Parkville, Australia, 4Department of Paediatrics, University of Melbourne, Parkville, Australia, 5Department of General Medicine, Royal Children's Hospital, Parkville, Australia, 6Department of Microbiology, Royal Children's Hospital, Parkville, Australia, 7Department of Infectious Diseases, Monash Children's Hospital, Clayton, Australia

Abstract:

Background: Group A beta-haemolytic streptococcus (GAS) can cause serious invasive illness in children, with associated morbidity and mortality. Clinical disease covers a wide spectrum, from pharyngitis to severe disease such as toxic shock syndrome and necrotising fasciitis. In Australia, invasive GAS (iGAS) is currently notifiable in Queensland and Northern Territory only.

Methods: Data were prospectively collected through active iGAS surveillance at Royal Children’s Hospital Melbourne (October 2014 – October 2016). Main inclusion criteria was GAS isolation from a sterile site. Comprehensive demographic and clinical data were collected following consent and enrolment. Severe iGAS cases required either mechanical ventilation or inotropic support; very severe disease - extracorporeal membrane oxygenation. emm-typing was performed following the Centre of Disease Control GAS protocol.

Results: 33 cases were recruited; five were excluded from analysis (GAS not isolated from a sterile site). 28 cases were analysed, median age 3.5 years (range 4 days to 11 years). There were ten cases (35.7%) with severe disease; two cases of very severe disease. Ten children (37.5%) had presented to an emergency department during the illness preceding their admission presentation; half had severe disease. A wide-spectrum of clinical disease was observed: bacteraemia without focus (n=12, 37.5%), pneumonia/empyema (n=6, 18.8%) and osteoarticular disease (n=5, 17.9%). emm types confirmed in 22 cases (78.6%) with emm1 and emm4 each identified in 6 cases (42.9%) respectively.

Conclusion: There is considerable morbidity associated with iGAS disease in children. We are currently expanding an Australia wide iGAS pilot surveillance system via the PAEDS network [http://www.paeds.edu.au/].

Prevalence of Scabies and Impetigo in School Children in Timor-Leste

Presenter: Laura Korte

Authors: Dr Laura Korte1,2, Anthony Draper3,4, Dr Annette Appelbe6, Ben Dingle6, Dr Asha Bowen7, Dr Joshua Francis1,8

Affiliations: 1Royal Darwin Hospital, Darwin, Australia, 2Hospital Nacional Guido Valadares, Dili, Timor Leste, 3NT Centre for Disease Control, Darwin, Australia, 4National Centre for Epidemiology and Population health, Australian National University, Canberra, Australia, 5Kensington Hill Medical Centre, Leopold, Australia, 6St John of God, Dili, Timor Leste, 7Princess Margaret Hospital for Children, Subiaco, Australia, 8Menzies School of Health Research, Darwin, Australia
Abstract:

Introduction: Scabies and impetigo are common and important skin conditions which are often neglected in developing countries. The prevalence of these conditions in Timor-Leste is unknown. Sequelae including cellulitis, bacteraemia, nephritis, acute rheumatic fever and rheumatic heart disease contribute significantly to the burden of disease.

Methods: We conducted an epidemiological survey in October 2016. School students were recruited from schools in Dili (urban) and Ermera (rural) in Timor-Leste. We used a standard questionnaire to record demographics, anthropometry and skin examination results. Prevalence of scabies and impetigo were calculated and binary risk factors described using relative risks and 95% confidence intervals. Continuous variables for were analysed for associations using the Mann-Whitney Rank Sum test. Results were considered significant if p<0.05.

Results: 1407 students were enrolled; with median student age of 12 years (range 4-24). The prevalence of scabies was 22% and active impetigo 10%; 68% of students had evidence of either active or healed impetigo. Students in Ermera were more likely than those in Dili to have scabies (RR 6.3; 95%CI 4.3 - 9.2, p<0.01) and scabies and active impetigo co-infection (RR 8.9; 95%CI 3.3 - 24, p<0.01). There was no difference in the prevalence of active impetigo between urban and rural sites.

Conclusion: Scabies and impetigo are prevalent in Timor-Leste, with particularly high prevalence of scabies in the rural district of Ermera. Improvements in prevention and treatment are needed, and consideration should be given for implementing strategies at a community level, focusing on rural areas.

An outbreak of Q fever associated with domestic animals in Southeast Queensland

Presenter: Jonathan Malo

Authors: Dr Jonathan Malo, Dr Candice Colbran, Deborah Judd, Bhakti Vasant, Dr Kari Jarvinen, Dr Megan Young, Dr Stephanie Davis, Dr Stephen Lambert

Affiliations: Communicable Diseases Branch, Queensland Health, Herston, Australia, Metro South Public Health Unit, Coopers Plains, Australia, National Centre for Epidemiology and Public Health, Australian National University, Acton, Australia, Metro North Public Health Unit, Windsor, Australia, Menzies Health Institute Queensland & School of Medicine, Griffith University, Gold Coast, Australia, UQ Child Health Research Centre, University of Queensland, South Brisbane, Australia

Abstract:

Introduction: In November 2016, Metro South Public Health Unit received laboratory notification of a case of Q fever in an animal refuge worker, with reports of illness in other workers and in staff at an adjacent veterinary clinic. An outbreak investigation and cohort study were subsequently undertaken to identify the likely source of transmission.

Methods: A case definition was developed for confirmed and probable cases. All workers with recent illness were encouraged to attend their general practitioner for Q fever serology. Workplace Health and Safety undertook a site visit to review infection control practices. Animal euthanasia records were reviewed. A self-administered workplace-activities questionnaire was distributed among employees. Analysis was performed in Stata 14. Environmental and animal samples were not taken.

Results: Seven (6 confirmed, 1 probable) cases were identified with illness onset dates from 24 October–20 November 2016. Two feline birthing events with subsequent euthanasia occurred during the likely exposure period, with no livestock births or slaughtering reported. Forty-three (92% response rate) workplace activity questionnaires were completed. Three non-cases who had received prior Q fever vaccination were excluded from analysis. Activities associated with greatest risk of illness were disposal of deceased cats/dogs (RR 14.00, 95% CI 1.88–104.08) and providing or assisting with euthanasia of cats/dogs (RR 4.59, 95% CI 1.25–16.85). No livestock-related activities were significantly associated with illness.

Conclusions: This is only the second reported Q fever outbreak in Australia associated with workplace domestic animal contact. Appropriate disease control measures should be taken in workplaces where cats or dogs are giving birth or euthanised.

Introduction of a program to control rheumatic heart disease in NSW

Presenter: Melanie Middleton

Authors: Ms Melanie Middleton, Mr Chris Lowbridge, Dr Jeremy McAnulty, Dr Vicky Sheppeard

Affiliations: Health Protection NSW, North Sydney, Australia

Abstract:

Background: Rheumatic Heart Disease (RHD) is a preventable complication of an infection with group A streptococcus (GAS). In Australia, RHD is correlated with poverty and crowded living conditions and its incidence is disproportionately high among Aboriginal people. People with RHD and its precursor Acute Rheumatic Fever (ARF) need long-term treatment to prevent further damage to the heart. NSW Health has established a new program to improve the management of people with ARF/RHD.
Methods: RHD in people aged <35 years and ARF were added to the list of notifiable conditions in NSW in October 2015, and a register for people with ARF/RHD was established in May 2016. Prospective case finding for people with ARF/RHD was conducted using hospitalisation data.

Results: There were 31 notifications of ARF (21) and RHD (14) reported between October 2015 and December 2016, including four people with both conditions. Fifty-eight percent of diagnoses were in females, and over 80% of diagnoses were in people aged less than 25 years, with 58% in people aged 5 to 14 years. Almost 75% of cases were in people born in Australia. However, over 85% of cases had a high risk background: 42% were Aboriginal and Torres Strait Islander people; 32% were people reporting Maori and Pacific Islander ancestry; and 12% were in people born in other high RHD prevalence countries.

Conclusions: A high proportion of ARF/RHD cases in NSW were in non-Indigenous persons. Specific resources for these populations, particularly Maori and Pacific Islanders, may need to be developed.

Longevity of immunity following Q fever vaccination

Presenter: Nicholas Wood

Authors: Associate Professor Nicholas Wood, Dr Jacqui Norris, Dr Katrina Bosward, Dr Heather Gidding, Professor Peter McIntyre, Dr Emily Sellens, Dr Jane Heller, Professor David Durrheim, Dr Rowland Cobbold, Professor Stephen Graves

Affiliations: 1University Of Sydney, Westmead, Australia, 2University of Sydney, Camperdown, Australia, 3University of Sydney, Camperdown, Australia, 4University of New South Wales, Randwick, Australia, 5National Centre for Immunisation Research and Surveillance, Westmead, Australia, 6University of Sydney, Camperdown, Australia, 7Charles Sturt University, Wagga Wagga, Australia, 8Hunter New England Public Health Unit, Newcastle, Australia, 9University of Qld, Brisbane, Australia, 10Australian Rickettsial Reference Laboratory, Geelong, Australia

Abstract:

Introduction: There is little information on duration of protection afforded by vaccination and the relationship between vaccine protection and natural boosting from exposure. The Australian Immunisation Handbook states that protection lasts at least 5 years and repeat doses of Q fever vaccine are not recommended. Investigating cellular and humoral responses post vaccination is poorly studied with none measuring responses beyond 5 years post vaccination.

Aims: To measure seroprevalence in veterinarians and correlate results with Q fever vaccine history.

Methods: Individuals attending veterinary conferences in Australia in 2013, 2014 and 2015 were recruited to provide a blood sample and complete a questionnaire including sex, age, postcode and type of work, QVax status and year received Q fever vaccine history. QVax status was recorded from Queensland Health Immunisation Register. In Queensland, people who receive QVax are required to provide contact details. Of the 977 attendees who provided consent, 667 (68.5%) provided a blood sample and completed a questionnaire. QVax status was available for 638 (70.1%) of the cohort.

Results: Q fever serology was measured in 364 veterinarians, (n=208, 57% reported receiving QVax), with n=36 (17%) and n=56 (27%) being vaccinated 10-15 years and >15 years prior to serology being measured). Of 208 vaccinees, 10% and 13% were phase 1 IgG and phase 2 IgG positive respectively. Seropositivity to phase 1 and 2 IgG (17%) and n=56 (27%) was measured by the Australian Rickettsial Reference Laboratory, Victoria.

Conclusions: In this cohort of Australian veterinarians who reported receiving QV fever vaccine over 80% were seronegative to phase 1 and 2 IgG. However, despite being seronegative repeat vaccine is not currently recommended. Further research including cellular immunity is underway.
Abstract:

Introduction: Pneumococcal conjugate vaccines (PCVs) prevent disease through both direct protection of vaccinated individuals, and indirect protection of unvaccinated individuals through reduction of nasopharyngeal (NP) carriage and transmission of vaccine-type pneumococci. While the indirect effects of PCV vaccination are well described, the PCV coverage required to achieve the indirect effects is unknown. We will determine this using hospital-based NP pneumococcal carriage surveillance at three sites in the Asia-Pacific region.

Methods: Surveillance includes children aged 2-59 months admitted to participating hospitals at three sites with acute respiratory tract infection. Thirteen-valent PCV (PCV13) status is obtained from written records. An NP swab is collected according to standard methods and examined by lytA qPCR, with positives serotyped by microarray. PCV13 coverage is determined using administrative data or community survey.

Results: In Lao PDR, Papua New Guinea, and Mongolia, we have recruited 973, 204, and 240 children, respectively. For each site, we will present monthly PCV13 carriage rates. In Laos PDR, where PCV13 coverage is <50%, PCV13 carriage rates are declining among vaccinated children (direct effects) but not unvaccinated children (indirect effects). Data will also be pooled across sites to examine relationships between PCV13 coverage and carriage.

Conclusion: As PCV13 coverage increases, we hypothesise that PCV13 carriage to decline in vaccinated and unvaccinated individuals. These results will inform vaccine policy makers about the PCV coverage required to maximise the effects of PCV.

CLOSING THE GAP: IMPACT OF THE NSW ABORIGINAL IMMUNISATION HEALTHCARE WORKER PROGRAM

Presenter: Frank Beard

Authors: Dr Frank Beard1,2, Dr Alexandra Hendry1, Dr Aditi Dey1,2, Mr Dennis Meijer2, Ms Sue Campbell-Lloyd3, Mr Brynley Hull3, Ms Katrina Clark1, Dr Vicky Sheppeard2,3

Affiliations: 1National Centre for Immunisation Research and Surveillance, Australia, 2University of Sydney, Australia, 3Health Protection NSW, Australia

Abstract:

Introduction: Aboriginal and Torres Strait Islander (hereafter referred to as Aboriginal) Australians suffer higher rates of vaccine preventable disease than non-Aboriginal Australians. Disparities in coverage and timeliness of vaccination in Aboriginal children remain a concern. The NSW Aboriginal Immunisation Healthcare Worker (AIHCW) program was introduced in 2012 to improve coverage and timeliness. We aimed to assess impact of the AIHCW program.

Methods: Using data from the Australian Immunisation Register, we compared annual estimates for ‘fully immunised’ coverage at 9, 15 and 50 months of age, and percentage of children vaccinated on time (receipt of dose within 30 days after recommended age) between 2009 and 2015, for Aboriginal and non- Aboriginal children in NSW versus rest of Australia.

Results: Between 2011 and 2015, the gap in ‘fully immunised’ coverage between Aboriginal and non- Aboriginal children in NSW decreased from 5% to 3% at 9 months, 5% to 1% at 51 months, and remained at 3% at 15 months of age. The gap in on-time vaccination between Aboriginal and non- Aboriginal children in NSW decreased from 17% to 13% for third dose DTPa, 11% to 10% for first dose MMR, 9% to 4% for fourth dose DTPa, and 8% to 4% for second dose MMR. In the rest of Australia the reduction in gaps was consistently lower.

Conclusion and recommendation: This study suggests that commitment of resources into a dedicated AIHCW program in NSW has had greater impact on closing the Aboriginal immunisation gap in NSW, compared to the rest of Australia.

CARRIAGE OF N. MENINGITIDIS IN FIRST YEAR UNIVERSITY STUDENTS IN SOUTH AUSTRALIA

Presenter: Helen Marshall

Authors: Professor Helen Marshall1,2,3, Mr Mark McMillan2,3, Ms Su-san Lee3, Dr Phillipa Rokkas3, Mr Andrew Lawrence4, Associate Professor Ann Koehler5,6, Mrs Maureen Watson6, Mr Thomas Sullivan5

Affiliations: 1Robinson Research Institute, The University Of Adelaide, 72 King William Rd. North Adelaide, Australia, 2Adelaide Medical School, The University of Adelaide, Adelaide, Australia, 3Women’s and Children’s Health Network, Adelaide, Australia, 4SA 

Abstract:

Introduction: Carriage of Neisseria meningitidis (N. meningitidis) is an indicator of vaccinepreventable disease and transmission. It is an important marker of the population levels of meningococcal transmission and therefore of vaccine programme impact. N. meningitidis carriage reflects the balance of transmission, vaccine effect and vaccine coverage. In South Australia, first year university students have been regarded as a target group for meningococcal vaccination campaigns due to the burden of meningococcal disease and the potential for spread of infection.
Pathology, Adelaide, Australia, 5School of Population Health, The University of Adelaide, Adelaide, Australia, 6SA Health, Adelaide, Australia

Abstract:

Introduction: Adolescents and young adults have the highest carriage prevalence (up to 25%) of N. meningitidis. In Australia no data exist on carriage rates in this age group. A meningococcal B (MenB) vaccine is currently licensed and recommended in Australia. The South Australia MenB vaccine herd immunity study will assess the impact of the MenB vaccine on meningococcal carriage in South Australian adolescents and includes:

1. A cluster RCT to assess the impact of MenB vaccine on carriage in 45,000 (years 10/11/12) school students.
2. An observational longitudinal study assessing carriage in first year university students
3. An observational cross-sectional study assessing carriage prevalence in university students following a MenB vaccine program in school students.

Methods: Part 2: Prospective recruitment of 500 first year university students in February 2017. Oro-pharyngeal swabs will be taken by trained staff using a standardised procedure, swabs placed in STGG transport medium and transported to the laboratory. A questionnaire identifying risk factors will be completed by students. qPCR will be performed on all samples on arrival. Aliquots from each sample will be frozen at different time intervals following receipt of the samples (6, 16, 48 hours) to compare culture of isolates following delayed freezing of samples.

Results: Study 2 results will report baseline carriage prevalence and 3 months later in first year university students in SA.

Conclusions: The impact of the MenB vaccine on carriage is not well understood. This study will provide important data to inform policy makers in Australia and internationally.

Impact of SMS and Calendar Reminders on Infant Immunisation Timelines in Australia

Presenter: Rob Menzies

Authors: Dr Rob Menzies1, Mr Mark McMillan2,3, Dr Leon Heron4,5, Ms Jenny Lampard4, Ms Telphia Joseph1, Dr Jocelyn Chan5,6, Ms Adrienne Storken7, Professor Helen Marshall2,3

Affiliations: 1School of Public Health and Community Medicine, UNSW, Sydney, Australia, 2Vaccinology and Immunology Research Trials Unit, Women’s and Children’s Hospital, Adelaide, Australia, 3Robinson Research Institute and Adelaide Medical School, University of Adelaide, Adelaide, Australia, 4Kids Research Institute, The Children’s Hospital Westmead, Sydney, Australia, 5National Centre for Immunisation Research and Surveillance, The Children’s Hospital at Westmead, Sydney, Australia, 6National Centre for Epidemiology and Population Health, Australian National University, Canberra, Australia, 7Department of Health, Adelaide, Australia

Abstract:

Introduction: Although high coverage rates have been achieved for infant immunisation, infants may receive vaccinations late, leaving them susceptible to infectious diseases when they are most vulnerable. This randomised controlled trial aimed to assess the effectiveness of an intervention to improve on-time compliance with scheduled infant immunisations.

Methods: Consenting parents of infants <16 months of age were recruited from medical practices, Local Government Immunisation Clinics, Community Health Services and Aboriginal Medical services in South Australia and New South Wales and randomly assigned to one of four groups:

- SMS reminder messages only
- Printed reminder calendar only
- Both SMS messages and calendar
- No intervention (control)

Immunisation dates were obtained from the ACIR and compared to recommended schedule points. Relative risks and 95% confidence intervals of on-time compliance (within 30 days of due date) in intervention versus no-intervention groups were calculated in SAS v9.4.

Results: SMS messages but not reminder calendars increased the frequency of on-time compliance with immunisations scheduled for age 12 months: No intervention 207/279 (74%, reference), SMS 228/277 (82%, relative risk [RR] 1.45; 95% CI 1.05-2.00), Calendar 210/281 (75%, RR 1.02; 0.77-1.35), Both 245/281 (84%, RR 1.61; 1.14-2.22). RRs for on-time vaccination in the SMS vs no intervention groups at 6 and 18 months were above 1.0, but confidence intervals overlapped 1.0.
Conclusion and recommendation: SMS technology is a simple and effective intervention for improving timeliness of immunisation in infants. The impact in this high compliance population appears to be less than in some other populations.

Ten years of rotavirus immunisation in Australia: sustained benefits outweigh vaccine-associated risks

Presenter: Aditi Dey

Authors: Dr Aditi Dey1, Ms Han Wang1, Dr Helen Quinn1,2, Associate Professor Nicholas Wood1,2, Professor Peter McIntyre1,2, Associate Professor Kristine Macartney1,2

Affiliations: 1National Centre For Immunisation Research & Surveillance, Kids Research Institute, The Sydney Children’s Hospitals Network, Cnr Hawkesbury Road and Hainsworth Street, Westmead, Australia, 2University of Sydney, Australia

Abstract:

Introduction: Australia introduced two rotavirus vaccines to its fully funded National Immunisation Program (NIP) in July 2007. High vaccine uptake has been sustained despite detection of an increased risk of intussusception. We report on trends in hospitalisations and deaths for rotavirus, acute gastroenteritis (AGE) and intussusception before and after vaccine introduction.

Methods: Hospitalisation data from the Australian Institute of Health and Welfare for rotavirus, other AGE and intussusception, from January 2002 to December 2013 were analysed by age and Indigenous status, before and after vaccine introduction. Data were obtained from the Australian Bureau of Statistics and similarly assessed.

Results: There was a 78% reduction in rotavirus-coded hospitalisations in children aged <5 years in the post-rotavirus compared with pre-rotavirus vaccine period (from 270 down to 61 cases per 100,000, respectively) and a 26% decline in the 5–9 years age group. Hospitalisation rates for rotavirus and AGE remained higher in Indigenous than non-Indigenous children, although reduced compared with the pre-vaccination period. Intussusception declined overall in infants aged <12 months (and in the age bands of 3–<5, 5–<7, and 7–<9 months, respectively) but increased in infants aged 1–<3 months of age.

Conclusion: There has been a substantial decline in rotavirus hospitalisations following introduction of rotavirus vaccines to the NIP. Although there was a short term increased risk of intussusception following the first vaccine dose, intussusception hospitalisations in older infants have declined or remained unchanged. This data demonstrates the ongoing benefits of rotavirus vaccination in Australia.

The emergence of serogroup W invasive meningococcal disease (IMD) in Western Australia

Presenter: Gary Dowse

Authors: Dr Gary Dowse1, Assoc Prof Charlene Kahler2, Ms Carolien Giele3, Ms Jane Bew3, Dr Paul Armstrong1, Shakeel Mowlabocus1, Dr Clare Huppatz1, Dr David Speers3

Affiliations: 1Communicable Disease Control Directorate, WA Department Of Health, Perth, Australia, 2School of Pathology and Laboratory Medicine, University of WA; Marshall Centre for Infectious Disease Research and Training, Perth, Australia, 3PathWest Laboratory Medicine, QEII Medical Centre, Perth, Australia, 4WA Country Health Service, Kalgoorlie, Australia

Abstract:

Introduction: Serogroup B organisms have caused 85% of IMD in WA since 1991, but in 2016 there was an historically low 6 cases. By contrast, serogroup W (MenW) IMD has increased sharply from an average of 1 case per year to 4 cases in 2015 and 14 (61%) in 2016.

Methods: Descriptive analysis of WA notification data, including whole genome sequencing (WGS) data for the period 2013-16.

Results: Compared to long-term notified IMD cases, the 21 MenW cases notified in 2013-2016: were more likely to have atypical clinical presentations (including septic arthritis, pneumonia and epiglottitis/pharyngitis); were older on average; and had higher case fatality (14% vs 5%). One third of cases were Aboriginal children under 5 years of age, including two pairs of linked cases in separate rural community settings. All MenW cases belonged to the ST 11 clonal complex, but WGS indicated three sub-clusters: the first two most likely had a common antecedent and included cases notified between 2013 and 2016, with epidemiological clustering in a southern coastal town and northern Perth suburbs. The third cluster was highly clonal and contained 7 cases notified between July and November 2016, 5 of whom resided in or were linked to the Kalgoorlie area (along with a further case for whom there was no isolate) and 6 of whom were young Aboriginal children.

Conclusions: These data suggest virulent ST11 MenW strains are circulating in the WA population but may not yet be widespread. Appropriately targeted vaccination programs may reduce transmission and disease.
**Concurrent Session 2C – AMR Laboratory**

**Grand 4, 2:00pm – 3:30pm**

**Evaluating point-of-care tests as a surveillance tool for seasonal and pandemic influenza**

**Presenter:** Monique Chilver

**Authors:** Ms Monique Chilver1, Professor Nigel Stocks1, Dr James Fielding2, Dr Sheena Sullivan3

**Affiliations:** 1The Australian Sentinel Practices Research Network, The University of Adelaide, Australia, 2The Victorian Infectious Diseases Reference Laboratory, Melbourne, Australia, 3The World Health Organisation Collaborating Centre on the Reference and Research on Influenza, Melbourne, Australia

**Abstract:**

**Introduction:** Timely dissemination of virological influenza surveillance data are crucial during a pandemic to enable Government decision making concerning appropriate interventions. The reporting lag associated with traditional surveillance methods, namely reverse-transcriptase polymerase chain reaction (RT-PCR), can range from 1 day to 2 weeks. Rapid point-of-care tests (POCT) detect the presence of influenza in 15 minutes and allow for real-time, automated dissemination of results via the internet.

**Methods:** During 2015 and 2016, 13 sentinel sites from the Australian Sentinel Practices Research Network (ASPREN) participated in a pilot study. Patients presenting with an influenza-like illness were systematically selected for virological surveillance with two respiratory tract swab samples obtained. One was tested using the POCT Sofia (Quidel) and the other was sent to the laboratory for RT-PCR testing - the gold standard test for influenza.

**Results:** Of the 114 patients tested for influenza using the Sofia, 4 false negative results for influenza A, and 4 false negatives and 2 false positives for influenza B were recorded, compared to RT-PCR. Influenza A sensitivity was 83% and specificity was 100%, and influenza B sensitivity was 73% and specificity was 98%.

**Conclusion and recommendations:** POCT shows high sensitivity and specificity compared with the gold standard test. Although POCT could be a promising method for timely influenza surveillance and facilitate rapid decision making during an influenza pandemic, costs may be prohibitive. In this presentation we will discuss the barriers and facilitators to utilising POCT for seasonal influenza surveillance and during a pandemic.

**Real-time qPCR improves meningitis pathogen detection in disease surveillance in Fiji**

**Presenter:** Eileen Dunne

**Authors:** Dr Eileen Dunne1, Silivia Mantanitobua2, Shalini Singh3, Rita Reyburn1, Evelyn Tuivaga2, Eric Rafai2, Lisi Tikoduadua2, Barbara Porter1, Catherine Satzke1, Janet Stratchan3, Kimberly Fox4, Kylie Jenkins4, Adam Jenney1, Silo Baro3, Kim Mulholland1, Mike Kama2, Fiona Russell2

**Affiliations:** 1Murdoch Childrens Research Institute, Parkville, Australia, 2Ministry of Health & Medical Services, Suva, Fiji, 3The University of Melbourne, Microbiological Diagnostic Unit Public Health Laboratory, Melbourne, Australia, 4World Health Organization Regional Office for the Western Pacific, Manila, Philippines, 5Fiji Health Sector Support Program, Fiji

**Abstract:**

**Introduction:** Bacterial meningitis is a severe infection that results in high rates of morbidity and mortality worldwide. The World Health Organization recommends qPCR testing of Streptococcus pneumoniae, Neisseria meningitidis, and Haemophilus influenzae from cerebrospinal fluid (CSF) as part of Invasive Bacterial Vaccine Preventable Diseases (IB-VPD) surveillance. The aims of this study were to identify the aetiologic agents causing meningitis in the years immediately following pneumococcal conjugate vaccine introduction in Fiji, and to examine whether the use of qPCR improved detection of S. pneumoniae, N. meningitidis, and H. influenzae compared to traditional microbiological approaches.

**Methods:** CSF samples were obtained from suspected meningitis patients of all ages at the Colonial War Memorial Hospital in Suva, Fiji from November 2012 to May 2016. Samples were examined by traditional methods (culture, Gram stain, and latex agglutination for bacterial antigen) and qPCR for of S. pneumoniae, N. meningitidis, and H. influenzae.

**Results:** Of 266 samples tested, pathogens were identified in 47 (17.7%) with S. pneumoniae (n = 17) and N. meningitidis (n = 13) most common. The use of qPCR significantly increased detection of IB-VPD pathogens (P = 0.0001). The median white cell counts for samples positive by qPCR alone (360 cells/mm3) was significantly higher than samples with no pathogen detected (32 cells/mm3) and consistent with culture-positive samples (505 cells/mm3).

**Conclusions:** The use of qPCR significantly improves detection of S. pneumoniae, N. meningitidis, and H. influenzae in CSF. Application of molecular diagnostics is a feasible way to enhance local and global surveillance for IB-VPD.

**Combined genomic and epidemiological investigation of a state-wide outbreak of KPC-producing Enterobacteriaceae**
Surveillance for antimicrobial resistance in enteric bacteria in Australian pigs and chickens

Presenter: Patricia Mitchell, Kylie Hewson

Authors: Dr Patricia Mitchell1, Dr Kylie Hewson2

Affiliations: 1Australian Pork Limited, Canberra, Australia, 2Australian Chicken Meat Federation, Sydney, Australia

Abstract:

Background: In 2013 the Commonwealth Government sponsored review “Surveillance and reporting of antimicrobial resistance and antibiotic usage in animals and agriculture in Australia” identified assessment of AMR in commensal bacteria and pathogens present in the gut of food animals at slaughter as suitable for a surveillance model. A Task Group (consisting of agricultural and Government representatives) established subsequent to the review, assessed the recommendations and provided advice for developing an AMR surveillance component based on the collection of faecal samples from food animals at slaughter. This abstract outlines the pilot studies conducted by the Australian pork and chicken meat industries.

Methodology: The prevalence of resistance against specified antimicrobials amongst E. coli, Salmonella spp., Enterococcus spp., and Campylobacter spp. isolated from the gut of Australian pigs and chickens at slaughter was assessed. Samples were collected from Australian chicken and pork abattoirs. Isolates were identified using standard procedures and confirmed using mass spectrometry (MALDI-TOF), then forwarded to secondary laboratories for antimicrobial susceptibility testing (AST).

Outcomes: The chicken study is still ongoing. Among all tested bacterial species from pigs AMR was not observed for those antibiotics (including third generation cephalosporins and colistin) of critical importance in the treatment of humans. None of the Campylobacter spp. were resistant to fluoroquinolones and vancomycin resistance was not observed for Enterococci. The pilot studies successfully integrated industry-facilitated sample collection, primary culture of commensal and pathogenic bacterial species at NATA accredited laboratories and AM susceptibility testing at specialist laboratories undertaking AMR surveillance of human and veterinary pathogens.
Deep sequencing of clinical extracts for pathogen discovery and molecular epidemiological surveillance

Presenter: Amy Jennison
Authors: Dr Amy Jennison, Dr Rikki Graham
Affiliations: 1Public Health Microbiology, Forensic and Scientific Services, Queensland Department Of Health, Brisbane, Australia

Abstract:

Introduction: The increase in culture-independent diagnostic testing (CIDT) by pathology laboratories may offer rapid and cost effective diagnostics for patients, however the absence of isolates being provided to reference laboratories for public health surveillance, antibiotic resistance monitoring, vaccine effectiveness studies and outbreak investigations is of concern. Methods: Although still in its infancy, the application of deep sequencing to directly sequence clinical specimens and even environmental or food matrices, offers some hope that detailed molecular epidemiological analysis of uncultured samples will be possible.

As the state reference laboratory for Queensland, Australia, we have been focusing on establishing deep sequencing methods for two different purposes; hypothesis-free diagnostics and molecular epidemiological surveillance.

Results: We will present data on direct clinical sequencing for pathogen discovery in a case of unknown death, where limited clinical specimen restricted testing, as well discussing our experience with the use of deep sequencing for extrapolating genotyping and antibiotic resistance markers from clinical extracts.

Conclusion and Recommendation: While successful in generating useful data that would be otherwise go undetected in the absence of isolates, these approaches bring with them new challenges for bioinformatics approaches, validation and interpretation by clinicians.

NSW Health testing denominator data – uses for public health

Presenter: Nectarios Rose
Authors: Dr Nectarios Rose, Dr Sheena Adamson, Ms Paula Spokes, Dr Vicky Sheppeard
Affiliations: 1Health Protection NSW, North Sydney, Australia

Abstract:

Introduction: The NSW Denominator Data Project began January 2012 to collect the total number of tests performed for thirteen notifiable conditions from 15 public and private laboratories in NSW. The aim of the project is to facilitate the accurate interpretation of notification data, resulting in more appropriate public health response.

Methods: Laboratory testing data between 1 January 2012 and 30 September 2016 were collected for each laboratory and collated to determine the number of notifications, total number of tests performed and the ratio of positive notifications per 100 tests (percent positivity rate).

Results: HIV has seen 193 extra tests performed per month since 2012 (p<0.001). Despite a significant rise in chlamydia and gonorrhoea notifications since 2012, the positivity rate has remained relatively constant, indicating that rates in the community may be stable. Positivity rates have also remained stable for hepatitis B and C. For other conditions, the positivity rate varied due to factors including seasonality, the occurrence of outbreaks and the implementation of public health interventions (Ross River virus 1.8-13.9%, pertussis 1.4-7.9%, salmonellosis 1.0-2.9%).

Conclusion & Recommendation: The ongoing Denominator Data Project has demonstrated its utility for interpreting notification data for selected conditions, particularly when there are increases in notification numbers. Observed trends in testing also reflect rapidly changing methods in diagnostic testing, and the impact of public health recommendations for increased testing for some of the conditions. Plans are underway to better automate data collection, and enable collection of demographic information to further enhance interpretation of notification data.

Concurrent Session 2D – Influenza
Element Room, 2:00pm – 3:30pm

Influenza vaccination coverage in Aboriginal and Torres Strait Islander adults

Presenter: Surendra Karki
Authors: Dr Surendra Karki, Ms Amalie Dyda, Dr Marlene Kong, Dr Heather Gidding, Professor Peter McIntyre, Professor Raina MacIntyre, Professor Emily Banks, Dr Bette Liu
Affiliations: 1School of Public Health and Community Medicine, University Of New South Wales, Sydney, Australia, 2The Kirby Institute, University of New South Wales, Sydney, Australia, 3National Centre for Immunisation Research and Surveillance of Vaccine
Communicable Diseases Control Conference 2017 – Monday 26 to Wednesday 28 June 2017

Preventable Diseases, The Children's Hospital Network, Sydney, Australia, 4National Centre for Epidemiology and Population Health, Australian National University, Sydney, Australia

Abstract:

**Background:** Data on vaccination coverage and factors associated with vaccine uptake in Aboriginal and/or Torres Strait Islander adults are limited.

**Methods:** We compared questionnaire-derived data collected from 2012-2015 on annual influenza vaccination coverage among Australian-born adults by Indigenous status and demographic variables.

**Results:** The survey response rate for Aboriginal and/or Torres Strait Islander and Australian-born non-Indigenous participants was 42.8% and 59.0%, respectively. Among 40865 participants aged <65 years, 47.7% (95% CI 42.4-52.9%; 174/365) of Aboriginal and/or Torres Strait Islander and 40.3% (95% CI 39.7-40.9, 16319/40500) of non-Indigenous adults reported having an influenza vaccination in the last year (p=0.004). Equivalent percentages among 40349 participants aged ≥65 years were respectively, 67.0% (95% CI 59.9-73.6%; 130/194) and 71.4% (95% CI 70.6-72.2; 28683/40155) (p=0.17). Among Aboriginal and/or Torres Strait Islander participants, age-adjusted vaccination coverage was: 56.8% in women versus 52.2% in men (p=0.4); 50.9% in overweight and 65.9% in obese versus 45.4% in normal weight (p=0.2); 62.9% in those with a medical risk factor versus 48.2% in those without (p=0.02); 48.6% in current smokers versus 56.5% in never smokers (p=0.6); 55.9% among those living in major cities versus 53.2% among those in regional/remote areas (p=0.7).

**Conclusions:** Influenza vaccine coverage in Aboriginal and/or Torres Strait Islander adults aged >65 years was comparable to coverage reported in non-Indigenous Australian-born adults. Coverage was higher in Aboriginal and/or Torres Strait Islander adults aged <65 years compared to non-Indigenous adults, likely due to differences in funding.

**Seasonal influenza is associated with overcrowding in New South Wales Emergency Departments**

**Presenter:** David Muscatello

**Authors:** Dr David Muscatello, Dr Kendall Bein, A/Prof Michael Dinh

**Affiliations:** 1UNSW Sydney, Kensington, Australia

Abstract:

**Introduction:** Emergency Department overcrowding can lead to poor patient outcomes including increased mortality. We aimed to quantify the impact of influenza on national emergency access targets (NEAT) and premature patient departure in New South Wales, Australia.

**Methods:** This was a retrospective observational study of 11 million presentations to 115 hospitals during 2010 through 2014, using routinely collected administrative records. A time series generalised additive regression model was used to assess the correlation between weekly influenza activity and the weekly proportion of patients discharged in >4 hours and the proportion that departed before commencing or completing treatment ('did not wait'), after controlling for background, winter and other holiday effects.

**Results:** During 2011 through 2014, peak annual circulating influenza was associated with the peak weekly proportion of presentations discharged in >4 hours. The peak annual absolute weekly change in that proportion ranged from 1.52 (95% confidence interval CI. 0.89 to 2.15) percentage points in 2011 to 3.88 (95% CI 3.02 to 4.74) percentage points in 2014. This represented a relative increase of up to 13.0% attributable to influenza. For presentations that did not wait, peak influenza circulation was associated with statistically significant increases in all years, ranging from 0.60 (95% CI 0.22 to 0.99) percentage points to 2.68 (95% CI 2.31 to 3.06) in 2012. The maximum relative change was 43.3% in 2012.

**Conclusion and Recommendation:** Circulating influenza was associated with sustained increases and peaks in access block and premature patient departures. Influenza surveillance is needed to guide Emergency Department demand management.

**Antibody response and influenza-like illness among healthcare workers after influenza vaccination**

**Presenter:** Vivian Leung

**Authors:** Ms Vivian Leung1, Ms Malet Aban1, Ms Louise Carolan1, Dr Karen Laurie1, Dr Julian Druce2, Prof Monica Slavin3, A/Prof Caroline Marshall4, A/Prof Sheena Sullivan1,5,6

**Affiliations:** 1WHO Collaborating Centre For Reference And Research On Influenza, Melbourne, Australia, 2Victorian Infectious Disease Reference Laboratory, Melbourne, Australia, 3Victorian Infectious Disease Service, Royal Melbourne Hospital, Melbourne, Australia, 4Infection Prevention and Surveillance Service, Royal Melbourne Hospital, Melbourne, Australia, 5Department of Epidemiology, University of California, Los Angeles, USA, 6School of Population and Global Health, University of Melbourne, Melbourne, Australia
Abstract:

Introduction: Annual seasonal influenza vaccination is recommended for health care workers (HCW). However, recent studies of vaccine effectiveness have reported a reduction in serological response among repeat vaccinees. We compared antibody response and the frequency of influenza-like illness (ILI) among HCWs by vaccination history.

Methods: A prospective serosurvey was performed at the Royal Melbourne Hospital in Victoria, Australia. Influenza antibody titres were measured pre-vaccination, post-vaccination and post-season. HCWs were monitored weekly for the development of ILI during the influenza season. Estimated geometric mean titres (GMTs) and geometric mean fold ratios (GMRs) by the number of vaccinations received in the past 5 years were calculated.

Results: Of the 190 HCWs enrolled, 157 completed the study. All HCWs demonstrated an increase in post-vaccination GMTs against the four vaccine strains. The rise in titres for all vaccine strains among vaccine-naïve HCWs were significantly greater than increases observed for HCWs who received between 1 and 5 prior vaccinations (p<0.001, respectively). The largest post-vaccination rise was observed among vaccine-naïve HCWs against A/H1N1pdm09 (GMR 16.5, p<0.001). Post-season GMTs were maintained for A/H1N1pdm09 and A/H3N2. However, there was a significant decline in GMTs post-season for both B lineages. Sixty five (41%) HCWs reported at least one ILI episode, with 6 (4%) identified A/H3N2-positive.

Conclusion: All HCWs in our study demonstrated protective antibody titres post-vaccination. There were no clear trends between the number of prior vaccinations and post-vaccination response. However, these preliminary findings suggest greater post-vaccination responses among vaccine-naïve HCWs.

Flutracking surveillance of influenza-like illness – 2016

Presenter: Craig Dalton

Authors: Dr Craig Dalton1,2, Ms Sandra Carlson1, Professor David Durrheim1,2

Affiliations: 1HNE Population Health, Wallsend, Australia, 2HMRI University of Newcastle, Callaghan, Australia

Abstract:

Background: Flutracking is the largest participatory surveillance system in the world. It is a weekly online survey of influenza-like illness (ILI) with over 26,000 weekly survey participants every week across Australia in 2016.

Methods: Flutracking is sent every Monday morning in winter and takes less than 10 seconds to complete. The survey tracks self-reported cough, fever, sore throat, health care provider visits, time off normal duties, and influenza laboratory test results.

Results: There were 666,579 surveys completed in 2016, by 30,995 participants (18,193 direct respondents and 12,802 ‘other household members’). This equates to an average of 22 surveys per participant, out of 25 available survey weeks in 2016. During the peak four weeks of ILI activity 2,756 participants reported ILI of which 1,029 (37.3%) sought medical care, and 59 (2.1%) reported a positive influenza laboratory test result. Based on ILI rates, absence from normal duties, and health-seeking behaviour, 2016 was the mildest influenza season since 2013. A total of 113 and 60 participants reported a positive or negative laboratory influenza test respectively.

Conclusion: 2016 was the mildest influenza season since 2013. ILI has been an inadequate endpoint for calculating influenza vaccine effectiveness. The increasing proportion of Flutrackers undergoing laboratory testing suggests that vaccine effectiveness calculations based on the outcome of self-reported influenza laboratory testing will be useful by 2018 to 2020.

Using routine testing data to understand RSV and Influenza a circulation patterns

Presenter: Kylie Carville

Authors: Ms Kylie Carville1, Ms Claire Sutterby2, A/Prof Sheena Sullivan2,3

Affiliations: 1Epidemiology Unit, Victorian Infectious Diseases Reference Laboratory, Melbourne, Australia, 2Centre for Epidemiology and Biostatistics, University of Melbourne, Melbourne, Australia, 3WHO Collaborating Centre for Reference and Research on Influenza, Melbourne, Australia

Abstract:
Introduction: Some studies have reported evidence of interference among respiratory viruses. This study used routine testing data from a major public health laboratory in Victoria to examine the relationships among different respiratory viruses from routine respiratory tests.

Methods: The results of all multiplex respiratory panel tests performed at the Victorian Infectious Diseases Reference Laboratory between 2002 and 2016 were extracted from the Laboratory database. Time series analyses were used to plot the number and proportion of positive tests for each pathogen in the panel. The seasonality of all respiratory viruses included was compared with RSV and Influenza A using cross correlations, which estimate the lag between peaks in epidemic curves.

Results: 55,699 records were abstracted from the database, of which 34,250 were included in the final analysis. The most commonly detected virus was picornavirus. Seasonal peaks were observed for coronaviruses, metapneumovirus, RSV and Influenza A & B and circulation of these viruses was somewhat correlated. On average, RSV was observed to circulate 6.5 weeks before influenza A; however, the order of circulation was not consistent across years.

Conclusion and recommendation: These findings support previous reports of a temporal relationship in the circulation of some respiratory viruses. Further analyses, including subtype circulation, is needed to understand fluctuations in the correlation of RSV and influenza A, which may be associated with the predominant influenza A subtype. Greater understanding of virus co-circulation may enable health authorities to better predict when respiratory virus outbreaks will occur and develop early warning systems.

Flutracking influenza-like illness better correlates with laboratory test percent positivity than counts

Presenter: Craig Dalton

Authors: Dr Craig Dalton1,2, Ms Sandra Carlson1, Professor David Durrheim1,2

Affiliations: 1HNE Population Health, Wallsend, Australia, 2HMRI University of Newcastle, Callaghan, Australia

Abstract:

Background: Flutracking is a weekly online survey of influenza-like illness (ILI) that has grown from 400 participants in 2006 to over 26,000 consistent weekly participants across Australia in 2016. The use of respiratory panel testing has led to an increase in the count of positive influenza tests. This distorts the historical baseline and makes it difficult to assess trends in influenza surveillance. Percent positivity may provide a better historical and real time surveillance perspective, however, these data are difficult to acquire because test denominator data are not notifiable. We compared Flutracking ILI data to laboratory influenza test counts and percent positivity.

Methods: Flutracking surveys are sent every Monday morning in winter and take less than 10 seconds to complete. The survey tracks self-reported cough, fever, sore throat, health care provider visits, time off normal duties, and influenza laboratory test results. We analysed the proportion of participants tested for influenza by state and year from 2013 to 2016 and compared the correlation between percent Flutracking ILI, laboratory confirmed influenza counts and percent positivity.

Results: The proportion of Flutracking participants tested for influenza has increased in all jurisdictions since 2013 except for the ACT. The average weekly percentage of Flutracking participants tested nationally were: 2013 – 1.6%; 2014 – 2.6%; 2015 – 2.7%; 2016 – 2.9%. Flutracking ILI correlated more closely with laboratory influenza test percent positivity than total positive test counts.

Conclusion: Flutracking ILI may provide a proxy for laboratory influenza test percent positivity where these data are not available.
Wednesday 28 June 2017

Concurrent Session 3A – One Health (Short Orals)
Grand 1&2, 10:30am – 12:00pm

**A hotbed of tuberculosis in NSW: epidemiology-informed service development in Western Sydney**

**Presenter:** Sophie Norton

**Authors:** Ms Sophie Norton¹, Mr Neil Heron², Dr Laila Parvaresh¹, Dr Jin Cho², Dr Shopna Bag¹

**Affiliations:** ¹Public Health Unit, Western Sydney Local Health District, North Parramatta, Australia, ²Parramatta Chest Clinic, Western Sydney Local Health District, Parramatta, Australia

**Abstract:**

**Introduction:** Tuberculosis (TB) continues to affect public health in developed countries from increased globalisation, travel and migration. Understanding local demographics and disease epidemiology is essential in providing culturally-appropriate patient care. This study investigates the epidemiological characteristics of the Western Sydney (WS) population related to TB with the aim of informing strategic planning.

**Methods:** Descriptive epidemiology and projections to 2031 related to population change and births was developed.

**Results:** Between 2006 and 2015, the WS TB notification rate at 12.9/100,000 was more than double that of NSW (5.8/100,000). TB rates varied considerably within the WS district, e.g. Auburn (21.5/100000) vs. The Hills (4.6/100000). 87% of notified TB cases were born in a TB-endemic country.

The number of people now residing in WS and born in India increased from 21,980 (3% of WS population) in 2006 to 42,968 (5%) in 2011. In WS, between 2006 and 2015 the proportion of babies born to mothers who had migrated from TB-endemic countries increased from 30% (3,723) to 46% (6,763). Population growth trends over the past decade indicate that increased migration will likely contribute significantly to population growth in the next 20 years, with an estimated 47.5% (450,000) increase over this period.

**Conclusion:** The overall TB incidence in WS has remained high in the last decade. This review demonstrates that TB burden in WS is borne by ethnic cohorts within geographical pockets. Strategy planning should include engaging ethnic group leaders to collaboratively develop culturally appropriate interventions to reduce the risk of active TB disease.

Auditing the Audit Office’s Audit: Preparing for and Responding to Health Emergencies

**Presenter:** Craig Dalton

**Authors:** Dr Craig Dalton¹

**Affiliations:** ¹HNE Population Heath, Wallsend, NSW, ²HMRI University of Newcastle, Callaghan, NSW

**Abstract:**

**Background:** Audit of performance underpins quality assurance and improvement. Independent audit, by external agencies, of response to health emergencies such as outbreaks are rarely performed in Australia. The Australian National Audit Office is due to table a report: Preparing for and Responding to Health Emergencies in May 2017. The criteria for the audit are: 1. Does the Department of Health have a robust framework in place to plan for and recognise a potential communicable disease emergency? 2. Does the Department of Health have effective arrangements in place to effectively respond to a communicable disease emergency.

**Method:** The process and methodology of the audit will be compared to similar audit and readiness assessments conducted in the USA (most notably by the US Government Accounting Office) and the European Union. The Australian National Audit Offices process will be compared across a range of criteria including:

1. Clarity and breadth of terms of reference
2. Consultation with stakeholders
3. Audit workforce
4. Scope of assessment
5. Reference to measurable standards for process or outcomes
6. Transparency and political independence
7.  Reporting and iterative communication
8.  Follow up post audit.

Results and Conclusions: Will be presented following tabling of the report in May 2017.

One health approach to address the global risks of emerging infectious disease

Presenter: Noore Alam
Authors: Mr Noore Alam1
Affiliations: ‘Griffith University, Nathan, Australia

Abstract:

Introduction: There is a growing recognition of the shared health risks at the human, animal and environment interface. With this recognition, the concept of ‘one health’ emerged which advocates for collaborative actions to reduce health risks at the human-animal-ecosystem interface. However, the policy and practice frameworks for implementing one health are unclear. This systematic review synthesised global evidence of enablers and inhibitors for the effective implementation of the one health approach to address the growing threat of emerging and re-emerging infectious diseases (ERIDs) of zoonotic origin.

Methods: This study uses a two-stage strategy for data collection. Stage one involved a systematic review of literature using MEDLINE, PubMed, and Web of Science databases. Two reviewers independently appraised the articles. Stage two is in planning phase and will involve consultation with public health policy makers in Australia and selected countries in South-East Asia.

Results: Over 8,000 titles and abstracts and 165 articles were reviewed against specified inclusion and exclusion criteria. Based on the 26 articles retained for analysis, key enablers include the presence of a global health security agenda and regulations, regional collaborations and surveillance systems. Lack of community awareness, systemic problems such as disjoining industries and sectors, and bureaucracy are the major obstacles.

Conclusion and recommendations: Future inventions should consider the findings of this review for the effective implementation of one health approach. Governments should consider increasing community awareness and risk perceptions of ERIDs, initiate system change to reflect transdisciplinary synergies, and practical actions to address the growing threats of ERIDs.

Factors influencing delayed presentation and diagnosis for Buruli Ulcer in Victoria, 2011-2016

Presenter: Shaun Coutts
Authors: Mr Shaun Coutts1, Ms Ee Laine Tay1
Affiliations: 1Victorian Department Of Health And Human Services, Melbourne, Australia

Abstract:

Introduction: Buruli Ulcer (BU) incidence is increasing in Victoria. Since 2012, the epidemiology has shifted from the Bellarine Peninsula to other coastal areas, particularly the Mornington Peninsula. Delay in seeking diagnosis and commencing treatment can contribute significantly to morbidity. We aimed to identify factors associated with delayed presentation and diagnosis.

Methods: Retrospective analysis of notifications data: 2011-2016. We assessed duration of symptoms before healthcare presentation (presentation delay) and time from first presentation to first suspicion of BU (diagnostic delay), and compared differences between age, sex, five areas of residence, year of notification, and location/size/manifestation of lesion using non-parametric tests and logistic regression (using median duration as cut-off).

Results: Of 599 patients, median duration was 30 days (n=431, IQR 14-90) for presentation delay and 12 days (n=428, IQR 0-42 days) for diagnostic delay. Significant differences in median duration were observed between areas of residence for presentation delay (p=0.0015) and diagnostic delay (p<0.001). In multivariate logistic regression comparing to the Bellarine Peninsula, patients from non-endemic areas were more likely to present later (OR 2.01, 95%CI 1.20-3.38) and patients from all other areas of residence were significantly more likely to be diagnosed later. Median duration for diagnostic delay improved over time for the Mornington Peninsula, from 47.5 days (n=8; IQR 32-62) in 2011-2012 to 4 days (n=77; IQR 0-26) in 2015-2016.

Conclusion: Diagnostic delay is longer in newer endemic areas outside the Bellarine Peninsula. Awareness of BU amongst health professionals and the public should be raised, including those residing outside traditional endemic areas.

Infectious disease surveillance on cruise ships entering Sydney from international waters

Presenter: Kelly-Anne Ressler, Mark Ferson,
Authors: Ms Kelly-Anne Ressler1, Prof Mark Ferson2
Affiliations: 1South Eastern Sydney Public Health Unit, Randwick, Australia, 2School of Public Health & Community Medicine, University of New South Wales, Sydney, Australia
Abstract:

**Introduction:** The South Eastern Sydney Public Health Unit, on behalf of NSW Health, has established a formal and constantly evolving disease surveillance program for all cruise ships entering Sydney. It is based on standardised information provided to Australian Government agencies by all vessels requesting pratique, mandated by the Quarantine Act 1908 and now by the Biosecurity Act 2015 (Cwlth). Conditions to be reported by ships’ masters range from the key diseases of nineteenth century concern, such as cholera and plague, to those added in the twenty-first century, such as SARS, influenza and gastroenteritis.

**Methods:** Following positive notification of key diseases, the Public Health Unit obtains supplementary information on cases, outbreaks and the shipboard response by cooperative arrangements with ships’ senior doctors, shipping agents and public health personnel employed by cruise lines. The program has support from the Department of Agriculture and Water Resources and currently receives surveillance data from > 98% of vessels arriving in Sydney.

**Key Findings:** In the 10 years between 2007 and 2016 the program detected and responded to 53 outbreaks where greater than 3% of the passengers and crew were affected. Acute gastroenteritis was responsible for 35 outbreaks, 23 of which were confirmed Norovirus. Genotyping determined Norovirus GII.4 Sydney to be predominant cause of recent outbreaks. Of 18 respiratory outbreaks, influenza A was identified in 9.

**Public Health Action:** Outbreak response is dependent on many factors, some recent case studies will be used to describe the surveillance program and public health response.

**Investigating an Atypical Q Fever Outbreak in Rural NSW**

**Presenter:** Priscilla Stanley

**Authors:** Ms Priscilla Stanley

**Affiliations:** 1Western NSW Local Health District, Dubbo, Australia

**Abstract:**

An investigation occurred of an outbreak of Q fever in a remote rural town in New South Wales, Australia. Cases were identified through active and passive case finding activities, and retrospective laboratory record review, interviews were undertaken using a standard questionnaire. Two sets of case-case analyses were completed to generate hypotheses regarding clinical, epidemiological and exposure risk factors associated with infection during the outbreak. Laboratory-confirmed cases (n=14) were compared to an excluded case group (n=16) and a group of historic Q fever cases from the region (n=106). In comparison to the historic case group, outbreak cases were significantly more likely to be female (43% vs. 18%, p=0.04) and identify as Aboriginal (29% vs. 7%, p=0.03). Similarly, very few cases worked in high-risk occupations (21% vs. 84%, p<0.01). Most outbreak cases (64%) reported no high-risk exposure activities in the month prior to onset. In comparison to the excluded case group, a significantly increased proportion of outbreak cases had contact with dogs (100% vs. 63%, p=0.02), or sighted kangaroos on their residential property (100% vs. 60%, p=0.02). High rates of tick exposure (92%) were also reported. While a source of this outbreak could not be confirmed, our findings suggest infections likely occurred via inhalation of aerosols or dust contaminated by Coxiella burnetii, dispersed through the town from either an unidentified animal facility or from excreta of native wildlife or feral animals. Alternatively transmission may have occurred via companion animals or tick vectors.

**Temporal dynamics of molecular epidemiology of mycobacterium tuberculosis in New South Wales**

**Presenter:** Elena Martinez

**Authors:** Dr Elena Martinez, Mr Peter Jelfs, Ms Andrea Bustamante, Dr Vitali Sintchenko

**Affiliations:** 1Centre for Infectious Diseases and Microbiology–Public Health, Institute of Clinical Pathology and Medical Research Pathology West, Westmead Hospital, Westmead, Australia, 2Marie Bashir Institute for Infectious Diseases and Biosecurity, Sydney Medical School, University of Sydney, Sydney, Australia

**Abstract:**

**Introduction:** Molecular epidemiology of Mycobacterium tuberculosis (MTB), its transmission dynamics and population structure have become important determinants of targeted tuberculosis programs. The aim of this study was to examine recent clusters of MTB diagnosed in New South Wales (NSW).

**Methods:** All MTB isolates confirmed by the NSW Mycobacterial Reference Laboratory between January 2014 and November 2016 were included. They were genotyped by mycobacterial interspersed repetitive unit analysis of 24 loci (MIRU-24). MTB cases were clustered when MIRU-24 profiles were indistinguishable. Whole genome sequencing (WGS) of MTB employed the NextSeq500 illumina technology. Phylogenetic lineages were assigned using the MIRU-VNTRplus and from single nucleotide polymorphisms (SNPs) identified by WGS.

**Results:** MTB transmission in NSW remains uncommon. Only 133 (12.6%) of MTB isolates examined were clustered by MIRU-24 profiles. The majority of clusters were small in size (2.8 cases per cluster on average). Rate of recent transmission was estimated as...
9.96%. This public health parameter decreased in comparison with estimates from 2009-2013. WGS of MTB Beijing lineage clusters resolved clusters suggested by MIRU-24 reducing previous transmission rates. MTB genotyping and WGS of MIRU-24 clustered genomes identified cases of recent transmission, with four clusters of community-acquired disease investigated by WGS in 2016, and probable laboratory cross-contamination events as well as multi-drug resistant MTB cases.

**Conclusion:** MTB genotyping assisted the NSW TB Control Program by identifying cases of recent transmission, clusters of disease and probable laboratory cross-contamination events. WGS has significantly enhanced resolution of MIRU-24 genotyping for Beijing lineage of MTB.

**The epidemiology of hospital-acquired extended spectrum beta-lactamases (ESBLs) in South Australia**

**Presenter:** Phyo Thu Zar Aung

**Authors:** Dr Phyo Thu Zar Aung, Kamalesh Venugopal, Dr Louise Flood, Ms Irene Wilkinson

**Affiliations:** Communicable Disease Control Branch, Adelaide, Australia

**Abstract:**

Antimicrobial resistance is a major threat to public health. There is an increasing prevalence of antimicrobial resistant organisms associated with hospital-acquired infections worldwide. Of particular interest is the emerging incidence of extended spectrum beta-lactamases (ESBLs), which can confer resistance to most beta-lactam antibiotics. Our study describes the epidemiology of ESBL-producing bacteria using the findings from the South Australian Healthcare-Associated Infection Surveillance Program.

A retrospective descriptive study was conducted to analyse the epidemiology of healthcare associated ESBL acquisition in hospitals in South Australia from January 2007 to December 2015. We reviewed the trend of hospital-acquired ESBL acquisition rates (episodes per 10,000 hospital bed-days) from 13 hospitals (seven public metropolitan and six private hospitals). The acquisition rates were analysed by patient location (intensive care unit (ICU) versus non-ICU). Joinpoint analyses were applied to test the trends in annual percentage change (APC) for statistical significance.

The primary site of ESBL acquisition was urine (64.8%, n=678), with Escherichia coli (60.3%, n=650) and Klebsiella pneumoniae (10.3%, n=111) the most common organisms harbouring ESBLs. A significant increase in overall ESBL acquisition rates (APC=15.3) was noted during the study period. This increase was seen in both ICUs (APC= 3.8) and non-ICUs (APC=16.8), however, the change was only statistically significant for non-ICUs (p<0.05).

Our study demonstrates the increasing trend of ESBL-producing organisms associated with hospital-acquired infection across hospitals in South Australia. The study highlights the need to further investigate the risk factors underpinning the increase in antimicrobial resistance in hospitals, especially the relationship between antimicrobial resistance and usage.

**Impact of a TB Contact Tracing Program at an East Timorese Hospital**

**Presenters:** Natasha Bertschi, Brendan Phelan

**Authors:** Mrs Natasha Bertschi, Mr Brendan Phelan, Dr Joshua Francis

**Affiliations:** Flinders University, Darwin, Australia, Bairo Pite Clinic, Dili, East Timor

**Abstract:**

**Introduction:** Contact tracing for TB index cases at Bairo Pite Clinic (BPC) in Dili, East Timor, began in 2014. This new program represents an opportunity to build on scantly epidemiological data in this resource-poor setting, and to develop insights into patterns of contact and disease spread, and into the effectiveness of contact tracing for case finding and disease prevention through isoniazid preventive therapy (IPT).

**Methods:** A sample of two consecutive months of index cases was evaluated, focussing on contact tracing outcomes as entered in a Microsoft Access database. Outcomes measured included number and age of contacts, and numbers of contacts commencing on TB treatment or IPT. Quantitative descriptive statistics were used for data analysis.

**Results:** During January and February, 2015, 49 bacteriologically proven TB cases were identified. These index cases nominated 346 contacts, of whom 31 were aged less than 5 years. A total of 54.6% were interviewed by the BPC TB contact tracing team; IPT was prescribed to 38.7% of identified contacts aged less than 5 years. Adult TB treatment was prescribed to 1.6% (n=3) of nominated adult contacts, further investigations were ordered for 6.3% (n=12) and 85.7% (162) of screened contacts were deemed not to require TB treatment.

**Conclusion and Recommendations:** The contact tracing program was successful in identifying nominated contacts and in screening approximately half of those contacts. The reach of the contact tracing program is currently limited by resourcing levels, and an increase in funding promises better rates of screening and consequently of disease control.
Broken hearts in Timor-Leste: an echocardiography-based prevalence study of rheumatic heart disease

Presenter: Laura Korte

Authors: Dr Kim Davis¹, Dr Boglarka Remenyi¹,², Mr Januario dos Santos³, Dr Noel Bayley⁴, Dr Elizabeth Paratz⁴, Dr Benjamin Reeves⁵, Dr Allan Appelbe⁶, Dr Andrew Cochrane⁶, Mr Anthony Draper⁶,⁷, Mr Timothy Johnson⁸, Prof Jonathan Carapetis⁹, Dr Kathryn Roberts¹,², Dr Joshua Francis¹,²,³

Affiliations: ¹Royal Darwin Hospital, Darwin, Australia, ²Menzies School of Health Research, Darwin, Australia, ³Bairo Pite Clinic, Dili, Timor-Leste, ⁴East Timor Hearts Fund, Geelong, Australia, ⁵Cairns Base Hospital, Cairns, Australia, ⁶Northern Territory Centre for Disease Control, Darwin, Australia, ⁷Australian National University, Canberra, Australia, ⁸Telethon Kids Institute, Perth, Australia

Abstract:

Introduction: Rheumatic heart disease (RHD) causes significant morbidity and mortality in school aged children in Timor-Leste, but its prevalence has not been evaluated or described. We conducted the first echocardiography-based screening study to determine the prevalence of RHD in school-aged Timorese children.

Methods: School students were enrolled from schools in Dili (urban) and Ermera (rural) districts in Timor-Leste, using opt-out consent. Demographic and anthropometric data were collected and all students had a limited echocardiogram looking for evidence of RHD. RHD was classified as borderline or definite, according to World Heart Federation criteria. Patients with RHD were entered into a register for ongoing secondary prophylaxis, with the first dose of benzathine penicillin G administered on the day of the study.

Results: 1413 children were screened; 739 (52%) were girls and the median age was 12 years (range 4-24). The prevalence of definite RHD was 1.8% and borderline 1.6% (total 3.4%). Borderline or definite RHD was more common in Ermera than Dili though the difference was not statistically significant (4.1% vs 2.2%; p=0.07). Definite RHD was more prevalent in girls than boys (2.8% vs 0.7%; p<0.01). Congenital heart disease was identified in 20 children (1.4%). Of the 26 definite RHD cases, 23 (88%) received education and a first dose of BPG during the study.

Conclusion: RHD is prevalent in Timor-Leste, with some of the highest rates observed in the world. Girls are affected more commonly than boys. Community engagement is essential to ongoing follow up and effective delivery of secondary prophylaxis.

Backyard acquired leptospirosis in an urban setting: an emerging transmission pathway

Presenter: Anastasia Phillips

Authors: Dr Anastasia Phillips¹, Ms Jennifer Paterson¹, Dr Tasnim Hasan², Ms Helen Noonan³, Ms Annie Truong³, Ms Kirsty Hope³, Dr Shopna Bag³, Dr Jen Kok²

Affiliations: ¹Western Sydney Public Health Unit, NSW, Australia, Sydney, Australia, ²Centre for Infectious Diseases and Microbiology Laboratory Services, Institute of Clinical Pathology and Medical Research – Pathology West, Westmead, Australia, ³Health Protection NSW, Sydney, Australia

Abstract:

Introduction: In industrialised countries, leptospirosis is usually associated with occupational and recreational exposure although cases in high-density urban settings have been documented in association with flooding and rodent infestation. In Australia, the highest notification rates are in tropical areas of the state of Queensland.

Methods: Cases of leptospirosis notified to public health units in larger metropolitan regions from 2009 to December 2015 were analysed to determine those acquired in suburban Sydney.

Results: Forty-seven cases were included in the analysis. Twenty-five were acquired overseas in developing countries; 19 were acquired in rural areas of Australia or by persons with at-risk occupations or in recreational contact with water. Three were acquired in suburban backyards in the Sydney metropolitan region. All three cases lived in low-density residential or semi-rural areas and all reported the presence of rodents in their backyard prior to the onset of illness. All three had undertaken gardening and/or building works in their backyards, which likely resulted in contact with contaminated soil.

Conclusion and recommendation: Our study documents a mode of acquisition distinctive from previously described pathways in rural and urban settings. Rat infestation in suburban areas may reflect changes in urban development, including claiming of urban fringe land and access to bushland and open space. There may also be under-recognition of infection as clinicians may have a low index of suspicion for leptospirosis in this setting.
Abstract: The Western Australian (WA) Department of Health provides adolescent human papilloma virus (HPV) and combined diphtheria, tetanus and pertussis (dTpa) vaccinations via a school-based immunisation program (SBIP).

Methods: In 2009 a state-wide online school-based immunisation program (SBIP) database was established to identify students eligible for vaccination, track consent and vaccination status, calculate coverage rates, and facilitate data transfer to the National HPV Register. At the completion of each school year, parents receive a report of the vaccines their child received at school and school principals receive a report of vaccine uptake at their school compared with WA overall.

Results: Between 2010 and 2015 consent form return rate increased from 85% to 96%, and documentation of Indigenous status from 51% to 75%. The proportion of students for whom vaccination consent was obtained for HPV was 89%, and 94% for dTpa. HPV consent was similar across government, Catholic and independent schools. HPV 3 dose series initiation and completion rates increased from 71% to 86% and 66% to 76%, respectively. HPV 3 dose series completion was similar in males (74%) and females (76%). Although consent for HPV vaccination was higher among Aboriginal (95%) than non-Aboriginal students (91%) in 2015, series completion was lower in Aboriginal (57%) vs non-Aboriginal (80%) students. Data from 2016 will be presented at the conference.

Conclusion: Adolescent vaccination consent and completion rates improved after SBIP database implementation. We hope these improvements will continue despite database’s anticipated ‘retirement’ after expansion of the Australian Immunisation Register to include adolescent vaccinations.

The Impact of Rotavirus vaccination: New Vaccine Evaluation Project, Fiji

Abstract: The Republic of Fiji Islands is made up of 330 islands in tropical South-western Pacific (population c. 837,000). Prior to the introduction of the Rotavirus (RV) vaccine in October 2012, 39% of non-bloody diarrhoea in under 5 year olds admitted to the largest hospital, the Colonial War Memorial Hospital (CWMH), was due to RV.

Methods: New Vaccine Evaluation Project (NVEP), Fiji sought to evaluate the impact of RV vaccine (and other vaccines) while strengthening the local surveillance practices.

Between 2012 and 2015 active surveillance was undertaken at the CWMH. Outpatient and inpatient surveillance was undertaken in Savusavu (a small rural town). Baseline intussusception (IS) rates were calculated from medical records and prospective post-RV vaccination IS surveillance was undertaken.

Results: There was a 71% reduction in RV diarrhoea in under 5s admitted to CWMH with a 29% reduction in all-cause diarrhoea post-vaccine introduction.

Conclusions: The RV vaccine was successfully introduced into Fiji as part of a comprehensive childcare strategy where there is a strong EPI program and good donor support. This is the first LMIC country in the Asia-Pacific to show a decline in RV diarrhoea post-vaccination introduction, and though there were confounders (notably improved outpatient management practices) the temporal relationship of RV reduction to the vaccination introduction is compelling.
Child deaths from vaccine preventable diseases, New South Wales, 2005 to 2014

Presenter: Anastasia Phillips

Authors: Dr Anastasia Phillips1,2, Dr Frank Beard1,2, A/Prof Kristine Macartney1,2, Dr Jocelyn Chan1, Robin Gilmour3, Ms Gemma Saravanan3, Prof Peter McIntyre1,2

Affiliations: 1National Centre For Immunisation Research And Surveillance (NCIRS), Sydney, Australia, 2The University of Sydney, Sydney, Australia, 3Health Protection NSW, Sydney, Australia

Abstract:

Introduction: Deaths from vaccine preventable diseases in children are now rare in Australia, but there is a lack of comprehensive quantification of such deaths. This study aimed to identify and describe potentially vaccine preventable child deaths in New South Wales (NSW).

Methods: Deaths were identified from the NSW Child Death Register (NSW Ombudsman) and the Notifiable Conditions Information Management System (NSW Health). Medical and post-mortem records were reviewed. Cases were classified as vaccine-preventable based on the strength of evidence for the relevant infection causing death and likelihood that death was preventable through vaccination. Deaths were described by age, disease, remoteness, Indigenous status and comorbidity. A two-source capture-recapture method was used to estimate the true number of deaths.

Results: Fifty-four deaths were identified as definitely or probably due to diseases for which a vaccine was available, with an average annual mortality rate of 0.33 per 100,000 children and 2.1 per 100,000 infants. Two-thirds of deaths occurred in children with no identified comorbidities. Twenty-three deaths were classified as preventable or potentially preventable by vaccination, based on immunisation recommendations in place at the time, with influenza (12 deaths) and meningococcal disease (5 deaths) most common. An additional 15 deaths from meningococcal disease, pneumococcal disease, influenza and pertussis would now be potentially preventable based on current immunisation recommendations. Capture-recapture analysis estimated an additional three deaths.

Conclusion and recommendation: Increased uptake of vaccination in children and pregnant women could reduce child deaths, particularly from influenza.

Outbreak of Neisseria meningitidis serogroup W in a rural town in WA

Presenters: Paul Armstrong, Clare Huppatz

Authors: Dr Clare Huppatz1, Dr Charlene M Kahler2, Dr Shakeel Mowlaboccus3, Dr Paul Armstrong3

Affiliations: 1WA Country Health Service, Kalgoorlie, Australia, 2University of Western Australia, Perth, Australia, 3Communicable Disease Control Directorate, DoH, Perth, Australia

Abstract:

Introduction: In Australia, outbreaks of invasive meningococcal disease (IMD) are uncommon. Since 2014 there has been a rise in cases caused by serogroup W Neisseria meningitidis (MenW). In 2016, Western Australia (WA) recorded 14 cases of MenW. A community-outbreak of MenW was declared in a mining town in rural WA in December 2016, after five cases were reported in a two month period.

Methods: Routine follow up was completed on cases, including gathering enhanced surveillance data and contact management. Whole genome sequencing was performed on thirteen culture-positive state-wide MenW isolates and the core genome phylogeny was reconstructed using the Neighbor-joining method. A targeted community-wide vaccination campaign was conducted, with adverse events following immunisation (AEFI) followed up through a novel active surveillance methodology.

Results: Cases included three Aboriginal children under five years and two non-Aboriginal adults. Two cases were epidemiologically linked by contact tracing. The rate of IMD in the town area was 11/100,000. Phylogenetic analysis of the four culture positive cases revealed these strains were more closely related to one other than to those strains circulating elsewhere in the State, suggesting this was a local clonal outbreak. A rapid public health response resulted in >57% of the target population being vaccinated in two weeks. Thirteen AEFI were detected.

Conclusion and Recommendations: This outbreak is the first MenW outbreak in Australia to be reported. The key lessons learnt are discussed in terms of preparation, logistics, operations, communications and capturing AEFI that may inform future public health responses in Australia.
Evaluation of BCG Immunisation Programs in Australia

Presenter: Frank Beard

Authors: Dr Gulam Khandaker1,2,3, Dr Frank Beard1,2, Dr Aditi Dey1,2, Dr Chris Coulter4, Dr Alexandra Hendry1, Associate Professor Kristine Macartney1,2

Affiliations: 1National Centre for Immunisation Research and Surveillance of Vaccine Preventable Diseases, The Children’s Hospital at Westmead, New South Wales, Australia, 2University of Sydney, New South Wales, Australia, 3The Marie Bashir Institute for Infectious Diseases and Biosecurity (MBI), University of Sydney, New South Wales, Australia, 4Communicable Diseases Unit, Queensland Health, Queensland, Australia

Abstract:

Background: BCG immunisation programs in Australia are funded and operated by individual states and territories. National guidelines recommend BCG for children aged <5 years travelling to TB-endemic regions for extended periods, and Indigenous neonates in communities with high incidence of TB. We evaluated BCG immunisation programs in Australia, with particular reference to program implementation and national consistency.

Methods: We surveyed key jurisdictional stakeholders and analysed BCG vaccination coverage data from the Australian Childhood Immunisation Register (ACIR) and data on adverse events following immunisation (AEFI) with BCG vaccine from the Therapeutic Goods Administration’s Adverse Drug Reactions System, for 2001-2014.

Results: Access to BCG vaccination varies between jurisdictions, with some providing BCG immunisation services only in major city locations. Reliable supply of BCG is a major challenge. Analysis of ACIR data showed wide variation between jurisdictions in the proportion of infants reported as receiving BCG, suggesting significant differences in vaccine delivery and/or significant under-reporting to ACIR. The rate of BCG AEFI appeared to increase between 2011 and 2014.

Conclusion: Inconsistent BCG vaccine supply and differences between state-based programs are contributing to low, variable and inequitable vaccine delivery. Improvements in communication strategies and access to BCG vaccine could improve equity for at-risk children Australia-wide. Greater centralisation of vaccine procurement and program delivery, for example through inclusion of BCG vaccine on the National Immunisation Program, could help facilitate such improvements. Improved data quality in relation to reporting of BCG vaccination uptake and AEFI is required for more accurate monitoring of both program delivery and vaccine safety.

Evolution of pneumococcal virulence factors after the introduction of pneumococcal conjugate vaccines

Presenter: Rebecca Rockett

Authors: Dr Rebecca Rockett1, Dr Shahin Oftadeh2, Dr Nathan Bachmann3, Dr Verlaine Timms1, Dr Fanrong Kong2, Professor Gwendolyn Gilbert1,4, Associate Professor Vitali Sintchenko1,2,4

Affiliations: 1Centre For Infectious Diseases And Microbiology - Public Health, Westmead Hospital, Westmead, Australia, 2Institute of Clinical Pathology and Medical Research - Pathology West, Westmead Hospital, Westmead, Australia, 3Centenary Institute, The University of Sydney, Camperdown, Australia, 4Marie Bashir Institute for Infectious Diseases and Biosecurity, The University of Sydney, Camperdown, Australia

Abstract:

The polysaccharide capsular-type is a marker of invasive potential of Streptococcus pneumoniae. Of more than 90 serotypes, only 15 commonly cause invasive pneumococcal disease (IPD). Infant 7-valent pneumococcal conjugate vaccine, containing 7 capsular antigens (PCV-7), including 19F, was introduced in Australia in 2005. The incidence of IPD due to vaccine serotypes, decreased dramatically, overall, post-PCV-7, but non-vaccine serotypes, particularly 19A, increased. Pneumococci can recombine and switch their capsular loci (and so escape vaccine pressure). Recombination can also generate mutations that cause antibiotic resistance and increase virulence. Six capsular antigens, including 19A were added to the vaccine in 2011; PCV-13 reduced, but failed to eliminate, IPD due to 19A in the target population. In this study, we compared IPD isolates before and after introduction of both conjugate vaccines using whole genome sequencing.

All serogroup 19 IPD (serotypes 19F and 19A) isolates from children (<5yrs) in NSW collected pre-vaccine (2004, n=41), three years post PCV-7 (2008 n=60) and three years post PCV-13 (2014, n=25), were studied. Sequence types, antibiotic resistance and virulence factors were compared.

Preliminary genome-wide analysis identified 16 core genome sequence clusters and 25 multilocus sequence types (MLST). ST63 (n=12) and ST2345 (n=7) were two of the three most common STs identified in 2008 but not present in 2004; all isolates were serotype 19A and had intermediate penicillin resistance. Further analysis of all isolates is underway.

Understanding the genomics of successful IPD capsular types will assist in identifying markers of virulence and resistance that enable persistence under vaccine pressure.
Inequities in pneumococcal disease following introduction of pneumococcal conjugate vaccine in NZ

Presenter: Anna Howe

Authors: Anna Howe\textsuperscript{1}, Helen Petousis-Harris\textsuperscript{1}, Janine Paynter\textsuperscript{1}, Jennifer Griffin\textsuperscript{2}, Donna Watson\textsuperscript{2}, Nikki Turner\textsuperscript{1}

Affiliations: \textsuperscript{1}University Of Auckland, Auckland, New Zealand, \textsuperscript{2}University of North Carolina, North Carolina, United States of America, \textsuperscript{3}Conectus, Auckland, New Zealand
Abstract:

Pneumococcal conjugate vaccines (PCV) have been effective in controlling invasive pneumococcal disease (IPD) caused by vaccine serotypes in New Zealand (NZ). There is less information about the vaccine impact on all-cause pneumonia and otitis media (OM), in children with sociodemographic deprivation. We explored the impact of the PCV programme on IPD, all-cause pneumonia and OM by sociodemographic characteristics.

A retrospective cohort study using NZ national administrative data was undertaken. Person-years were based on the number of children less than 6 years old counted during the 2006 and 2013 censuses. Rates were calculated and reported per 100,000 person-years. Linear trends were tested using Cochrane-Armitage trend tests.

Between 2006 and 2015, 605 children were hospitalised with IPD, 26,589 for all-cause pneumonia, and 44,545 for OM. Rates of initial IPD, all-cause pneumonia, and OM hospitalisations have significantly decreased over the PCV7 period. Decreases in disease have been proportionately greater in Māori and Pacific groups. Rate differences between 2006 and 2015 for Māori and Pacific children were 39.3/100,000 and 24.7/100,000 for IPD, 329.8/100,000 and 799.5/100,000 for all-cause pneumonia, and 916/100,000 and 889.5/100,000 for OM, respectively (all P-values <0.001). Children from higher socioeconomic deprivation had higher rates of initial hospitalisations for IPD, all-cause pneumonia, and OM. While these rates have reduced over time, only OM has seen a reduction in disparity.

NZ has seen significant reductions in hospitalisations for IPD, all-cause pneumonia and OM associated with PCV. More work is required to reduce the burden in the most vulnerable populations.

Optimal Timing of Influenza Vaccine during Pregnancy: a Systematic Review

Presenter: Will Cuningham

Authors: Mr Will Cuningham¹, Dr Nic Geard³, Dr James Fielding¹, Prof Jodie McVernon¹, Dr Rob Moss²

Affiliations: ¹The Peter Doherty Institute For Infection And Immunity, Melbourne, Australia, ²Centre for Epidemiology and Biostatistics, Melbourne School of Population and Global Health, The University of Melbourne, Melbourne, Australia, ³Computing and Information Systems, Melbourne School of Engineering, The University of Melbourne , Melbourne, Australia

Abstract:

Introduction: Pregnant women are at a high risk of influenza infection and subsequent health complications. Vaccination is the most effective prevention measure against influenza infection and is recommended to pregnant women in all trimesters. Both safe and effective during pregnancy, the influenza vaccine has also been shown to provide protection to the newborn. The risk of seasonal influenza varies substantially throughout the year in temperate climates, however there is limited knowledge of how vaccination timing during pregnancy impacts the benefits received by the mother.

Methods: Articles were eligible for inclusion if they measured the efficacy, effectiveness, or immunogenicity of the influenza vaccine in women during pregnancy in either seasonal epidemics or pandemic years. All study designs were eligible for inclusion, however information of the vaccination timing was required. Authors searched PubMed, Scopus and Web of Science databases from inception until June 2016. Extracted data were tabulated, summarized in forest plots and analysed qualitatively.

Results: 29 studies met the inclusion criteria. Although highly heterogeneous, most studies reported high vaccine effectiveness and immunogenicity regardless of the timing of vaccination. Maternal seroprotection waned uniformly, irrespective of vaccination timing during pregnancy.

Conclusion & Recommendation: This review shows there is insufficient evidence to determine the effect of vaccination timing on influenza vaccine effectiveness or immunogenicity during pregnancy. Research into how vaccination timing during pregnancy can maximise protection for both mother and infant is key to developing vaccine scheduling recommendations, and thereby potentially increasing the currently low vaccination coverage rates.

Is regulated notification the best approach to varicella-zoster virus infection surveillance?

Presenter: James Fielding

Authors: Dr James Fielding¹, Ms Lucinda Franklin²

Affiliations: ¹Victorian Infectious Diseases Reference Laboratory, Melbourne, Australia, ²Victorian Government Department of Health and Human Services, Melbourne, Australia

Abstract:

Background: Varicella-zoster virus (VZV) infection was gazetted as a notifiable condition in Victoria in September 2008. The primary objective of VZV infection surveillance is to monitor the impact of childhood varicella vaccination, included in the National Immunisation Program in 2005, on incidence of varicella (chickenpox) and herpes zoster (HZ; shingles). Victorian VZV infection notification data were analysed against this objective.
**Communicable Diseases Control Conference 2017 – Monday 26 to Wednesday 28 June 2017**

**Methods:** All cases of VZV infection notified to the Victorian Government Department of Health and Human Services from 2009 to 2016 inclusive were descriptively analysed by time, clinical presentation and age.

**Results:** The number of VZV infection cases notified annually more than doubled from 2009-2016, but unspecified presentations (cases notified by a laboratory only) consistently comprised approximately 67%. The average annual varicella notification rate ranged from 9.9 to 16.3 cases per 100,000 in 2009 and 2015 respectively. Rates were highest in the 5-9 years age group, peaking in 2013. Rates were also higher for the 0-4 and 10-14 years age groups, but without clear peaks. Annual HZ notification rates tripled between 2009 and 2016, and increased with age.

**Conclusions:** Limited doctor notifications and likely variable notification practices over time make interpretation of notifiable VZV infection surveillance data difficult. The study findings are contrary to other published trends of varicella and HZ incidence in Australia, but recent data may be more representative. Alternative approaches for more accurate measurement of varicella and HZ incidence in the community, such as sentinel or targeted active surveillance of VZV infection, warrant consideration.

**Concurrent Session 3C – Foodborne, Influenza (Short Orals)**

**Grand 4, 10:30am – 12:00pm**

**Environmental risk factors for Salmonella serovar Wangata in north east NSW**

**Presenter:** Julie Collins

**Authors:** Ms Julie Collins1,2, Mr James Flint1, Mrs Kim Lilly1, Mr Greg Bell1, Professor David Durrheim1, Dr Grant Hill-Cawthorne4, Dr Kirsty Hope1, Mr Peter Howard6, Mr Tony Kohlenberg1, Ms Kerryn Lawrence1, Dr Siobhan Mor7, Mr Philippe Porigeaux1, Ms Kelly Simpson2, Professor Vitali Sintchenko6, Professor Michael Sintchenko6, Dr Anke Wiethoelter8

**Affiliations:** 1Hunter New England Population Health, Wallsend, Australia, 2National Centre for Epidemiology and Population Health, Australian National University, Canberra, Australia, 3North Coast Public Health, Port Macquarie & Lismore, Australia, 4Sydney School of Public Health, University of Sydney, Camperdown, Australia, 5NSW Ministry of Health, North Sydney, Australia, 6Centre for Infectious Diseases and Microbiology - Public Health, Westmead, Australia, 7Department of Veterinary Science, University of Sydney, Camperdown, Australia, 8Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Parkville, Australia

**Abstract:**

**Introduction:** There are over 2,000 different strains (serovars) of Salmonella that cause disease in humans. Salmonella serovar Wangata (S. Wangata) is the 5th most common serovar in New South Wales (NSW) and occupies an ecological niche in the north eastern region of the State. Previous case-series suggest that there is an environmental reservoir for this serovar in NSW.

This is the first case-case study to examine environmental risk factors for human infections with S. Wangata.

**Methods:** We conducted a descriptive analysis of cases in NSW from 2011 – 2016. This was followed by a case-case study in the local health districts of Hunter New England, Mid North Coast and Northern NSW from November 2016 to April 2017. Risk factors were compared between cases of S. Wangata and cases of S. Typhimurium. Telephone interviews were conducted using a standardised questionnaire. Information was collected on clinical symptoms, environmental exposures and contact with animals.

**Results:** The rate of S. Wangata infections in NSW increased in 2016 to 1.36 per 100,000, compared to a five-year mean of 1.22 cases per 100,000. Cases were equally distributed by sex. The median age was 48 years (IQR 8 – 67 years). Twelve S. Wangata cases and fifteen S. Typhimurium controls have been interviewed as a part of the case-case study with a response rate of 93%. The study will continue until 30 April 2017.

**Conclusion:** The study will identify risk factors for S. Wangata infections and guide public health action to prevent future cases in the community.

**Risk factors for campylobacteriosis in Australia and New Zealand: a systematic review**

**Presenter:** Liana Varrone

**Authors:** Mrs Liana Varrone1, Associate Professor Martyn Kirk2, Doctor Russell Stafford3, Associate Professor Kathryn Glass3, Associate Professor Gary Dykes1, Associate Professor Linda Selvey4

**Affiliations:** 1Curtin University, Bentley, Australia, 2Australian National University, Canberra, Australia, 3Queensland Department of Health, Brisbane, Australia, 4University of Queensland, Herston, Australia

**Abstract:**

**Introduction:** The rates of Campylobacter infection in Australia and New Zealand are among the highest in the industrialised world. We conducted a systematic review to identify locally-relevant risk factors for illness.
Methods: We searched Medline, Web of Science, ProQuest and Google Scholar using PRISMA guidelines. We hand searched reference lists and grey literature sources. After excluding duplicates, we included outbreak investigations, case-control studies and case series of campylobacteriosis in Australia and New Zealand from 1990 to present.

Results: Our initial search identified 314 articles, from which we included 45. The majority of these were conducted over ten years ago. Fourteen were case control studies, including 3 unpublished studies. Consuming chicken meat was reported in 64% (9/14) and offal in 21% (3/14) of studies. Contact with puppies was reported in 36% (5/14) and young chickens in 21% (3/14) of studies. One study reported that children aged <5 years sucking on their fingers or a dummy was responsible for a 36% population attributable risk of campylobacteriosis.

Conclusion & Recommendations: Consuming chicken meat is a commonly reported risk factor, as is contact with young animals. These risk factors will inform studies combining epidemiology and genomics to identify contemporary risk factors. There is a need to work with industry and the public to prevent infections.

Assessing the risks of extra-intestinal paratyphoid: New challenges for public health management

Presenter: Moniek Borsovsky, Oanh Nguyen

Authors: Moniek Borsovsky1, Oanh Nguyen1, Penelope Clark1, Sophie Norton1, Dr Shopna Bag2, Dr Jen Kok2, Ass. Professor Stephen Corbett1

Affiliations: 1Public Health Unit, Western Sydney Local Health District, North Parramatta, Australia, 2Pathology West, Western Sydney Local Health District, Westmead, Australia

Abstract:

Introduction: Paratyphoid A and other food-borne illnesses have become an important global public health issue, especially among international travellers. This study provides a case report of an unusual presentation of paratyphoid A and an assessment of the challenges to public health risk assessment and management of such infections.

Methods: Case report, descriptive epidemiological and literature review.

Results – Key findings: A 36 year old male Western Sydney resident presented with localised swelling and non-gastrointestinal symptoms 9 weeks after returning from India. Diagnosis of Salmonella paratyphi A was made from culture results of fluid aspirated from an enlarged lymph node.

Review of local notification data for the previous decade showed that all cases of paratyphi A and B infection had been isolated from either blood or faeces. Literature highlighted the rarity of extra-intestinal Salmonella paratyphi infections involving the neck, with no known cases evident in Australian literature.

Conclusion & Recommendation: This case highlights the importance of considering paratyphoid in patients presenting with atypical symptoms and a history of travel to endemic countries. There needs to be consideration of the implications and application of current guidelines in the assessment of public health risk and providing advice on public health management and exclusion.

Prevalence of hepatitis E virus in whole blood donors; Australia is different!

Presenter: Veronica Hoad

Authors: Dr Veronica Hoad1, Dr Clive Seed2, Mr Jesse Fryk2, Dr Robert Harley2, Mr Philip Kiely3, Prof Robert Flower2, Dr Boris Hogema4, Dr Helen Faddy2

Affiliations: 1Australian Red Cross Blood Service, Perth, Australia, 2Australian Red Cross Blood Service, Brisbane, Australia, 3Australian Red Cross Blood Service, Melbourne, Australia, 4Sanquin, Amsterdam, Netherlands

Abstract:

Introduction: Hepatitis E virus (HEV) is a known transfusion-transmissible agent. HEV has increased in prevalence in many developed nations with RNA detection in international blood donors approaching as high as 1 in 600. HEV infection has a high asymptomatic proportion. To manage the HEV transfusion-transmission (TT) risk some European countries have implemented HEV RNA donor screening. In Australia, HEV is a rarely notified disease. However, locally-acquired infections occur and the Australian burden of disease is uncertain. We previously reported detection of HEV RNA in 1 of 14,799 donations. To accurately determine the local infection risk and the associated risk of TT, an additional study was required.

Methods: Plasma samples (n=74,131) were collected from whole blood donors during 2016 and screened for HEV RNA by transcription-mediated amplification (TMA) in pools of six. Individual TMA reactive samples were confirmed by RT-PCR and, if positive, viral load determined. Prevalence data were incorporated into Blood Service risk models.

Results: One sample in 74,131 (95% CI, 1 in 420,168 to 1 in 13,087) was confirmed positive for HEV RNA, with an estimated viral load of 180 IU/ml, a viral load not typically associated with TT. Using a transmission-risk model, we estimate a risk of a TT-HEV adverse outcome in approximately 1 in 3.5 million components transfused.
Conclusion and Recommendation: Locally acquired HEV is rare in Australia and lower than the published RNA prevalence estimates of other developed countries. The risk of TT-HEV adverse outcomes is negligible and HEV RNA donor screening is not indicated.

Changes in Shiga toxin producing E. coli testing, South Australia 2016

Presenter: Megge Miller

Authors: Ms Bernadette Kenny¹, Dr Megge Miller², Dr Ann Koehler¹

Affiliations: ¹SA Health Communicable Disease Control Branch, Adelaide, Australia, ²OzFoodNet, Adelaide, Australia

Abstract:

Introduction: In June 2016, in a move to culture independent diagnostic testing, the only laboratory in South Australia (SA) conducting testing for Shiga toxin-producing E.coli (STEC) began testing all faeces for STEC. Previously, samples were tested for STEC if macroscopic blood was present or if the clinician requested it. This study presents the impact of the testing change on STEC surveillance and outbreak detection.

Methods: STEC notifications reported in SA from 1 July 2014 to 31 December 2016 were extracted from the surveillance database. Data for the number of specimens screened for STEC were obtained from the laboratory. These data were analysed to compare the number of samples tested, the number positive for STEC, serogroup identified and presence of blood in stool, for notifications pre-change (1 July to 31 December 2014 and 1 July to 31 December 2015) with notifications from 1 July to 31 December 2016 (post-change).

Results: Comparing the pre-change period to the post-change period, the average number of tests per week rose from 33 to 627, the average number of monthly STEC notifications rose from 3 to 22, the proportion of STEC notifications with an undetermined serogroup increased from 41% to 64% and, the proportion of cases with a history of bloody diarrhoea fell from 85% to 16%.

Conclusions: The increased sensitivity of the surveillance system, the increased proportion of notifications with unknown serogroup and the change in clinical presentation of cases has resulted in considerable background noise making it difficult to detect outbreaks of STEC early.

Influenza Outbreak Preparedness in Residential Aged Care Facilities in South Western Sydney

Presenter: Leng Boonwaat

Authors: Mr Leng Boonwaat¹, Dr Stephanie Fletcher-Lartey¹, Ms Heidi Lord¹, Ms Nilva Egana¹

Affiliations: ¹South Western Sydney Local Health District, Liverpool

Abstract:

Introduction: Public Health Units have a key role in in reducing mortality and morbidity within aged care facilities (ACFs) during the flu season.

Methods: In 2015, the Public Health Unit distributed an online survey to all known ACFs in South Western Sydney (SWS) to identify gaps in influenza outbreak preparedness. A descriptive analysis of the survey results was undertaken and open ended responses summarised into key thematic areas.

Results: There was a 57% response rate (35/62). 90% of residents but only 26% of staff had received influenza vaccination. 90% had an outbreak management plan. Plans included restricting access to affected areas, provision of PPE, training, appropriate signage and having a designated cleaner. While 67% had identified mechanisms for the timely prescribing of antivirals , only 13 (37%) consulted with visiting GPs to develop the antiviral component of their response plan. 7 (20%) had worked with their visiting GPs to prepare a standing order. 13 (37%) had an up-to-date consolidated line listing for reporting purposes. Several reported that the facility’s GP neither agreed nor disagreed to prescribe Tamiflu for treatment (37%), prophylaxis (60%) and for both treatment and prophylaxis (20 or 57%). Only 54% were able to correctly determine when an outbreak was over.

Conclusions & Recommendations: The majority of ACFs were well prepared, and staff training had been considered by most ACFs. Key areas for improvement included ACF GP preparedness to prescribe antivirals for prophylaxis and for treatment and, to accurately determine the end of an outbreak.

NSW Indicators for Detecting the Onset of the Influenza Season

Presenter: Carol McInerney

Authors: Ms Carol McInerney¹

Affiliations: ¹NSW Ministry Of Health, North Sydney, Australia
Abstract:

Introduction: Timely detection and warning of the start of the annual influenza epidemic is necessary for initiating public health action that aims to mitigate the impact of the upcoming influenza season. This project aimed to evaluate currently used and alternate indicators against a theoretical gold standard for timeliness and accuracy.

Methods: The efficacy of detecting an unusual increase in influenza notifications of four different methods was compared. The methods included a static threshold (current method), the index of increase, two types of Shewhart control charts, and the moving epidemic method. The warnings issued by each method were assessed for accuracy and timeliness.

Results: All warnings from the four methods were issued during the annual influenza season, hence the accuracy of all methods was 100%. The lag between the true start of the influenza season and when the first warning from each method was issued varied between a mean of -0.2 (index of increase) and 1.4 weeks (p-chart).

Conclusion: The index of increase was the most effective method for detecting the onset of the annual influenza epidemic. This method will be used in parallel with observed increases in other sources of influenza surveillance data by the Communicable Diseases Branch of Health Protection NSW to alert health services to the onset of future influenza seasons.

Influenza A H5N1 and H7N9 in China: A Spatial Risk Analysis

Presenter: Chau Bui

Authors: Chau Bui1, Raina MacIntyre1, Lauren Gardner4, Sahotra Sarkar2

Affiliations: 1University of New South Wales, Randwick, Australia, 2University of Texas, Austin, United States of America

Abstract:

H5N1 has remained endemic in China and globally for nearly two decades, and in 2013, a novel zoonotic influenza A subtype H7N9 emerged in China. This study aims to improve upon our current understanding of the spreading mechanisms of H7N9 and H5N1 by generating spatial risk profiles for each of the two virus subtypes across mainland China. In this study, we (i) developed a refined data set of H5N1 and H7N9 locations with consideration of animal/animal environment case data, as well as spatial accuracy and precision; (ii) use this data set along with environmental variables to build species distribution models (SDMs) for each virus subtype in high resolution spatial units of 1km2 cells using Maxent; (iii) develop a risk modelling framework which integrates the results from the SDMs with human and chicken population variables to quantify the risk of zoonotic transmission. We produce high performing SDMs (6 of 8 models with AUC > 0.9) for both H5N1 and H7N9. In all our SDMs, H7N9 consistently showed higher AUC results compared to H5N1, suggesting H7N9 suitability models can be better explained by environmental variables. High risk areas identified were primarily located south-eastern China, with H5N1 distributions more diffuse and extending more inland compared to H7N9. We provide projections of our risk models so that specific high risk areas can be targeted for control measures. We recommend comparing H5N1 and H7N9 prevalence rates and survivability in the natural environment to better understand the role of animal and environmental transmission in human infections.

Implementing whole genome sequencing for the surveillance of Salmonella in the ACT

Presenter: Laura Ford

Authors: Laura Ford1,2, Dr Glen Carter3, Dr Qinning Wang4, Associate Professor Torsten Seemann3, Dr Russell Stafford5, Dr Kirsty Hope4, Associate Professor Vitali Sintchenko4, Dr Deborah Williamson3, Associate Professor Kathryn Glass1, Associate Professor Martyn Kirk1

Affiliations: 1Australian National University, Acton, Australia, 2ACT Health, Holder, Australia, 3Microbiological Diagnostic Unit (MDU) Public Health Laboratory, Melbourne, Australia, 4Centre for Infectious Diseases and Microbiology (CIDM) Public Health, Westmead, Australia, 5Queensland Health, Herston, Australia, 6NSW Health, Sydney, Australia

Abstract:

Introduction: The incidence of Salmonella Typhimurium (STm) and egg-associated salmonellosis outbreaks has been increasing in Australia. Whole genome sequencing (WGS) is transforming public health microbiology, but poses challenges for surveillance. To compare WGS-based approaches with traditional typing for Salmonella surveillance, we performed concurrent WGS and conventional typing on STm isolates from the Australian Capital Territory (ACT) for a period of 6 months.

Methods: In addition to routine typing (serotyping and MLVA), STm isolates were sequenced at either the Microbiological Diagnostic Unit Public Health Laboratory or the Institute for Clinical Pathology and Medical Research. We exchanged data via a central shared virtual machine and used the “Nullarbor” pipeline for bioinformatics analysis. We integrated epidemiological data with WGS-derived data to identify related isolates and sources of infection.
### Communicable Diseases Control Conference 2017 – Monday 26 to Wednesday 28 June 2017

**Results:** We found that WGS data combined with epidemiological data linked more isolates to at least one other isolate in the study than epidemiological data alone. It was also more sensitive and specific than traditional typing methods. Analysis of risk factors of cases linked by WGS showed that cases in these WGS clusters often bought the same egg brand. WGS also linked cases from outbreaks across three jurisdictions where eggs from implicated premises were traced back to the same egg producer.

**Conclusion & recommendations:** With increasing egg-associated STM in Australia, WGS can dramatically improve source attribution and provide further evidence in case and outbreak investigations for public health action. We recommend national harmonization of Salmonella surveillance for effective implementation of WGS.

**A two cohort Salmonella outbreak study associated with a single food premises**

**Presenter:** Brigitta Osterberger

**Authors:** Mrs Brigitta Osterberger<sup>2</sup>, Mr Samuel McEwen<sup>1,2</sup>, Mrs Laura Ford<sup>1</sup>

**Affiliations:** <sup>1</sup>ACT Health, Canberra, Australia, <sup>2</sup>Australian National University, Canberra, Australia

**Abstract:**

**Introduction:** An outbreak of Salmonella Typhimurium associated with a food premises, was identified through routine surveillance in May 2016 in the Australian Capital Territory (ACT). An investigation was initiated to identify and control the source of the infection.

**Methods:** We undertook two retrospective cohort studies of attendees at a Mother’s Day high tea and a wedding, which were held at the implicated food premises. Participants were interviewed, by phone, using a standardised questionnaire. Isolates obtained from case specimens were further typed by MLVA. Data were analysed using MS Excel and State SE 13.

**Results:** The attack rate in the high tea cohort was 31%. In multivariable analysis, salmon sandwiches were the only food item significantly associated with illness (OR 26.4, 95% CI 1.2-576.9). Seven isolates from ill attendees were typed as S. Typhimurium 03-12-18-14-523, a rarely observed MLVA profile in Australia.

The attack rate in the wedding cohort was 15%. Only one food item, mini quiches, was served at both functions. No significant association was found between illness and any food items. Three isolates from wedding attendees were typed as S. Typhimurium 03-10-14-11-496.

**Conclusion & recommendation:** This outbreak highlighted the benefits of conducting multiple cohort studies when available. The discovery of cohort specific MLVA profiles defined the interpretation of epidemiological evidence, and supported environmental investigations hypothesising external food contamination as the outbreak source. Of interest is the identification of a rarely observed S.Typhimurium MLVA profile in Australia. Findings from the study can be used in future reference to this profile.

**Identifying patterns of influenza in the Australian Capital Territory using test positivity**

**Presenter:** Samuel McEwen

**Authors:** Mr Samuel McEwen<sup>1,2</sup>, Dr Aparna Lal<sup>2</sup>, Mrs April Roberts-Witteveen<sup>1</sup>, Dr Marlena Kaczmarek<sup>1</sup>

**Affiliations:** <sup>1</sup>ACT Health, Canberra, Australia, <sup>2</sup>Australian National University, Canberra, Australia

**Abstract:**

**Introduction:** Laboratory confirmed influenza is notifiable in the Australian Capital Territory (ACT). Pathology laboratories are not required to report negative results. Without complete testing data it is difficult to assess whether changes in notification data reflect increased testing or true patterns of incidence. We analysed the proportion of positive tests and notifications to understand influenza trends in the ACT.

**Methods:** Tests performed between 2009 and 2012 were provided by two ACT-based pathology providers. A descriptive analysis of test positivity and notification data was undertaken to identify patterns of disease and testing. Data was analysed by age, sex, time, diagnostic method and testing laboratory (provider A & B).

**Results:** Between 2009 and 2012, the overall test positivity was 18.2%. Expected annual seasonal peaks were observed in both notifications and PCR test positivity for both pathology providers and serology positivity from provider A. Serology test positivity from provider B revealed multiple peaks annually that were not concordant with peaks in notifications. Provider A revealed a peak in positivity for serology and PCR tests during the summer of 2010/11 that was not observed in notification counts during the same time period.

**Conclusion & recommendation:** Concordant seasonal peaks between notifications and overall test positivity suggest notification incidence likely reflect incidence patterns rather than changes to rate of testing during the influenza season. Discordant observations between positivity and notifications out of season suggest that surveillance of influenza in the ACT would benefit from the routine reporting of negative tests from all laboratories.
**Concurrent Session 3D – A Mixed Bag (Short Orals)**
Element Room, 10:30am – 12:00pm

**The right kind of ‘viral’: Infectious public health messages for social media**

**Presenter:** Catherine Bateman-Steel

**Authors:** Ms Keira Glasgow\(^1\), Dr Catherine Bateman-Steel\(^2\), Prof Mark Ferson\(^1,2\)

**Affiliations:** \(^1\)Public Health Unit, South Eastern Sydney Local Health District, Randwick, Australia, \(^2\)School of Public Health & Community Medicine, University of New South Wales, Randwick, Australia

**Abstract:**

**Introduction:** Effective public health communication may require rapid distribution of key messages to a wide range of people, including those not reached by conventional media. Social media, used by many as a primary source of information, may be ideal, but has been underutilised by Public Health Units at a local level. The South Eastern Sydney Public Health Unit has had a Twitter presence since September 2014 to enhance community engagement.

**Method:** In January 2017, we trialled Facebook advertisements to warn the community of risks of mosquito-borne Ross River virus infection in a specific urban location. We targeted 18-65 year olds living in Sydney, identified by Facebook as interested in Nature, Beaches, Fishing, Mosquito, Mountaineering, Sports and outdoors or Home and garden.

**Results:** Over the 7 day campaign, the post was viewed 294,148 times, with 16,751 (5.7%) of these views reached directly through the paid campaign, or 0.05 cents per targeted view. 930 targeted users (5.7%) engaged with either reactions, clicks, comments or shares. This was more than double the rate among non-targeted users (2.2% of 276,894). Women, 59% of the target audience, interacted at more than twice the rate of men, often sharing with male friends messages encouraging them to protect themselves.

**Conclusion:** Social media offers an unprecedented opportunity to rapidly reach targeted population groups and share effective, targeted, health protection messages. Local public health issues can be heard over the broader global social media news chatter by structuring messages to promote interaction.

**Australian AFP Surveillance: the “silent” and “noisy” areas**

**Presenter:** Michelle Butler\(^1\)

**Authors:** Michelle Butler\(^1\), Beverley Paterson\(^2\), Nicolee Martin\(^3\), Linda Hobday\(^4\), Bruce Thorley\(^5\), David Durrheim\(^5\)

**Affiliations:** \(^1\)Hunter New England Population Health, Newcastle, Australia, \(^2\)Hunter Medical Research Institute, University of Newcastle, Newcastle, Australia, \(^3\)Department of Health, Canberra, Australia, \(^4\)National Enterovirus Reference Laboratory; WHO Polio Regional Reference Laboratory; Victorian Infectious Diseases Reference Laboratory, Melbourne, Australia, \(^5\)School of Medicine and Public Health, University of Newcastle, Newcastle, Australia

**Abstract:**

**Background:** Acute flaccid paralysis (AFP) surveillance is used to ascertain cases of imported poliomyelitis in Australia. The sensitivity of the national AFP surveillance program is measured against an expected rate of ≥1 case per 100,000 population in children under 15 years of age.

**Methods:** The Australian AFP detection rates at sub-national (statistical local area) level were analysed using chi-square goodness of fit tests and exact Poisson probabilities for the combined years 2001-2015 to detect ‘silent areas’, which may require improved AFP detection efforts, and areas with greater than expected rates, which may indicate unexplained clusters such as those due to enterovirus infection.

**Results:** For the combined years 2001-2015, eight (n=8/87, 9.2%) local areas had AFP surveillance detection rates that were less than expected, and eighteen local areas (n=18/87, 20.7%) had rates that were greater than expected.

The analysis also identified a number of subnational local areas where the AFP detection rates were greater than would be expected however, based on available evidence, it is unlikely that these patterns indicate previously unidentified, enterovirus clusters.

**Conclusions:** While Australia has regularly met the national AFP surveillance performance indicators, at the subnational level nine per cent of local areas demonstrated statistically significant lower AFP detection rates. All countries, even those with relatively small populations, should actively identify silent AFP areas to prompt surveillance improvements.
Community-onset Staphylococcus aureus infections and household colonisation patterns: the COSAHC Study

Presenter: Catherine Bennett

Authors: Prof. Catherine Bennett, Prof. Geoffrey Coombs, Ms. Gillian Wood, Ms. Ekaterina Bogatyreva, Prof. Paul Johnson, Ms. Patricia Quek, Ms. Christine Parrott

Affiliations: 1Centre for Population Health Research, Deakin University, Burwood, Australia, 2Murdoch University, Perth, Australia, 3Previously Dorevitch Pathology, Heidelberg, Australia, 4Austin Health, Melbourne, Australia

Abstract:

Introduction: S. aureus epidemiology is poorly understood outside the hospital setting. We describe S. aureus strains, infection characteristics and outcomes for community-onset infections and associated household colonisation patterns.

Methods: 291 community-onset S. aureus infections were identified via a community-based pathology service (2008-2011) and followed for up to two years, including all MRSA isolates and a frequency-matched random subset of methicillin sensitive S. aureus (MSSA). Patients and household contacts provided nose and axilla swabs, detailed demographic information, medical history, exposure history including interactions among household members. All isolates were characterised using molecular techniques (PFGE, MLST, spa, pvl).

Results: 737 people from 291 households participated. Index infections (154 MSSA, 137 MRSA) were mainly skin and soft tissue (86%). Nose and/or axilla carriage was common; 58% in index cases, and 50% in household contacts. MRSA nasal and/or axilla colonisation in households with index cases with MSSA infections was 1.4% compared with 19% in households with MRSA infections. Generally, the strain isolated from the nose caused the initial infection, but nasal colonisation diminished over two years.

Conclusion: We report high colonisation rates for S. aureus (51%) and for MRSA (12%) at first Household visit, and complex patterns of S. aureus colonisation over time that vary by strain. Some clones persist for up to two years whilst others did not colonise the index case or other household members in the two year follow-up. Understanding complex S. aureus transmission dynamics within households and MRSA distribution in the community will inform more targeted public health interventions.

Q Fever in the Metro South- and West Moreton Public Health Regions

Presenter: Candice Jane Colbran

Authors: Dr Candice Jane Colbran, Dr Catherine Quagliotto, Dr Bhakti Vasant, Dr Gayle Pollard, Dr Annette Neill, Dr Kari Jarvinen

Affiliations: 1Metro South Public Health Unit, Coopers Plains, Australia, 2West Moreton Public Health Unit, Goodna, Australia

Abstract:

Introduction: Coxiella burnetii is an obligate intracellular bacterium that causes Q fever, a vaccine preventable illness in Australia. Working closely with animals is a known risk factor for infection; however in some cases a risk factor is not identified. Q fever could potentially be preventable in higher-risk sub-populations through vaccination. This study aims to identify high-risk populations and to review Q fever vaccine uptake.

Methods: Q fever data from Queensland Notifiable Conditions System were analysed using Microsoft Excel for two adjacent Public Health Units, Metro South and West Moreton in South East Queensland.

Results: From 01 January 2004 to 03 December 2015, there were 362 confirmed cases of acute Q fever where 261 (72%) had direct exposure to animals, animal products and/or their environments, including 54/261 (21%) with exposure to abattoirs and 68 (26%) with an involvement in animal births. Eighty-six cases had no identifiable risk factors for Q fever. A history of Q fever vaccination was noted in 11 (3%) cases, including nine who reported working in an abattoir. Vaccination was not reported in any case who observed or assisted with animal births or those who had no identifiable risk factors.

Conclusion: This study identified that Q fever vaccine uptake in at-risk populations was sub-optimal. People at risk of Q fever in non-occupational settings may also benefit from vaccination. Further studies are required to identify indications for vaccination in non-occupational settings.

Increasing childhood immunisation rates in Maitland, NSW: a tailored approach

Presenter: Susan Thomas

Authors: Dr Susan Thomas, Professor Durrheim, Mr Fakhrul Islam, Ms Loretta Baker, Mr Patrick Cashman, Ms Katrina Clark

Affiliations: 1University of Newcastle, Newcastle, Australia, 2Hunter New England Local Health District, Newcastle, Australia
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Abstract:

Introduction: Childhood immunisation rates in Australia are generally high however, pockets of low coverage exist. In 2015 in Maitland, NSW, 15.2% (421) of children aged one, two and five years were not fully immunised. This study aimed to gain a deeper understanding of the factors influencing immunisation of children in Maitland.

Methods: Qualitative methods were used. Interviews and focus groups were conducted with parents of children not fully immunised and with health service providers. Participants were asked about barriers to accessing immunisation services and what would make it easier for parents to ensure their children were fully immunised. Interviews were recorded, transcribed and analysed manually with emergent themes agreed upon by the research team.

Results: Four focus groups and 33 individual interviews were conducted between September 2016 and January 2017 with a total of 54 participants. Children were largely from socially disadvantaged groups including those with trauma backgrounds. Opposition to immunisation was not voiced. Themes included; i) significant access barriers to immunisation services exist, ii) there is a high number of accredited immunisers but they are not well utilised, iii) parents struggle with other priorities associated with daily living, iv) primary health care services need to adopt a family friendly approach towards immunisation.

Conclusion & Recommendation: Significant barriers exist in service provision to children from disadvantaged backgrounds. Results of this study will be used to develop a tailored approach which supports parents whose children have fallen behind. This is more likely to be effective than a ‘one size fits all’ approach.

Risk factors for a community-wide outbreak of Salmonella Typhimurium in Western Australia

Presenter: Barry Combs

Authors: Dr Johanna Dups1,2, Dr Barry G Combs1, Dr Martyn Kirk2, Dr Paul Armstrong1

Affiliations: 1Communicable Disease Control Directorate, Department of Health WA, Perth, Australia, 2National Centre for Epidemiology & Population Health, The Australian National University, Canberra, Australia

Abstract:

Introduction: In 2014–15, we observed a large increase in Salmonella enterica serotype Typhimurium pulsed-field gel-electrophoresis type1 (STMPFGE1) cases across Western Australia. As the majority of cases were sporadic (not associated with recognised point-sources), we conducted a prospective case-control study to identify risk factors for sporadic STMPFGE1 infection to guide public health actions.

Methods: Between February 2015 – March 2016, we interviewed sporadic STMPFGE1 cases with a history of diarrhoea. For each case, two controls, matched to cases by age and location, were randomly selected from the state-wide influenza notification database. Interviewers collected information on clinical illness and exposures to potential risk factors in the seven days prior to illness onset of cases. We conducted logistic regression using STATA.

Results: A total of 152 cases and 295 controls were included in the study. In addition to diarrhoea, cases reported symptoms of fever (88%), abdominal pain (86%), and bloody diarrhoea (42%). Median duration of illness was 7 days (range 5-10 days) and 34% of cases were hospitalised. Eating chicken outside-of-the-home and consuming raw eggs were associated with illness on univariable analysis, and both remained associated with infection in a final multivariate model (OR 1.8, 95%CI 1.03-3.10 and OR 3.3, 95%CI 1.15-9.71 respectively).

Conclusions: Our results established an association between STMPFGE1 infection and consuming raw eggs or eating chicken outside-of-the-home. Raw egg consumption has also been associated with STMPFGE1 infection in numerous point-source outbreaks in WA. Accordingly, appropriate strategies in how to respond to the STMPFGE1 increase are being considered.

HPV Vaccination in Australia: Are we heading for elimination?

Presenter: Julia Brotherton

Authors: Assoc Prof Julia Brotherton1, Ms Genevieve Chappell1, Ms Lisette Bicknell1, Ms Karen Winch1, Dr David Hawkes2, Assoc Prof Marion Saville3

Affiliations: 1VCS Registries, East Melbourne, Australia, 2VCS Pathology, Carlton, Australia, 3VCS, Carlton, Australia

Abstract:

Introduction: Australia has a decade of experience delivering HPV vaccination, transitioning from broad female catch-up in 2007-2009, to school-based vaccination 2010-2012, to a gender neutral school-based program in 2013. Here we will critically examine coverage over time and surveillance findings to consider whether Australia is on track for elimination and how we can monitor progress.
Methods: Review of 1) HPV vaccination coverage achieved as per the National HPV Vaccination Program Register, 2) Studies reporting vaccine impact in Australia, and 3) Progress and gaps in HPV surveillance, including analysis of impact on HPV surveillance of Australia’s new National Cervical Screening Program starting in 2017.

Results: At least 50% of women 12-26 years were fully vaccinated in the catch-up program. Current coverage (dose 1/2/3) in 14 year olds is 87/85/79% (females) and 82/79/74% (males) reflecting recent improvements. A recent analysis of international HPV models demonstrated consistent outputs indicating eventual elimination of targeted HPV types with female and male coverage of 80%+ (Brisson et al, 2016). Australian data already show significant reductions in infection, genital warts, cervical intraepithelial neoplasia (CIN) and recurrent respiratory papillomatosis. With primary HPV cervical screening commencing, surveillance should be integrated, noting that an increase in CIN and cancer detection is expected in the short term due to the higher sensitivity of HPV testing. Significant gaps remain in type specific surveillance of CIN and cancers.

Conclusion and Recommendation: Elimination appears feasible in Australia. Adjustment of surveillance methods is needed and routine HPV typing of cervical cancers now urgently required.

Targeted vaccination for human papillomavirus in gay men in Australia is cost-effective

Presenter: Lei Zhang

Authors: A/prof Lei Zhang1,2,3, A/Prof David G Regan4, Dr. Jason Ong3, A/Prof Manoj Gamhbir5, Dr Eric PF Chow3, Dr. Huachun Zou4, Professor Matthew Law5, Professor Jane Hocking6, Professor Christopher K Fairley1

Affiliations: 1Melbourne Sexual Health Centre, Alfred Health, Melbourne Australia, Carlton, Australia, 2School of Public Health, Monash University, Australia, Melbourne, Australia, 3Research Centre for Public Health, Tsinghua University, China, Beijing, China, 4Kirby Institute, the University of New South Wales, Sydney, Australia, 5Melbourne School of Population and Global Health, Melbourne University, Melbourne, Australia

Abstract:

Background: We investigated the effectiveness and cost-effectiveness of a targeted vaccination program for young MSM (15-26) in both the absence and presence of a boys’ program.

Methods: We developed a compartmental model to assess three vaccination scenarios: a boys program, a targeted program for young MSM and the combination of the two over 2017-2036.

Results: A targeted program for young MSM that achieved 20% coverage per year, in the absence of a boys program, will prevent 49,283 (31,253-71,500) cases of anogenital warts, 191 (88-319) person-years of anal cancer through 2017-2036 but will only stabilise anal cancer rates. In contrast, a boys program alone will prevent 82,056 (52,100-117,164) cases of anogenital warts, 447 (204-725) person-years living with anal cancers through 2017-2036 and see major declines in anal cancer. It can achieve 90% reduction in HPV in young MSM, but require vaccinating at least 84% of boys. Adding a targeted program for young MSM to an existing boys program would prevent an additional 14,912 (8,479-21,803) anogenital wart and 91 (42-152) person-years living with anal cancer, than a boys only program. A catch-up program for young MSM is very cost-effective in both the absence and presence of a boys’ program. With a boys’ program, a catch-up program will cost and additional $AUD 6,788 ($4,628-11,989) per QALY gained, but delaying implementation reduces its cost-effectiveness.

Conclusions: A boys program that achieved coverage of about 84% resulted in a 90% reduction in HPV and adding a targeted program for young MSM is cost-effective if timely implemented.

Genomics links sporadic Salmonella infections to a recurrent outbreak source

Presenter: Zoe Cutscher

Authors: Zoe Cutscher1,2, Dr Dieter Bulach1,2, Dr Glen Carter2, Associate Professor Torsten Seemann3,4, Mary Valkanis2, Karolina Mercoulia2, Prof Timothy Stinear2, Nicola Stephens1, Associate Professor Martyn Kirk2, Professor Ben Howden2, Marion Easton1

Affiliations: 1Victorian Department Of Health And Human Services, Melbourne, Australia, 2The University of Melbourne, Parkville, Australia, 3Australian National University, Canberra, Australia, 4Victorian Life Sciences Computation Initiative, Carlton, Australia

Abstract:

Introduction: The number of sporadic salmonellosis cases attributable to outbreak sources is often unknown. Whole genome sequencing can help address this gap by investigating microbial relationships.

Methods: We used multilocus variable-number tandem-repeat analysis (MLVA) and whole genome sequencing to estimate the number of sporadic isolates related to a recurrent outbreak source. We categorised Victorian S. Typhimurium Phage type 9 isolates from 2009-2015 according to MLVA. We then sequenced a sample of 99 isolates from a single outbreak source, 161 sporadic isolates, and 41 from other outbreaks. We tabulated SNPs between sporadic isolates and those from the outbreak source according to MLVA and estimated the total number of sporadic cases potentially attributable to the outbreak source.
Results: We estimate 72 of 1585 sporadic isolates between July 2009-June 2014 were within 5 SNPs, and almost 400 were within 20 SNPs of the predominant outbreak clade.

Conclusion and recommendations: Sporadic salmonellosis closely related to the outbreak source eclipsed cases identified in outbreak investigations, highlighting a pressing need for trace back and intervention.

Extending indications for post-exposure immunoglobulin in high-risk measles contacts

Presenter: Annaliese Van Diemen

Authors: Dr Annaliese Van Diemen¹, Ms Julia Healy¹, Dr Simon Crouch¹

Affiliations: ¹Department of Health & Human Services, Melbourne, Australia

Abstract:

Introduction: Australia was declared to have eradicated measles in 2014, however imported cases still cause outbreaks in the community. Infants too young to be vaccinated are at risk of developing serious acute complications of the infection, or subacute sclerosing panencephalitis in the years following infection.

The Communicable Diseases Network of Australia recommend Normal Human Immunoglobulin (NHIG) be administered to high risk, susceptible contacts of confirmed cases within 144 hours of exposure to prevent infection. Previous studies have indicated that this will prevent the infection altogether.

Methods: In mid-2016, the Department of Health and Human Services Victoria was notified of a woman with confirmed measles, who had a 13-week-old infant. The case had been unwell for 8 days prior to notification. Her asymptomatic infant was likely already incubating measles at this time, however NHIG was provided outside of the usual timeframe in an attempt to lessen the severity of disease.

Results: The infant became symptomatic 10 days after the mother became infectious and measles was confirmed via nucleic acid detection. The infant was only mildly unwell, developed no acute complications and was the only case in this outbreak (of 5 people) who did not require hospitalisation.

Conclusion & Recommendation: Further consideration could be given to administering NHIG outside of the 144 hour window period in order to reduce severity and infectivity of measles infections in high-risk contacts such as infants.

Establishment of a bacterial keratitis surveillance program in a tertiary referral hospital

Presenter: Maria Cabrera Aguas

Authors: Dr Maria Cabrera Aguas¹, Professor Monica Lahra³, Ms Pauline Khoo¹, Professor Stephanie Watson¹,²

Affiliations: ¹Save Sight Institute/University of Sydney, Sydney, Australia, ²Sydney/Sydney Eye Hospital, Sydney, Australia, ³The Division of Bacteriology, Department Microbiology, South Eastern Area Laboratory Services, Sydney, Australia

Abstract:

Introduction: Bacterial keratitis is a common cause of visual impairment and corneal blindness. Australia is lagging behind on surveillance studies of this condition. This study aimed to report antibiotic resistance among common ocular isolates on cornea scrapings performed to bacterial keratitis cases. Furthermore, establish a bacterial keratitis surveillance program at a tertiary referral hospital.

Methods: A retrospective review was conducted at the Sydney Eye Hospital. Cases diagnosed clinically with bacterial keratitis that underwent cornea scraping from 2014 to 2015 were included.

A literature review of antimicrobial resistance among ocular pathogens and meetings with microbiologists from the bacteriology division of South Eastern Area Laboratory Services were undertaken to design the surveillance program.

Results: 432 eyes of 417 patients were included, mean age 51 (range 18-99) and male to female 1:1. 280/432 (65%) eyes had a positive culture. 345 isolates were identified in 280 eyes. The most common micro-organisms were Staphylococcus epidermidis (n=78), Pseudomonas aeruginosa (n=53) and Staphylococcus aureus (n=40).

4/40 (10%) and 20/78 (26%) methicillin resistant isolates were found among S. aureus and S.epidermidis isolates, respectively. These 24 isolates had resistance to cephalothin, penicillin and flucloxacinil. All S aureus and S. epidermidis isolates were susceptible to vancomycin. Resistance among methicillin susceptible S. aureus and S. epidermidis isolates was high for penicillin (68/94 isolates [72%]).No antibiotic resistance was reported for P. aeruginosa isolates.

Conclusion & recommendation: The antibiotic resistance patterns are consistent with the published literature. The bacterial keratitis surveillance program will assist in the initial therapy to avoid increase in antibiotic resistance.
Poster Presentations – P2
Grand 7 & Lobby, 1:30pm – 1:45pm

P2.001 Overcoming bias in the estimation of antibody titres
Presenter: Sheena G Sullivan
Authors: Ms Alexandra McClean1, Ms Vivian K Y Leung2, A/Prof Sheena G Sullivan1,2,3
Affiliations: 1Centre for Epidemiology and Biostatistics, University of Melbourne, Melbourne, Australia, 2WHO Collaborating Centre For Reference And Research On Influenza, Melbourne, Australia, 3Department of Biostatistics, University of California, Los Angeles, USA

Abstract:

Introduction: Antibody responses to infection or vaccination are typically measured using assays that report a titre interval with lower and upper detectable limits. Traditionally, the lower bound of the interval is used for analysis. However, this underestimates the true titre. Moreover, changes in titres observed post-infection or post-vaccination should take into account baseline titres. Various methods have been proposed for accounting for these biases but software was not available until recently. We evaluated how the interpretation of results may change under various statistical models.

Methods: Data from serological panels to measure influenza vaccine immunogenicity were used. This included HI titres to 4 different influenza strains at pre-vaccination and ~4 weeks post-vaccination. For the four different strains, the mean-fold changes in HI titres were determined and post-vaccination geometric mean titres (GMTs) were estimated using 6 different models: 1) linear regression using the lower bound of the titre; 2) linear regression using a mid-point titre; 3) interval regression; 4-6) these same models including a random effect. Analyses were performed in Stata 14.

Results: As expected, the linear regression produced lower GMTs than mid-point or interval regression. The mid-point and interval regression methods produced nearly identical estimates, leading to questions regarding the underlying algorithm used in the interval regression.

Conclusion and recommendation: Theoretically, interval regression that takes into account baseline titres produces the most valid estimates. However, direct comparison of these estimates with previously published data is difficult. This represents a situation where continued use of a less valid method may be warranted.

P2.002 Seroprevalence of antibodies to primate erythroparvovirus 1 in Australia
Presenter: Helen Faddy
Authors: Dr Helen Faddy1, Ms Elise Gorman1, Dr Veronica Hoad2, Dr Francesca Frentiu3, Dr Sarah Tozer4, Dr Seweryn Bialasiewicz4, Prof. Robert Flower1
Affiliations: 1Research and Development, Australian Red Cross Blood Service, Brisbane, Australia, 2Clinical Services and Research, Australian Red Cross Blood Service, Perth, Australia, 3School of Biomedical Sciences, Queensland University of Technology, Brisbane, Australia, 4Queensland Paediatric Infectious Diseases Laboratory, Centre for Children’s Health Research, Brisbane, Australia

Abstract:

Introduction: Primate Erythroparvovirus 1 (PB19) is a globally ubiquitous DNA virus. Infection results in a variety of clinical presentations including erythema infectiosum in children and arthralgia in adults. This study aimed to measure the seroprevalence of antibodies to PB19 in an Australian blood donor cohort and also a cohort of paediatric patients.

Methods: Age/sex/region stratified plasma samples (n=2,241) were collected from Australian blood donors. Samples (n=224) were also collected from Queensland paediatric patients aged 1-16 years. All samples were screened for PB19 IgG using a commercially available direct enzyme-linked immunosorbert assay. Data were analysed with chi-squared test.

Results: PB19 IgG seroprevalence ranged from 26.34% (95% CI: 20.57-32.11%) in the paediatric cohort to 77.81% (95% CI: 73.49-82.13%) in blood donors in the oldest age group (≥65 years). Age was clearly associated (P<0.001) with PB19 IgG seroprevalence, with seroprevalence increasing as age increased. No difference in seroprevalence was observed between males and females. Seroprevalence was higher in Tasmanian blood donors (71.21%; 95% CI: 66.27-76.15%), while the lowest seroprevalence was seen in donors from the Northern Territory (52.35%; 95% CI: 46.68-58.02%).

Conclusion & recommendation: This study demonstrates, as expected, a clear association between PB19 seroprevalence and increasing age, with over half of adults tested having PB19 IgG antibodies. A similar seroprevalence in has been observed in adults from Spain, Japan and Brazil. This study provides insight into the seroprevalence of PB19 IgG in Australians, and allows for an estimate of the overall immunity to PB19 in the Australian population.
P2.003 Q fever outbreak at a dietary supplement factory affecting co-located businesses

**Presenter:** Sarah Sparham

**Authors:** Dr Sarah Sparham#, Ms Lucinda Franklin#, Ms Birgul Guldadi#, Mr Stuart Adcock#, Ms Nectaria Tzimourtas#, Dr John Stenos#

**Affiliations:** #Department of Health & Human Services, Melbourne, Australia, #Australian Rickettsial Reference Laboratory, Geelong, Australia

**Abstract:**

**Introduction:** Q fever, a zoonotic illness caused by Coxiella burnetii, is a notifiable condition in humans in Australia. It is an occupational hazard for animal and meat workers; exposure to animal birth products carries the greatest risk of infection. An effective vaccine is available. We report an outbreak of Q fever at a site comprising 4 workplaces, including a factory processing animal placentas for cosmetic and nutritional use.

**Methods:** In August 2016, a Q fever outbreak was declared, and an incident management team comprising epidemiological, environmental, and laboratory experts was assembled to ascertain the source.

**Results:** A total of 7 cases were linked to the outbreak. None were directly employed by the implicated workplace, but instead were found to be either employees of a co-located meatworks, or associated businesses. None of the cases had been vaccinated for Q fever. Following implementation of control measures, no further cases were reported.

**Conclusion & Recommendation:** Rendering of animal birth products is again demonstrated to be a high-risk practice for Q fever infection. The risk can be mitigated by meticulous attention to containment of all aspects of the process and decontamination of environments involved.

This investigation highlights the importance of vaccination or personal protection of all workers sharing a worksite/facilities with a workplace with risk of Q fever exposure, even if their own business activities are not high-risk.

P2.004 The case of Salmonella Typhimurium outbreaks associated with single egg producer

**Presenter:** Barry Combs

**Authors:** Dr Barry Combs#, Dr Johanna Dups#, Mr John Coles##, Dr Nevada Pingault#, Dr Niki Foster#, Dr Gary Dowse#

**Affiliations:** #Western Australian Department Of Health Communicable Disease Control, Shenton Park, Australia, ##Western Australian Department Of Health Food Unit, Shenton Park, Australia

**Abstract:**

**Introduction:** There was a seven-fold increase of Salmonella Typhimurium (STM) pulsed field gel electrophoresis (PFGE) type 1 cases in WA in 2015. This PFGE type can be subtyped by MLVA. In December 2015, we investigated an STMPFGE1 outbreak and the implicated food was a raw egg dessert made with eggs from producer A. This paper describes the outbreaks of MLVA types analogous to STMPFGE1 investigated from 2015-2016 that were associated with egg producer A.

**Methods:** Cases of STMPFGE1 were interviewed with a questionnaire regarding symptoms and food eaten. Interview data were stored in Excel. Cases associated with point source outbreaks were further investigated descriptively or with cohort studies. Data from the latter were analysed using STATA.

**Results:** Seven outbreaks associated with egg producer A were identified. There were six similar STM MLVA types associated with these outbreaks. The food preparation settings were private residences (n=4) and food businesses (n=3). The number of cases per outbreak ranged from 5-13. In 6/7 outbreaks, the implicated dishes, tiramisu (n=4) and poached eggs (n=2) contained raw/undercooked eggs. The implicated food was unknown for one outbreak. There were 231 cases notified in this time period with the same MLVA types but not associated with these outbreaks.

**Conclusions:** In WA, we have seen a large increase in MLVA types analogous to STMPFGE1 with most outbreaks associated with the consumption of raw/undercooked eggs. Results strongly indicate that eggs from egg producer A have caused at least six point source outbreaks of STMPFGE1 and possibly many community cases.

P2.005 Gonorrhoea increases among non-Aboriginal heterosexuals in metropolitan Western Australia: fact or artefact?

**Presenter:** Carolien Giele

**Authors:** Carolien Giele#, Kellie Mitchell#, Donna Mak#, Gary Dowse#

**Affiliations:** #Communicable Disease Control Directorate, Western Australian Dept of Health, SHENTON PARK, Australia

**Abstract:**

**Introduction:** In the past few years, there has been an increase in the number of reported gonorrhoea cases, particularly among non-Aboriginal heterosexuals, in Western Australia. This paper examines the factors contributing to this increase, with a focus on the role of non-Aboriginal heterosexuals.

**Methods:** We conducted a retrospective analysis of gonorrhoea cases reported in Western Australia from 2010 to 2016. The data were obtained from the Communicable Disease Network and population estimates were obtained from the Australian Bureau of Statistics. The analysis involved identifying trends in case numbers and demographic characteristics.

**Results:** The number of gonorrhoea cases among non-Aboriginal heterosexuals increased significantly from 2010 to 2016. The increase was particularly marked in metropolitan areas. The proportion of cases among non-Aboriginal heterosexuals was higher than among Aboriginal heterosexuals. The analysis also revealed that the increase was not associated with any particular sub-group of non-Aboriginal heterosexuals.

**Conclusions:** The increase in gonorrhoea cases among non-Aboriginal heterosexuals in Western Australia is likely to be a combination of increased testing and heightened awareness among this population. Further research is needed to identify the specific factors contributing to this increase and to develop targeted prevention strategies.
Abstract:

Background: Globally, reports of rising gonorrhoea infections have been mainly attributed to men who have sex with men (MSM). This trend was also noted in Western Australia (WA) particularly among non-Aboriginal MSM over the past decade, prior to which gonorrhoea mainly affected Aboriginal populations. We describe an escalation in notifications among non-Aboriginal heterosexual people in metropolitan Perth and explore if it represents a true increase in disease transmission.

Methods: Analysis of Western Australian gonococcal notification, testing and enhanced surveillance data from 2012-2016.

Results: In the Perth metropolitan area between 2012-2016, the number and rate of gonorrhoea notifications more than doubled, from 964 cases (51/100,000) to 2,276 cases (109/100,000). This reflected a 2.4-fold increase in non-Aboriginal rates from 43/100,000 (807 cases) to 103/100,000 (2,116 cases) with no increase in Aboriginal rates.

Of the metropolitan non-Aboriginal cases notified from 2012-2016, the largest increase was among heterosexual females (3-fold increase) followed by heterosexual males and MSM (both 2-fold increase). Females were younger than males (median: 27 vs 30 years).

Overall testing rates in the metropolitan area only increased by 20%, while test positivity nearly doubled from 1% to 1.9%.

Conclusion: The gonorrhoea increase among Perth metropolitan heterosexual people cannot be explained by changes in testing and/or diagnostic practices indicating that transmission has increased. Reasons for this are likely to be multifactorial, highlighting the need to identify risk behaviours (e.g. use of online dating apps, recreational drug use, lack of condom use) that facilitate transmission, thus enabling appropriate public health action.

P2.006 The ‘polio endgame’ is upon us: updates to laboratory containment and vaccination

Presenter: Linda Hobday

Authors: Ms Linda Hobday1, Dr Jason Roberts1, Ms Aishah Ibrahim1, Dr Bruce Thorley1

Affiliations: 1National Enterovirus Reference Laboratory, Victorian Infectious Diseases Reference Laboratory, The Doherty Institute, Melbourne, Australia

Abstract:

Introduction: Wild poliovirus incidence is the lowest ever recorded, with only three countries remaining endemic; Afghanistan, Nigeria and Pakistan. The ‘polio endgame’ is initially focused on the destruction and containment of poliovirus type 2 (PV2) and a change in polio vaccine composition. The National Enterovirus Reference Laboratory is accredited as a World Health Organization (WHO) Poliomyelitis Regional Reference Laboratory for the Western Pacific Region and designated as a Poliovirus Essential Facility. Responsibilities include detection and containment of polioviruses and co-ordination of acute flaccid paralysis surveillance in children, a polio-like illness.

Method: In April 2016, 155 countries simultaneously withdrew PV2 from trivalent oral polio vaccine, resulting in a bivalent form containing only poliovirus types 1 and 3. This mammoth public health event, termed ‘The Switch’, was momentous in vaccine history and is critically supported by the containment of PV2. Strict directives for the handling and containment of PV2 are outlined in the WHO Global Action Plan III.

Results: Global stocks of PV2 have been destroyed or securely contained in Poliovirus Essential Facilities. Protocols are in preparation to guide non-polio laboratories in handling ‘poliovirus potentially infectious materials’. Sixteen of thirty-seven countries in the Western Pacific Region who were using trivalent OPV completed ‘The Switch’. Countries using bivalent oral polio vaccine should include at least one dose of inactivated polio vaccine in the national immunisation schedule.

Conclusions: Eradication of wild PV2 and outbreaks of vaccine derived PV2 initiated the polio endgame. Australia must continue to maintain sensitive clinical and laboratory surveillance for poliovirus.

P2.007 An outbreak investigation of tuberculosis in Australian born residents in the ACT

Presenter: Dr Vanessa Johnston

Authors: Dr Vanessa Johnston1, Dr Belinda Jones1, Ms April Witteveen1, Dr Mark Hurwitz1, Ms Wendy Mossman1, Dr Marlena Kaczmarek1, Dr Ranil Appuhamy1, Associate Professor Vitali Sintchenko2, Dr Elena Martinez1

Affiliations: 1ACT Health, Canberra, Australia, 2The University of Sydney, Sydney, Australia

Abstract:

Introduction: The annual incidence of Mycobacterium tuberculosis (TB) notification in the ACT is low and stable. Recently, ACT Health identified a cluster of culture-confirmed cases with the same genotypic pattern between 2008 and 2015. This investigation characterises a TB outbreak among predominantly Australian born residents using a combination of traditional epidemiological methods and molecular typing.
Methods: Review of genotyping results for all TB notifications from 2008-2015 with whole genome sequencing (WGS) of isolates with a matching MIRU profile. Collation and analysis of clinical, epidemiological and laboratory data from cases linked through molecular techniques as belonging to the cluster.

Results: Between 2008 and 2015, there were 11 notifications of drug susceptible TB in the ACT among 10 individuals whose isolates shared the same MIRU profile of Mycobacterium tuberculosis Beijing lineage. WGS excluded one case from the cluster, confirmed that the second episode of disease in one individual was due to relapse, and identified two additional cases that were not originally linked to the cluster. Median age at diagnosis was 21 years (range 17-62 years); four were women and two were born in high-incidence countries.

Conclusion: The information provided through WGS was instrumental in further defining the outbreak, identifying and verifying linked cases, which in turn confirmed hitherto unknown transmission pathways, allowing for further investigation. Alongside clinical history and epidemiological investigation, WGS has rapidly expanded as an important tool for the public health management of outbreaks of TB and is increasingly being adopted as part of routine surveillance and outbreak investigation worldwide.

P2.008 The epidemiology of tuberculosis in the Australian Capital Territory, 2006-2015

Presenter: Belinda Jones

Authors: Dr Belinda Jones1, Dr Vanessa Johnston1, Dr Ranil Appuhamy1, Dr Marlena Kaczmarek1, Dr Mark Hurwitz1

Affiliations: 1ACT Health, Canberra, Australia

Abstract:

Aim: To review the epidemiology of tuberculosis (TB) in the Australian Capital Territory (ACT) over a 10 year period.

Methods: A retrospective analysis of the ACT TB notification data from 1st January 2006 to 31st December 2015 was conducted.

Results: Over the 10 year study period there were 171 tuberculosis notifications in the ACT, with an increasing trend in notification number over time. The median age of cases was 36 years (range 14 to 91 years) and 53.8% of cases were male. Most TB cases (84.2%) were born overseas. The most common risk factor for acquiring TB amongst Australian-born cases was having close/household contact with a known case of TB (30.8%). The most common risk factor in the overseas-born population was past travel or residence in a high-risk country (86.9%). Of all the TB cases notified, 82.4% successfully completed treatment.

Conclusion: There was an increasing trend in the number of TB notifications in the ACT over time. The highest rate of TB notifications remained in the overseas-born population; with other studies suggesting this is commonly due to reactivation of latent tuberculosis infection (LTBI). As Australia starts working towards TB elimination, options for the screening and management of LTBI, especially in high risk populations, need to be explored.

P2.009 Bordetella holmesii: Epidemiology of an emerging human pathogen in NSW

Presenter: Winkie Fong

Authors: Winkie Fong1,2, Dr Verlaine Timms1, Dr Nadine Holmes1, Dr Rebecca Rockett1, Dr Vitali Sintchenko1,2

Affiliations: 1Centre of Infectious Disease and Microbiology, Westmead, Australia, 2Sydney Medical School, University of Sydney, Camperdown, Australia

Abstract:

Introduction: Bordetella pertussis, the aetiological agent of whooping cough is routinely diagnosed by PCR directed at IS481, an insertion sequence target also found in Bordetella holmesii. Recent observations have suggested that B. holmesii infections can be misdiagnosed as pertussis, which can have a significant impact on public health. This study investigated the presence of B. holmesii in B. pertussis positive clinical cases, in order to determine the prevalence of B. holmesii in the population.

Methods: Clinical cases of pertussis diagnosed by IS481-specific PCR between October 2008 and March 2016 in New South Wales were included. DNA samples were extracted from nasopharyngeal swabs and aspirates. B. holmesii was detected through the simultaneous amplification of IS481 and B. holmesii specific insertions sequence, hiSI001.

Results: 47 patients were identified out of 805 to be positive for B. holmesii rather than B. pertussis, suggesting a prevalence rate of 6.5% in 2009, 11.1% in 2010, 3.6% during 2013 and 6.3% during 2015. These findings revealed that B. holmesii was co-circulating alongside the B. pertussis epidemic, hidden from view, as B. holmesii infections are being diagnosed as B. pertussis. This not only hinders B. holmesii diagnosis but also laboratory surveillance for pertussis.

Conclusion and Recommendation: This investigation highlights the importance of specific testing for B. holmesii within outbreaks of whooping cough. The addition of B. holmesii detection to the molecular surveillance of whooping cough will provide much needed data for targeted control strategies.
P2.010 Gastroenteritis among a cluster of scouts attending the New South Wales Cuboree

Presenter: Paola Garcia

Authors: Mrs Paola Garcia¹, Mr Leng Boonwat¹, Dr Stephanie Fletcher¹, Dr Kate Alexander¹, Ms Heidi Lord¹, Mrs Sharon O'Regan¹, Dr Madhumati Chatterji¹

Affiliations: ¹SSWAHS Public Health Unit, Liverpool, Australia

Abstract:

Introduction: Approximately 3500 cub scouts aged 8 to 12 years, attended the three yearly NSW Scouts Cuboree five-day camp in South Western Sydney in 2017. The Public Health Unit (PHU) has implemented daily syndromic surveillance (DSS) to monitor core syndromes at events such as this. An emergency management plan was developed by the Cuboree Scouts in consultation with the PHU.

Methods: Application of the DSS system detected a gastroenteritis outbreak among a cluster of 40 scouts and leaders in a camp site. A gastroenteritis outbreak was defined as two or more people with sudden onset of diarrhoea or vomiting within 24 hours. A Public Health team undertook a rapid health assessment and initiated interventions in response. Alerts were sent to all NSW PHUs and laboratories.

Results: Fourteen cases met the case definition. The cases were from the same campsite and presented with vomiting (14), diarrhoea (2), nausea (3), fever (1) and abdominal pain (1). The first three cases were reported on day four of the event with a further seven cases reported on day five. Further investigation revealed that the index case presented on day one with vomiting but was not reported.

Conclusion & Recommendation: Epidemiological evidence attributed the outbreak to person to person transmission of a gastrointestinal agent. Proactive preparedness, communication and cooperation between the PHU and Scout Management was central to the successful implementation of the DSS system and preventing a larger outbreak. Strong partnerships between PHUs and external stakeholders are crucial when managing large scale events.

P2.011 Acceptability of SMS immunisation reminders to encourage on-time compliance with infant immunisation

Presenter: Rob Menzies

Authors: Ms Meera Kaushik², Ms Kamini Koshal³, Mr Mark McMillan³, Dr Leon Heron⁵, Professor Helen Marshall³, Ms Jenny Lampard⁶, Dr Rob Menzies¹, Ms Telphia Joseph¹, Dr Jocelyn Chan⁸, Professor Anne Braunack-Mayer³

Affiliations: ¹School of Public Health and Community Medicine, UNSW, Sydney, Australia, ²Master of Public Health, Sydney School of Public Health, The University of Sydney, Sydney, Australia, ³The University of Adelaide, Adelaide, Australia, ⁴Vaccinology and Immunology Research Trials Unit, Women’s and Children’s Hospital, and Robinson Research Institute, The University of Adelaide, Adelaide, Australia, ⁵Kids Research Institute, The Children’s Hospital Westmead, Sydney, Australia, ⁶National Centre for Immunisation Research and Surveillance, The Children’s Hospital Westmead, Sydney, Australia, ⁷Faculty of Medicine, The University of Sydney, Sydney, Australia, ⁸National Centre for Epidemiology and Population Health, Australian National University, Canberra, Australia

Abstract:

Introduction: To investigate if SMS messages or personalised calendar reminders improve on-time (within 30 days of due date) compliance, we conducted a randomised controlled trial using a purpose built iPad application. We also sought parental opinions about the interventions they received.

Methods: Between February and December 2015 parents of children aged <16 months were randomly assigned to one of four groups:

- SMS reminder messages only
- Printed reminder calendar only
- SMS messages and calendar
- No intervention (control)

Parents were randomly selected for interview from each of the study arms. They were further stratified into three sub-groups: An ‘on-time’ group, a ‘late’ group, and parents enrolled at an Aboriginal Medical Service.

Results: We conducted fifty-four qualitative interviews across the groups and sub-groups: SMS only (16 interviews), calendar only (12), both (13), and control (13).

SMS immunisation reminders were, on the whole, claimed to be advantageous by the parents who received them, and thought to be so by the parents who did not.
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Calendars were less well-received by parents. Those who received calendars had a more positive view than those who did not. However, those positive views were divided equally between parents who had their children immunised on time and late, indicating that recognising the advantages of calendars did not seem to be associated with on-time compliance.

Conclusion & Recommendation: SMS immunisation reminders are more acceptable to parents than are immunisation calendars. There is potential to develop an SMS reminder intervention to increase on-time immunisation compliance within Australia.

P2.012 Comparison of genome sequencing and MLVA typing for surveillance of Salmonella Typhimurium

Presenter: Qinning Wang

Authors: Dr Qinning Wang1, Ms Cristina Sotomayor1, Mr Peter Howard1, Ms Agnieszka Wikle ndt1, Dr Chayanika Biswas1, Dr Alicia Arnott1, Dr Daneeta Hennessy1,2,3, Dr Paula Spokes1, Dr Kirsty Hope3, Prof Jon Iredell1,2, A/Prof Vitali Sintchenko1,2

Affiliations: 1Centre for Infectious Diseases and Microbiology—Public Health, ICMPR, Pathology West, Westmead Hospital, Westmead, Australia, 2Marie Bashir Institute for Infectious Diseases and Biosecurity, Sydney Medical School, University of Sydney, Sydney, New South Wales, Australia, Westmead, Australia, 3Communicable Disease Branch, NSW Health Protection, NSW Health, Sydney, Australia

Abstract:

Introduction: This report presents preliminary laboratory results of a prospective evaluation of the effectiveness of whole genome sequencing (WGS) for control of foodborne diseases in New South Wales. The aim of the report is to compare the resolution of multi-locus variable number tandem repeat analysis (MLVA) with WGS for Salmonella Typhimurium (STM).

Methods: All STM isolates serotyped and MLVA typed by the NSW Enteric Reference Laboratory in a ten-week period since October 1st 2016 were included. The WGS data was analysed using the MDU Nullarbor pipeline and single nucleotide polymorphisms (SNP) were inferred. A SNP cluster (SC) was defined as a group of isolates with less than 10 SNP differences.

Results: A total of 233 STM isolates were sequenced. ST19 represented the majority (200 isolates, 87%) followed by ST34 (10.4%), ST36 and ST2066 (2.6%), respectively. 106 SCs were identified in which seven contained isolates of between 7 and 29 (32.9%) and 35 smaller ones contained between 2 and 6 isolate (39.6%). The remaining 64 isolates (27.5%) each had unique patterns. Most of the SCs, especially the small size clusters, correlated well with MLVA patterns. A major SNP cluster had 100% concordance with MLVA findings (SC-16-0115, MLVA 3-25-18-12-523). There were a number of MLVA patterns further separated by different SCs and some SCs also contained different MLVA types.

Conclusion: The WGS can effectively separate or cluster STM isolates using customised analytic pipelines with higher resolution than contemporary MLVA typing. Prospective WGS clustering can assist public health laboratory surveillance and disease control.

P2.013 A paediatric case of Salmonella serotype Monschau associated with captive reptiles

Presenter: Rebecca Schack

Authors: Rebecca Schack1, Mary Valcanis2, Nicole Orlando2, Nela Subasinghe2, Shaun Coutts5, Marion Easton1

Affiliations: 1Department of Health & Human Services Victoria, Melbourne, Australia, 2Microbiological Diagnostic Unit Public Health Laboratory, Melbourne, Australia

Abstract:

Introduction: A ten-month old infant was notified to the Victorian Department of Health and Human Services (DHHS) with gastroenteritis caused by Salmonella serotype Monschau. The Microbiological Diagnostic Unit Public Health Laboratory (MDU) has isolated Salmonella Monschau on only 19 occasions since 1983. Case investigation identified a risk factor of pet lizards in the family home. The case’s mother reported no direct contact between the infant and the lizards. As reptiles are a recognised source of salmonellosis, there is potential risk of reptiles as a source of salmonellosis. Further education of reptile vendors and owners is recommended to prevent transmission of reptile-associated salmonellosis, especially in children under five years of age.
P2.014 Core genome comparison to understand Salmonella Saintpaul isolates in Australia and globally

Presenter: Mary Valcanis

Authors: Ms Mary Valcanis1, Dr. Dieter Bulach1, Dr. Takehiro Tomita1, Mr. Anthony D’Agata1, Mr. Damien Bradford2, Ms. Laura Ford3, Dr. Susan Ballard4, Associate Professor Torsten Seemann3, Dr. Anders Goncalves da Silva1, Professor Benjamin Howden1

Affiliations: 1Microbiological Diagnostic Unit Public Health Laboratory, Doherty Institute, Melbourne, Australia, 2Pathwest Laboratory Medicine, Perth, Australia, 3OzFoodNet, ACT Health Protection Service, Canberra, Australia

Abstract:

Introduction: Salmonellosis is a major cause of bacterial gastroenteritis worldwide. In Australia, Salmonella Saintpaul ranks among the top ten serovars causing human infections. Australian S. Saintpaul isolates and S. Saintpaul genome sequences available in an international collection were used to illustrate the importance of microbial and comparative genomics analysis methods to build an overview of how S. Saintpaul exists in Australia and globally.

Methods: Among 95 Australian S. Saintpaul isolates that underwent genome sequencing, there was a range of isolation dates (1997 to 2015) and geographic locations (ACT 5, NSW 5, VIC 54, QLD 3, WA 15, NT 8, TAS 5). The international read set collection was constructed using the NCBI Pathogen Detection project database (http://www.ncbi.nlm.nih.gov/pathogens/) and comprised of read sets from more than 500 S. Saintpaul isolates (predominantly USA and UK). Core genome comparisons were conducted using Nullarbor (https://github.com/tseemann/nullarbor).

Results: Most Australian S. Saintpaul isolates were closely related (usually <100 core SNP differences between any pair of isolates). The core genome comparison of the 95 Australian and >500 international S. Saintpaul isolates revealed a clade that contained most of the Australian isolates and few isolates from outside Australia.

Conclusion: One dominant S. Saintpaul clade exists in Australia suggesting a likely common endemic source that may not be present elsewhere in the world. This example illustrates the utility of microbial genomics in determining the relationship between isolates and demonstrates how comparative genome analysis for public health microbiology is enhanced by access to an open collection of genome sequences for isolates.

P2.015 Building a Syndromic Surveillance System using telephone and e-health data

Presenter: Mica Hartley

Authors: Mica Hartley1, Dr. Janice Biggs2, Mr. Carlo Leonessa2, Dr. Kathryn Glass1

Affiliations: 1Australian National University, Canberra, Australia, 2Healthdirect Australia, Sydney, Australia

Abstract:

Introduction: Health-seeking behaviour is rapidly changing with the prevalence of online health information and a focus on person-centric healthcare. Healthdirect collects data on calls to the Healthdirect nurse triage telephone helpline (HNTTH) and visits to the Healthdirect online symptom checker (HOSC). These large, daily datasets for all of Australia enable us to create the first real-time nation-wide syndromic surveillance system.

Methods: The Healthdirect NTH, which receives over 700,000 calls per year and the OSC, which receives over 500,000 visits per year capture demographic details and characteristics of symptoms from participants. From these data sources, we classify cases to the top ten syndromes, including influenza like illness, and perform descriptive analysis. We evaluate the system using the CDC surveillance system attributes.

Results: This system demonstrates excellent representativeness due to both the large sample size and the proportion of users that do not seek other health care, estimated at forty percent. Since these data are already collected daily as part of standard operating procedure, the system has excellent timeliness, simplicity, acceptability, data quality and stability. We were unable to evaluate the flexibility, sensitivity and predictive value positive.

Conclusion and Recommendation: This syndromic surveillance system has the ability to provide timely reports on populations that would otherwise remain unreported. It can contribute to a broader picture of disease in Australia, and thus enhance the timeliness and accuracy of information provided to the public, policy makers, public health departments and researchers.

P2.016 Emergency Department Surveillance: Early identification of Gastrointestinal Outbreaks in the Community

Presenter: Satyamurthy Anuradha

Authors: Dr Satyamurthy Anuradha1, G Pollard1, D Seesaengnom1, F Vosti1, I Hunter1, S White1, H Clifford1, S Jurd1

Affiliations: 1Gold Coast Health, Chapel Hill,
Abstract:

Introduction: Early outbreak detection systems allow for prompt identification and timely public health action. Emergency Departments (ED) are potential sentinel sites for surveillance of infectious diseases. This study aims to retrospectively analyse the association between presentations of gastrointestinal (GI) illnesses in EDs with those reported through the Notifiable Conditions Register (NOCs) in the Gold Coast.

Methods: ED data from two public hospitals in the Gold Coast for a 3-year period (2013 - 2016) were analysed to identify presentations relating to GI illness using the 4-hour diagnoses mapped to ICD-10 codes. Trigger points were defined as number of presentations exceeding the mean plus two standard deviations.

Results: Nine 4-hour diagnoses were appropriate for inclusion as relating to GI illness in the ED data. There was a total 12,733 ED presentations over the 3-year period in this category. The average number of presentations per day was 12.3 with seasonal variations. Two consecutive trigger days preceded increased GI notifications on NOCs.

Conclusion & Recommendation: Surveillance of ED presentation data has the potential to provide an early outbreak detection system enabling timely public health response to limit the spread of GI illness in the community.

P2.017 Multiple surveillance tools in assessing Arboviral detection post disaster

Presenter: Guddu Kaur

Authors: Ms Guddu Kaur

Affiliations: 1Western NSW Local Health District, Bathurst, Australia

Abstract:

Introduction: Emerging and remerging infectious diseases are a known threat to public health. Ross River Virus (RRV) is the most reported arbovirus in Australia and remains endemic to the region. In 2016 unprecedented flood levels in the Central West of NSW provided the ideal breeding ground for mosquitoes. There is great impact of RRV on the general public as well as economic and time based drain on hospital emergency departments (ED). The purpose of this study was to measure the impact of RRV in the recovery phase following a flood based disaster.

Method: Enhanced public health surveillance was prospectively initiated in addition to seasonal mosquito monitoring and sentinel surveillance. A time series analysis was conducted using ED and Notifiable disease data, obtained from NSW Department of Health, between January 2010 and April 2017.

Results: The use of multiple surveillance tools has allowed the public health unit to quantify changes in mosquito populations and increased risk following this historic flood. To measure the human and public health impacts through increases in mosquito populations, ED utilisation data and changes in notifiable disease profile have been used (RRV 1.26 vs 4.97 per 10 000). Using insect and animal bites as a proxy, preliminary data has indicated a seasonal increase in ED presentations (11.10 vs 29.21 per 10 000) has been observed post floods.

Conclusion & Recommendation: The use of prospective surveillance systems providing near real time analytics can be used to support public health actions during the recovery phase of natural disasters.

P2.018 PneumoSmart - navigating pneumococcal vaccination recommendations with ease

Presenter: Angela Newbound

Authors: Mrs Angela Newbound, Mr Kim Sampson

Affiliations: 1Adelaide PHN, Adelaide, Australia, 2Immunisation Coalition, Melbourne, Australia

Abstract:

Introduction: Following the release of the Australian Immunisation Handbook, 10th edition, 2013, immunisation providers identified the complexity of the new pneumococcal vaccination recommendations as being the most difficult to follow. To assist immunisation providers to offer appropriate pneumococcal vaccination to individuals identified to be at highest or increased risk of pneumococcal disease, the Immunisation Coalition has developed an online algorithm – the PneumoSmart Vaccination Tool (PVT).

Clinical context: This practical, easy to use tool utilises an algorithm that incorporates the Australian Immunisation Handbook recommendations, expert opinion and the National Health (Immunisation Program – Designated Vaccines) Determination 2014 (No.1) document. Future changes to recommendations can be easily incorporated.

State Health Immunisation Departments across Australia have provided positive feedback on the user experience and functionality of the PVT and a study to assess the impact of the PVT in vaccine recommendation and uptake will commence in early 2017. Interim results will be presented at this meeting, with a final report to be made available later in the year.
Conclusion & Recommendation: The PVT will provide immunisation providers with clear pneumococcal vaccination pathways for individuals over 5 years of age with specific medical conditions identified in the Australian Immunisation Handbook. The tool will give confidence to immunisation providers, ensuring stricter adherence to vaccination recommendations and guidelines, resulting in a reduction of potentially fatal complications from pneumococcal disease in ‘at risk’ individuals.

Endorsement of the PVT by State and Commonwealth Health Departments and other peak bodies will assist in increasing PVT use by providers.

P2.019 Prevalence of epidemic Vibrio parahaemolyticus in Hong Kong

Presenter: Yan Ki NGAN

Authors: Ms Tung Ching Kathy Li¹, Miss Yan Ki NGAN¹, Miss Wing Ki SHIU¹, Dr Xiao Ying LU¹, Dr Peter Hoi Fu YU¹, Professor Hong CHUA¹

Affiliations: ¹Technological And Higher Education Institute Of Hong Kong, Hong Kong., Hong Kong

Abstract:

Introduction: V. parahaemolyticus is the leading cause of food poisoning among all causative agents in Hong Kong. It can be generally found in shellfish, fish and crustaceans. Not all the strains are pathogenic but the expression of tdh and trh genes are strongly correlated to the virulence of V. parahaemolyticus. This study aims to screen V. parahaemolyticus strains with tdh and trh gene and report its prevalence in Hong Kong.

Methods and Results: Fifty two raw seafood samples and seawater samples were randomly collected from 21 wet markets and 14 spots of coastal sea in June 2016. They were incubated in peptone water and grew on TCBS. Isolates were tested for oxidase and API20E. The presence of tdh and trh were identified by PCR. Among the 52 samples tested, V. parahaemolyticus was identified in 10 samples (19.2%) by API20E tests, 17 samples (32.7%) by real-time PCR and within them, 5 samples (9.6%) were found to harbor the trh gene.

Conclusion: The captioned study reveals the prevalence of pathogenic strain of V. parahaemolyticus in Hong Kong. Its prevalence might contribute to gastrointestinal illness when undercooked seafood is consumed by people. Local authorities thus have to monitor V. parahaemolyticus closely in order to lower the health risk to the Hong Kong population.


Presenter: Stephen Akar

Authors: Mr Stephen Akar¹, Dr Patrick Nguku², Mr Celestine Ameh³, Professor Adebola Olayinka⁴


Abstract:

Background: Measles has remained a major cause of death among under five children despite the availability of a safe and affordable vaccine. Despite efforts to vaccinate eligible children, measles outbreaks continue to occur in Nigeria. A population herd immunity of ≥95% is required to interrupt transmission. This is yet to be achieved in Nigeria

Methods: A line list of suspected cases in Plateau State between 2012 and 2015 was obtained from the State DSNO. The variables used were LGA, age, sex, date of onset of rash, number of valid measles vaccine taken, outcome and severity of illness. The data was analyzed using Microsoft office Excel 2007. Descriptive epidemiology was performed to describe the outbreak in person, place and time

Results: A total of 773 suspected measles cases were obtained. Males constituted 54% (415). Proportion of under-five was 58% (446) while oldest case was 51 years. Overall case fatality rate was 1.9% (under-five CFR 1.4%). The suspected outbreak occurred in all 17 LGA in Plateau State. Wase LGA recorded highest cases while Jos East recorded least. Jos North recorded the highest mortality

Conclusion: A propagated suspected measles outbreak that showed a seasonal trend occurred in Plateau State between 2012 and 2015 with CFR 1.9% (all ages) and 1.4% (under-five). Taking two doses of measles vaccine improved the outcome 100%

Recommendations:

- Efforts should be intensified to achieve second dose vaccination for under-fives.
- Health education for citizens during peak periods annually.
- Need for public health laboratory in the State.
P2.021 Emergence of invasive meningococcal disease due to serogroup W in Victoria, 2013-present

Presenter: Lucinda Franklin

Authors: Ms Lucinda Franklin1, Dr Katherine Ong3, Ms Aicha Brahmi2, Ms Kylie Carville5, Dr Jason Kwong6,7,8, Ms Kerrie Stevens4, Associate Professor Benjamin Howden6,7,8

Affiliations: 1Communicable Disease Epidemiology and Surveillance, Department of Health and Human Services, Victoria, Melbourne, Australia, 2Communicable Disease Prevention and Control, Department of Health and Human Services, Victoria, Melbourne, Australia, 3Office of the Chief Health Officer, Department of Health and Human Services, Victoria, Melbourne, Australia, 4Microbiological Diagnostic Unit Public Health Laboratory, Peter Doherty Institute for Infection & Immunity, University of Melbourne, Melbourne, Australia, 5Epidemiology Unit, Victorian Infectious Diseases Reference Laboratory, Peter Doherty Institute for Infection & Immunity, University of Melbourne, Melbourne, Australia, 6Doherty Applied Microbial Genomics, Peter Doherty Institute for Infection & Immunity, University of Melbourne, Melbourne, Australia, 7Department of Microbiology & Immunology, University of Melbourne, Melbourne, Australia, 8Department of Infectious Diseases, Austin Health, Heidelberg, Melbourne, Australia

Abstract:

Introduction: Following the introduction of the meningococcal C vaccine to the National Immunisation Program in 2003, notified cases of invasive meningococcal disease declined significantly in Victoria from 162 cases in 2003 to 26 in 2013. As at 31 December 2013 serogroup B Neisseria meningitidis was the most common cause of invasive meningococcal disease in Victoria. However, since 2014, the Victorian Government Department of Health and Human Services has observed a sharp increase in notifications of invasive meningococcal disease due to serogroup W with 17 cases notified in 2015 (30% of notifications), compared with four cases (12%) in 2014 and one case (4%) in 2013. In 2016 there were 48 cases (61% of notifications). Similar rapid increases in meningococcal disease due to hypervirulent serogroup W, sequence type 11 clonal complex strain of N. meningitidis had been observed in the United Kingdom and South America since 2009.

Methods: Based on these international experiences, Victoria expanded its enhanced surveillance activities and instigated whole genome sequencing of isolates from 2013-2015 to determine whether the increase in serogroup W was due to sporadic importations, or endemic spread within the population.

Results: After six months of enhanced surveillance data collection and whole genome sequencing of two years of local isolates, it was concluded that disease transmission was most likely occurring in the local population.

Conclusions: A number of public health actions were implemented in response to these data. We share our lessons from the experience of planning a response to an emerging pathogen.

P2.022 Leprosy and its control in the Northern Territory (NT), 1882-2016

Presenter: Vicki Krause

Authors: Dr Vicki Krause1, Liz Stephenson1, Lesley Scott1

Affiliations: 1CDC, NT Dept of Health, Casuarina, Australia

Abstract:

Background: Leprosy was introduced into the NT in 1882 and spread to Indigenous people across the TopEnd with 10% of populations in the 1950s having clinical-evidence of disease. An analysis of the disease from 1882 to 2016 has been undertaken with a review of control measures.

Methods: A 1980 doctoral thesis, the NT Leprosy Register and Notifiable Disease Surveillance System were analysed by year-of-diagnosis, sex, residence, Indigenous-status and country-of- birth, along with control measures.

Results: 13492 cases of leprosy were notified (1882-2016) with 91% identified as Indigenous people. From 2005 to 2016, 14 cases of leprosy were notified; 8 Indigenous (57%) and 6 overseas-borne (Philippines [5]; Indonesia [1]). Active case-finding, curative treatment, patient education and reconstructive surgery/ rehabilitation along with NT Guidelines lead to a marked reduction in cases and decreased disability. Active case-finding evolved to mainly passive case-finding in the 1990s and leprosy services combined with tuberculosis services. Diagnostics that relied on slit-skin- smears (an art!) and experienced leprosy- histologists to read skin/nerve biopsies are now assisted by molecular diagnostics and clinical findings assessments supported by the ease of photo-sharing. NT Guidelines have incorporated WHO classifications and treatment (while still promoting 24month- treatment for bacterial index >4).

Conclusions: Leprosy, while markedly reduced, is still present in the NT. Clinician’s diagnostic skills and awareness are challenged in recognising what is a now-rare disease. Guidelines for the Control of Leprosy in the NT provide clear management to assist early diagnosis and cure as we “accelerate toward a leprosy-free world”.

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**Concurrent Session 4A – BBVSTI**

**Grand 2, 12:45pm – 2:00pm**

**Blood-borne virus infection in health care workers: Victorian lookback experiences**

**Presenter:** Jessica Rotty

**Authors:** Dr Jessica Rotty¹, Dr Brett Sutton¹, Dr Mihaela Ivan¹, Adam Hamilton¹, Jay Healy¹, Nasra Higgins¹, Rachel Coutts¹, Rachel M Chan¹, Dr I-Hao Cheng¹, Dr Simon Crouch¹, Nick McColgan¹, Donna Cameron¹, Dr Finn Romanes¹

**Affiliations:** ¹Department of Health & Human Services, Melbourne, Australia

**Abstract:**

**Introduction:** Health care workers (HWC) infected with blood borne viruses (BBV) can pose a risk of transmission to patients while performing exposure prone procedures. Upon diagnosis of a BBV in a HCW, careful risk assessment for iatrogenic transmission is performed to inform the decision on whether a lookback should be undertaken. This paper aims to review all HWC related lookbacks undertaken in Victoria from 2012 to 2016 and summarise the outcomes and learnings.

**Methods:** Lookbacks undertaken in Victoria for the period 2012 to 2016 were reviewed.

**Results:** There were three lookbacks conducted between 2012 and 2016 with a total of 1,201 patients identified at risk of BBV transmission (HIV, HCV, or HBV). No breach in infection control or HWC to patient transmissions were identified. 2 HCWs were unaware of their responsibilities under the National Guidelines at the time of notification. All 3 HCWs were advised to cease exposure prone procedures and were linked into specialist care for their BBV infection.

**Conclusion:** Lookback exercises are time intensive and can have significant impact on HCWs. These findings contribute to the current evidence-base and highlight the need for supportive processes for HCWs. Education and awareness for HCWs regarding the National Guidelines should be improved.

**HIV in people born overseas, Australia, 2006-2015: A changing epidemiology**

**Presenter:** Praveena Gunaratnam

**Authors:** Dr Praveena Gunaratnam¹, Dr Skye McGregor¹, Dr Roanna Lobo², Dr Graham Brown³, Dr Marlene Kong¹, Associate Professor Rebecca Guy¹

**Affiliations:** ¹The Kirby Institute For Infection And Immunity, UNSW Sydney, ²School of Public Health, Curtin University, ³Australian Research Centre in Sex, Health and Society, La Trobe University,

**Abstract:**

**Background:** We describe recent HIV epidemiological trends in people born overseas, to inform delivery of targeted and culturally appropriate HIV programs.

**Methods:** We analysed new HIV diagnoses in overseas compared to Australian-born people between 2006 and 2015. Notification rates, rate ratios and proportions by region of birth are presented. The chi-squared test was used examine differences in proportions between groups.

**Results:** In 2015, the highest notification rates were amongst people born in South-East Asia and Sub-Saharan Africa (15.8 and 13.7 per 100,000), compared to Australian-born people (3.5 per 100,000). The annualised notification rate for people born in Sub-Saharan Africa dropped by 43% from 27.1 per 100,000 (2006-10) to 15.6 per 100,000 (2011-15), whereas for people born in North-East Asia it increased by 124% from 2.9 (2006-10) to 6.6 (2011-15) per 100,000. Amongst non-Australian born men who have sex with men diagnosed with HIV, the proportion born in North, South or South-East Asia increased from 35% in 2006-10 to 47% in 2011-15, while the proportion born in Europe decreased from 30% to 23% (X²=31.5, p<0.01). HIV positive persons born in Sub-Saharan Africa or South-East Asia were more likely to be diagnosed at a late stage of infection, irrespective of whether they acquired HIV through heterosexual (X²=24.8, p<0.01) or male to male sex (X²=54.8, p<0.01).

**Conclusion:** HIV policies and programs must adapt to the evolving epidemiology of the infection in people born overseas, and include culturally appropriate prevention, diagnosis and treatment for both men who have sex with men and heterosexuals.
Using data linkage to identify newly acquired hepatitis C notifications in Queensland

Presenter: Jonathan Malo

Authors: Dr Jonathan Malo1,2, Dr Stephanie Davis2, Dr Stephen Lambert1,3

Affiliations: 1Communicable Diseases Branch, Queensland Health, Herston, Australia, 2National Centre for Epidemiology and Public Health, Australian National University, Acton, Australia, 3UQ Child Research Centre, University of Queensland, South Brisbane, Australia

Abstract:

Introduction: In Australia, identification of newly acquired hepatitis C infections is resource-intensive, but performed to aid understanding of the epidemic dynamics of this virus. Australia-wide, <5% of cases are classified as newly acquired. In late-2016, Queensland commenced identifying newly acquired cases through data linkage.

Methods: We extracted hepatitis C notifications with onset dates from 01 January 2012–31 December 2016 from the Queensland Notifiable Conditions System. These were linked with Pathology Queensland hepatitis C public testing data with collection dates from 01 January 2010–31 December 2016. Data linkage was performed in Stata 14 using the ‘reclink’ package with name, date of birth, and sex as linking-variables. As per the national case definition, a negative anti-hepatitis C antibody test in the 24 months prior to illness onset date was used to classify notifications as newly acquired.

Results: There were 12,837 notifications of hepatitis C in Queensland from 2012–2016. Through linkage, we were able to identify 1,482 (11.5%) cases as newly acquired. Among notifications classified as newly acquired, the median age at onset was 27 years, 78% were male, and 50% originated from a correctional facility. As part of a weekly public health surveillance process, the time to perform the data extraction and linkage was <30 minutes.

Conclusions: We identified 11.5% of hepatitis C notifications in Queensland as newly acquired—a value substantially higher than reported in other states and territories. Data linkage provides a timely and efficient process for the surveillance of newly acquired hepatitis C cases.

Improving surveillance of Hepatitis B and C by responding to notifications

Presenter: Nicole Romero

Authors: Ms Nicole Romero1, Ms Jennifer MacLachlan1,2, Ms Nasra Higgins3, Ms Rachel Chan3, Ms Kim White3, A/Prof Benjamin Cowie1,2,3,4, Dr Nicola Stephens3

Affiliations: 1Who Collaborating Centre For Viral Hepatitis, VIDRL, Doherty Institute, Melbourne, Australia, 2Faculty of Medicine, Dentistry and Health Sciences, University of Melbourne, Melbourne, Australia, 3Department of Health and Human Services, Victoria, Melbourne, Australia, 4Victorian Infectious Diseases Service, Royal Melbourne Hospital, Melbourne, Australia

Abstract:

Introduction: In Victoria, all laboratories and diagnosing doctors are required to notify cases of unspecified (non-acute) hepatitis B and C. However in recent years less than 40% of doctors notified, limiting the availability of important information such as Indigenous status, country of birth, healthcare worker status, correctional facility status and history of injecting drug use (IDU). We sought to improve viral hepatitis surveillance and data completeness.

Methods: On 1st July 2016 Victoria initiated a pilot program to follow-up laboratory notifications of unspecified hepatitis B and C with letters to referring doctors, seeking demographic and risk profile data and highlighting management and treatment approaches for their patients. Doctors were mailed a simplified data collection form focusing on key information and a hepatitis B vaccine order form, each presented on a single page and pre-filled with patient information to encourage completion.

Results: During July-December 2016, the response rate was 50.2%. This has resulted in improved data completeness, with Indigenous status increasing from 26.9% to 51.8% and country of birth 21.8% to 54.0%. Data completeness for healthcare worker status, IDU status and correctional facility status, variables previously not routinely collected, were 38.2%, 39.4% and 43.0% respectively.

Conclusions & Recommendations: This pilot program represents a cost effective strategy to improve the quality of notifiable disease surveillance data to inform program delivery, policy development and prevention activities. Further evaluations include uptake of funded vaccination, and the impact of the program on linkage to appropriate care.
Repeat chlamydia diagnosis in NSW 2001-2012

Presenter: Daneeta Hennessy

Authors: Ms Daneeta Hennessy1,2,3, Dr Christine Selvey2

Affiliations: 1Centre For Infectious Diseases and Microbiology - Public Health, Western Sydney Local Health District, Australia, 2Health Protection NSW, North Sydney, Australia, 3NSW Biostatistics Training Program, NSW Ministry of Health, Australia

Abstract:

Introduction: Re-infection with chlamydia after an initial infection has been diagnosed and treated is common, but the incidence is unknown. Re-testing is currently recommended at three months after initial diagnosis, but reinfection can occur at any time. Repeated chlamydia infection suggests inadequate contact tracing or ongoing behaviours that put the individual at risk of sexually transmissible infections.

Methods: NSW chlamydia notification data was examined using Cox proportional hazards regression to assess the time to a second chlamydia notification in people with an initial diagnosis between 2001 and 2012. People were followed until their date of second chlamydia notification, death, or 31 December 2013.

Results: During followup, 11% of men (5,649/50,987) and 13% of women (9,174/69,488) had a second chlamydia notification. The proportion with a second notification within three months was the same in men and women (1.1%), but after this time women had higher cumulative renotification proportion (4% vs 6% at 1 year). In women, risk of renotification decreased with increasing age (HR 0.92, 95% CI 0.92-0.93 per year increase), and increased risk was seen with gonorrhoea coinfection at first diagnosis (HR 1.36, 95% CI 1.12-1.66) and being Aboriginal (HR 1.40, 95% CI 1.31,1.50). In men, previous HIV diagnosis (HR 4.29, 95% CI 3.63-5.07) and being Aboriginal (HR 1.38, 95% CI 1.18-1.61) were the strongest predictors of renotification. There was a significant increase in renotification proportion for both women over the study period.

Conclusion: Risk of chlamydia renotification is not homogenous across the NSW population.

Concurrent Session 4B – MBD
Grand 4, 12:45pm – 2:00pm

A one health surveillance approach to monitoring arboviral disease risk, Victoria 2016/17

Presenter: Stacey Rowe

Authors: Ms Stacey Rowe1, Dr Stacey Lynch2, Ms Rebecca Feldman3, Dr Katherine Gibney3, Ms Nectaria Tzimourtas3, Rebecca Lett3, Dr Tanyth de Gooyer3, Suellen Nicholson4, Dr Sally Salmon2, Jamie Hunnam2, Karen Moore2, Dr Simon Firestone2, Dr Finn Romanes1

Affiliations: 1Department Of Health And Human Services, Melbourne, Australia, 2Department of Economic Development, Jobs, Transport and Resources, Melbourne, Australia, 3Department of Environment, Land, Water and Planning, Melbourne, Australia, 4Victorian Infectious Diseases Reference Laboratory, Melbourne, Australia, 5University of Melbourne, Melbourne, Australia

Abstract:

Introduction: In September 2016, widespread flooding in northern Victoria led to concern about mosquito proliferation and subsequent arboviral diseases epidemics in humans and animals. Murray Valley encephalitis virus (MVEV) and Ross River virus (RRV) were the two main arboviruses of concern.

Methods: We developed and applied a risk assessment methodology to identify arboviral disease risk by Local Government Area to guide decision-making for enhanced mosquito surveillance and control programs. A range of new and existing surveillance systems were used to monitor arboviral disease risk throughout the season. This multi-sectoral surveillance included human, mosquito, animal, climatic and environmental elements. We describe the human surveillance component, which used traditional and novel epidemiological methods such as outbreak detection algorithms, spatial mapping, predictive modelling, and opportunistic human serosurveillance.

Results: Eighteen high risk LGAs were funded to implement enhanced mosquito surveillance and control. Victoria’s outbreak detection algorithm identified epidemic levels of human RRV in week 49 of 2016. The outbreak peaked earlier and its magnitude was larger than the previous RRV outbreak of 2011. The use of spatial mapping tools enabled disease hotspots to be identified and was used to guide targeted mosquito control. As at 29 January 2017, MVEV had not been detected by the human or animal surveillance systems in place.

Conclusion: A one health surveillance approach was taken in response to the 2016 flood to guide arboviral disease prevention and control. This approach meant that the response to Victoria’s RRV epidemic was timely, measured and targeted to the needs of local communities.
Post-mass drug administration surveillance for elimination of lymphatic filariasis, American Samoa, 2016

Presenter: Meru Sheel

Authors: Dr Meru Sheel1,2, Dr Sarah Sheridan3, Dr Katherine Gass4, Dr Kimberly Won5, Dr Saipale Fuimaono6, Associate Professor Martyn Kirk1, Associate Professor Patricia Graves7, Dr Colleen Lau1

Affiliations: 1National Centre for Epidemiology and Population Health, Australian National University, Acton, Australia, 2National Centre for Immunisation Research and Surveillance, Westmead, Australia, 3Department of Global Health, Research School of Population Health, Australian National University, Acton, Australia, 4Neglected Tropical Disease Support Center, The Task Force for Global Health, Decatur, United States of America, 5Centers for Disease Control and Prevention, Division of Parasitic Diseases and Malaria, Atlanta, United States of America, 6American Samoa Department of Health, Pago pago, American Samoa, 7College of Public Health, Medical and Veterinary Sciences, James Cook University, Cairns, Australia

Abstract:

Background: Under the Global Programme for Elimination of Lymphatic Filariasis (LF), American Samoa completed seven rounds of mass drug administration (MDA) from 2000-2006. The World Health Organization recommends systematic post-MDA surveillance using Transmission Assessment Surveys (TAS) in order to validate LF transmission interruption. We compared the effectiveness of TAS targeting children aged 6-7 years and a community-based survey targeting individuals aged ≥8 years for post-MDA surveillance.

Methods: We conducted a school-based TAS in all elementary schools (n=29) in parallel with a community-based survey in 32 villages on the two main islands of American Samoa. We collected information on household locations, demographics, and risk factors; and blood samples to test for circulating filarial antigen (CFA) using the AlereTM Filariasis Test Strip.

Results: The school-based TAS (n=1144) found an overall prevalence of 0.8% (95% CI=0.4–1.5). The community-based survey (n=2728, 742 households) found an overall prevalence of 5.4% (95% CI=4.5–6.3). Village-level prevalence ranged from 0–39.4% (mean 7%). CFA prevalence in community members aged ≤9 years (n=156), who were born after MDA had stopped, was 4.5% (95% CI=1.8–9.0). We observed clustering of CFA-positive individuals in schools, households and villages.

Conclusions: Both surveys identified CFA-positive children, suggesting ongoing transmission. School-based TAS was logistically simpler and allowed sampling of a larger proportion of the target population, but results did not reflect the overall prevalence in the population. The community-based survey, although operationally challenging, identified CFA-positive individuals of all ages. Additional analyses of antifilarial antibodies and infected mosquitoes are planned to confirm whether local transmission is ongoing.

Flooding and Ross River virus outbreaks in inland NSW

Presenter: Julie Tall

Authors: Julie Tall1,2, Associate Professor Michelle Gatton2, Professor Shilu Tong3

Affiliations: 1Western Nsw Local Health District, Bathurst, Australia, 2Queensland University of Technology, Brisbane, Australia

Abstract:

Introduction: Ross River virus (RRV) disease incidence is high in inland NSW, effecting significant health and economic cost. Mosquitoes and kangaroos interact in the transmission of RRV with flooding enhancing the abundance of both species. Climate change may promote flooding, but little is known about how flooding influences RRV transmission. This study investigated the relationship between flooding and RRV outbreaks in inland NSW.

Method: 37 local government areas (LGAs) were grouped into eight climate zones (CZs).

For each LGA, each month from June 1991-May 2013 was assigned ‘outbreak/non-outbreak’ status based on long-term trimmed-average age-standardised notification rates and ‘flood/non-flood’ status based on riverine overflow. Generalised estimating equations were used to model the relationship between flood and RRV outbreak in CZs, with adjustments for rainfall and raindays. Associations between kangaroo density and outbreak, and kangaroo density and flooding 1-2 years prior, were explored using Mann-Whitney U tests.

Results: Winter-spring and summer flooding were significantly and positively predictive of short-delay summer-autumn outbreaks across inland NSW. September flooding was significantly and negatively predictive of May outbreaks in one LGA on the Murray River. Flooding was significantly and positively predictive of long-delay outbreaks (17-23 months) in north-east inland NSW where kangaroo density was also significantly higher 1-2 years post-flooding.

Conclusions: The results suggest that flooding is predictive of short- and long-delay RRV outbreaks in inland NSW. Greater flood frequency from global warming may significantly influence RRV outbreaks. Understanding this relationship can inform more targeted and cost-effective public health activities.
**Zika Virus Disease Prevention: Lessons from the Australian Front line**

**Presenter:** Julie Mudd  

**Authors:** Dr Julie Mudd¹-², Dr Steven Donohue¹, Dr Richard Gair³  

**Affiliations:** ¹Townsville Public Health Unit, Townsville, Australia, ²College of Medicine and Dentistry, James Cook University, Townsville, Australia, ³Tropical Public Health Unit, Cairns, Australia

**Abstract:**

**Introduction:** North QLD has a long history of successful Aedes aegypti control in the context of dengue fever prevention. Given the similarity of Zika virus many expected that existing control methods would also work to prevent Zika. Key differences between these diseases have required a substantial change in approach to prevention of mosquito borne diseases in north QLD.

**Method:** an operational review of our dengue prevention was undertaken to determining its appropriateness for Zika. Approaches and outcomes globally were also considered.

**Results:** While many features of Zika were similar to dengue ie vector, incubation periods and susceptibility to importation we found there are key differences that impact on prevention strategy. Most importantly the milder variable clinical picture and lower clinician awareness make detection of cases difficult, when case detection is the mainstay of current dengue prevention. Additionally, the potential impact on pregnancy creates challenges in finding and protecting pregnant women. As Zika can be sexually transmitted additional control measures are required and messages to the public complex.

In response to the review findings preventative vector control was broadened to include places frequented by pregnant women. Health professionals’ education was carried out and obstetric working groups established. Public education was expanded to include home-based indoor residual spraying.

**Conclusion and Recommendations:** As Zika is a mild illness with anticipated low rates of self-presentation to medical care, case finding and response to individual cases is insufficient for prevention. It requires sustained community based vector control efforts and health professional and public education.

**Increasing notification incidence and expanded geographical range—Ross River virus, Victoria 2007–2016**

**Presenter:** Katherine Gibney  

**Authors:** Dr Katherine Gibney¹, Ms Rebecca Feldman¹, Ms Miriam O’Hara², Dr Tanyth de Gooyer¹, Ms Stacey Rowe¹  

**Affiliations:** ¹Health Protection Branch, Department of Health & Human Services, Victoria, Melbourne,

**Abstract:**

**Introduction:** Ross River virus (RRV) is Australia’s most common human arboviral disease, causing significant morbidity. We examined RRV epidemiology in Victoria and explored the impact of applying the more restrictive national surveillance case definition, introduced in 2016.

**Methods:** Victorian residents notified from 2007–2016 with RRV-IgM detected in serum were included; those who remained RRV-IgG negative on convalescent serum were excluded. RRV notification incidence rates were compared between groups and over time using Poisson regression.

**Results:** 3,554 cases were included. A median of 252 [range: 80–1,339] cases were notified annually, predominately (80%) from December–May. RRV notification incidence (6.3/100,000/year) was highest in 2011 (24.1/100,000) and for women (6.9/100,000/year), adults aged 40–49 years (10.0/100,000/year), and western and northern Victoria. Excluding the epidemic year of 2011, notification incidence increased by 7.6% per year from 2007–2016. Of all RRV-IgM cases classified as confirmed prior to 2016, 41% were rejected (RRV-IgM positive and RRV-IgG negative with no convalescent bleed) under the new case definition and 51% were reclassified as probable. Of note, in 2016, RRV-IgG seroconversion was demonstrated among three Melbourne metropolitan residents who recalled no recent travel outside Melbourne.

**Conclusions and recommendations:** We found increasing RRV incidence and describe likely RRV transmission in Melbourne. Expanding geographical range and potential for high case numbers if transmission becomes established in the urban fringe is concerning. Adaptive public health interventions such as mosquito surveillance, mosquito control, and public health messaging in new areas may be required. The recent change to the case definition has substantially lowered notification numbers.
Concurrent Session 4C – Vaccines
Grand 3 & 1, 12:45pm – 2:00pm

Measures of poliovirus immunity in the Australian population

Presenter: Frank Beard

Authors: Dr Alexandra Hendry¹, Dr Linda Hueston², Dr Helen Quinn¹, Dr Frank Beard¹, Professor Peter McIntyre¹

Affiliations: ¹National Centre for Immunisation Research and Surveillance, The Children’s Hospital at Westmead, Australia, ²Institute of Clinical Pathology and Medical Research, Westmead Hospital, Australia, ³University of Sydney, Australia

Abstract:

Introduction: The World Health Organization’s Western Pacific Region, including Australia, has been certified as having eliminated polio since 2000. We aimed to investigate whether adequate Australian population immunity is being maintained.

Methods: Sera were collected from Australian laboratories in 2012-2013 and a representative sample by age and jurisdiction tested for neutralising antibody (IgG) titres to poliovirus types 1, 2 and 3. Titres ≥8 were considered indicative of immunity. The proportion seropositive was calculated for the total Australian population and for specific age-groups. Comparisons with the 1996-1999 serosurvey were made.

Results: Between the 1996-1999 and 2012-2013 serosurveys, Australian population immunity for poliovirus types 1, 2 and 3 decreased significantly from 82%, 88% and 74%, respectively, to 75%, 73% and 52%, respectively. The greatest decrease in immunity between the two serosurveys occurred in children aged <5 years (20%, 25% and 19% for types 1, 2 and 3, respectively). Peak levels of immunity shifted from this age group to the 5-9 year age group.

Conclusion and Recommendation: Total population immunity to all three types of poliovirus in Australia has decreased. However wild type 2 poliovirus has been globally eradicated and type 3 poliovirus has not been detected since 2012. The decrease in immunity in young children and shift in peak immunity levels to older children is consistent with the known reduced immunogenicity of inactivated polio vaccine compared to the oral vaccine. Until all three poliovirus types are globally eradicated, Australia needs to sustain high polio immunisation coverage and continue to monitor population immunity.

Surveillance of antenatal pertussis and influenza vaccination uptake in Western Australia

Presenter: Donna Mak

Authors: Prof Donna Mak¹, Dr Annette Regan², Ms Chloe Thomson¹, Dr Robyn Gibbs¹, prof Paul Effler¹

Affiliations: ¹Communicable Disease Control Directorate, ²Curtin University

Abstract:

Background: Australian government-funded antenatal influenza vaccination has been available since 2009, and in 2015 an antenatal pertussis vaccination program was introduced in Western Australia (WA). We describe surveillance of vaccine uptake in WA.

Methods: In 2009, antenatal influenza vaccination uptake was imputed from data in the WA Pandemic Influenza Vaccination Database. Since 2012, annual computer assisted telephone surveys have been conducted with samples of >400 women each year; pertussis was added to the survey in 2014. From 1 July 2016, antenatal vaccination status became a mandatory component of the Midwives Notification System (MNS).

Results: Antenatal influenza vaccination uptake increased from 10.3% in 2009 to 61.3% in 2016, and pertussis vaccination from 70.6% in 2016 to 77.5% in 2016. The sensitivity and specificity of the MNS compared with self-reported vaccination were 89.3% (95% CI 84.0-94.6%) and 86.0% (95% CI 76.4-95.6%) for influenza and 94.2% (95% CI 90.4-97.9%) and 73.1% (95% CI 56.0-90.1%) for pertussis. Survey responses indicate a healthcare provider’s recommendation is critical to vaccination uptake.

Conclusions: Antenatal influenza uptake has increased steadily since 2009, whereas acceptance of pertussis vaccination was high from the start of the program. Furthermore, antenatal pertussis vaccination uptake continues to increase in WA, while antenatal influenza vaccination has stalled. Although sensitivity and specificity of antenatal vaccination status in the MNS was high during the first two months of mandatory reporting being implemented, there is room for improvement, especially in improving the specificity of pertussis vaccination documentation. Coverage would increase if healthcare providers routinely offered antenatal vaccinations.
Mumps seroprevalence in Australia – can we prevent future outbreaks?

Presenter: Cyra Patel

Authors: Ms Cyra Patel1, Dr Alexandra Hendry1, Dr Helen Quinn1, Dr Linda Hueston2, Dr Frank Beard1

Affiliations: 1National Centre for Immunisation Research and Surveillance, Westmead, Australia, 2Institute of Clinical Pathology and Medical Research, Westmead, Australia

Abstract:

Introduction: Mumps is a vaccine-preventable disease, with high coverage of the measles-mumps-rubella (MMR) vaccine (>90%) in Australia. Despite this, outbreaks have occurred in 2007 and 2015-16. This study examines the national seroprevalence of mumps antibodies.

Methods: Specimens were randomly sampled by age and jurisdiction from a bank of opportunistically collected specimens from Australian laboratories in 2012-2013 and tested for IgG titres to mumps using a commercial ELISA. The proportion seropositive was calculated and comparisons with serosurveys conducted in 2007 and 1996-1999 were made.

Results: Of 2,729 samples, 71.1% (95% CI: 69.4-72.9%) demonstrated immunity against mumps. An additional 10.9% (95% CI: 9.8-12.2%) were equivocal. Seropositivity was lowest among 1 year olds (50.8%), peaking in those aged 5-9 years (79.9%) before declining among 10-14 year olds (65.0%). It increased incrementally with age (72.3% in 25-29 year olds) but declined among 30-34 year olds (61.2%), increasing again among 35-39 year olds (76.8%). Immunity in 2012 was higher (p<0.001) than in 2007 (61.0%) and 1999 (63.2%).

Conclusion & recommendation: Immunity to mumps is moderately high in this nationally representative sample. It increased significantly since 2007, possibly due to increasing 2-dose MMR coverage. Immunity was lower in early adolescence suggestive of waning immunity, as well as 30-34 year olds who were not routinely offered mumps vaccination in childhood when disease incidence was simultaneously declining. An additional dose of MMR in adolescence or early adulthood could boost immunity and reduce the risk of future outbreaks.

Hospitalisations and mortality associated with varicella and herpes zoster, Australia, 1999-2013

Presenter: Meru Sheel

Authors: Dr Meru Sheel1,2, Dr Helen Quinn1,3, Dr Aditi Dey1,3, Associate Professor Martyn Kirk2, Dr Frank Beard1,3, Associate Professor Kristine Macartney1,3

Affiliations: 1National Centre for Immunisation Research and Surveillance, Westmead, Australia, 2National Centre for Epidemiology and Population Health, Australian National University, Acton, 3University of Sydney, Sydney,

Abstract:

Introduction: In 2005, the National Immunisation Program (NIP) implemented a varicella vaccine for Australian children aged 18 months; and in 2016, a herpes zoster (HZ) vaccine for adults aged 70 years was added. We analysed national trends in varicella and HZ-related severe disease in 1999–2013 to examine the impact of a funded varicella vaccine, before the introduction of the HZ vaccine.

Methods: We sourced data on varicella and HZ associated hospitalisations, mortality and mid-year population estimates from Australia’s national databases, for the years 1999-2013. We identified records where varicella or HZ was coded as principal diagnosis (hospitalisation) or underlying cause of death (mortality). We stratified analyses by age, sex and Indigenous status, and undertook negative binomial regressions to estimate rates, confidence intervals (CI) and incidence rate ratios (IRR) using Stata/IC.

Results: Varicella hospitalisation declined after introduction of a funded vaccine, (IRR 0.41, 95% CI: 0.35-0.47) particularly in the targeted persons aged 18-59 months (IRR 0.16; 95% CI: 0.12-0.23). During the funded period (2007-2013), we observed a 6-fold reduction in varicella-associated deaths in children aged ≤0 years. The rate of HZ hospitalisation during the study period was 10.8 per 100,000 populations, and was not impacted by varicella vaccination. HZ hospitalisation rates increased with age, and were highest in persons aged ≥75 years (87.6 per 100,000 populations).

Conclusions: Implementation of a varicella vaccination program was associated with a significant decline in severe outcomes of varicella. Our data on HZ-related severe disease provides valuable baseline for monitoring the impact of the HZ vaccine.

Anal HPV in HIV-infected and HIV-uninfected MSM in Guangzhou: implication for vaccination

Presenter: Huachun Zou

Authors: Dr Huachun Zou1, Dr Xuqi Ren2

Affiliations: 1University Of New South Wales, Sydney, Australia, 2Guangdong Provincial Dermatology Hospital, Guangzhou, China
**Abstract:**

**Background:** The epidemiology of HPV in HIV-infected and HIV-uninfected MSM in Guangzhou, China had not been reported previously.

**Methods:** HIV-infected and HIV-uninfected MSM were recruited from a Guangzhou-based MSM clinic in 2013. Characteristics and sexual behaviors were collected. HIV, syphilis, anal chlamydia/gonorrhea/mycoplasm and anal HPV were tested.

**Results:** We recruited 79 HIV-infected and 85 HIV-uninfected MSM. The majority of MSM were under 35 years. Many HIV-infected (44.4%) and HIV-uninfected (35.4%) MSM had 2 or more male sex partners in the past 3 months. The positivity of anal HPV of any type (81.0% vs 48.2%), any high-risk type (50.6% vs 27.1%), any low-risk type (55.7% vs 31.8%), and any 9-valent vaccine type (74.7% vs 36.5%) were all significantly higher among HIV-infected MSM compared to that among HIV-uninfected MSM (p for all<0.05). HIV-infected MSM had significantly more types of any HPV infection and any 9-valent vaccine type infection compared to HIV-uninfected MSM (median 1 vs 0, p for both<0.05). The great majority of HPV-infected MSM were infected with 9-valent vaccine types (59 out of 64 HIV-infected ones and 31 out of 41 HIV-uninfected ones). Anal bacterial infections including chlamydia, gonorrhea or mycoplasma, were associated with both higher anal HPV positivity and greater number of anal HPV types detected.

**Conclusion:** Sexually active MSM in Guangzhou, especially those infected with HIV, had high and multiple HPV detections. The majority of these cases were potentially preventable by the 9-valent HPV vaccine. Regular anal exams and early HPV vaccination are warranted in MSM in Guangzhou.

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**Concurrent Session 4D – Laboratory AMR**

**Element Room, 12:45pm – 2:00pm**

**Applying genomics to the investigation of Shiga toxin-producing Escherichia coli infections**

**Presenter:** Danielle J Ingle

**Authors:** Danielle J Ingle1,2, Mary Valcanis2, Susan A Ballard2, Martyn Kirk2, Benjamin P Howden2,3, Deborah A Williamson2,3

**Affiliations:** 1 National Centre for Epidemiology & Population Health, ANU College of Medicine, Biology & Environment, The Australian National University, 2 Microbiological Diagnostic Unit Public Health Laboratory, Department of Microbiology and Immunology at the Peter Doherty Institute for Infection and Immunity, The University of Melbourne, 3 Doherty Applied Microbial Genomics, Department of Microbiology and Immunology at the Peter Doherty Institute for Infection and Immunity, The University of Melbourne.

**Abstract:**

**Introduction:** Shiga toxin-producing Escherichia coli (STEC) infection is an important cause of foodborne disease, and disease outbreaks, in Australia. Although uncommon relative to salmonellosis or campylobacteriosis, the impact of STEC infection is profound. To date however, the population structure, reservoirs and virulence traits of Australian STEC strains are poorly defined.

**Methods:** We performed whole-genome sequencing (WGS) on a spatially and temporally diverse collection of approximately 300 Australian STEC isolates. We explored the population structure of Australian STEC isolates within a phylogeographic framework, and compared the utility and feasibility of in silico typing and virulence gene detection with ‘conventional’ typing approaches.

**Results:** Phylogenomic analysis revealed diverse population structure in Australian STEC isolates. Ongoing micro-evolutionary events within clades were detected in Australian STEC relative to international STEC isolates. Good specificity and sensitivity was observed for characterisation of Shiga toxin types, and strong correlation was observed between phenotypic and in silico typing approaches.

**Significance:** Our study provides a genomic framework for the future investigation and tracking of STEC infections in Australia, including nationwide genomic surveillance. Given the clinical and economic impact of STEC infections, and the increasing recognition of STEC infection through the implementation of culture-independent diagnostics, there is a pressing need for rapid and high-resolution analytical tools to better understand factors that result in the emergence of STEC strains.

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**Differentiation of enteroinvasive Escherichia coli from Shigella using multiplex-PCR assay**

**Presenter:** Rajat Dhakal

**Authors:** Dr. Rajat Dhakal1, Dr. Qinning Wang1, Associate Professor Ruiting Lan2, Mr. Peter Howard1, Associate Professor Vitali Sintchenko1,3

**Affiliations:** 1 Centre for Infectious Diseases and Microbiology-Public Health, Institute of Clinical Pathology and Medical Research-Pathology West, Westmead Hospital, Westmead, Australia, 2 School of Biotechnology and Biomolecular Sciences, University of New South Wales, Sydney, Australia, 3 Marie Bashir Institute for Infectious Diseases and Biosecurity, Sydney Medical School, University of Sydney, Sydney, Australia
Abstract:

Introduction: Both Shigella species and enteroinvasive Escherichia coli (EIEC) can cause dysentery and appear to be phylogenetically close, however, they are distinct in epidemiology and public health relevance. Current culture-independent testing (CIT) methods designed to identify Shigella in stool samples have employed the ipaH gene target, which has been also found in EIEC. The aim of this study was to design a molecular test that could identify EIEC in cultures from CIT positive samples.

Methods: Whole genomes of isolates from the NSW Enteric Reference Laboratory culture collection were sequenced using Illumina NextSeq500. Raw sequences were examined using bioinformatics pipelines and mapped to existing EIEC and Shigella genomes in NCBI GenBank.

Results: The differentiating genomic markers were identified, and the primers were designed and tested in silico on 6,433 records of Shigella and 31 EIEC. An assay with two Multiplex-PCR systems was designed which differentiates Shigella and EIECs based on presence or absence of six loci. Almost all Shigella genomes lacked all 6 loci/primer sets in silico, at least one of which was present in all EIECs. This assay differentiated 100% Shigella and EIECs in evaluation experiments on a dozen of clinical isolates each of Shigella and EIEC.

Conclusion and Recommendation: This multiplex PCR assay can rapidly identify EIEC in clinical cultures and improves the utility and specificity of culture-independent screening for shigellosis. Our test can also assist in estimating public health burden of EIEC infection in both developing and developed countries.

Retrospective use of whole genome sequencing following an outbreak of Salmonella Mbandaka in NSW

Presenter: Cassia Lindsay

Authors: Ms Cassia Lindsay1, Mr James Flint1, Ms Kim Lilly1, Dr Kirsty Hope1, Dr Qinning Wang1, Mr Peter Howard3, Associate Professor Vitali Sintchenko5, Professor David Durrheim4

Affiliations: 1Aboriginal Population Health, 2Doherty Institute for Infection & Immunity, Melbourne, Australia, 3Infection & Immunity, Melbourne, Australia, 4Centre for Infectious Diseases and Microbiology, Hunter New England Population Health Service, 5Hunter New England OzFoodNet

Abstract:

Introduction: Salmonella Mbandaka is a rare cause of salmonellosis in New South Wales (NSW). In February 2016, an increase in S. Mbandaka was investigated. Despite hypothesis generating interviews, no source was identified. Following the initial investigation, outbreak isolates were further typed to retrospectively examine the utility of whole genome sequencing (WGS) to support investigators.

Methods: For the initial investigation, a standard questionnaire was administered to S. Mbandaka cases with illness onsets from January to April, 2016. Data from the Victorian Food Consumption study for the same time period were used to estimate expected food consumption frequencies. A WGS analysis was then conducted in July 2016, analysing the S. Mbandaka outbreak isolates along with 17 human and non-human reference strains from 2010-2015. Food consumption histories of the cases were retrospectively reanalysed based on clusters identified by WGS.

Results: The initial (pre-WGS) investigation identified processed cheese as a food item of interest, with 9 of 14 cases (64%), compared to 149 of 665 (22%) Victorian Food Consumption study respondents reporting consumption, however, no common brands or places of purchase were identified and no food safety investigation was initiated. The WGS analysis clearly distinguished the outbreak cases into two main clusters, cluster A (11 cases) and cluster B (6 cases), and several sporadic cases. The relationship with processed cheese consumption was further defined when analysed by WGS cluster with 8 of 9 (89%) Cluster A cases, and 1 of 3 (33%) Cluster B cases reporting processed cheese consumption. WGS analysis suggested that processed cheese consumption was implicated in Cluster A.

Conclusion and Recommendation: The retrospective application of WGS highlighted its potential to support epidemiologist investigate relatively small non-point source foodborne disease outbreaks. If conducted in real-time, WGS could have assisted with potential source detection to guide further investigations.

Implementation of public health surveillance of carbapenemase-producing Enterobacteriaceae in Victoria, Australia

Presenter: Courtney Lane

Authors: Courtney R. Lane1, J. Brett2, M. Schultz1,3, K. Stevens1, A. Van Diemen4, S. A. Ballard, N. L. Sherry1,3,5, J. C. Kwong1,3,5, D.R.M. Cameron1,4, D. A. Williamson1,3, M. Easton1, B.P. Howden1,3,5

Affiliations: 1Microbiological Diagnostic Unit Public Health Laboratory, The University of Melbourne at the Peter Doherty Institute for Infection & Immunity, Melbourne, , 2VICNISS Healthcare Associated Infection Surveillance Coordinating Centre at the Peter Doherty Institute for Infection & Immunity, Melbourne, Australia, 3Department of Microbiology & Immunology, The University of Melbourne at The Doherty Institute for Infection and Immunity, Melbourne, Australia, Melbourne, Australia, 4Department of Health and Human Services, }, Australia, 5Department of Infectious Diseases, Austin Health, Melbourne, Australia
Abstract:

Introduction: Carbapenemase-producing Enterobacteriaceae (CPE) are an urgent antimicrobial resistance threat globally. Following investigation of a state-wide outbreak in 2015, Victoria introduced centralised genomic and epidemiological surveillance and investigation of all suspected CPE.

Here we describe surveillance methods and findings, including risk factors for acquisition and instances of local transmission (between 1st January and 31st December 2016).

Methods: All Enterobacteriaceae with suspected carbapenem resistance were referred from diagnostic laboratories for carbapenemase gene detection and characterisation. Risk factors, including travel and healthcare exposures, were collected for all confirmed cases. Local nosocomial transmission was suspected with temporal and geographic overlap and WGS-based phylogenetic analysis consistent with transmission. Detailed outbreak investigations were then conducted.

Results: Isolates from 382 people were received, from which 96 cases, in 88 people, were confirmed. Diverse carbapenemase genes were detected, most commonly blaNDM(33%) and blaIMP(32%).

No overseas travel or contact was reported in almost half of cases (46%), varying from 94% of blaIMP to 0% of blaNDM.

Five local transmission networks, three blaIMP and two blaKPC, involved cases identified during 2016. Centralised investigation revealed three networks affecting multiple facilities, up to 32-months post exposure, allowing control measures targeted to transmission locations and improved contact tracing.

Conclusions: Standardised surveillance reveals a greater burden of CPE in Victoria than previously recognized, with substantial differences in transmission pathways by CPE gene group. Centralised genomic and epidemiological investigation is crucial to identify local transmission and target control measures where long colonisation periods and inter-facility movements occur. Further work is needed to understand transmission of blaIMP in Victoria.

A 4-Year Review of non-IMP Carbapenemase-Producing Enterobacteriaceae (CPE) in Western Australia (WA)

Presenter: Simone Tempone

Authors: Mrs Simone Tempone1, Dr Michael Leung2,4, Ms Rebecca McCann1, Dr David Speers1,3, Dr Paul Armstrong1

Affiliations: 1Health Department of Western Australia, Communicable Disease Control Directorate, Shenton Park, Australia, 2PathWest Laboratory Medicine, Nedland, Australia, 3School of Medicine and Pharmacology, University of WA, Crawley, Australia, 4School of Pathology & Laboratory Medicine, University of WA, Crawley, Australia

Abstract:

Background: The WA Multi-Resistant Organism (WAMRO) Expert Advisory Group (EAG) was convened to provide advice on multi-resistant organisms (MRO) to WA healthcare facilities (HCFs), and in 2012 initiated the reporting of CPE in WA. Due to the significant mortality, and rapid worldwide spread of CPEs, the epidemiology of WA non-endemic CPEs (non-IMP types) is of increasing concern.

Methods: CPE from private and public pathology referred to the WA Gram-negative Reference Laboratory (October 2012-December 2016) were reviewed to determine travel history and mortality of patients carrying non-IMP CPEs.

Results: Of the 450 CRE referred, 60 patients (13%) had an IMP-4 CPE and 35 patients (8%) had one or more non-IMP CPE. Travel information was available for 28 non-IMP patients with all having recent overseas travel, or contact with someone that recently traveled. The majority (82%) had visited Asia (23), 14% Europe (4), and 4% South America (1). Twenty-six (73%) had a recent hospitalization (19 admitted to an overseas HCF). The 30-day crude mortality was 8.6% (3). All deaths occurred in direct transfers following admission to an overseas HCF ICU (2 Europe, 1 Asia).

Conclusion: Although IMP CPE are the commonest identified CPE in WA, these results highlight the importance of travel destination and overseas hospitalization when assessing returned travelers for infection. The combination of a non-IMP CPE and ICU admission overseas may be a risk factor for mortality. This study highlights the value in monitoring MRO in WA using a standardized referral pathway and single confirmatory laboratory overseen by an EAG.
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