Communicable Diseases Control Conference 2019

Controlling communicable diseases – mobilising evidence, action and partners

Tuesday 19 to Thursday 21 November 2019
Hyatt Hotel Canberra, ACT

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Poster Presentations – P1
The Gallery, Level 1, 1:45pm – 2:00pm

P1.001 - How do you slice the pie? Prioritising public health projects in Victoria

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Abstract:
Introduction: Priority setting is a process of adjudication among competing programs to guide distribution of resources commensurate with need. Globally, there is no agreed best practice methodology to prioritise public health projects, nor is there consensus on the values used to inform the prioritisation process. We developed a tailored prioritisation approach to support resource allocation in the Health Protection Branch of the Victorian Department of Health and Human Services.

Methods: A consensus-based methodology to prioritise public health research and surveillance projects was developed. Methodological components included: project identification and documentation; development of an assessment criteria and scoring system; and facilitation of a multidisciplinary workshop of internal and external public health specialists. Workshop attendees assessed projects using the criteria, which were scored, ranked and assigned implementation categories.

Results: There were 26 projects developed spanning communicable disease and environmental health portfolios. The criteria assessed projects against five categories: public health importance; feasibility; relevance to policy; cost and time; and equity. Projects were assessed and assigned four implementation groups ranging from: low priority (interesting, but not essential) to highest priority (consider implementing immediately). The output of the prioritisation process was compiled and provided to decision makers to support funding decisions.

Conclusion: The prioritisation method enabled a fair and evidence-based decision-making process for prioritising discrete public health projects in Victoria. The process was welcomed by the assessment team for its consensus-based methodology and multidisciplinary approach. The results will be adapted and applied for future planning and resource allocation.

P1.002 - Utilizing the communicable disease surveillance system to process mandatory anaphylaxis notifications, Victoria

Authors: Jess Encena¹, Erica Clifford¹, Fiona Jones², Joy Gregory¹, Caillean Michael¹, Trevor Lauer¹, Dr Angie Bone¹

Affiliations: ¹Department of Health and Human Services Victoria, Melbourne, Australia, ²Dairy Food Safety Victoria, Melbourne, Australia

Abstract: Utilizing the communicable disease surveillance system to process mandatory anaphylaxis notifications, Victoria.

Context: On 1 November 2018, the Victorian Anaphylaxis Notification System commenced following amendments to the Public Health and Wellbeing Act 2008. These amendments were in response to a Victorian coronial report on a child’s death due to anaphylaxis following consumption of a mis-labelled food, and subsequent delayed recall of the product from the market. The primary objectives of the system are: to identify mis-labelled packaged foods in the marketplace and poor allergen management at council-registered food premises serving unpackaged food; and, to implement timely and appropriate public health action to reduce public health risks.

Process: The Act requires Victorian hospitals to notify the Victorian Government Department of Health and Human Services of all anaphylaxis presentations to emergency departments, in a prescribed method and timeframe. To capture and process anaphylaxis notifications, a system was developed which utilizes established communicable disease surveillance processes, tools and infrastructure.

Implementation evaluation: A four-month implementation phase evaluation determined the notification system had been designed and delivered in accordance with legislation; was simple, effective and efficient in capturing and processing food-caused anaphylaxis notifications and enabled timely response when necessary. The evaluation also identified several areas for improvement.

Outcomes: In the first seven months of implementation, 1,355 notifications were received, with 251 (18 percent) related to packaged food, and 315 (23 percent) related to unpackaged food from food premises. Case investigations resulted in one packaged food recall and 47 local council referrals for appropriate action.
P1.003 - Applied field epidemiology in the investigation of adverse events of medical devices

Authors: Dr Mario Vittorino1, Dr Ben Polkinghorne1, Dr Simon Singer2

Affiliations: 1ANU, Canberra, Australia, 2TGA, Canberra, Australia

Abstract:

Background: Intraocular lens (IOL) opacification is a rare complication after cataract surgery. However, it constitutes an important adverse event which can significantly reduce the vision of affected patients, resulting in explantation or exchange of the medical device. We report an investigation of an “outbreak” of cases that occurred in Australia, detected by the vigilance system of the Therapeutic Goods Administration (TGA).

Methods: This is a descriptive case series which explores the applicability of the standard 10 steps of disease outbreak investigation within the regulatory environment of medical devices.

Results: After detecting three incident reports for the same product implanted during a period of 5 months, an investigation of relevant adverse event reports was instigated accordingly. During a period of less than 1 year, 11 cases of IOL opacification were reported to the TGA. The adverse event notification rate in Australia was higher than the worldwide figure. The manufacturer of the device conducted additional investigations in the material and the manufacturing processes. No root cause has been identified to date. No new cases have been identified since 2018.

Conclusion: It is important to understand the difficulties and roadblocks in applying the methods to investigate infectious diseases outbreaks to medical devices. There are several limitations in the data available from adverse events reports related to IOLs, but by following a consistent method for investigation, a clearer perspective of the problem can be made, and the likelihood of understanding a medical device “outbreak” is increased.

P1.005 - Expert perspectives on dealing with outbreaks in areas with high anti-vaccination sentiment

Authors: Dr Penelope Robinson1, Dr Kerrie Wiley1, Professor Julie Leask2, Dr Chris Degeling2

Affiliations: 1University Of Sydney, , Australia, 2University of Wollongong, , Australia

Abstract:

Background: Communities with low vaccination rates are at greater risk during vaccine preventable disease outbreaks. As part of a project to develop policy options to address vaccine refusal, we sought the perspectives of public health experts on the key issues faced when dealing with a measles outbreak in an area with high anti-vaccination sentiment.

Methods: A measles outbreak scenario formed the basis of a 3-round modified Delphi process to identify key practitioner concerns in relation to parents/carers who don’t follow the recommended vaccination schedule. We investigated the perceptions, attitudes and experiences of experts in the field: policymakers, infectious disease experts, immunisation program staff, and others involved in delivering childhood vaccinations.

Results: Preliminary findings indicate the biggest concern is the potential for a large disease outbreak and highest priority during an outbreak is to isolate infected children. The two most highly ranked practical issues are mistrust from non-vaccinating members of the community and combating misinformation about vaccines. Trying to change minds of such individuals is not a priority during an outbreak, nor is vaccinating their children. Using media and social media to provide information about vaccination and disease risk was a focus.

Conclusion: Our findings provide a deeper understanding of the challenges faced during an outbreak and priorities for communicating with communities with low vaccination coverage. Expert views and priorities will inform the design of deliberative processes involving vaccinating and non-vaccinating Australians which aim to develop ethical and publicly acceptable policy options for addressing vaccine refusal.

P1.006 - Indigenous vaccination – do continuous quality improvement programs result in higher coverage?

Authors: Ms Fleur Webster1, Dr Veronica Matthews2, A/Professor Heather Gidding3,4, Professor Richard Taylor5, Dr Robert Menzies1

Affiliations: 1School of Public Health and Community Medicine, University of NSW, Sydney, Australia, 2The University Centre for Rural Health, University of Sydney, Lismore, Australia, 3Clinical and Population Perinatal Health Research, The University of Sydney Northern Clinical School, Faculty of Medicine and Health, University of Sydney, Sydney, Australia, 4National Centre for Immunisation Research and Surveillance, Westmead, Australia

Abstract:

Background: Coverage for vaccines specifically aimed at Aboriginal and Torres Strait Islander (hereafter respectfully referred to as Indigenous) people is substantially lower than for the non-Indigenous population. The effectiveness of continuous quality improvement (CQI) programs in health care to improve coverage is unclear. The study aimed to compare influenza and pneumococcal vaccination coverage among Indigenous adult clients of health services participating in a CQI program (OneTwentySeventy) (n=3,445) with coverage from the 2012-13 National Aboriginal and Torres Strait Islander Health Survey (NATSIHS; n=6,037).
Methods: Coverage for clients attending Northern Territory and Queensland One2seventy services in 2012 were analysed separately by age, and compared to NATSIHS data. All participants had ≥1 risk factor for influenza or invasive pneumococcal disease.

Results: Vaccination coverage was higher among adult clients of services participating in One2seventy compared to the NATSIHS among those aged ≥15 years for influenza (Northern Territory: 79.8% vs. 65.7%; Queensland: 49.7% vs. 39.2%) and for pneumococcal in the Northern Territory only (49.7% vs. 29.1%). The exception was some older age groups (≥50 years) and pneumococcal vaccination in Queensland which were lower than national survey data across all age groups.

Conclusion: The study showed that while there is room for improvement and some variation, coverage for vaccines recommended specifically for Indigenous adults are higher among clients of health services participating in a CQI program, in age groups that include younger adults, compared to national coverage estimates for Indigenous adults. This research demonstrates the potential of CQI programs in Indigenous service delivery to improve health outcomes.

P1.007 - Insights into the burden of influenza in Indigenous Australians, 2018

Authors: Ms Sandra Carlson¹, Ms Kristy Crooks²,³, Dr Craig Dalton¹,³, Professor David Durrheim¹,³,⁴

Affiliations: ¹Hunter New England Health, Wallsend, Australia, ²Menzies School of Health Research, Charles Darwin University, Casuarina, Australia, ³University of Newcastle, Callaghan, Australia, ⁴James Cook University, Townsville, Australia

Abstract:
Background: Aboriginal and Torres Strait Islander Australians have an increased risk of adverse outcomes due to influenza, however national influenza surveillance does not comprehensively monitor influenza activity and severity by Indigenous status. Flutracking, an Australian and New Zealand online influenza-like illness (ILI) surveillance system, has collected Indigenous status data since 2012. We provide insights into the burden of influenza in Indigenous Australians, using Flutracking 2017 and 2018 ILI data.

Methods: We report on 2018 vaccination coverage, cumulative ILI results, and health seeking behaviour, stratified by Indigenous status, and compared to prior years.

Results: In 2018, the total incidence of ILI for Indigenous participants (40.1%) was 1.5 times higher than non-Indigenous participants (27.1%). In 2017, the total incidence of ILI for Indigenous participants (38.4%) was similar (only 1.1 times higher) to non-Indigenous participants (35.5%). In 2018, the percentage of Indigenous participants seeking health advice for influenza (50.6%) was higher than non-Indigenous participants seeking advice (40.7%). During 2012-2018, the percentage of Indigenous Flutracking participants who reported being vaccinated against influenza was consistently lower than non-Indigenous participants.

Conclusion: At the national level, 2017 and 2018 were considered exceptionally severe and mild influenza years, respectively. However, Indigenous Flutracking participants experienced equally high ILI activity and severity in both years. Higher ILI levels and severity in Indigenous Australians is likely to be due to a combination of lower vaccination rates, higher prevalence of comorbidities and sociodemographic factors in some communities.

P1.008 - Determining the household-level impact of antenatal vaccination for respiratory syncytial virus

Authors: Dr Patricia Campbell¹,², Dr Alexandra Hogan³, Dr Nicholas Geard³

Affiliations: ¹The University Of Melbourne, Melbourne, Australia, ²Murdock Children’s Research Institute, Parkville, Australia, ³Imperial College London, , United Kingdom

Abstract:
Background: Respiratory syncytial virus (RSV) is a major cause of respiratory morbidity in young children, with premature infants and infants younger than six months at the greatest risk of severe disease. While results for a phase 3 clinical trial of an antenatal vaccine have been released, the population- and household level impacts of such a vaccine in a high-income setting remain unknown.

Methods: We simulated RSV transmission within an individual-based framework with household structure, parameterized to match Australian conditions. We compared the infection incidence across different levels of vaccination coverage, and between infants born to vaccinated and non-vaccinated mothers. We analysed model sensitivity to assumptions about the duration and strength of natural- and vaccine-induced immunity.

Results: The greatest benefit of vaccination was observed in infants younger than 3 months, with 70% coverage reducing the population infection incidence by 16.6% (IQR 14.2–19.8). Over the first six months of life, the incidence rate ratio (IRR) between infants born to unvaccinated versus vaccinated mothers was 1.26 (IQR 1.23–1.30) at 70% vaccination coverage. This IRR increased to 1.39 (IQR 1.33–1.41) when vaccination was more effective at preventing infection than our baseline assumption, but was relatively invariant to changes in vaccination coverage or the duration of immunity.

Conclusion: Controlling RSV in infants with antenatal vaccination alone, where protection from vaccination is anticipated to be imperfect and short-lived, is challenging. While a substantial individual benefit may be obtained from RSV vaccination, population-level reductions are likely to be more modest.
P1.009 - HIV surveillance in NSW: Understanding a divergent epidemic

Authors: Dr Steven Negro1, Ms Kwendy Cavanagh1, Ms Vicki Bowden1, Ms Julie Darnell1, Dr Christine Selvey1, Dr Vicky Sheppard1

Affiliations: 1Health Protection NSW, Sydney, Australia

Background: NSW has set an ambitious goal of virtually eliminating HIV transmission by 2020. HIV notifications are reported quarterly to inform progress of intervention strategies and help implement policy.

Processes: Laboratory, demographic and clinical information notified to NSW Health are collected at diagnosis with additional information on treatment uptake and retention in care collected six months post HIV infection. Testing denominator data is obtained from laboratories. These data are used in descriptive analyses, updated each quarter.

Analysis: During January to March 2019, 65 NSW residents were newly diagnosed with HIV infection, 22% less than the 5 year average for quarter 1 (Q1). Fifty-two (80%) were men-who-have-sex-with-men (MSM), an overall reduction of 22%. Seventeen of 52 MSM were Australian-born and 35 were overseas-born, a 48% reduction and 4% increase, respectively, compared to the Q1 2014-2018 averages. Of 17 Australian-born MSM, 65% had evidence of early stage infection and 18% were diagnosed late. Of 35 overseas-born MSM, 29% had early stage infection but 43% were diagnosed late, a 29% increase. Of 193 new diagnoses between January and September 2018, now followed up 6 months post diagnosis, 84% had initiated treatment within 6 weeks. The median days from diagnosis to treatment fell from 45 in 2013 to 19.5.

Conclusions: There have been significant declines in HIV notifications for Australian-born MSM, suggesting current messaging and prevention strategies, like PrEP, are succeeding. However, these reductions have not been seen in overseas-born men and the increasing proportion of late diagnoses in this group warrants targeted initiatives.

P1.010 - Invasive Haemophilus influenzae type b disease epidemiology and vaccine failures, Australia 2000–2017

Authors: Ms Julia Maguire1,2, Ms Kelley Meder1, Dr Aditi Dey1,2, Professor Peter McIntyre1,2, Professor Kristine Macartney1,2, Dr Frank Beard1,2

Affiliations: 1National Centre for Immunisation Research and Surveillance, Westmead, Australia, 2The University of Sydney, Wetsmead, Australia

Abstract: Background: Invasive Haemophilus influenzae type b (Hib) disease incidence in Australia fell sharply after Hib vaccine introduction on the National Immunisation Program (NIP) in 1993. Two deaths in vaccinated children in 2017, and moving the fourth vaccine dose from 12 to 18 months in 2018, prompted this review.

Methods: Invasive Hib cases born 2000–2017 and notified to the national Hib Case Surveillance Scheme were eligible. Notification rates, incident rate ratios (IRR), trends and case-fatality ratios (CFR) were calculated. Relative incidence was calculated comparing unvaccinated children and children with ≥1 vaccine dose recorded on the Australian Immunisation Register.

Results: There were 153 cases born and notified in 2000–2017; notification rate was highest in infants (1.5 per 100,000), with 87% aged ≤5 years. Notification rates decreased in Indigenous and non-Indigenous children over time, rate disparity remained high (IRR 13.3). Overall CFR was 12.4%. Estimated Hib incidence in unvaccinated children was 7.2-fold and 9.8-fold higher than children who had received ≥1 dose of PRP-OMP and PRP-T, respectively. 65/153 cases (42.5%) were classified as vaccine failures, with no increasing trend over time; 11 (17%) were aged 12–17 months.

Conclusion: Invasive Hib disease rates in Australia are low and declining. However, it is important to continue monitoring epidemiology especially in Indigenous children who experience more disease and at a younger age than non-Indigenous children. Continued surveillance of vaccine failures, which consistently occur at a low rate, is also essential as is long-term monitoring of any impact following the 2018 NIP schedule change.

P1.011 - Value of data aggregation to inform Australia’s response to infectious disease emergencies

Authors: Ms Priyanka Pillai1, Professor Jodie McVernon1

Affiliations: 1The Peter Doherty Institute For Infection And Immunity, The University Of Melbourne, Melbourne, Australia

Abstract: Background: The infectious diseases data ecosystem is comprised of information from surveillance, clinical research, primary care, diagnostic laboratories, epidemiology and genomics. Past public health emergencies have demonstrated the challenges associated with rapid sharing of data to inform response. It is essential to improve data collection, facilitate data sharing and support data usage for decision-making in the communicable diseases community.

Method: A literature review was undertaken to summarise existing practices in infectious diseases data management in Australia and internationally. The scoping work includes expert contributions from infectious diseases research, health informatics, bioinformatics and information systems.

Results: Australia’s health and medical research strategic plans emphasise on enhanced data collection, efficient reporting systems and building advanced infrastructure. There is global support for making data available under F.A.I.R. (Findable,
Accessible, Interoperable and Reusable) Principles to support knowledge integration, innovation and discovery. The Five Safes Framework (Projects, People, Data, Outputs and Settings) is an accountability framework to inform decisions about data usage. There are international exemplars of platforms that rapidly collect and disseminate data to inform public health responses. Ethically approved and harmonised protocols are essential tools for rapid collection, sharing and aggregation of data to support decision-making during an outbreak.

Conclusion: The challenges in sharing and aggregating data can be addressed by building trust among data custodians, promoting collaboration and implementing data stewardship practices. The infrastructure solutions to leverage big data in infectious diseases should be agile, comply with ethical requirements and legislation, facilitate equitable data access and expedite cross-jurisdictional data sharing in Australia.

P1.012 - Evaluation of the Haemophilus influenzae type b Case Surveillance Scheme

Authors: Ms Kelley Meder1, Dr Aditi Dey1,2, Professor Peter McIntyre1,2, Dr Frank Beard1,2

Affiliations: 1National Centre For Immunisation Research & Surveillance, Westmead, Sydney, Australia, 2The University of Sydney, Australia

Abstract:
Background: Invasive Haemophilus influenzae type b (Hib) disease is a serious disease with high death rate. Prior to vaccine introduction disease rates in Indigenous Australians were amongst the highest in the world. Following Hib vaccine introduction on the National Immunisation Program in 1993 there was a sharp decrease in disease notifications. The Hib Case Surveillance Scheme (HCSS) is an enhanced surveillance system established in 1994, currently managed by the National Centre for Immunisation Research and Surveillance. We aimed to evaluate the usefulness of the HCSS.

Methods: We reviewed the HCSS’s simplicity, flexibility, data quality, acceptability, sensitivity, representativeness, timeliness, and stability. To review these key attributes we analysed HCSS and National Notifiable Diseases Data Surveillance System (NNDSS) Hib disease datasets from 2000–2016, and surveyed eleven stakeholders involved in the HCSS through questionnaire or interview.

Results: From 2000–2016, rates of Hib disease notification to the NNDSS ranged from 0.06 to 0.15 per 100,000 population. The HCSS was 91% sensitive. Completeness of data fields in the HCSS ranged from 73-90%. Stakeholders considered the strengths of the HCSS to be simplicity, longevity, and consistency over time, with limitations being use of paper forms and limited published reports on the data. Recommendations included electronic reporting, more regular publication of reports, and national serotyping for all invasive Haemophilus influenzae isolates to monitor for serotype replacement.

Conclusion: Further engagement with stakeholders is required to determine how best to implement recommendations of this evaluation and ensure processes are better streamlined and coordinated.

P1.013 - Rapid influenza testing enhances outbreak responses and strengthens partnerships with Residential Care

Authors: Ms Fiona Vosti1, Ms Rachael Young1, Ms Kay Jones1, Mrs Deena Malloy1, Dr Satyamurthy Anuradha2

Affiliations: 1Gold Coast Public Health Unit, Carrara, Australia, 2Pathology Queensland, Southport, Australia, 3Metro South Public Health Unit, Coopers Plains, Australia

Abstract:
Influenza is highly infectious and can result in severe consequences including permanent disability or death. Influenza can spread quickly amongst people living and working in Residential Care Facilities (RCF) and effective outbreak control relies on early suspicion and diagnosis of influenza as well as timely notification to Public Health Units.

Any delay in collection or analysis of samples impedes the outbreak management response which may lead to avoidable hospital admissions. Two GeneXpert machines were introduced to the Gold Coast Hospital and Health Service (GCHHS) prior to the Gold Coast 2018 Commonwealth Games and have been shown to provide reliable and rapid results when testing for influenza. Information about the availability and benefits of rapid testing was provided to RCF staff in an education session held in early 2019. Rapid testing of swabs collected from residents enables the Gold Coast Public Health Unit (GCPHU) to provide appropriate and timely guidance and recommendations for control of influenza outbreaks.

A case series analysis will be conducted reviewing clinical records describing the differences where rapid testing was utilised or not. We will also compare the timeliness of notification to GCPHU, the number of hospitalisations and deaths as well as the length of each influenza outbreak.

Use of rapid testing for influenza demonstrates value and improves the management of influenza outbreaks in RCF. Promoting RCF access to this rapid testing enables GCPHU to better support RCFS in outbreak management and strengthens partnerships between the organisations involved.
P1.014 - Assessing immunisation service utilisation for Aboriginal Children in Victoria using AIR data

Authors: Ms Kylie Carville1, Ms Catherine McNamara2, Ms Chelsea Taylor3, Ms Lucinda Franklin2

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Abstract:
Background: The National Immunisation Program (NIP) can be delivered by a range of services, including general practice, councils, and for Aboriginal people, by Aboriginal Community Controlled Health Organisations (ACCHOs). Understanding where Aboriginal children are immunized can help target immunisation policy and programs, and other health messages.

Methods: Australian Immunisation Register (AIR) reports are available to the Immunisation Section of the Victorian Government Department of Health and Human Services to assist with best practice immunization. Data on provider type was analysed for Aboriginal children aged <7 years who had received at least one immunisation during 2016. All prior immunisations received by these children were included.

Results: Immunisation records from 6,632 Aboriginal children were analysed. The provider type variable was found to mix individual provider and service type, ie immunisations delivered by a ‘Medicare GP’ could be in general practice or ACCHO (both services are also categories of the variable). Address fields were used to recode service type. Of 14,760 immunization events in 2016, 19.2% were delivered by Council, 18.0% by ACCHOs, and 58.5% in general practice. Using the AIR provider type variable, only 10.2% of immunisations were delivered at ACCHOs. Older children were increasingly likely to receive immunisations at an ACCHO, from 16.9% of <1 year olds to 27.2% of 5-<7 year olds. Data on pattern of service use will be presented.

Conclusion: Caution must be used reporting with the AIR provider type variable, which underestimates the proportion of Aboriginal children immunized at ACCHOs, and thus their value in immunization delivery.

P1.015 - Modelling of optimal vaccination strategies in response to a re-emergent smallpox outbreak

Authors: Ms Valentina Costantino1

Affiliations: 1Kirby Institute Unsw, Sydney, Australia

Abstract:
The re-emergence of smallpox is now an increasing and legitimate concern. Advances in synthetic biology have now made it possible for the virus to be synthesized in a laboratory, with methods publicly available. Smallpox introduction into a susceptible population, with increased immunosuppression and elderly rates, raises questions of how vaccination should be used in an epidemic situation when supply may be limited.

We constructed three modified SEIR models to simulate targeted, ring and mass vaccination in response to a smallpox outbreak in Sydney. We used age specific distribution of susceptibility, infectivity, contacts rates and tested results under different assumptions. Number of doses needed of second and third generation vaccine are estimated with the total number of deaths at the end of the epidemic. Results show that a faster response is the key and ring vaccination tracing contacts is the most effective strategy with the smaller number of doses. However in the case of not being able to trace a high proportion of contacts, mass vaccination with at least 125000 doses delivered per day could prevent more deaths. This study supports a better preparation and response planning in case of smallpox outbreak in a setting as Sydney.

P1.016 - Determinants of antenatal influenza and pertussis vaccination uptake in Canberra

Authors: Mr Callum Thirkell1,2, Associate Professor Vanessa Johnston1,2, Dr Ben Polkinghorne3, Dr Marlena Kaczmarek4

Affiliations: 1ACT Health, Canberra, Australia, 2Australian National University, Canberra, Australia

Abstract:
Background: Antenatal influenza and pertussis vaccination is recommended in Australia for every pregnancy, however uptake is not systematically documented.

Methods: All women with a live birth between 1 October 2018 and 30 September 2019 at the largest public hospital in the ACT are being invited to participate in an online survey 4-6 weeks post-birth. Up to three invitation text messages are sent. Interim descriptive and univariate analysis of 6-months data are presented.

Results: During the six-month period, 1,669 women were invited. Of the 796 (48%) respondents: 593 (74%) consented and at least partially completed the survey; 35 (4%) consented but did not complete; and 168 (21%) declined.

Self-reported antenatal vaccination uptake in mothers surveyed was 94% (559) for pertussis and 69% (398) for influenza. The majority (85%) of influenza vaccinations were administered during the first and second trimesters.

Mothers who received a healthcare provider recommendation to vaccinated reported significantly higher uptake of both pertussis (534/555 [OR 9.5, 95% CI 3.95-23.02, p<0.001]) and influenza vaccination (354/450 [OR 7.4, 95% CI 4.72-11.52, p<0.001]).
Mothers expecting their first child also reported significantly higher uptake of both pertussis (244/252 [OR 2.6, 95% CI 1.13-5.91, p=0.025]) and influenza vaccination uptake (187/252 [OR 1.5, 95% CI 1.05-2.22, p=0.027]).

**Conclusion:** Self-reported antenatal vaccination uptake among recruited participants was high for pertussis, particularly when vaccination was recommended by a health professional. Having a first child may be associated with higher likelihood of vaccination. A systematic method to record antenatal vaccinations should be considered.

**P1.017 - Microbiological susceptibility testing for urinary tract infections in Australian general practice**

**Authors:** Mr Zhuoxin Peng\(^1\), Prof. Andrew Hayen\(^2\), A/Prof Bette Liu\(^3\)

**Affiliations:** 1UNSW, Kingsford, Australia, 2University of Technology Sydney, Ultimo, Sydney, Australia

**Abstract:**

**Background:** Microbiology testing is recommended in many conditions when antibiotics are prescribed for urinary tract infection (UTI). However, to what extent clinical practice matches recommendations in real-world primary care is unknown.

**Methods:** We examined electronic health records from NPS MedicineInsight, a de-identified database collected from 3.6 million patients and 3300 Australian general practices. Records of clinical encounters for UTI with antibiotic prescribing between January 1 2013 to July 31 2018 were extracted. Our primary outcome is the proportion of encounters where urine microbiology testing was performed. We examined and compared this proportion in the population overall, and by age, sex, pregnancy condition and whether patients were living in residential aged care facilities (RACF) using generalised estimating equations, adjusting for clustering by patient and practice.

**Results:** There were 96,237 first-onset UTI encounters, i.e., no UTI encounter record in the 365 days prior; 87% (84,113/96,237) had antibiotics prescribed on the same day. Among them 63% (52,929/84,113) had urine microbiology testing requested on the same day. The proportion of test was unexpectedly lower in those populations recommended to receive test: men (57%) vs women (64%), pregnant women (53%) vs women without a pregnancy record aged 22-45 years old (66%), children aged under 5 years (52%) vs adults aged over 20 years (63%), and people living in RACF (28%) vs those not living in RACF aged over 75 years (55%). These differences were all significant after adjusting for clustering and other individual characteristics.

**Conclusion:** Microbiology susceptibility testing for UTI may not correspond to recommendations.

**P1.018 - Response to a syphilis outbreak in remote Aboriginal communities: a partnership approach**

**Authors:** Ms Rudie Marshall-Lang\(^1\), Dr Paul Armstrong\(^2\), Ms Briannan Dean\(^3\), Dr Marianne Wood\(^4\)

**Affiliations:** 1Sexual Health and Blood-borne Virus Program, Western Australian Department of Health, East Perth, Australia, 2Communicable Disease Control Directorate, Western Australian Department of Health, East Perth, Australia, 3Aboriginal Health Council of Western Australia, Highgate, Australia

**Abstract:**

**Context:** There is an ongoing outbreak of infectious syphilis affecting young Aboriginal adults in remote Australia. Since the outbreak was identified in the Kimberley (June 2014), Pilbara (February 2018) and Goldfields (January 2019) regions, there have been 210, 68 and 8 notifications, respectively (to the end of March 2019).

**Process:** The Western Australian Syphilis Outbreak Response Group (WA SORG) was formed to coordinate the state-wide response to this outbreak. The WA SORG aims to control the outbreak of syphilis among Aboriginal communities in WA using partnership strategies that, wherever possible, are applicable to the sustainable control measures for sexually transmitted infections (STIs) and promotion of sexual health in Aboriginal communities. The group is co-chaired by the WA Department of Health and the Aboriginal Health Council of WA.

The WA SORG is linked to relevant networks including the Multijurisdictional Syphilis Outbreak Working Group (MJSO), the (national) Enhanced response addressing sexually transmissible infections (and blood-borne viruses) in Indigenous populations Governance Group, and networks in the outbreak affected regions.

**Analysis:** The WA SORG has developed a Syphilis Outbreak Response Action Plan and a Monitoring Framework to guide activity and measure performance. Five working groups have been established to progress the Action Plan. Interim outcomes of the response will be available by the time of the conference.

**Outcomes:** The WA SORG plays an integral role to coordinate the state-wide response to the outbreak in partnership with regional health services and key stakeholders.
P1.019 - Incorporating qualitative inquiry into the public health investigation of a disease outbreak.

Authors: Prof Donna Mak1,2, Dr Roanna Lobo3, Ms Josephine Shearer4, Dr Johnathan Hallett5

Affiliations: 1Communicable Disease Control Directorate, Perth, Australia, 2Curtin University, Bentley, Australia, 3School of Medicine, University of Notre Dame, Fremantle, Australia

Abstract: Introduction: In metropolitan Perth, Western Australia, notifications of gonorrhoea in heterosexual adults were 50% higher in 2017 than the preceding five-year mean. Communicable disease surveillance data are typically collected using a quantitative paradigm and describe cases in terms of epidemiological categories including age, gender, geographic location and exposure to known risk factors. Qualitative data about sexual behaviours was identified as a knowledge gap that could not be addressed by statutory disease notification and enhanced surveillance data.

Method: Qualitative research was initiated involving prospective recruitment by clinicians, of heterosexual adults aged 18-34 years diagnosed with gonorrhoea. Ethics approval for one site took nine months. After seven months no patients were recruited. A female with qualitative inquiry experience was employed by the Health Department to conduct telephone interviews with recently notified gonorrhoea cases as part of a public health outbreak investigation.

Results: Ten male and eight female patients participated in telephone interviews (median duration 23 minutes). Two patients declined an interview; no participants requested a male interviewer. Participants discussed openly and in detail their sexual behaviours including condom use, numbers of sexual partners, and risk assessment strategies used to avoid infection.

Conclusion and recommendations: Qualitative data can complement quantitative surveillance data when tailoring a public health response to an infectious disease outbreak. Disease control services should include staff with qualitative inquiry as well as quantitative, epidemiological skills. Artificial silos of quantitative vs qualitative inquiry and timeframes required for ethics approval do not support development and implementation of timely public health outbreak responses.

Behavioural insights into case notifications data: Flutracking and community-level surveillance

Authors: Rob Moss,1 Alexander Zarebski, Sandra Carlson, James McCaw

Affiliations: 1Melbourne School of Population and Global Health, The University Of Melbourne, Parkville, Australia, 2Department of Zoology, The University of Oxford, Oxford, England, 3Hunter New England Population Health, Health Ministry of NSW, Newcastle, Australia, 4School of Mathematics and Statistics, The University of Melbourne, Melbourne, Australia, 5Murdoch Children’s Research Institute, The Royal Children’s Hospital, Melbourne, Australia, 6Victorian Infectious Diseases Reference Laboratory Epidemiology Unit, The Peter Doherty Institute for Infection and Immunity, Melbourne, Australia

Abstract: Background: Australia experienced a particularly large and severe influenza season in 2017, and an increased perception of risk in the community may have affected healthcare-seeking behaviour and clinical decision-making. The objective of this study was to determine if accounting for changes in population and clinician behaviours could improve the performance of our near-real-time seasonal influenza forecasts, which predict future influenza case notification counts.

Method: We used weekly Flutracking surveillance data to estimate the probability that a person with influenza-like illness would seek healthcare and have a specimen collected for testing. We then used this estimated probability to calibrate our forecasts at each week of the influenza season, and assessed the change in forecast performance using Bayes factors.

Results: While the weekly Flutracking data typically include very few self-reported influenza tests, the data for 2017 revealed a substantial change in healthcare-seeking behaviour and clinical decision-making: the probability of a person with ILI being tested increased by 125–250%. This change was evident prior to the epidemic peak. By calibrating our forecasts at each week to account for this trend, the forecast performance was greatly improved.

Conclusion: Community-level surveillance systems such as Flutracking are unique in their ability to provide insights into perceived risk and attitudes to seeking healthcare. We have shown that these insights can improve how we interpret case notifications data. This is particularly relevant to “unusual” influenza seasons and to pandemic influenza, where patient and clinician behaviours are likely to change markedly.

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Affiliations: 1Melbourne School of Population and Global Health, The University Of Melbourne, Parkville, Australia, 2Department of Zoology, The University of Oxford, Oxford, England, 3Hunter New England Population Health, Health Ministry of NSW, Newcastle, Australia, 4School of Mathematics and Statistics, The University of Melbourne, Melbourne, Australia, 5Murdoch Children’s Research Institute, The Royal Children’s Hospital, Melbourne, Australia, 6Victorian Infectious Diseases Reference Laboratory Epidemiology Unit, The Peter Doherty Institute for Infection and Immunity, Melbourne, Australia

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Conclusion: Community-level surveillance systems such as Flutracking are unique in their ability to provide insights into perceived risk and attitudes to seeking healthcare. We have shown that these insights can improve how we interpret case notifications data. This is particularly relevant to “unusual” influenza seasons and to pandemic influenza, where patient and clinician behaviours are likely to change markedly.

1A - Genomics and foodborne diseases

Genomic surveillance for Salmonella Enteritidis in Victoria –implementation and evaluation

Authors: Ms Danea Hennessy1, Marion Easton1, Zoe Cutcher1, Joy Gregory1, Siobhan St George1,2, Mary Valcanis1, William Pitchers1, Anders Gonçalves Da Silva1, Ben Howden1, Deborah Williamson1

Affiliations: 1Victorian Department Of Health And Human Services, Melbourne, Australia, 2Microbiological Diagnostic Unit Public Health Laboratory, Parkville, Australia

Abstract:
Background: Whole genome sequencing (WGS) is increasingly used for public health surveillance as it provides a higher level of discrimination than other pathogen typing methods. However, storage and interrogation of combined genomic and epidemiologic data is a challenge when using an event-based public health database. We used Salmonella Enteritidis to determine the best way to report and record genomic information for use in routine surveillance activities in Victoria and evaluated the concordance between genomic cluster results and epidemiologic data.

Methods: All Salmonella Enteritidis isolates submitted to the Microbiological Diagnostic Unit Public Health Laboratory from 1st July 2018 were sequenced, and genomic analysis was used to identify clusters of closely-related isolates. Over the same period, an enhanced questionnaire was used to obtain detailed travel histories from cases.

Results: Genomic clusters identified using a single-linkage approach with a threshold of 20 single nucleotide polymorphisms correlated well with travel history at the country level. This approach was able to accurately distinguish between travel-associated cases and cases acquired in Australia. However, the single linkage definition meant that clusters occasionally merged or split due to the changing isolates in the six-month rolling window for analysis. This required a change in approach to interpretation of typing results when compared to static typing methods such as phage typing. New fields were created in the notifications database for recording genomic cluster results, and interactive surveillance reports incorporating genomic information were developed using Power BI.

Conclusion: Genomics has been successfully integrated into surveillance for Salmonella Enteritidis in Victoria.

Controlling the first outbreak of Salmonella Enteritidis in Australian eggs

Authors: Ms Keira Glasgow1,2, Ms Debbie Chia3, Ms Ashleigh Armanasco3, Mr Craig Shadbolt4, Dr Qinning Wang5, Prof Vitali Sintchenko5, Dr Bronwyn Hendry6

Affiliations: 1Health Protection NSW, St Leonards, Australia, 2OzFoodNet NSW, Sydney, Australia, 3NSW Ministry of Health, St Leonards, Australia, 4Biosecurity and Food Safety, NSW Department of Primary Industry, Newington, Australia, 5Institute of Clinical Pathology & Medical Research (ICPMR), NSW Health Pathology, Westmead, Australia, 6Animal Biosecurity, NSW Department of Primary Industry, Orange, Australia

Abstract:
Background: Salmonella enterica serovar Enteritidis (SE) is one of the most common causes of salmonellosis internationally. It is endemic in poultry layer flocks around the world and until recently, Australian egg farms were considered free of SE. In mid-2018, the first outbreak of SE linked to Australian eggs was detected in New South Wales (NSW). OzFoodNet initiated a multi-jurisdictional response to investigate sources of human infections and coordinate control.

Methods: The investigation followed a One Health approach. Notified cases were interviewed using the standardised Salmonella Hypothesis Generating Questionnaire. Food enforcement agencies investigated food handling practices and conducted traceback of food supply. Animal health authorities implemented biosecurity measures on farms. Whole genome sequencing characterised linkages between human, food and environmental isolates.

Results: At 17 June 2019, 235 cases of SE were identified and linked to the outbreak. The majority were notified in NSW (82%) and over a third (35%) were hospitalised. The causative strain represented Sequence Type 11, phage type 7A. Eggs were the most frequently reported food consumed (89%). The first affected farm was identified in September 2018, and ten additional affected egg farms were linked by egg sales, farm distribution networks and environmental sampling. Control measures included prohibition orders in restaurants, egg recalls, and biosecurity directions on farms.
Conclusion: The introduction of SE to Australian eggs farms has been a significant threat to public health, food safety and animal biosecurity. The One Health approach was essential to detect and prevent transmission at all stages of the food chain.

Establishing a pragmatic framework for the implementation of genomic-led Salmonella Typhimurium surveillance

Authors: Dr Patiyen Andersson\(^1\), Dr William Pitchers\(^1\), Daneeta Hennessy\(^1\), Dr Zoe Cutcher\(^1\), Dr Danielle Ingle\(^1\), Mary Valcanis\(^1\), Marion Easton\(^2\), Professor Benjamin Howden\(^3\), Associate Professor Deborah Williamson\(^4\)

Affiliations: \(^1\)Microbiological Diagnostic Unit Public Health Laboratory at The Peter Doherty Institute for Infection and Immunity, University of Melbourne, Melbourne, Australia, \(^2\)Department of Health and Human Services, State Government of Victoria, Melbourne, Australia

Abstract:

Background: Whole genome sequencing (WGS) provides a comprehensive and highly discriminatory tool for characterising pathogens of public health importance. In Victoria, WGS-based analysis of Salmonella Typhimurium (STM) clusters is initiated based on traditional, less discriminatory typing methods and epidemiological data. We investigated the potential to add value through routine use of WGS analysis for STM surveillance.

Methods: All STM isolates from humans sent to the Microbiological Diagnostic Unit PHL in Victoria between 1st July 2018 and 30th June 2019 were included (n=2000). Isolates were sequenced using an Illumina Nextseq platform, and bioinformatic analysis was performed using in-house pipelines. Identification of potential clusters was performed using a single-linkage nearest-neighbour algorithm testing different thresholds of genetic variability (5, 10, 20 single nucleotide polymorphisms (SNPs)) and, where possible, correlated with epidemiological data.

Results: A total of 132 genomic clusters, containing up to 256 isolates, were identified. Clustering was most informative at the 5 SNP level. Temporally and geographically defined clusters were observed. Two large clusters persisted throughout the entire study period, representing nearly 30% of the total disease burden. WGS provided improved discrimination of these compared to current traditional typing.

Conclusions: WGS provides critical information that can assist prioritisation of resources for public health follow-up. Prospective analysis of all STM isolates could guide investigation of large, ‘slow-burning’ clusters. Genomic discrimination between highly-related and less-related isolates within such clusters could support targeted epidemiological investigations to identify a source.

Whole genome sequencing for investigation of a foodborne Salmonella Typhimurium outbreak

Authors: Dr Niki Foster\(^1\), Mr Ty Chiu Chew\(^2\), Dr Qinning Wang\(^3\), Mr John Coles\(^1\), Dr Nevada Pingault\(^4\)

Affiliations: \(^1\)Department Of Health, Western Australia, Perth, Australia, \(^2\)City of Melville, Perth, Australia, \(^3\)NSW Health Pathology, Sydney, Australia

Abstract:

Background: WA Health coordinated an outbreak investigation after two groups of diners ate at a restaurant in mid-2018. A total of seven people became ill with diarrhoea and/or vomiting, with four people diagnosed with Salmonella Typhimurium (STM) MLVA 03-17-09-12-523.

Methods: A case control study was conducted using ill people as cases and well people who dined with the cases as controls. Genotyping by Multi Locus Variable number tandem repeat Analysis (MLVA) and Whole Genome Sequencing (WGS) were performed on STM isolates from human and food samples.

Results: The analytical study, comprising seven cases and five controls, identified consumption of deep-fried ice-cream and sweet and sour pork as statistically associated with illness (both consumed by 5/7 cases and 0/5 controls; OR undefined, 95% CI 1.989 - undefined, \(P = 0.028\)). The two step cooking method used to prepare the sweet and sour pork meant it was a less biologically plausible vehicle than the deep-fried ice-cream.

Samples of egg wash, desiccated coconut, uncooked fried ice cream and cooked fried ice-cream collected during the environmental health investigation were positive for the same STM MLVA type as cases. WGS of clinical and food isolates identified 0-2 SNP difference between the isolates, confirming the cases were genomically linked.

Conclusion: This is the first application of WGS in WA to link human and food samples in a foodborne outbreak. WGS identified a very close genomic link between STM isolates, and supported the epidemiological data that illness was caused by contaminated fried ice-cream consumed at the premises.
Combining epidemiological and genomic data to describe Shigella transmission in NSW

Authors: Mr Neil Franklin

Affiliations: 1Nsw Health, Ozfoodnet, Sydney, Australia

Abstract:
Background: In NSW, Shigellosis infection occurs primarily in returning overseas travellers returning and in men who have sex with men (MSM) locally. Peaks in Shigellosis notifications occur due to increases in travel or clusters of localised MSM transmission. The numbers of multi-drug resistant (MDR) Shigella cases in returned travellers and MSM both increased in 2018. Here, we combine epidemiological and genomic data to describe the spread of MDR Shigella lineages in NSW.

Methods: Shigella sonnei G isolates collected in NSW between 2017 and 2019 were analysed. Whole-genome sequencing (WGS) and bioinformatic analyses was performed by ICPMR. Antibiotic resistance was collected form primary laboratories and risk factor information on travel and sexual exposure were collected through case interviews.

Results: WGS revealed 6 separate genetic clusters. There were strong associations between epidemiology, and phylogeny. Clusters occurred both temporally and spread over a number of years, showing both potentially point source outbreaks and long-term transmission. Two of the clusters also contained overseas acquired isolates, indicating the potential for multiple introductions of shigella species with similar homology. Resistance information was available for 76% of cases, with 88% potentially resistant to Ciprofloxacin, Cotrimoxazole, Ampicillin and Azithromycin, but susceptible to Ceftriaxone and cefotaxime. The pattern of antibiotic resistance coincides strongly with WGS clustering.

Conclusion: This data demonstrates the high levels of antibiotic resistance in Shigella infections in NSW through local circulation as well as importation. Constant monitoring and reporting of antibiotic sensitivity is required to ensure treatment remains appropriate and local outbreaks are controlled.

Source Attribution of Campylobacter infections in Australia

Authors: Angus McLure, Dieter Bulach, Mary Valcanis, Amy Jennison, Rhiannon Wallace, Nigel French, Martyn Kirk, Kathryn Glass

Affiliations: 1National Centre For Epidemiology And Population Health, Australian National University, Canberra, Australia, 2Melbourne Bioinformatics, University of Melbourne, Melbourne, Australia, 3Microbiological Diagnostic Unit Public Health Laboratory, The Peter Doherty Institute, Melbourne, Australia, 4Forensic and Scientific Services, Queensland Health, Australia, 5NZ Food Safety Science & Research Centre, Massey University, Palmerston North, New Zealand

Abstract:
Background: Campylobacter species are a major cause of food-borne illness in Australia, leading to approximately 200,000 infections and 4,000 hospitalisations per year. Campylobacter species are regularly isolated from food animals but the relative contributions of each animal source to human disease is unknown.

Data: The multi-locus sequence typing (MLST) profiles of 523 Campylobacter isolates from retail chicken, pork, beef, and lamb and 509 isolates from human cases collected in ACT, NSW, Queensland and Victoria between 2017 and 2018 as part of the national CampySource project.

Methods: We used a Bayesian asymmetric island model of source attribution, implemented in the R package islandR, that estimated the mutation and recombination rates of Campylobacter and the movement of Campylobacter types between sources to infer the sampling distribution of MLST profiles in each source. The inferred sampling distributions in the source were compared to observed MLST profiles in humans to estimate the attribution proportions at the sequence type and species level.

Results: Chicken was the leading source, accounting for 90.3% (95% CrI: 78.5-97.7%) of C. coli infections and 51.2% (38.1-63.2%) of C. jejuni infections. Pork and lamb may also have been considerable sources of C. jejuni, accounting for 27.6% (7.4-42.9%) and 17.1% (0-27.7%) of infections respectively.

Conclusion: Our analysis of retail meat products suggests that in mainland East Australia C. coli infections primarily originate in chicken, but that C. jejuni infections have diverse origins. However, we cannot rule out transmission from unsampled animal and environmental sources or the possibility of transmission from cross-contaminated products.
1B – Influenza and other respiratory viruses
Mount Ainslie Room, 11:30am – 1:00pm

Drivers of a summer influenza epidemic – New South Wales, Australia, 2018-2019.

Authors: Ms Celeste Marsh1,2,3, Professor Ross M Andrews1,4, Dr Vicky Sheppeard1, Ms Robin Gilmour3, Dr Sean Tobin1

Affiliations: 1National Centre for Epidemiology and Population Health, Australian National University, Canberra, Australia,
2Immunisation Branch, Office of Health Protection, The Australian Government Department of Health, Canberra, Australia,
3Communicable Diseases Branch, Health Protection, NSW Health, St. Leonards, Australia,
4Menzies School of Health Research, Charles Darwin University, Tiwi, Australia

Abstract:
Background: There was an unusually high incidence of influenza during the summer of 2018-2019 in New South Wales (NSW), with almost double the notifications from the previous summer. We aimed to test the hypothesis that inter-seasonal influenza was associated with factors such as travel and influenza vaccination status.

Methods: We undertook a case-control study using the NSW notifiable diseases database; a ‘case’ was defined as laboratory-confirmed influenza with illness-onset between 1 December 2018 and 21 March 2019. Those notified with pertussis over the same time-frame served as the control group. Individuals with listed mobile numbers (n=3632, 37%) were sent an online survey via text message. Logistic regression analyses were used to assess associations between self-reported influenza illness and various exposures.

Results: There were 7225 individuals who met the influenza case definition; the highest rates occurred in those aged <5 years and those aged 85+ years. Among the respondents (n=961), cases were more likely to report pre-illness overseas travel or contact with an ill overseas visitor (135/649, 21%) than controls (17/259, 7%); the association was strong in early summer (Dec-Jan: AOR=7.10, p=<0.001) but not in later months (Feb-Mar: AOR=1.69, p=0.152). There was no difference in self-reported influenza vaccination status between groups.

Conclusions: The incidence of summer influenza appears to be increasing in Australia; for the 2018-2019 NSW summer, overseas travellers played a role in introducing infection. Results could prompt a re-evaluation of current recommendations for pre-travel vaccination or the timing for the seasonal influenza vaccine in NSW and other temperate zones.

Rapid expansion of Flutracking in New Zealand 2018

Authors: Dr Craig Dalton1,3, Dr Hernando Acosta2, Ms Sandra Carlson3, Dr Sarah Moberley3, Professor David Durrheim1,3

Affiliations: 1University Of Newcastle, Wallsend, Australia, 2New Zealand Ministry of Health, Wellington, New Zealand,
3Flutracking, Hunter New England Population Health, Wallsend, Australia

Abstract:
Introduction: Flutracking, an online community-based influenza-like illness surveillance system in Australia, is the largest participatory surveillance system in the world. It grew from 400 participants in a regional health service in 2006 to over 45,000 participants in 2018 through a range of promotional techniques and experiments conducted over the last 12 years. New Zealand joined Flutracking in March 2018. We demonstrate below the success of this expansion, and implications for expansion to other countries.

Method: We leveraged prior learnings from Australia and New Zealand’s own innovation to achieve rapid implementation and recruitment. Successful techniques included active social media use, asking participants to invite their friends, inviting participants to report on household members, minimal survey questions, and use of ‘obvious design’ principles. The first New Zealand surveys were sent within 2 months of the agreement to implement.

Results: In 2018, there were approximately 4000 New Zealand participants per week; a participation rate of 1 per 1200 residents. This contrasts with longer running systems that have typical weekly participation rates of Australia at 1 in 630, USA FluNearYou at 1 in 27,000, and the UK Flusurvey 1 in 26,000.

Conclusions: The collaboration in New Zealand resulted in a recruitment level in the first year of operation that exceeded many other countries’ levels over 5 to 10 years of operation. The system could be successfully expanded to other countries.
Self-reported influenza testing behaviour among Flutracking participants

Authors: Ms Sandra Carlson¹, Mr Zachary Howard¹, Dr Craig Dalton¹²

Affiliations: ¹Hunter New England Health, Wallsend, Australia, ²University of Newcastle, Callaghan, Australia

Abstract:

Background: Each year laboratory confirmed influenza counts are reported in the media, and often used to dramatize current activity and severity of the season. However, reporting only counts of positive results without reference to the denominator of total laboratory tests performed, may bias results because of changes to testing practices over time.

Methods: Flutracking, an Australia/New Zealand influenza-like illness (ILI) surveillance system, collects self-reported data on influenza tests. We calculated the annual average proportion of Australian participants with ILI that reported having an influenza test, by state, age and medical facility, from 2014 to 2018. We calculated an approximate adjustment factor for laboratory notification counts, to account for testing practice changes from 2018 to 2019.

Results: The average proportion of self-reported tests increased each year from 2014 (2.6%) to 2017 (5.0%), and decreased in 2018 (3.2%). Self-reported testing for 2014 to 2018 was generally highest in the elderly, lowest in school-aged children, and highest in South Australia. Self-reported testing increased markedly in the GP setting from 2018 to 2019, compared to emergency department and hospital testing. While absolute notifications have increased by over 400% from 2018 to 2019 (to epiweek 22), adjusting for the 2.1 times increase in self-reported testing from 2018 to 2019 would reduce this increase to 137%.

Conclusion: Laboratory testing rates may change in response to severity of influenza seasons but practice also evolves over time. Flutracking provides insights into testing behaviour changes by demographics and medical facilities, and how this might bias absolute influenza notification counts.

Influence of rapid emergency department influenza testing on hospital admission rates.

Authors: Dr Katherine Todd¹, Mr Paul Cook¹, Ms Lucy Cook¹, Ms Kirsty Graham¹, Dr Peter Lewis¹

Affiliations: ¹Central Coast Local Health District Public Health Unit, Gosford, Australia, ²Central Coast Local Health District Infection Prevention and Control Unit, Gosford, Australia

Abstract:

Background: In 2017, NSW Health Pathology introduced rapid diagnostic testing for influenza and respiratory syncytial virus. PCR results were provided within 4 hours of a nasopharyngeal swab being collected. Within Central Coast Local Health District the test was available from Gosford Hospital from mid-July 2017. Wyong Hospital had access to the test via Gosford Hospital; however this usually involved some delay. On-site testing in Wyong Hospital began in July 2018, creating a natural experiment of the influence of the timing of a test result on emergency department outcomes.

Methods: Emergency, hospital and critical care unit admission data for both hospitals for the period 2015-2018 was examined, including the years preceding and inclusive of the rapid diagnostic trial. Test positivity and admission rates were reviewed and compared over time and between hospitals. A random sample of inpatient records were reviewed.

Results: Initial data review suggests that admission rates among confirmed influenza patients rose disproportionately in Gosford Hospital compared with Wyong Hospital during the 2017 pilot study. Further review of the data will explore this correlation including whether a rapidly-available positive test result was associated with hospital admission in the absence of other clinical factors.

Conclusions: Rapid diagnostic testing for influenza can improve patient flow in emergency departments as well as facilitate timely administration of antivirals. Any unintended consequences that arise following the introduction of new tests should be identified and strategies developed to address these. In this setting this could include decision support tools on the management of acute influenza.

Influenza vaccine effectiveness when the season doesn’t end

Authors: A/Prof Sheena Sullivan¹, Ms Monique Chilver²

Affiliations: ¹WHO Collaborating Centre For Research And Research On Influenza, Melbourne, Australia, ²University of Adelaide, Adelaide, Australia

Abstract:

Background: The 2018 influenza season in Australia was late and mild and in stark contrast to the 2017 season, which was characterised by very high activity. However, it appears that the minimal activity seen in 2018 has continued throughout spring and into summer and autumn, and has been associated with outbreaks in the tropical north, dozens of deaths in late summer/early autumn and elevated presentations to emergency departments and GPs. It is unclear whether the 2018 vaccine offered any residual protection beyond the end of the 2018 season.

Methods: Data from the Australian Sentinel Practices Research Network were used to estimate vaccine effectiveness (VE). VE was calculated from the odds ratio comparing VE was compared for the 2018 season (March-September 2018) and the inter-seasonal period (October 2018-March 2019). Interim estimates will also be reported for the 2019, as these data become available.
Results: The overall VE for the 2018 season was estimated at 60% (95%CI: 38-75), but was only 13% (95%CI: -25-40) during the inter-seasonal period.

Conclusions: This preliminary analysis suggests that the residual effectiveness of the 2018 vaccine during the inter-seasonal period may have been reduced compared with during the season, consistent with observations from elsewhere that the vaccine’s effectiveness wanes over time. The implications for Australia, especially for the tropical north which frequently experiences inter-seasonal activity, will be discussed.

The Reliability of Point of Care testing in Aged Care Facilities

Authors: Mr Christian Jones1,2, Miss Elizabeth Ridgway1, Mrs Elizabeth Clarke1, Mrs Penelope Clark1, Mrs Sophie Norton1, Dr Shopna Bag1,2, Dr Jen Kok1,5, Professor Richard Lindley1,2, Professor Dominic Dwyer4,5, Professor Robert Booy2,3,5

Affiliations: 1Centre for Population Health, Western Sydney Local Health District, Australia, 2Sydney Medical School, University of Sydney, Sydney, Australia, 3National Centre for Immunisation Research and Surveillance, Westmead, Australia, 4Centre for Infectious Diseases and Microbiology Laboratory Services, NSW Health Pathology, Westmead Hospital, Westmead, Australia, 5Marie Bashir Institute for Infectious Diseases and Biosecurity, School of Biological Sciences and Sydney Medical School, The University of Sydney, Sydney, Australia

Abstract:
Background: Residents in aged care facilities (ACFs) are at higher risk of influenza and other respiratory pathogens. Early detection of influenza can prompt earlier intervention to reduce morbidity and mortality. Rapid diagnostic polymerase chain reaction (PCR) Point of Care (POC) platforms can screen for influenza within 30-60 minutes.

A study was commenced in the Western Sydney Local Health District (WSLHD) in 2018 to measure the sensitivity and specificity of POC testing in ACF’s against the laboratory-based multiplex PCR.

Methods: ACF residents with an influenza like illness routinely notified to the WSLHD Public Health Unit from August 2018 to May 2019, received on-site POC PCR testing of nasopharyngeal swabs using the Cepheid GeneXpert. This is a reverse transcriptase PCR assay that can detect and differentiate between influenza A, B and RSV. The remainder of the swab was delivered to the laboratory for confirmatory testing.

Results: Rapid POC testing was carried out on 73 specimens from 16 ACF’s, yielding 20 positive results (19 Flu A, 1 Flu B). Three ILIs were epi-linked and low positive (Ct>30), all resulting in laboratory false negatives. This provided a sensitivity of 100% and specificity of 100%. Morbidity and mortality will be presented.

Conclusion: The study has found the POC test to be extremely reliable and practical in early identification of influenza, enabling timely use of anti-viral treatment/prophylaxis to decrease transmission and prevent hospitalisations. Improving outbreak management is critical in reducing the burden of respiratory disease in the elderly.
1C – Meningococcal disease
Murrumbidgee Room, 11:30am – 1:00pm

Invasive meningococcal disease 2016–2018 – implications for vaccination policy

Authors: Ms Cyra Patel1, Associate Professor Nigel Crawford2,3, Professor Peter McIntyre1,4, Ms Catherine Tran1, Dr Clayton Chiu1,4

Affiliations: 1National Centre For Immunisation Research And Surveillance, Westmead, Australia, 2Murdoch Children’s Research Institute, Melbourne, Australia, 3Department of Paediatrics, University of Melbourne, Melbourne, Australia, 4University of Sydney, Sydney, Australia

Abstract:
Introduction: Invasive meningococcal disease (IMD) rates, particularly serogroups W and Y, have increased in recent years, leading to various jurisdictional vaccination responses. We monitor the changing epidemiology of IMD.

Methods:
IMD cases recorded in the National Notifiable Diseases Surveillance System between 2016 and 2018 were used to calculate incidence and case-fatality ratios (CFRs) by serogroup, age and Aboriginal and/or Torres Strait Islander (Indigenous) status.

Results: IMD incidence increased from 1.0/100,000 (2016) to 1.5/100,000 (2017), then declined to 1.1/100,000 (2018). Rates for MenACWY rose from 2016 (0.6/100,000) and peaked in 2017 (0.9/100,000), declining back to 0.6/100,000 in 2018. MenB IMD rates fluctuated between 0.38 and 0.56/100,000. IMD incidence was highest in <12 months (10.9/100,000), 12-23 months (4.7/100,000), and 15-19 years (2.6/100,000), with MenB (5.7, 2.4 and 1.4/100,000, respectively) more common than MenACWY (4.6, 1.8 and 1.1/100,000, respectively) in these age groups. CFR was higher for MenW (9.5%) than MenB (4.0%) or MenY (4.4%). High rates of MenB IMD were observed among young Indigenous children (<12 months: 26.1/100,000; 1-4 years: 7.0/100,000), with a substantial disparity between Indigenous (4.9/100,000) and non-Indigenous children aged <15 years (0.7/100,000). The rate disparity for MenW IMD was larger (9.0 vs. 0.2/100,000 in Indigenous and non-Indigenous children aged <15 years, respectively), and persisted in 2018 even after the outbreak in central Australia was controlled (7.8 vs. 0.1/100,000).

Conclusion: Current epidemiology supports the nationally-funded MenACWY vaccination program for toddlers and adolescents. Ongoing consideration for MenB vaccination strategies is supported by the epidemiology, particularly for Indigenous children and adolescents.

Genomic surveillance of Invasive Meningococcal Disease (IMD) in Australia 2017-2018

Authors: Ms Emily Sotheran1,2, Prof Jodie McVernon3,4, Assoc/Prof Deborah Williamson1,2, Ms Courtney Lane1,2, Dr Kristy Horan1, Ms Kerrie Stevens1, Ms Marion Easton1, Ms Janet Strachan4, Assoc/Prof Nicola Stephens4, Ms Kerryn Lodo4, Ms Faline Howes1, Prof Benjamin Howden1,2

Affiliations: 1Microbiological Diagnostic Unit Public Health Laboratory, The University of Melbourne at the Peter Doherty Institute for Infection & Immunity, Melbourne, Australia, 2Department of Microbiology & Immunology, The University of Melbourne at The Peter Doherty Institute for Infection and Immunity, Melbourne, Australia, 3Doherty Epidemiology, The University of Melbourne at The Peter Doherty Institute for Infection and Immunity, Melbourne, Australia, 4Centre for Epidemiology and Biostatistics, Melbourne School of Population and Global Health, The University of Melbourne, Melbourne, Australia, 5Communicable Diseases Branch, Victorian Department of Health & Human Services, Melbourne, Australia, 6School of Medicine, The University of Tasmania, Hobart, Australia, 7Menzies Research Institute, The University of Tasmania, Hobart, Australia, 8Communicable Diseases Prevention Unit, Department of Health & Human Services Tasmania, Hobart, Australia

Abstract:
Introduction: Invasive meningococcal disease (IMD) represents a constant public health threat. Yet, its transmission is poorly described through traditional characterisation. Whole-genome sequencing (WGS) provides high-resolution information on the genetic relationship between IMD isolates and elucidates transmission networks. Here we present findings from two years of national genomic surveillance of IMD.

Methods: Between 2017 and 2018, all national IMD cases (for which an isolate could be obtained) underwent WGS at jurisdictional reference laboratories. Sequence and associated metadata, including age, sex and state of residence were collated, and phylogenetic analysis performed.

Results: A total 441 IMD isolates were included (VIC: 111, QLD: 102, NSW/ACT: 92, WA: 58, NT: 27, SA: 26, TAS: 25). Phylogenetic analysis identified ongoing expansion of a serogroup W (finetyping P1.5;2:F1-1;ST11 (CC11)) clone which first emerged in Australia in 2014, including expansion of a sub-cluster from remote Western Australia, Northern Territory and Queensland. Additionally, a cluster of eight South Australian serogroup B isolates (finetyping B:P1.7-2;4:F1-5;ST154) spanning 2017/2018 was identified.

Finally, analyses identified a cluster of serogroup C (finetyping C:P1.5-1,10-8:F3-6;ST11(CC11)) in Victorian men aged 25-49, possibly consistent with international serogroup C outbreaks amongst men who have sex with men. This sub-population grouping was not evident through finetyping methods alone.
Conclusion: WGS provides unparalleled insight into the genetic relatedness between IMD isolates. Putative clusters and at-risk populations that would have been missed by traditional typing and ‘shoe leather’ epidemiology were identified through phylogenetic analyses. Genomic IMD surveillance system has the potential to provide earlier, more targeted, and more effective intervention.

Characterisation of meningococcal serogroup E invasive disease in Australia: a case series

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Abstract:

Background: Globally, invasive meningococcal disease (IMD) due to serogroup E (MenE) is rare, though carriage is not uncommon. IMD is nationally notifiable in Australia, and in Queensland laboratories are also asked to report isolation of N. meningitidis from eye/conjunctiva. We describe the first cases of IMD due to serogroup E in Queensland.

Methods and Results: Between April and July 2018, two cases of MenE IMD and one MenE conjunctivitis were reported in Queensland. Public health follow-up of cases and contacts revealed no prior IMD exposure. Following infection, one MenE IMD case had complement C7 deficiency detected and was recommended meningococcal ACWY and meningococcal B vaccination.

Isolates and a DNA extract from cases were referred to the Queensland state reference laboratory for routine molecular serogrouping and typing. Retrospective laboratory investigations revealed a Queensland IMD case typed as serogroup X in 2007, to be molecularly consistent with MenE. Molecular typing revealed the genotype of the 2007 and one of the 2018 strains to be E:P1.21-7,16:F5-36-ST1157 (clonal complex 1157); when analysed phylogenetically, compared to international cc1157 strains, they were relatively unrelated to each other. Although insufficient specimen was available for the second 2018 case, finetyping results indicated it would likely belong to clonal complex 1157.

Conclusions: Phylogenetic analysis suggests that the emergence of MenE IMD in Queensland is most likely due to rare sporadic disease incursions of a circulating cc1157 clone. The three cases of MenE IMD highlight the need for continued molecular surveillance of Australian N. meningitidis strains, including by whole genome sequencing.

A randomised controlled trial to assess impact of 4CMenB on meningococcal carriage

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Abstract:

Background: Neiseria meningitidis is the cause of invasive meningococcal disease, primarily affecting young children and adolescents. Meningococcal B (MenB) vaccine (4CMenB) has been shown to be effective against disease but its role in preventing transmission by impacting on meningococcal carriage is uncertain.

Methods: In a cluster randomised controlled trial, 237 (>95%) schools in South Australia (SA) were randomised to 4CMenB vaccination at baseline (intervention) or 12 months (control), for year 10-12 students. Primary outcome was oropharyngeal carriage of disease-causing N. meningitidis, in students identified by porA and genogroup PCR assays. Risk factors for carriage were assessed.

Results: April-June 2017, 34,489 students were enrolled. At 12 months, there was no difference in carriage prevalence of disease-causing N. meningitidis between vaccinated (2.55%) and control (2.52%) students (aOR = 1.02; 95%CI 0.80, 1.31; p=0.85). A 29% reduction in non-typeable N. meningitidis was identified in the vaccinated group compared to control group (1.65% vs 2.23%; aOR=0.71; p=0.008). Acquisition of invasive genogroups was the same in vaccinated (2.0%) and unvaccinated (2.0%) groups. Significant risk factors for carriage of disease-causing N. meningitidis included: year of schooling (aOR year <2 vs >2: 2.75); upper respiratory tract infection (aOR=1.35); smoking cigarettes (aOR=1.91); smoking a water-pipe (aOR=1.82); attending pubs/clubs (aOR=1.54); and recent intimate kissing (aOR=1.65). There was a 72% reduction in meningococcal disease in 17–19 year olds in SA.

Conclusions: With no discernible carriage impact, 4CMenB immunisation programs should focus on direct (individual) protection against invasive disease. The MenB vaccine program in SA is targeted for direct protection for highest risk age groups.
Evaluation Matters: Findings that Reoriented the ACT Year 10 MenACWY Vaccination Program

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Background: In 2018, in response to the emergence of meningococcal W disease nationally, the ACT government introduced a school-based meningococcal ACWY (MenACWY) vaccination program for year 10 students, with a time-limited catch-up campaign for 16- to 19-year-olds through general practitioners.

Methods: A mixed methods process and impact evaluation was undertaken. Quantitative data on vaccine distribution, administration and adverse events were analysed. Semi-structured interviews were conducted with immunisation staff to identify barriers and enablers to program implementation, using thematic analysis to draw out common themes.

Results: A mid-year analysis of vaccination coverage in the year 10 cohort was 78.9%, above the target coverage of ≥75.0%. However, vaccination coverage of 16- to 19-year-olds in the ACT at the mid-point of the catch-up campaign was only 14.1%; well below the target coverage of ≥35.0%. As a result of this finding, several strategic interventions were introduced. A final evaluation of the catch-up campaign at the end of 2018, revealed that vaccination coverage had significantly increased to 51.0%. Enablers to vaccination included ease of vaccine access through the school-based program, while barriers included obtaining consent and vaccine misconceptions.

Conclusion: The ACT year 10 MenACWY vaccination program and catch-up campaign exceeded vaccination coverage targets and demonstrated the effectiveness of school-based settings in facilitating vaccine access among adolescents. It also reinforced the importance of intersectoral collaboration and utilising monitoring and evaluation findings to reorient public health programs, if required.

Public health response to a community outbreak of Invasive Meningococcal Disease (IMD)

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Abstract:

Context: Tasmania typically has about 6 cases of Invasive Meningococcal Disease (IMD) a year. From 2016, Meningococcal W disease notifications increased. In response, a state-funded Meningococcal ACWY vaccination program commenced in 2017 for 15-19 year-olds.

In July 2018, a fatal case of serogroup W IMD in a teenager was notified to the Communicable Diseases Prevention Unit (CDPU). In the following fortnight, 3 further cases of serogroup W IMD were notified; all lived in northern suburban Hobart. No epidemiological links were identified between cases. These cases fulfilled the CDNA definition of a community outbreak of IMD.

Process: CDPU established a state-wide response, extending the Meningococcal ACWY immunisation program to all Tasmanians aged from 6 weeks to 20 years. The response provided vaccine urgently in the outbreak area, before being extended state-wide.

A cooperative effort from all sectors delivered the program. Four large public clinics were held over two weekends in the outbreak area; where vaccine was also provided through schools. Public clinics were then held in the North and North-West of the state. GPs and councils ran additional clinics.

Public concern and media interest created challenges but also helped achieve our aim.

Analytics: We collaborated with the Australian Immunisation Register (AIR) to monitor vaccine uptake.

Outcome: Between July 2017 and December 2018, 71% of the Tasmanians in the eligible cohort were recorded on AIR as immunised. In Hobart’s northern suburbs 89% of the eligible cohort was immunised. Two cases of serogroup W IMD since July 2018 were aged over 60 years.
Privileging First Nations voices in public health emergencies

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Abstract:

Background: The 2009 influenza pandemic, along with previous pandemics, had an inequitable impact on First Nations peoples. The current Australian pandemic plan suggests that equity and two-way communication and engagement with First Nations communities are important. Yet there are no current recommendations on how to communicate and engage with First Nations peoples in order to reduce risk and inequities together.

Drawing on Citizens’ Jury methods, Community Panel processes have been designed to allow decision-makers to hear First Nations people’s considered opinions, values and preferences on a particular issue. Community Panels may be a way to enhance communication with First Nations peoples on issues such as pandemic vaccination prioritisation.

Methods: This study operates within an Indigenist research approach using the citizens’ jury model. The modified Community Panels process will include safer spaces for conversations and circles of communication with communities. The study, designed and conducted largely by First Nations researchers, will be implemented with four First Nations communities. First Nations Community Panels and findings will be recorded, transcribed, analysed and recommendations reported.

Results: Themes and significant issues from the First Nations Community Panels will be presented and discussed.

Conclusion: We will draw understandings of the perspectives and values of First Nations communities and make recommendations on pandemic influenza vaccine prioritisation. If found to be culturally appropriate and acceptable, this way of working with First Nations peoples in two-way communication with public health researchers and practitioners could inform engagement with First Nations peoples in public health emergencies in the future.
Clinic factors associated with better delivery of secondary prophylaxis in ARF management

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Abstract: Background: Acute Rheumatic Fever (ARF) is a serious immune-mediated complication of infection with highly contagious Group A Streptococcus (GAS) pharyngitis or impetigo. The first episode of ARF triggers a long-term regime of antibiotic secondary prophylaxis (SP) to reduce risk of recurrent ARF due to continuing GAS exposure. NT register data have recently demonstrated the dose-response relationship between SP coverage and rates of recurrent ARF. In response, we developed a weighted measure of SP performance by primary healthcare clinics of their client population prescribed intramuscular penicillin injections to reduce ARF recurrence. As reported here, this weighted measure was used to determine clinic-level factors associated with better SP performance for their own clients.

Methods: We accessed a national primary healthcare database to obtain de-identified clinic audit data. We determined statistical associations between clinic factors (explanatory variables) and each clinic’s SP performance (outcome measure) using regression analysis. Complete data were available for 36 primary health care clinics including 496 audit records for clients.

Results: Better SP performance was significantly associated with “systematic processes of follow-up” at the clinic. Clinic accreditation, jurisdiction and workforce were not associated with SP performance. Every one unit increase in “systematic approach to follow-up” increased the median level of SP performance by 30% (95% CI: 2% to 66%).

Conclusions: Clinic managers are encouraged to critically review their follow-up and electronic reminder systems as these are strongly associated with known health benefits for clients and within their control as health leaders to improve.

Establishing the new National Rheumatic Heart Disease Data Collection

Authors: Ms April Roberts-witteveen1, Ms Tracy Dixon1, Ms Prajali Dangol1

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Abstract: Background: Timely, accurate and comprehensive data about acute rheumatic fever (ARF) and rheumatic heart disease (RHD) cases are essential for targeted and effective prevention and treatment programs. The Australian Government’s Rheumatic Fever Strategy (RFS), established in 2009, supports control programs including clinical registers in NT, QLD, WA and SA. In 2018, the Australian Institute of Health and Welfare (AIHW) was funded under the RFS to manage a national data collection and report annually against the 11 Key Performance Indicators (KPIs) in the Australian Guidelines for prevention, diagnosis and management of acute rheumatic fever and rheumatic heart disease.

Methods: The AIHW established an advisory committee and worked closely with jurisdictions to de-duplicate, process and analyse data. All data items in the collection were assessed for usefulness, quality, coverage, consistency in meaning and accuracy of interpretation.

Results: The first National RHD Data Collection annual report showed that as at 31 December 2017, almost 6,400 people in the 4 jurisdictions had a reported diagnosis of ARF and/or RHD. Most cases were young Indigenous Australians (89%). Data were provided against 7 KPIs although poor data quality impeded reporting by some recommended disaggregations. The advisory committee improved the consistency and accurate interpretation of several data items. Other items of poor quality were excluded from the report to prevent inaccurate conclusions being drawn.

Conclusions: The first report from the new collection used quality ARF and RHD data and will help policy development and service delivery to reduce the unacceptable burden of these preventable diseases.

‘It’s just Mumps’ – or is it? Outbreak preparedness in Aboriginal communities

Authors: Ms Bobby Maher1, Associate Professor Raymond Lovett1, Dr Katherine Thurber1, Dr Jason Agostino1,2

Affiliations: 1Australian National University, Canberra, Australia, 2Gurriny Yealamucka Health Service Aboriginal Corporation, Yarrabah, Australia

Abstract: Background: Yarrabah’s vaccination coverage is high, yet the community experienced a rise in mumps cases from December 2017 to March 2018.

Our aim was to describe this outbreak and recommend public health action, considering the context and complexities of a discrete Aboriginal community.
Methods: We cross-checked mumps case notifications in the community-controlled health service’s Communicare system, and the Queensland Health – Notifiable Conditions System for the dates 18/12/2017 to 07/03/2017. We co-designed and administered a questionnaire with Aboriginal health workers to follow-up case-patients knowledge on mumps, symptom severity and overcrowding.

Results: There were 36 confirmed cases and 25 probable cases from December 2017 to March 2018, the index case presented in December 2017. Completed questionnaires from 24.5% of cases (n=15/61) indicated that overcrowding was prevalent (n=9/15) and some cases specified a lack of understanding of health information relating to the disease (n=2/15). We identified systemic communication and systems issues in the public health approach and response.

Conclusion: The public health importance of outbreak investigations in Aboriginal communities have implications beyond the outbreak itself. Building relationships on trust and respect between community, the clinic and government health service is paramount. Aboriginal health workers were vital in the follow-up of case-patients. There is an opportunity to build and utilise this workforce in responding to outbreaks in Aboriginal communities where resources are limited, and they are ideally placed to contribute to disease control management strategies.

Permission has been provided by Yarrabah and Gurriny Yealemucka Health Service to publicise the study’s research findings.

Novel TB care with barrmarrany (family), for barrmarrany

Authors: Mrs Sue Devlin¹, Ms Kirsty Browne¹, Ms Kerryn Lawrence¹, Mr Richard Widders¹, Mr Greg McAvoy¹

Affiliations: ¹North Coast Public Health Unit, , Australia

Abstract:

Background: We describe an action-project within Participatory Action Research (PAR) which aims to amplify the voices of Aboriginal people affected by a tuberculosis outbreak, and to identify with Aboriginal people effective and empowering strategies. We aimed to prevent tuberculosis transmission by supporting a large barramarrany (family) facing recurring tuberculosis to regain the control necessary for good health and wellbeing.

Methods: Our project was founded on the PAR finding that for Aboriginal peoples ‘family must be central to tuberculosis care’. Aboriginal partners provided leadership that ensured Aboriginal peoples’ worldviews and cultural perspectives drove actions. Functionality assessment and repair work on the family’s house focused on the bathroom, kitchen and laundry. Food hampers were provided as a supplement to tuberculosis treatment and a vegetable garden was resurrected.

Results: We identified positive outcomes in interrelated social, health and tuberculosis-specific domains. The family regained the ability to deal with day-to-day challenges and stresses. This enabled the family to sustain healthy eating and to participate in healthcare and tuberculosis-specific prevention activities. Four family members completed tuberculosis treatment and there was an early tuberculosis diagnosis (prior to being highly infectious).

Conclusion: Our project adapted the WHO End TB Strategy to the on the ground situation: we put patients at the heart of service delivery; addressed social determinants of tuberculosis through partnerships; and used research and innovation to break the tuberculosis outbreak trajectory. Dialogue, research and policy focus on partnerships with discrete Aboriginal families and communities are required to address the complex interactions influencing tuberculosis transmission.
Emergence of Mycobacterium abscessus as a new “SuperBug” of public health relevance

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Abstract:
Background: Mycobacterium abscessus complex (MabC) can cause chronic, high-burden infections, especially in immunocompromised. Recently, this rapidly growing mycobacterium has emerged as increasingly virulent and drug-resistant pathogen. This study applied whole genome sequencing (WGS) to characterise MabC and examine their drug resistance mechanisms.

Methods: Isolates identified as MabC from NSW Mycobacterium Reference Laboratory were subjected to WGS using Illumina NextSeq500. Their genomes were examined and drug resistance conferring variants of genes erm, rrl, gyrA, gyrB and 16S rRNA were identified. Genomic predictions of drug resistance were compared with broth micro dilution susceptibility testing.

Results: 120 MabC isolates were included. Phylogenetic analysis confirmed M.abscessus subsp. abscessus (MabA) (82%) accounted for most of the MabC culture isolates received in the MRL. The dominant circulating clone of MabA contained an intact erm41 gene indicating inducible macrolide resistance, which was confirmed with phenotypic results. 19 isolates identified as M.abscessus subsp. massiliense (MabM) had a shortened erm41 gene and were clarithromycin susceptible. One isolate showed acquired resistance in the rrl gene (23S rRNA). Analysis of the 16S rRNA confirmed 115 isolates were susceptible to amikacin with the exception of 4 isolates that had discrepant genotypic and phenotypic results. No genomic mutations were present in gyrase genes that could explain the ciprofloxacin resistant phenotype in 117 isolates.

Conclusion: WGS can reliably speciate and characterise species within MabC and identify markers of resistance to macrolide and aminoglycoside antibiotics. However, there is no clear correlation of in vitro resistance to ciprofloxacin and variation in the gyrase genes.

Defining the role of genome sequencing in detecting drug resistant tuberculosis

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Background: Whole genome sequencing (WGS) of Mycobacterium tuberculosis has offered new insights into mechanisms of drug resistance. This study examined benefits of prospective genomic testing of M. tuberculosis for detection of drug resistant (DR) and multi-drug resistant tuberculosis (MDR-TB) in a low-incidence country.

Methods: All isolates confirmed as M. tuberculosis in the New South Wales Mycobacterium Reference Laboratory in Sydney between October 2016 and May 2019 were sequenced using Illumina NextSeq500. Phenotypic susceptibility for antituberculous agents was determined by MGIT960 (Becton Dickinson) and broth microdilution methods.

Results: Genome-wide analysis of 1200 prospectively strains identified DR in 13.9% and MDR-TB in 2% of cases, respectively. Negative predictive value of resistome detection reached 100%. While the majority of MDR-TB were associated with katG315T and rpoBS450L genotypes, two (25% of MDR-TB) cases of ‘occult MDR-TB’ with Xpert negative isolates and risk of treatment failure could have been missed without genomic analysis. No drug resistance markers were observed in cases of recurrent tuberculosis following completed treatment and only 17% of these were reinfections by a distinct strain. The majority of strains belonged to East African Indian (30%) and Beijing (34%) lineages. In addition, changes of heteroresistance in distinct subpopulations over time were documented in one case of MDR-TB.

Outcomes: The prospective longitudinal analysis of M. tuberculosis genomes in a low-incidence country can improve the recognition of borderline DR strains with risk of recurrence and enhance the case definition of MDR-TB that inform key performance indicators for tuberculosis control programmes.
Epidemiology of CPE in Victoria: Risk Factors for Acquisition in Community-Identified Cases

Authors: Siobhan St George1, Courtney Lane1, Judith Brett1, Dr Mark Schultz3, Kerrie Stevens1, Dr Annaliese van Diemen1, Dr Susan Ballard1, Dr Norelle Sherry1,2, Donna Cameron1,2, Marion Easton4, Associate Professor Deborah Williamson1, Professor Ben Howden1,4

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Abstract:
Introduction: Carbapenemase-producing Enterobacteriales (CPE) are an urgent antimicrobial resistance threat. Victoria introduced state-wide surveillance of CPE from December 2015. We will describe the epidemiology of CPE in Victoria, with a focus on community-identified cases.

Results to 31/12/2018 are presented here, but will be updated to 30/06/2019.

Methods: Screening of patients at highest risk of CPE acquisition was implemented in hospitals state-wide. Suspected CPE were referred from diagnostic laboratories for carbapenemase gene detection and characterisation. Risk factors, including travel and healthcare exposures, were collected for all confirmed cases.

Results: There were 162 cases in 2018, an increase of 14% on 2017, driven by a single-facility IMP-4 outbreak. Diverse carbapenemase genes, most commonly blaNDM, blaOXA-48-like and blaIMP were observed, along with rare CPE including blaGES, blaIMI, and blaNMC-A.

Risk factors for acquisition varied by carbapenemase gene and location at identification. From 2016-2018, overseas travel was reported by 57% of cases overall, but varied from 25% in blaIMP cases to 96% in blaNDM. 20% of cases were community-identified, most commonly in general practice (52%). A higher proportion of community-identified cases reported overseas travel compared to those hospitalised (66% vs 55%), though the proportion who reported overseas hospitalisation was similar (32-34%). 50 cases of putative overseas community acquisition were observed.

Conclusions: State-wide centralised surveillance of CPE is essential in identifying cases that may otherwise go undetected in the community and in determining risk factors for acquisition. Cases reporting overseas travel without hospitalisation remain a concerning sub-group who may not be identified by screening programs.

Incorporating a gonococcal antimicrobial resistance alert into the NSW notifiable diseases database

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Abstract:
Background: Australian national guidelines recommend the prompt public health follow-up of all gonococcal infections with resistance or decreased susceptibility to ceftriaxone and/or high-level resistance (MIC≥256 mg/L) to azithromycin. NSW Health established a gonococcal antimicrobial resistance (AMR) alert system within the NSW Notifiable Conditions Information Management System (NCIMS).

Methods: Since 1 April 2019, culture-based Neisseria gonorrhoeae antimicrobial susceptibility results sent via electronic laboratory reporting from the NSW Neisseria reference laboratory are uploaded into corresponding NCIMS notifications weekly. Every notification with non-susceptibility to ceftriaxone or resistance to azithromycin is automatically sent to an electronic workflow within NCIMS and e-mailed to an inbox monitored by NSW Communicable Disease Branch staff. A descriptive analysis of alerts for NSW residents to 12 June 2019 was conducted.

Results: A total of 41 alerts were received out of 858 notifications with culture (35% of 2423 notifications). All had low-level (MIC≤8 mg/L) resistance to azithromycin and were ceftriaxone susceptible. The majority (21/41; 51%) were males residing in inner Sydney. The median age of females was higher (32.5 years; range 21-50 years) compared with males (28.5 years; range 21-66 years). The proportion of females residing in regional areas was higher compared with males (50% vs. 12.5%). Median time from specimen collection to alert was 15 days (range 3-34 days).

Conclusion: The gonococcal AMR alert system provides a systematic and proactive approach for the detection of, and response to ceftriaxone and azithromycin non-susceptible strains in addition to identifying populations with emerging gonococcal AMR. Daily AMR data upload would improve timeliness.
Antimicrobial resistance of Salmonella Typhi in Australia: An increasing problem

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Abstract:
Background: Increasing antibiotic resistance in Salmonella Typhi (S. typhi) is a growing global concern. Multi-drug resistance (MDR) is increasingly common and the effectiveness of current first-line treatments -fluoroquinolones, azithromycin and third generation cephalosporins- is threatened by widespread use and recent outbreaks of extensively-drug resistant strains.

Methods: All isolates submitted to the Microbiological Diagnostic Unit Public Health Laboratory (MDU PHL) undergo antimicrobial resistance testing and are captured in the National Enteric Pathogen Surveillance System (NEPSS). Analysis of resistance data of S. Typhi isolates reported to NEPSS between 2008 and 2019(YTD) was undertaken to ascertain whether antimicrobial resistance is increasing. Differences in proportion were assessed using chi square and Fischer Exact tests.

Results: 1164 cases were reported to NEPSS, representing 78% off all cases notified to the National Notifiable Disease Surveillance System (NNDSS). Since 2008 increasing rates of resistance to first-line antibiotics including trimethoprim-sulfamethoxazole (p<0.001) were observed. Ciprofloxacin resistance increased markedly from 0% to 20% between 2008 and 2018 (p=0.001), and to 40% in the first half of 2019 (p= 0.004). Most notable however were the 21 isolates with resistance or reduced susceptibility to third generation cephalosporins or Azithromycin, 16 of which were recorded in the past three years.

Conclusions: Current therapeutic guidelines suggest the use of azithromycin, cephalosporins or ciprofloxacin as the preferred treatments of Typhoid. However increasing resistance to these first line antimicrobials, including those to which resistance has been previously rare, demonstrates the necessity for the detailed reporting of antimicrobial resistance testing and surveillance for Salmonella Typhi.

A population level genomic snapshot study of Vancomycin-Resistant Enterococci, Victoria, November 2018

Authors: Dr Sophia Bowman-Derrick1,2,3, Dr Claire Gorrie1, Dr Emma Field1, Ms Marion Easton1, Ms Courtney Lane2, Ms Kerrie Stevens2, Professor Benjamin Howden1

Affiliations: 1National Centre for Epidemiology and Population Health, Australian National University, Canberra, Australia, 2Microbiological Diagnostic Unit Public Health Laboratory, Melbourne, Australia, 3Victorian Department of Health and Human Services, Melbourne, Australia

Abstract:
Background: Vancomycin-resistant Enterococcus faecium (VREfm) colonises patients and causes serious infections, particularly within healthcare facilities. We conducted a cross-sectional study to investigate the genetic diversity and prevalence of VREfm within Victoria, in 2018 and compared findings to a similar 2015 study. Combining whole genome sequencing (WGS) and epidemiological data, evidence for transmission within and between healthcare facilities was assessed.

Methods: During November 2018, diagnostic microbiology laboratories submitted all VREfm cultures for WGS. In silico multi-locus sequence types (STs) and van genotypes were identified. Phylogenetic relatedness of isolates was analysed and compared with healthcare facility.

Results: In total, 311 isolates from 304 patients were identified. The incidence of VREfm infection in November 2018 was 1.7 per 100,000 population, similar to 2015 results (1.9 per 100,000) (p=0.92). ST796 was the dominant clone in both years (182 [59%] of 311 VREfm isolates, 2018, predominantly vanB). Among patients with VREfm, vanA was detected in 64 (21%) of 311 isolates, compared to 55 (19%) of 293 isolates in 2015 (p=0.58).

ST1424 vanA isolates were identified in Victoria for the first time, present in 11 (27%) of 41 healthcare facilities. Of the 33 ST1424 vanA isolates, 31 (94%) fell within a closely-related genomic cluster, involving nine healthcare facilities.

Conclusions: The incidence of VREfm and the prevalence of vanA VREfm were similar in 2015 and 2018 studies. The limited genetic diversity of ST1424 suggests possible transmission occurring between healthcare facilities, indicating the need for additional patient screening and management to prevent further spread of VREfm.
2B – Re-emerging VPDs
Mount Ainslie Room

Joining the dots: enhancing NSW measles surveillance with Nucleotide Sequencing

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Affiliations: 1Health Protection NSW, St Leonards, Australia

Abstract:
Context: In an elimination setting, being able to classify measles cases as either imported or import-related is vital. Between January and May 2019, NSW had multiple imported measles cases, resulting in three small local outbreaks. In addition to limited secondary cases among identified contacts were several other locally acquired cases whose epidemiological links to known cases was less clear or direct.

With fewer globally circulating measles strains (B3, D8 and H1), measles genotyping is now less useful in confirming epidemiological links between cases in the setting of multiple imported cases with overlapping infectious periods and exposure sites than in the past. Combined with poor patient/carer histories, definitive classification of locally acquired cases as import-related can be challenging.

Process: NSW routinely sends measles specimens to the Victorian Infectious Diseases Laboratory (VIDRL) for confirmation and typing. VIDRL conduct 450 nucleotide sequencing on all measles specimens and submit these to the WHO MeaNS Database for comparison with globally submitted sequences. We combined epidemiological data and strain sequencing results from NSW measles cases in 2019 to try to identify the source of locally acquired cases.

Analysis: Three small, distinct measles outbreaks were identified. Nucleotide sequencing confirmed transmission links for locally acquired cases, where epidemiological links to related source case were uncertain.

Outcome: Despite an increased number of imported cases, there was limited transmission within NSW. In an elimination setting, measles nucleotide sequencing is an important tool in definitively classifying the source of locally acquired cases, particularly when contact exposures are indirect or unclear.

Are vaccinated measles cases less likely to result in secondary cases?

Authors: Ms Hannah Vogt1, Dr Paul Armstrong2, Dr Aparna Lal1, Ms Thilini Perera3, Dr Erica Parker3, Dr Benjamin Scalley6

Affiliations: 1National Centre for Epidemiology and Population Health, Australian National University, Canberra, Australia, 2Department of Health, Western Australia, Perth, Australia, 3North Metropolitan Health Service, WA Health, Perth, Australia

Abstract:
Background: The proportion of measles cases who have previously been vaccinated with measles-containing vaccine has increased in Western Australia (WA) in recent years. Globally, there is paucity of information regarding the infectivity of these cases.

This study aims to review cases of measles within WA to determine if there is a difference in infectivity in those who have documentation of having received zero, one and two or more measles-containing vaccines.

Methods: All measles cases notified from 1/1/2014 to 30/5/2019 were extracted from the Western Australia Notifiable Infectious Disease Database (WANIDD). For each case, the number of measles-containing vaccines they received (written documentation confirmed through an immunisation register, health record or verbal advice from a health provider of 0, 1 or 2 or more vaccines, and the number of secondary cases that resulted from that case, were recorded.

Results: One hundred and thirty seven cases were reported, 74 of which had documentation of the number of vaccines received. Of the 44 who received no measles-containing vaccines, 30 secondary cases resulted (mean 0.68 secondary cases per index case); 7 received one vaccine (1 secondary case; 0.14 per index case); and 23 received two or more vaccines (3 secondary cases; 0.13 per index case).

Conclusion: WA data suggests that measles cases who have received one or two measles-containing vaccines may have reduced infectivity. Analysis of Australia-wide notification data would provide more certainty about the conclusion, which may inform whether measles control guidelines need to be tailored for this specific situation.
Modified clinical presentation of IgG positive measles cases

Authors: Ms Jay Healy¹, Dr Lucy Atwood¹, Janet Strachan¹, Ms Carrie Barnes¹

Affiliations:¹Victorian Department Of Health And Human Services, Melbourne, Australia, ²Austin Health, Heidelberg, 3084

Abstract:

Background: Sporadic measles cases and outbreaks continue to occur in Australia despite achieving measles elimination due to imported cases from endemic countries. The current immunisation schedule in Victoria provides two measles vaccine doses by 18 months. Although, prior to 1996 many of the population may have received only one measles-containing vaccine. There has been an observed increase in measles cases with mild or atypical clinical presentations since 2010.

Methods: A retrospective review was conducted or measles cases recorded on the Victorian Public Health Event Surveillance System whom exhibited evidence of measles IgG at disease onset and were PCR positive.

Results: Thirty-three cases of measles were recorded from 2010 to June 2019 in patients with a positive measles IgG at rash onset or within two days of rash onset. All cases were measles PCR positive and aged between 13 and 58 years, with half aged between 30 and 45 years. Five cases (15%) had no classical prodromal symptoms. Ten cases (30%) had an atypical rash that appeared first on the trunk or arms. Two further cases reported only a light, sparse or fine rash. Thirteen cases (39%) required hospitalisation due to illness.

Conclusion: Fourteen IgG positive measles cases (42%) had an atypical clinical presentation. Medical practitioners and public health officials should be aware of possible attenuated measles presentations in the population born between 1966 and 2000. If there is an epidemiological link or history of travel, then confirmation of measles should be made using PCR testing.

Measles in a previously vaccinated adult - a case report

Authors: Ashleigh Butler¹, Troy McNeil¹

Affiliations: ¹Northern Sydney Public Health Unit, Hornsby, Australia

Abstract:

Background: Since December 2018, there have been 38 measles cases reported in New South Wales; 24 have been identified as being overseas acquired and 14 cases identified as locally acquired. A young female (A) who was identified as a waiting room contact of an imported case of measles, was provided advice to watch for symptoms of measles in line with the Measles Control Guideline for Public Health Units after confirming she had been fully vaccinated with 2 doses of measles containing vaccine which had been documented on the Australian Immunisation Register (AIR).

Clinical Presentation: On day 14 following A’s exposure, she developed conjunctivitis, coryza, cough and a fever followed by a fine red, raised non itchy rash the next day. She presented to her GP advising she was a measles contact. Pathology collected on the day of rash onset showed that A was non immune (IgG negative), despite a documented history of vaccination. Subsequent pathology confirmed her as a case of measles, with a positive IgM and positive nose/throat and urine swabs by PCR.

Conclusion: This case demonstrates the importance of providing information to all contacts of measles cases regardless of vaccination status and raises questions. During A’s infectious period she attended work, multiple public places and used public transport during peak transit times. Ongoing surveillance did not reveal any additional cases of measles following their exposure to A. Are vaccinated cases less contagious even if no immunity is detected?

Pertussis vaccine impact in Queensland children born in 1998 and 1999

Authors: Ms Mohana Rajmokan¹, Prof Robert Ware², Dr Sarah Sheridan¹, Prof Keith Grimwood², Dr Stephen Lambert⁴

Affiliations: ¹Communicable Diseases Branch, Queensland Health, Herston, Australia, ²Menzies Health Institute Queensland, Griffith University, Gold Coast, Australia, ³National Centre for Immunisation Research and Surveillance of Vaccine Preventable Diseases (NCIRS), Children’s Hospital at Westmead, Westmead, Australia , ⁴Child Health Research Centre, The University of Queensland, Brisbane, Australia

Abstract:

Introduction: In Australia, acellular pertussis vaccines (DTPa) replaced whole-cell vaccines (DTPw) for the funded primary course for children at 2, 4, and 6 months of age in March 1999. We sought to expand upon previous analyses to assess the impact of receipt of at least one dose of acellular or whole cell pertussis vaccine in Queensland children.


Results: We identified 105,119 children born in 1998/1999 on the Queensland vaccination register. Of these, 99,612 (94.8%) had received any doses of a pertussis containing vaccine during their first year of life, and 91,564 (87%) received at least three doses.

For all three time periods: 3-dose DTPa primary course recipients had higher rates of pertussis than 3-dose DTPw primary course recipients; in the three-dose mixed course cohort, DTPa as the first dose resulted in higher rates compared to first dose DTPw.
This pattern was similar for the overall time period when we included children who had received at least one dose of pertussis-containing vaccine: rates of notification were higher in first dose DTPa recipients (IRR: 2.0 (95% CI: 1.8–2.3)).

Conclusions: When compared with DTPa, DTPw as a first dose provided more durable protection against pertussis infection up to the twentieth birthday.

Effectiveness of acellular pertussis vaccine in older adults: nested matched case-control study

Authors: A/prof Bette Liu1, Dr Wenqiang He1, A/prof Anthony Newall1, Dr Helen Quinn1, Mr Mark Bartlett1, Prof Andrew Hayen1, Dr Vicky Sheppeard1, Dr Nick Rose1, Raina MacIntyre5, Peter McIntyre4

Affiliations: 1School of Public Health UNSW, Kensington, Australia, 2National Centre for Immunisation Research and Surveillance, 3Sax Institute, 4University of Technology, 5Health Protection NSW Ministry of Health, 6Kirby Institute, UNSW

Abstract:
Background: Despite recommendations that older adults receive acellular pertussis vaccines, data on direct effectiveness in adults aged over 50 years are sparse.

Methods: Case-control study nested within an adult cohort. Cases were identified from linked pertussis notifications. For each case, three controls matched on age, sex and cohort recruitment date were selected and cases and controls were invited to complete a questionnaire, with verification of vaccination status by their primary care provider. Vaccine effectiveness (VE) was estimated by conditional logistic regression, with adjustment for reported contact with children and area of residence.

Results: Of 1112 notified cases in the cohort, we had complete data for 333 cases and 506 controls. Among 172 PCR-diagnosed cases (mean age 61 years), 11.2% versus 19.5% of matched controls, had confirmed receipt of pertussis vaccine, on average 3.2 years earlier. Adjusted VE against PCR-diagnosed pertussis was 52% (95%CI 15 to 73%); it was non-significantly higher in those vaccinated within 2 years (63%, 5 to 87%). VE did not differ significantly between adults aged <65 and 65+ years (adjusted VE: 55% (7 to 78%) versus 49% (-32% to 80%); p=0.8). In serologically diagnosed cases, adjusted VE was -55% (-177 to 13%).

Conclusion: Among older adults, either with presumed infection-acquired immunity or priming with whole-cell pertussis vaccine, we estimated modest but significant direct protection against PCR-confirmed pertussis. In cases notified on the basis of single titre serology, there was no evidence of vaccine protection, casting doubt on the validity of serologic diagnosis, especially in vaccinated cases.
2C – Outbreak investigations
Murrumbidgee Room

Poliovirus in Papua New Guinea: a Public Health Emergency of International Concern

Authors: Ms Linda Hobday1, Ms Janlyn Kumbu2, Dr Mathias Bauri3, Mr Berry Ropa, Dr Bruce Thorley4

Affiliations: 1Victorian Infectious Diseases Reference Laboratory, The Doherty Institute, Melbourne, Australia, 2Central Public Health Laboratory, Port Moresby, Papua New Guinea, 3National Department of Health, Port Moresby, Papua New Guinea

Abstract:
Context: The Western Pacific Region was declared polio-free from indigenous wild poliovirus in 2000. The NERL is designated as the World Health Organization National Poliomyelitis Reference Laboratory for Papua New Guinea and tests stool specimens from children with acute flaccid paralysis (AFP).

In June 2018, a circulating vaccine-derived poliovirus type 1 (cVDPV1) was reported from a child in Morobe Province. The virus had 1.5% sequence divergence in the VP1 genomic region compared to prototype Sabin 1, which inferred circulation for ~ 1.5 years. VDPV outbreaks have been reported in areas with conditions conducive to poliovirus transmission including low polio vaccine coverage and inadequate AFP surveillance.

Process: The WHO recommends the collection of two stools >24 hours apart from AFP cases and within 14 days of the onset of paralysis for virus culture. Virus isolates are characterised by RT-PCR to differentiate wild and vaccine strains of poliovirus. Further characterisation of vaccine strains is performed by sequencing the VP1 genomic region to identify deviations from prototype sequence.

Analysis and outcomes: As of June 2019, 26 cases of cVDPV1 have been reported in Papua New Guinea, with 1,199 stool specimens tested from 422 AFP cases and their contacts. An extensive nationwide public health outbreak response involving global collaborations was implemented to increase polio vaccine coverage and improve AFP surveillance. Sensitive AFP surveillance, including the timely testing of stool specimens, and supplementary activities such as environmental surveillance are crucial to rapidly detect poliovirus in case a comprehensive public health response is required.

Lessons from a multi-stakeholder, multi-intervention response to an outbreak of hepatitis A

Authors: Dr Naveen Tenneti1

Affiliations: 1Victorian Department Of Health And Human Services, Melbourne, Australia

Abstract:
Introduction: There has been an ongoing outbreak of hepatitis A in Victoria with approximately 250 outbreak cases notified since March 2017. Key populations affected are men who have sex with men (MSM), people who use injectable drugs (PWID), adult prisoners and homeless rough sleepers. The Victorian Department of Health and Human Services has coordinated a multi-stakeholder, multi-intervention response to this outbreak which has helped to mitigate further outbreak cases and develop new strategies for prevention.

Methods: This was a mixed-methods study. It involved a quantitative analysis of hepatitis A notifications (disaggregated by age, gender, sex, location and risk factors) and vaccine ordering data (disaggregated by location and provider). This was supplemented by a descriptive analysis of various interventions and models of stakeholder engagement which included the offer of free vaccine, behavioural psychology approaches, communications campaigns and provider and risk group outreach and education.

Results: MSM, PWID, homeless rough sleepers and adult prisoners accounted for most of the outbreak cases. The geographical distribution of vaccine ordering suggests that high incidence areas are associated with higher rates of ordering. This data-driven approach has permitted the targeting of interventions to specific areas, types of providers and risk groups.

Conclusion: The Victorian public health response to the hepatitis A outbreak has been rapid and intervened in critical transmission pathways. The outbreak has also provided an opportunity to test new measures and reiterate key messaging around the prevention of hepatitis A and other food-borne and sexually transmissible diseases.

A third wave: infectious syphilis in metropolitan heterosexual people, Perth, Western Australia

Authors: Prof Donna Mak1,2, Ms Kellie Mitchell1, Ms Carolien Giele3, Ms Lisa Bastian1, Dr Benjamin Scalley1

Affiliations: 1Communicable Disease Control Directorate and University of Notre Dame, Nedlands, Australia, 2University of Notre Dame, Fremantle, Australia, 3Metropolitan Communicable Disease Control, Perth, Australia

Abstract:
Background: In Western Australia, infectious syphilis has primarily affected Aboriginal people in remote areas and men who have sex with men in metropolitan Perth (Perth). However, since 2016, infectious syphilis notifications have been increasing in heterosexual people in Perth.

Approach: Statutory notification data from 2009 to 31/03/2019 were analysed to describe the epidemiology of infectious syphilis in heterosexual people in Perth.
Outcomes: Syphilis rates in 2019 in Perth are projected to be 15/100 000 in non-Aboriginal people representing a 5-fold increase since 2009, with a similar trend in Aboriginal people. This is unlikely to be due to increased testing alone as test positivity rates in metropolitan males and females increased by >2-, and >3-, fold, respectively between 2014 and 2018. Three-quarters (76%) of female cases were >45 years. The first case of congenital syphilis in Perth since 2013 was notified in late 2018; the neonate was symptomatic at birth.

Implications for public health practice: Similar to the situation in New Zealand and Canada, heterosexual people contracting syphilis in Perth do not appear to have any particular risk factors making it difficult to identify who should be offered opportunistic syphilis testing. WA Health has responded by broadening on-line resources and social marketing aimed at STI prevention to include syphilis and reviewing antenatal STI testing guidelines. Qualitative interviews may be useful to collect risk behaviour information which patients may be reluctant to divulge to their GP, e.g. heterosexual-identifying males who have sex with men. Further information will be provided during the presentation.

Understanding the rebound in syphilis notifications in 2000-2006 in Victoria, Australia

Authors: Miss Kym Wilkins, Professor Joshua Ross, Doctor Robert Cope, Doctor Rachel Sacks-Davis

Affiliations: 1The University Of Adelaide, Adelaide, Australia, 2Burnet Institute, Melbourne, Australia, 3Department of Epidemiology and Preventive Medicine, Monash University, Melbourne, Australia

Abstract:
Notifications of infectious syphilis in Victoria, Australia declined to a nadir of two cases in 1999, but have since rebounded. The majority of notifications for infectious syphilis during its re-emergence were among gay, bisexual and other men who have sex with men (GBM) (particularly those living with Human Immunodeficiency Virus (HIV)). Victoria was not the only state in Australia, nor industrialised country, to observe the rebound. However, Victoria observed distinctive trends in syphilis notifications due to the extremely low nadir in 1999.

Hypothesised factors to explain the rebound are: (i) the effect of decreased mortality (and morbidity) among high-risk HIV infected MSM; (ii) biological factors relating to syphilis/HIV co-infection; (iii) sexual behaviour change due to HIV treatment optimism; (iv) increased testing rates of syphilis; and/or, (v) HIV treatment impairing immunity to the syphilis-causing Treponema pallidum bacterium.

A mathematical model describing the transmission of syphilis and HIV (including co-infection) through a GBM community was constructed. The model incorporates the complex behavioural and social dynamics. The dynamics were solved numerically under the five hypotheses noted above, to determine which hypothesis (or set of hypotheses) correlates best to syphilis notifications in Victoria from 1998 to 2006.

This is the first study using models to evaluate competing hypotheses from the public health literature explaining the rebound of infectious syphilis in the GBM population. Being able to provide support for a particular hypothesis will increase our understanding of the complex interactions driving the incidence of sexually transmitted infections.

Human Metapneumovirus (hMPV) Outbreaks in Western Sydney Aged-Care Facilities in 2018

Authors: Mr Christian Jones, Ms Elizabeth Ridgway, Mrs Elizabeth Clarke, Mrs Penelope Clark, Dr Shopna Bag, Mrs Sophie Norton, Dr Jen Kok, Professor Richard Lindley, Professor Dominic Dwyer, Professor Robert Booy

Affiliations: 1Sydney Medical School, The University Of Sydney, Australia, 2Centre for Population Health, Western Sydney Public Health Unit, North Parramatta, Australia, 3Marie Bashir Institute for Infectious Diseases and Biosecurity, School of Biological Sciences and Sydney Medical School, The University of Sydney, Australia, 4Centre for Infectious Diseases and Microbiology Laboratory Services, NSW Health Pathology, Westmead Hospital, Westmead, Australia, 5The George Institute for Global Health, Sydney, Australia, 6National Centre for Immunisation Research and Surveillance of Vaccine Preventable Diseases, The Children’s Hospital at Westmead, Westmead, Australia

Abstract:
Human metapneumovirus (hMPV), first described in 2001, is a cause of acute respiratory tract infection in the elderly, with symptoms ranging from mild to severe, and complications including pneumonia.

Methods: Between 1 July and 31 December 2018, 14 outbreaks of Influenza-like Illness (ILI) were monitored in aged-care facilities (ACFs) and a subsequent epidemiological investigation undertaken by the Western Sydney Local Health District Public Health Unit.

Results: hMPV was the main causative pathogen in 3 (21%) outbreaks (27, 28, and 15 cases respectively) in late winter and early spring. 1 Fifty five residents and 15 staff were identified as ILI cases, with hMPV detected in 11 of 63 specimens tested. Of the total ILI cases, 8 were hospitalised (15%), 6 with pneumonia/viral pneumonia as the primary diagnosis. Five residents died (9%); 1 had confirmed hMPV, 3 were epidemiologically-linked to a hMPV case, with a primary diagnosis of pneumonia/viral pneumonia and 1 was incidental. The maximum attack rate observed was 11/36 i.e. 31%.

Conclusion: hMPV was an important cause of morbidity and mortality in this study. A major challenge was the lack of testing for, and awareness of, hMPV as a viral cause of ILI by ACFs, laboratories, and emergency departments, which generally opt for rapid testing only for influenza and RSV. There is no licenced vaccine or approved treatment. Our findings highlight the need for accurate diagnosis, additional prevention measures and surveillance, typically only reserved for influenza outbreaks, to be extended to the control of other respiratory viruses.
Learnings from After-Action Reviews of 14 Regional and National Outbreaks, Australia 2006-2016

Authors: Dr Craig Dalton¹

Affiliations: ¹University Of Newcastle, Wallsend, Australia

Abstract:

Background: Every outbreak is a lesson in prevention and for improving performance in future outbreaks. After-action reviews of outbreaks have become more common in Australia over the last 20 years.

Methods: Insights and recommendations for improvement from 14 public health after-action reviews facilitated between 2006 and 2016 were analysed for common themes. The outbreak debriefs cover a range of scenarios including foodborne, respiratory and vaccine preventable diseases.

Results: Common challenges repeatedly identified in the reviews included:

- Incident Command System (ICS): ICS was often implemented late, incompletely, and with inadequate training prior to or during implementation resulting in obstacles to span of control, clarity of leadership and surge capacity.

- Clarification of Roles: within public health agency hierarchies and between different agencies e.g. food safety versus public health. Multiple outbreaks in which it was not clear who the lead investigator was.

- Communication: External - issues between agencies and general practitioners, laboratories, and emergency departments, and clarifying lead agency for public comment. Internal - New IT communication/portals with legal clarity required to share information.

- Surge capacity: review of capacity and triggers for surging epidemiological, environmental health/food, laboratory, and communication personnel is required.

- Rapid Risk Assessment: Delays in decision-making suggest a need for structured and reproducible methods to estimate the scale and uncertainty of threats to inform public health actions and communications.

Conclusion: Exercises across local, state, and national agencies are required to address issues identified above. They should have a frequency based on an evidence-base for achieving a prescribed response performance standard.
2D – Table Top Presentations
Federation Ballroom Sth

Genomic analysis identifies multiple incursions and local transmission of Candida auris, Victoria

Authors: Courtney R Lane1, Torsten Seemann2, Leon J Worth2,3,4, Marion Easton5, Jenny Wong5, Donna Cameron1,5, Francesca Azzato1, William Pitchers1, Richard Bartolo6, Cristina Mateevici6, Caroline Marshall7,8, Monica A Slavin1,4,7, Benjamin P Howden1,9, Deborah A Williamson1,9

Affiliations: 1Microbiological Diagnostic Unit Public Health Laboratory, The University of Melbourne at the Peter Doherty Institute for Infection & Immunity, Melbourne, Australia, 2VCI NiSS Coordinating Centre at the Peter Doherty Institute for Infection & Immunity, Melbourne, Australia, 3University of Melbourne, Parkville, Australia, 4Peter MacCallum Cancer Centre, Melbourne, Australia, 5Victorian Department of Health and Human Services, Melbourne, Australia, 6Darevitch Pathology, Western Health, Footscray, Australia, 7Royal Melbourne Hospital at the Peter Doherty Institute for Infection & Immunity, Melbourne, Australia, 8Western Health, Footscray, Australia, 9Royal Melbourne Hospital, Parkville, Australia, 10Austin Health, Heidelberg, Australia

Abstract:
Background: The fungal pathogen Candida auris (C. auris) is an emerging global health threat. Often resistant to multiple antifungals, it is associated with outbreaks in healthcare settings. In July 2018, following identification of C. auris in a hospitalised patient, the Victorian Department of Health and Human Services recommended increased screening and introduced centralised reporting of all cases.

Methods: Isolates of C. auris identified between July 1st and December 31st, 2018 were referred to the Victorian Infectious Diseases Reference Laboratory for identification and antimicrobial susceptibility testing, and the Microbiological Diagnostic Unit Public Health Laboratory for whole genome sequencing and phylogenomic analysis. Publicly available international isolates were included for context. Epidemiological data was provided by admitting healthcare facilities.

Results: C. auris was isolated from four patients. All patients reported overseas hospitalisation and all isolates fell within the previously described South Asian clade on phylogenomic analysis. Local transmission was suspected between two patients with a concurrent hospital stay, which was supported by phylogenomic analysis. Isolates from the remaining two patients were not closely related to each other, or any other included isolate, consistent with independent overseas acquisition.

The Victorian C. auris Guideline for Health Services was subsequently developed, providing recommendations for the identification and management of C. auris cases.

Conclusion: Multiple introductions and putative transmission of C. auris have been observed in Victoria, resolved through the combined analysis of genomic and epidemiological data. Vigilant screening and isolation of patients hospitalised overseas is required to prevent further introduction to local healthcare facilities.

Barriers to High Immunisation Coverage in Perth’s Aboriginal Children: a Midwives Study

Authors: Ms Rebecca Carman1, Dr Lesley Andrew1, Professor Amanda Devine1

Affiliations: 1Edith Cowan University, Perth, Australia

Abstract:
Background: Aboriginal children living in Perth, Western Australia experience low immunisation coverage compared to the national target. Where this occurs, there is a heightened risk of disease outbreak and potential for reduced life-expectancy. Midwives within the hospital setting are a trusted source of evidence-based information; their scope of practice ensures that they are well positioned to generate vaccine demand through early parental engagement. As a result of this critical rapport, and in an attempt to identify factors which may serve to increase immunisation coverage within this population and location, a study exploring the behavioural attributes of midwives was undertaken in 2018.

Methods: A purpose-designed survey, based on theory was distributed to 80 midwives working in two public hospitals in Perth that provide maternity services to a high proportion of Aboriginal women. In addition, three semi-structured interviews were conducted concurrently on key informants via a mixed-methods approach.

Results: Preliminary survey results indicated that 85% of midwives were unaware of the low immunisation coverage in Perth’s Aboriginal children; 38% reported some concern over the efficacy of vaccines, 81% felt there was inadequate immunisation content within their undergraduate degree, while 48% do not discuss childhood immunisations with parents prior to discharge. Further statistical analysis is planned. Key barriers identified in the interviews were immunisation education and awareness.

Conclusion: A lack of awareness of the rates, coupled with insufficient immunisation discharge education and an ambivalence concerning vaccine efficacy appear to be hampering sustainable immunisation coverage improvements in Aboriginal children living in metropolitan Perth.
An introduction to Australia’s first National Microbial Genomics Framework

Authors: Ms Amy Black¹, Tuyet Hoang¹, Ms Sandra Gebbie¹

Affiliations: ¹Australian Government Department of Health, Canberra, Australia

Abstract:
The first Australian National Microbial Genomics Framework presents a collaborative commitment to integrating microbial genomics into the Australian laboratory and public health systems. Microbial genomics is revolutionising the diagnosis, surveillance and control of communicable diseases. It reveals at the highest possible resolution, the identity and ancestry of a pathogen, the way in which it infects humans and how it evades both the immune system and antibiotic treatment.

Microbial genomics can contribute to the detection of pathogens and provide high resolution typing and characterisation data for the identification of clusters of transmission for communicable disease surveillance and outbreak investigation. Globally, the use of microbial genomics is increasing rapidly, driven by accessible and advanced sequencing technologies and efficient bioinformatics data analysis.

The introduction and implementation of microbial genomics in Australian laboratories has been sporadic, with varying capability and capacity across jurisdictions. The framework was developed by the Australian Government, in close consultation with states and territories, to provide a nationally consistent and strategic view for integrating microbial genomics in the Australian public health system and seeks to highlight key policy issues and challenges.

This framework provides guidance for the development and implementation of microbial genomic related policies, strategies, actions and services and is directed at policy and decision-makers at national, state and territory and health service levels. It is designed to drive national effort on agreed strategic priorities and will evolve and adapt to the advancing of technology and practices to ensure that Australia stays at the forefront of this innovative public health practice.

Seasonal influenza vaccination for children at increased risk: does policy meet practice?

Authors: Ms Jane Tuckerman¹, A/Prof Nigel Crawford², Prof Helen Marshall³

Affiliations: ¹University Of Adelaide & Robinson Research Institute, North Adelaide, Australia, ²Murdoch Children’s Research Institute (MCRI) & Department of General Medicine, Royal Children’s Hospital, Melbourne, Australia, ³University Of Adelaide, Robinson Research Institute & Vaccinology and Immunology Research Trials Unit, Women’s and Children’s Hospital, North Adelaide, Australia

Abstract:
Background: Understanding the influenza vaccination practices of medical practitioners caring for children with special risk medical conditions (SRMC) is imperative for determining strategies to improve uptake.

Methods: A Cross-sectional survey was undertaken with paediatric specialists and general practitioners who were the treating medical practitioners (MPs) of children with confirmed SRMCs to determine influenza vaccination practices. Multivariable regression examined characteristics associated with providing a recommendation.

Results: 190 participants had complete data. While 98% were aware of the recommendation, only 38.4% reported they ‘always’ routinely recommended influenza vaccine and a moderate number (52.6%) were confident in understanding all of the conditions considered ‘medically at risk’, less (19.5%) were very confident. MPs were more likely to provide a recommendation always or mostly if they received the vaccine themselves yearly (aOR 4.13, CI 1.09-15.69), had confidence in understanding all of the conditions considered ‘medically at risk’ (aOR 1.77, CI 0.96-3.24) and perceived ownership of the responsibility to provide the recommendation (aOR 7.55, CI 1.71-33.30). Those practicing in a regional location were less likely to provide a recommendation (aOR 0.25 CI 0.09-0.70).

Conclusions: Improving MPs knowledge through reminders and access to consistent and concise information about what constitutes a SRMC is required. Increasing MPs engagement in the influenza vaccination program could also provide a sense of responsibility fostering provider endorsement.
Household item sharing and transmission of staphylococcus aureus in Australian community setting

Authors: Ms Xi Cook\textsuperscript{1}, Ms Christine Parrot\textsuperscript{1}, Dr Elyse Dunn\textsuperscript{1}, Dr Gillian Wood\textsuperscript{1}, Prof Geoffrey Coombs\textsuperscript{2}, Prof Paul Johnson\textsuperscript{3}, Prof Catherine Bennett\textsuperscript{1}

Affiliations: \textsuperscript{1}Deakin University, Centre for Population Health Research, Burwood, Australia, \textsuperscript{2}Antimicrobial Resistance and Infection Control Research Laboratory, Murdoch University, Perth, Australia, \textsuperscript{3}Austin Health, University of Melbourne, Parkville, Australia

Abstract:

Aim: To compare common household item sharing and evidence of transmission in households with community-onset S. aureus infections.

Methods: The Community-Onset Staphylococcus aureus Household Cohort study investigated households in Melbourne, Australia (2008-2012) with laboratory-confirmed S. aureus infections (291 index cases, 446 household contacts). For shared households (204), S. aureus colonisation (nasal and axilla) and self-reported data on sharing of 13 common household items were collected quarterly. Transmission events were defined as two individuals sharing strains (colonising or infecting) matched on PFGE. Multilevel mixed-effects logistic regression was used to model transmission events and household sharing.

Results: S. aureus transmission occurred in 137 households (67.2%) and 393/881 pairs (44.6%); most often in couples (75.4% 95%CI 66.8-82.8) and between parent and child (51.5% 95%CI 46.3-56.7). Hand towel was the only item associated with transmission adjusted for baseline colonisation status, relationship, index case and duration of pairs present in the study (OR: 3.4 95%CI 1.2-10.0 p=0.026). Methicillin resistant S. aureus (MRSA) transmission was less frequent, seen in only 17/61 households with MRSA present (27.9%), and in 45/292 of pairs (15.4%). MRSA transmission was most common between parent and child (55.6% 95%CI 41.1-70.1) or within couples (17.8% 95%CI 6.6-29.0), and independently associated with sharing a hair brush (OR: 4.5 95%CI 1.2-17.8, p=0.03). Clustering effects (p<0.0001) suggest high correlation among transmission events within households.

Conclusions: We cannot confirm items as vehicles for transmission or simply markers of other interactions, however these data do identify sharing behaviors and relationships that are at greater risk of transmission.
Thursday 21 November 2019

Poster Presentations – P2
The Gallery, Level 1, 12:45pm – 1:00pm

P2.001 - Meningococcal C Carriage survey, Western Division, Fiji:2018

Authors: Mr Isireli Koroioku, Miss Mere Taufa, Ms Jokaveti Tadrau, Mr Peni Dovi, Ms Rejeli Yuniduva, Dr Jimaima Kailawadoko, Dr Daniel Faktaufon, Mrs Talica Cabemaiwai, Mr Sakiusa Baleivanualala, Dr Susana Nakalevu, Dr Devina Nand, Dr Mike Kama, Dr Aalisha Sahu Khan, Mr Samuel McOwen

Affiliations: 1Fiji Center for Communicable Diseases Control, Suva, Fiji, 2Ministry of Health & Medical Services, Suva, Fiji

Abstract:
Background: Antibiotic sensitivity testing of cases identified rifampicin resistance in one school-aged case. The identification of Neisseria Meningitidis(NM) rifampicin resistance is a public health concern in Fiji. After resistance to ciprofloxacin was widely identified in N. meningitidis isolates from 2017-18. Rifampicin became the primary antibiotic of choice for chemoprophylaxis of close contacts, and for use as MDA in institutional outbreak settings. Ceftriaxone is not widely available in Fiji.

Method: A carriage-survey of the resistant case’s contact and school-aged children conducted in a division in Fiji using oral swabs. Participants were sampled pragmatically from schools near the case’s residence and were logistically viable for sample collection and transportation. Initial sample preparation was conducted by the Fiji Centre for Communicable Disease Control and samples were sent to the Microbiological Diagnostic Unit Public Health Laboratory for sensitivity testing.

Results: Using a pragmatic approach 220 samples were collected. NM was identified in 15 (6.8%) of samples. Serotyping identified carriage of serotypes B(n=6), C(n=3) and W(n=1). Five samples could not be serotyped. Rifampicin resistance was not identified in any samples. The three serotype C samples were found to show ‘less susceptible’ resistance patterns to Ciprofloxacin.

Conclusion: This carriage survey provides an example of using available resources in a timely manner to conduct operational research to answer a pressing public health question. Ongoing sensitivity testing for cases of meningococcal in Fiji is of vital importance. These findings support the continued use of rifampicin as the first line chemoprophylactic contact management treatment for meningococcal disease in Fiji.

P2.002 - Meningococcal outbreak investigation and risk assessment in a school in Fiji: 2018

Authors: Mr Isireli Koroituku, Ms Mere Taufa, Miss Jokaveti Tadrau, Ms Rejeli Yuniduva, Mr Peni Dovi, Dr Jimaima Kailawadoko, Dr Daniel Faktaufon, Mrs Silvia Matanitobua, Mrs Talica Cabemaiwai, Ms Lusiana Waqailiti, Dr Devina Nand, Dr Mike Kama, Dr Josaia Tiko, Dr Aalisha Sahu Khan, Mr Samuel McOwen

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Abstract:
Introduction: Meningococcal disease incidence has increased in Fiji over the past decade. High-school-aged children are a high-risk group for transmission. In Fiji, Boarding schools are common, and overcrowding is common providing settings that favor outbreaks of meningococcal disease in this high-risk group. In March 2018, an outbreak of the meningococcal disease was identified amongst students who attended a boarding school, and their contacts in Eastern division. After identification of the outbreak, an investigation and response were initiated by the Fiji Centre for Communicable Disease Control.

Method: The investigation and response included retrospectively analyzing disease data, interviewing cases, contact tracing, conducting an environmental health investigation, directly observed treatment short course chemoprophylaxis and risk communication activities.

Findings: Nine confirmed cases of Meningococcal C were identified in boarding school students over a seven month period. A transmission tree created from case interviews and contract tracing provided plausible epidemiological evidence of an association between all cases. The environmental investigation found overcrowding in dorms and no handwashing stations for boarding students. School-wide chemoprophylaxis (four dose rifampicin course) for boarders attained 93% coverage. Household and family contact chemoprophylaxis was given to all identified contacts. A health awareness presentation covered causative agent, mode of transmission, signs and symptoms and preventative measures to be undertaken for meningococcal disease.

Conclusion: This outbreak response details a comprehensive investigation to an institutional outbreak of meningococcal C in Fiji. Using the holistic approach the investigation was able to identify the scale of the outbreak, risks and mitigation strategies and public health interventions.
P2.003 - Lost opportunities for paediatric influenza vaccination: a cross-sectional study

Authors: Ms Samantha Carlson¹, Dr Helen Quinn³, Professor Kristine Macartney³, Professor Julie Leask⁴

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Abstract:

Background: More children are hospitalised in Australia due to influenza than any other vaccine preventable disease, with approximately 1700 children aged <15 years hospitalised annually. Most of these children have no history of influenza vaccination. Our objective was to understand attitudes about and access to influenza vaccination, experienced by those most affected by the disease.

Methods: Parents of children hospitalised for laboratory-confirmed influenza in 2018 were invited to participate in an online survey. The survey was developed according to previous qualitative interviews, published literature, and the Capability, Opportunity, Motivation, Behaviour (COM-B) theoretical model.

Results: Of the 69 children aged 26 months, only 28% of their parents recalled receiving a health care provider (HCP) recommendation to vaccinate, despite 81% having taken their child to a general practitioner at least twice in the previous 12 months. Few (12%) were vaccinated prior to hospitalisation. Overall, parents did not report difficulties in accessing influenza vaccination, but parents of vaccinated children reported easier access. Many parents (69%, 41/59) had some degree of hesitancy about influenza vaccination. There was no significant difference between the median scores of specific influenza vaccine concerns between parents of vaccinated and unvaccinated children. One third (32%, 21/65) were undecided about future influenza vaccination – many stated a discussion with a HCP was required.

Conclusion: Parents have concerns about influenza vaccine safety and efficacy, even after witnessing the severity of the disease in their hospitalised children. It is important for HCPs to clarify concerns and strongly recommend influenza vaccination to all patients.

P2.004 - Prioritizing influenza vaccine allocation during a pandemic – a review

Authors: Dr Frank Beard⁶, Dr James Fielding⁴, Prof Angus Dawson¹, Prof Kristine Macartney³, Prof Jodie McVernon⁵, A/Prof Peter Massey⁵, Dr Rob Moss⁴, Prof Kanta Subbarao¹,², A/Prof Sheena Sullivan¹,²

Affiliations: ¹Who Collaborating Centre For Reference And Research On Influenza, Melbourne, Australia, ²National Centre for Immunisation Research and Surveillance, Sydney, Australia, ³Victorian Infectious Diseases Reference Laboratory, Melbourne, Australia, ⁴Sydney Health Ethics, University of Sydney, Sydney, Australia, ⁵Peter Doherty Institute for Infection and Immunity, Melbourne, Australia, ⁶Hunter New England Population Health, Newcastle, Australia

Abstract:

Background: In future influenza pandemic, vaccination will be key to controlling transmission, morbidity and mortality. However, pandemic vaccine development takes several months and will become available in batches, thereby requiring staged allocation. The World Health Organization (WHO) recommends that nations establish goals for pandemic influenza vaccine use and identify priority groups for vaccination. The purpose of this study was to review pandemic plans to inform vaccine prioritisation for Australia.

Methods: We reviewed current national pandemic plans for Organisation for Economic Co-operation and Development (OECD) countries. Secondly, we conducted semi-structured interviews with representatives from the United States, Canada, New Zealand, the United Kingdom, the WHO and the European Centres for Disease Control to clarify the process of creating/updating those plans.

Results: Only 12 of 34 possibly relevant pandemic plans could be retrieved, and only six had been published or updated (in English) since 2009. Updated plans recommended a flexible vaccine prioritisation strategy that responds to the epidemiology of the pandemic; this was also a key point raised during interviews. Groups prioritised for vaccine tended to be those at high risk of death and complications from influenza infection, including Indigenous populations, pregnant women, age-defined risk groups (e.g. children), and individuals working in high-risk settings (e.g. health care workers and essential service providers). Interviewees emphasized the importance of clear communication to ensure acceptability of any prioritisation plan among the populace.

Conclusion: The availability of updated plans that reflect the agreed values of the country are a valuable resource for informing pandemic preparedness.
P2.005 - ARF/RHD in a regional area of NSW: striving to do better

Authors: Ms Julie Kohlhaagen¹, Ms Helen Stevens¹, Mr Peter Massey¹, Miss Kirsten Williamson¹

Affiliations: ¹Hunter New England Population Health, Newcastle, Australia

Abstract:
Background: Hunter New England Local Health District (HNELHD) has higher rates of Acute Rheumatic Fever (ARF) and Rheumatic Heart Disease (RHD) than most Local Health Districts (LHDs) in New South Wales (NSW). The majority of HNELHD cases are in non-metropolitan areas, including a cluster of cases in a small rural community. ARF/RHD disproportionately affects disadvantaged populations, especially Aboriginal families.

There is opportunity to prevent further cases, improve health outcomes, and reduce inequity underlying ARF/RHD through provision of coordinated care focused on preventative medicine, clinical excellence, family and community support, cultural competence, partnership building and operational research.

Methods: Epidemiological and service reviews were conducted.

Findings: Since ARF/RHD became notifiable (2015), HNELHD has had 15 ARF and 11 RHD cases reported but this is likely an undercount of the true burden. The mean age at ARF notification was 11 years old (range: 3-27); the mean age at RHD diagnosis was 18 years old (range: 4 to 34). The youngest child requiring valve repair from ARF/RHD was 6 years. ARF/RHD notification rates in HNELHD are higher than the NSW average (0.6 vs. 0.2 cases per 100,000 per year for ARF, and 0.4 vs. 0.1 cases per 100,000 per year for RHD, respectively) and appear to be increasing.

Conclusions: ARF/RHD is an uncommon but important health challenge in HNE. Cultural governance combined with increasing commitment by health services/systems in developing primordial, primary and secondary preventative programs with Aboriginal communities is essential in working towards excellence in long-term care of children and adults with ARF/RHD.

P2.006 - Going viral: social media and public health messaging in NSW

Authors: Ms Meredith Wickens¹, Dr Sean Tobin¹, Dr Vicky Sheppeard¹

Affiliations: ¹Health Protection NSW, St Leonards, Australia

Abstract:
Context: Effective public health messaging, whether related to health promotion or urgent health alerts, requires timely directing of information to those who most need to receive it. Used appropriately social media is a particularly useful tool, especially when used in conjunction with more traditional media and communication methods.

In recent years, NSW Health has increasingly incorporated social media into our communications toolkit, with a well-established presence on Facebook and Twitter. Within the vaccine preventable diseases portfolio social media use has been ramped up in the past 18 months, with expansion onto different platforms, development of more target audience specific content, and wider application of its use into areas such as urgent health alerts.

Process: We developed and ran the first NSW Health campaign using Snapchat (for meningococcal disease), enlisted social media in distribution of measles alerts, and developed a series of targeted campaigns combining social media and more traditional media platforms.

Analysis: Evaluation of campaigns was undertaken using a combination of communications (eg: click-through) and disease related (eg: vaccine distribution) data. We collated and assessed feedback and queries received on social media (moderation).

Outcomes: Snapchat performed well with the youth audience, delivering 3x the expected impressions. Facebook remains a powerful platform, particularly when content is audience specific, and can be more cost effective than other media. Evaluation outcomes and social media moderation content is being used to inform future campaigns, and further develop public facing resources and communications. We are investigating additional platforms to further increase our targeting and reach.

P2.007 - The incidence of leprosy in Australia is on the rise

Authors: Dr Harrison Edwards¹

Affiliations: ¹University Of Queensland, Herston, Australia

Abstract:
Background: Leprosy is a notifiable infection of skin and nerves caused primarily by Mycobacterium leprae. In Australia, leprosy occurs mainly in indigenous populations in northern Australia and immigrants from endemic regions of the world. Treatment lasts many months, and the disease carries significant stigma.

211,009 incident cases of leprosy were reported globally in 2017. Multidrug treatment (MDT) has been highly successful in decreasing the incidence, but that trend has reversed in Australia. Although leprosy is endemic in many parts of the world, the goal in Australia should be complete eradication.

Methods: The Australian National Notifiable Disease Surveillance System was examined, and incident cases of leprosy were grouped in four-year periods for analysis.
Results: The data show that 1991-1994, the beginning of reporting, had the highest incidence with 58 cases. In the next four-year period, 1995-1998, the incidence was 36 cases. By 1999-2002, the number decreased to 23. Subsequently, the incidence has risen every four-year period: in 2003-2006, 32 cases were reported; 2007-2010, 40 cases; 2011-2014, 41 cases; 2015-2018, 50 cases. Incidence has continually risen and now has more than doubled since 2002.

Conclusion: Communicable disease control is a process initiated by data collection which signals the emergence or re-emergence of communicable diseases. Vigilance is important to identify trends. Globally, leprosy incidence has been greatly reduced since the WHO-MDT initiative in 1995, but is increasing in select Australian at-risk populations. Surveillance, treatment protocols, education and support for local primary care services are essential in ensuring this disease is eradicated in Australia.

P2.008 - Donovanosis, a sexually transmitted skin disease: gone, but let’s not forget

Authors: Dr Harrison Edwards

Affiliations: ¹University Of Queensland, Herston, Australia

Abstract:

Background: Donovanosis (granuloma inguinale) is a notifiable disease caused by Klebsiella granulomatis, characterised by granulomatous genital ulcers. In Australia, it was found almost exclusively in indigenous populations in northern Australia, and it has been eliminated nationwide since 2014. Persisting endemic regions of the world include Papua New Guinea, Southeast India, Southern Africa and Central and South America.

Methods: The Australian National Notifiable Disease Surveillance System was examined, and incident cases of donovanosis were grouped in four-year periods for analysis.

Results: The data show that 1991-1994, the beginning of reporting, had the highest incidence with 346 cases. In the next four-year period, 1995-1998, incidence was 237 cases. By 1999-2002, the number decreased to 88. The decrease continued in every four-year period: in 2003-2006, 45 cases were reported; 2007-2010, 7 cases; 2011-2013, 2 cases; and 2014-2018, zero cases.

Conclusion: Study of successful eradication campaigns can inform implementation of similar efforts in other endemic areas. In Australia, the position of donovanosis project officer was created in 1997 to manage surveillance, diagnosis and treatment in Northern Territory, South Australia and Western Australia. In 2001, the National Donovanosis Advisory Eradication Committee was established to develop and provide surveillance, treatment protocols, education and support for local primary care services. This multidisciplinary model involving both government and nongovernment agencies with a centralised expert liaison with primary carers resulted in an effective model for the elimination of the disease, defined as three years with zero incidence. It created a pathway that may be helpful for other endemic regions.

P2.009 - The NSW Health CPE surveillance program – Early insights and future directions

Authors: Dr Renee Tuddenham, Dr Elizabeth Ellis, Dr Tara Smith

Affiliations: ¹Health Protection NSW, St Leondards, Australia

Abstract:

Context: Carbapenemase-producing Enterobacterales (CPE) can cause severe, often untreatable infections, primarily in people who are hospitalised with other conditions. While CPE is common in many parts of the world, Australian patients appear to mainly acquire CPE overseas. In NSW, Health Protection NSW (HPNSW) and the Clinical Excellence Commission (CEC) have developed a surveillance system for CPE to understand its epidemiology, detect clusters and outbreaks early, and support facilities with prompt investigation and control.

Process: CPE became notifiable by laboratories in 2019. During the first months of surveillance, minimal data available to the laboratory was collected on each case and entered into a bespoke database. Patients who were apparently clustered, very young or facilities with little CPE experience were further investigated to identify risks factors and ensure control measures were in place.

Analysis: Routinely collected notification data do not capture sufficient information to understand risks for CPE. Enhancements have been made to improve the breadth of data collected on each case, including carriage status and transmission risk factors. Whole genome sequencing of each isolate has begun.

Outcomes: From March to May 2019 80 notifications from 72 cases were received, including one outbreak. The enhanced surveillance will likely provide useful information about local epidemiology and outbreak management. This surveillance system will inform future directions of the NSW MRO surveillance and control.
P2.010 - The status of antimicrobial resistance in Campylobacter jejuni and coli in Australia

Authors: Dr Rhiannon Wallace1, Dr Dieter Bulach2,3, Dr Amy Jennison4, Mrs Liana Varrone5, Mr Angus McLure4, Dr Mary Valcanis6, Dr Benjamin Polkinghorne6, Dr Kathryn Glass7, Dr Martyn Kirk7

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Abstract:

Aim: The aim of this study was to investigate the prevalence of resistance in Campylobacter coli and Campylobacter jejuni to aminoglycoside, macrolide, fluoroquinolone, beta-lactam and tetracycline antibiotics using phenotypic susceptibility testing and whole genome sequencing.

Methods: C. coli and C. jejuni (n = 164) isolates were collected from patients with campylobacteriosis from all eight Australian states and territories and tested for susceptibility to six antimicrobials using E-test and EUCAST methodology. Isolates were also sequenced using the Illumina NextSeq platform. Short-reads and de novo assemblies were used to produce draft genomes using MEGAHIT and comparative genomic analysis was performed using the Nullarbor pipeline. Draft genomes were screened for known antimicrobial resistance genes using ResFinder and sub-species classification was determined using multilocus sequence typing (MLST) using the Campylobacter jejuni/coli typing scheme (PubMLST).

Results: MLST indicated significant diversity among isolates with 13 and 43 sequence types (STs) identified for C. coli and C. jejuni, respectively; one new ST was identified for C. coli and four new STs for C. jejuni. The most common STs observed were C. coli ST 1181 and C. jejuni ST 50. Phenotypically, 14.0, 20.1, 1.8 and 14.6% of isolates were resistant to ampicillin, ciprofloxacin, erythromycin and tetracycline, respectively. Six isolates (3.7%) were resistant to three or more antibiotics and one isolate was resistant to four antibiotics including ampicillin, ciprofloxacin, erythromycin and tetracycline.

Conclusion: The results highlight that 20.1% of isolates were resistant to ciprofloxacin, but the majority of isolates (98.2%) were susceptible to erythromycin, the drug of choice for treating Campylobacter infection.

P2.011 - Medical record review of influenza activity and management in emergency departments (ED).

Authors: Ms Robin Gilmour1, Miss LJ Garcia1, Dr Anthea Katelaris1, Dr Sean Tobin1, Dr Vicky Sheppard1

Affiliations: 1Health Protection NSW, St Leonards, Australia

Abstract:

Background: In 2019 (up to and including March) the ED presentation rate for Respiratory illnesses, fever and unspecified infections was 14.7% higher than for the same period in 2018. Presentations which fall under this category have historically been used an indicator of influenza activity in NSW. This category includes a wide variety of respiratory infections including influenza and other conditions such as rhinovirus, bronchiolitis, and community acquired pneumonia.

The unseasonal increase in unplanned respiratory presentations to emergency departments together with an unusually high number of cases of influenza notified in NSW prompted further investigation into the testing and clinical course through ED of patients classified in the Respiratory illnesses, fever and unspecified infections category.

Methods: A targeted medical record audit was conducted on a random sample of patients presenting to EDs in the Respiratory illnesses, fever and unspecified infections category in 3 local health districts in NSW.

Results: A total of 302 patient ED events and medical records were reviewed by LHD PHUs. Of these 24% (73/302) of cases were included for audit. Of the 302 cases there were 171 (56.5%) ILI, 97 (32.1%) with fever and unspecified infections and 34 (11.2%) with fever and respiratory illness. The unseasonal increase in unplanned respiratory presentations to emergency departments together with an unusually high number of cases of influenza notified in NSW prompted further investigation into the testing and clinical course through ED of patients classified in the Respiratory illnesses, fever and unspecified infections category.

Conclusion: Management of people presenting with ILI symptoms to EDS is varied. Testing and treatment protocols are needed to assist clinicians implement best practice management.

P2.012 - Beyond Secondary Prevention of Rheumatic Heart Disease

Authors: Dr Kate Hardie1, Ms Jessica de Dassel1

Affiliations: 1NT Centre For Disease Control, Darwin, Australia

Abstract:

RHD control efforts in Australia have to date focused on secondary prevention of ARF and progression to RHD by recommending long-acting benzathine penicillin G injections every 28 days for a minimum of 10 years.

For the first time, NT data is presented describing the proportion of patients being diagnosed with RHD without a previous diagnosis of ARF and without the option of having accessed BPG preventive treatment.

These results highlight the absolute necessity of taking action on the social and environmental determinants of health in order to eliminate RHD in the NT and the rest of Australia.
P2.013 - Mumps surveillance in NSW - where are we up to?

Authors: Rachel Latta¹, Peter Massey¹, Meredith Wickens²

Affiliations: ¹Hunter New England Local Health District, Newcastle, Australia, ²Health Protection NSW, St Leonards, Australia

Abstract:

Background: Mumps in New South Wales (NSW) is uncommon, notification rate <1.0 per 100,000, 197 notifications in NSW 2017-2018. During 2017 more than double the number of notifications were received. There has been a recent resurgence of notifications in Australia, similar to other highly-vaccinated countries, which disproportionately affects teenagers, young adults, and Aboriginal people. Waning immunity or lower vaccine effectiveness may be occurring. Previous review shows variability in mumps follow up and surveillance data completeness.

Interpreting mumps laboratory results in highly-vaccinated populations is complex, and affected by timing of testing, choice of laboratory methods and previous vaccinations. This study examines current mumps surveillance across public health units (PHUs) in NSW and will be used to inform NSW approaches to mumps surveillance.

Methods: A retrospective audit of 2017-2018 mumps notifications in NSW Notifiable Conditions Information Management System (NCIMS). Data includes demographics; laboratory results; vaccination history; recorded clinical symptoms; and other relevant epidemiological data. Summary statistics will be used to describe the data, which will be compared to state control guidelines to highlight gaps and differences.

Results: Initial review of 20 mumps notifications showed variability in application of the case definition. The results of the full study will be presented at the CDC conference.

Conclusion: It is hypothesised the study will highlight variability in case investigation and data completeness in NSW. Importantly the study may indicate whether changes to the investigation and data collection of mumps notifications are required.

P2.014 - Shot in the dark: process and purpose in protracted vaccine cold-chain breaches

Authors: Dr Sarah Khanlari¹, Dr Zeina Najjar¹, Claire Pearson¹, Dr Emma Quinn¹, Travers Johnstone¹, Dr Dunja Vekic¹, Dr Elaine Tennant¹, Dr Isis Maitland-Scott¹, Dr Shireen Durrani¹, Dr Leena Gupta¹

Affiliations: ¹Sydney Local Health District Public Health Unit, Camperdown, Australia

Abstract:

Background: Cold-chain maintenance is an essential consideration for the National Immunisation Program, with its application standardised in the ‘Strive for 5’ guidelines. Cold-chain breaches (CCB) are reportable to Public Health Units (PHU). We describe a recent PHU investigation of a protracted CCB, and the processes involved in issue identification, risk characterisation and action.

Process and outcomes: The investigation determined irregular temperature monitoring and inadequate domestic refrigeration over a prolonged time period. Vaccine packaging demonstrated signs of condensation suggestive of significant temperature excursions. Some vaccines were expired.

There is limited evidence to guide best public health practice following protracted CCBs, in particular determining a justifiable timeframe in which to recommend revaccination. If available, General Practice accreditation against vaccine storage standards may present one such point in time. Characterising the risk associated with receiving compromised vaccines should account for: the broader context in which immunisation programs have evolved, changing vaccine storage standards, a complex regulation and governance environment; and shifting expectations of documentation and data accessibility. Furthermore, the potency of each vaccine is differentially affected by temperature excursions, which may allow advice to revaccinate with specific vaccines. In practice however, a range of patient, population and risk-perceptive factors limit prioritising vaccines.

Affected patients, who could be identified through the Australian Immunisation Register, were contacted in phases based on risk categories, with revaccination recommended.

Conclusions: Protracted CCBs present numerous process issues including uncertainty in risk-benefit analyses, accessibility and accuracy of vaccine records, application of untested legislation and maintaining confidence in immunisation programs.
P2.015 - Visualising year to year severity of influenza-like illness
Authors: Michelle Butler¹, Craig Dalton¹,²,³, Sandra Carlson¹,², David Durrheim¹,²,³
Affiliations: ¹Hunter New England Population Health, Wallsend, Australia, ²Hunter Medical Research Institute, Lambton, Australia, ³Newcastle University, Newcastle, Australia

Abstract: Background: The WHO (World Health Organisation)'s communication of the severity of the 2009 H1N1 influenza pandemic was controversial and led to confusion. This highlighted the need for a shared conceptual model that allows for the rapid severity assessment of both seasonal and pandemic influenza.

The impact of influenza at population level is monitored by a range of surveillance systems. However, it is often difficult to describe the severity of influenza seasons and compare them with previous seasons. Is it highly transmissible? Does it have low transmissibility but high morbidity? A shared conceptual model would assist public health authorities and researchers to communicate and explore variations in influenza severity, and respond to and adapt control measures and communication during a pandemic.

Methods: Flutracking is an online surveillance program that monitors influenza-like illness (ILI) weekly across Australia’s influenza season from over 40,000 participants. Using WHO Pandemic Influenza Severity Assessment definitions we analysed the Flutracking data from Australia’s most populous state, New South Wales, between 2009 and 2018 inclusive, for transmissibility and seriousness to create three different data visualisations by age group and year.

Results: The visualisations produced an intuitive insight into the relative severity of influenza seasons. The visualisations overcome some biases and misperceptions regarding the severity of a particular influenza season. For example, younger participants having higher transmissibility and older participants having lower transmissibility but more serious illness.

Conclusion: Using the Flutracking data, the visualisations succinctly illustrated the relationships between transmissibility and severity between and within the age-cohorts across time.

P2.016 - Challenges in latent TB screening in primary care in Australia: mobilizing partnerships
Authors: Dr Madhumati Chatterji¹, Prof Guy Marks¹, Prof Teng Liaw², Prof Mieke Van Driel¹
Affiliations: ¹University Of Queensland, Herston, Australia, ²University Of New South Wales, Sydney, Australia

Abstract: A global public health problem with approximately 10 million cases and 1.6 million deaths annually, tuberculosis (TB) kills more people than HIV and malaria combined. In low-incidence countries such as Australia most cases of active TB result from progression of latent TB infection (LTBI). Estimated to infect about one-third of the global population, the at-risk population for LTBI in Australia largely includes people born overseas in high TB burden countries, immune compromised persons and Aboriginal and Torres Strait Islander people. While Australia is in an enviable position with approximately 6 new cases of active TB per 100,000 population annually, there is no room for complacency. Innovative strategies in preventing emergence of active TB from its latent stage is a strong recommendation in policy statements of low TB burden countries, to respond to WHO’s target for TB elimination (<1 case per million population by 2050) and United Nation’s United to End TB high level meeting in September 2018.

My research explores a model of care for LTBI screening and treatment in primary care, a timely, topical and relevant area of research for Australia. The aim of my research is to develop a conceptual framework for LTBI screening and treatment in primary care using qualitative methods of co-design, and designing a pilot to test the conceptual framework. In my presentation I shall present the challenges in the implementation of LTBI screening and treatment in primary care in Australia and the need for mobilizing partnerships across primary and secondary care and public health.

P2.017 - Western Sydney: Hot Spot for Enteric Fever
Authors: Dr Ling Lim¹, Penelope Clark¹, Moniek Borsoszky¹, Jennifer Paterson¹, Jennifer Lampard¹, Alison Mills¹, Sophie Norton¹, Keira Glasgow², Dr Venkata Lavu¹,², Dr Shopna Bag¹,²
Affiliations: ¹Western Sydney Local Health District, , Australia, ²NSW Ministry of Health, , Australia, ³Westmead Hospital, , Australia, ⁴University of Sydney, , Australia

Abstract: Background: Over the past decade, enteric fever cases within Western Sydney Local Health District (WSLHD) have increased by 50%, double the rate of population growth (25%).

Methods: Analysis of WSLHD surveillance data and Public Health documentation.
**Results:** Between 1 Dec 2018 and 31 May 2019, 23 typhoid and 17 paratyphoid cases were notified in WSLHD, more than half of the total cases in NSW. All cases had an overseas source with 90% from the Indian subcontinent (33 India, 2 Pakistan, 1 Nepal) related to visiting friends and relatives (VFR). Case ages ranged from 4 to 54 years with 48% in children. 78% of cases were hospitalised for enteric fevers with an average length of stay of 7 days. Cases were managed according to the NSW Health Typhoid/Paratyphoid public health guidelines. An average of 19 days (range 4-60 days), from notification to case closure, was required to manage cases and their contacts which included three cases in high risk occupations. Whilst the majority of the cases were in first or second generation migrants, only three cases required interpreter services. Amongst the 23 typhoid cases, 3 cases reported prior typhoid immunisation (>=3 years ago); most were either unaware of the vaccine availability or had not considered immunisation prior to travel.

**Conclusion:** Measures to mitigate the increasing demand on healthcare services include targeting VFR travellers to the Indian subcontinent, with culturally appropriate communication of risks for enteric fever and measures to prevent infection including food and water hygiene and immunisation against typhoid.

**P2.018 - Collaborative effort to provide a public health response in a disadvantaged community**

**Authors:** Ms Angela Russell¹, Ms Nicola Mulcahy¹

**Affiliations:** ¹Communicable Diseases Prevention Unit, Department of Health, Hobart, Australia

**Abstract:**

**Context:** People with considerable socio-economic disadvantage face barriers to accessing health care. In response to a notifiable disease, Public Health Units may find it difficult to facilitate the necessary contact management, and overcome barriers to providing high quality, equitable, accessible and affordable care.

**Process:** We describe the adoption of a place-based public health response to deliver high quality care to people of socio-economic disadvantage in response to a case of Invasive Meningococcal Disease (IMD). We coordinated a multidisciplinary effort that included the Public Health Unit, the manager of the residential facility and a non-government organisation that provides health care services to people of socio-economic disadvantage.

**Outcomes:** The residential facility accommodated people with a range of health issues associated with homelessness, including mental ill health and low literacy. 36 people were identified as household-like contacts of the case, requiring clearance antibiotics and immunisation. With all three organisations working together, 34 people provided informed consent and were given prophylaxis within 24 hours of the initial confirmation of the case. No secondary cases of IMD occurred in this cohort.

**Conclusion:** This is an example of a successful collaborative effort that overcame barriers to the delivery of high quality health care to people with considerable socio-economic disadvantage. The public health response provided equitable care and successfully mitigated the risk of secondary cases of IMD amongst a group of high-risk contacts.
3A – Vaccine preventable diseases
Federation Ballroom Nth

Maternal characteristics and pregnancy outcomes associated with pertussis and influenza

Authors: Dr Jane Frawley, Professor Peter McIntyre, Dr Wengiang He, Associate Professor Heather Gidding, Dr Lisa McCallum, Professor Elizabeth Sullivan, Professor Andrew Haven, Associate Professor Bette Liu

Affiliations: 1University Of Technology Sydney, Ultimo, Australia, 2University of Sydney, Sydney, Australia, 3University of New South Wales, Randwick, Australia, 4NSW Health, Newcastle, Australia, 5University of Newcastle, Newcastle, Australia

Abstract:
Aim: While there is a growing body of evidence about the impact of influenza infection during pregnancy, much less is known about pertussis. We aimed to 1) determine the proportion of pregnant women notified with influenza and pertussis during pregnancy; and 2) examine a range of maternal and infant outcomes for women diagnosed with pertussis or influenza during pregnancy compared to women without such a diagnosis.

Methods: We linked three NSW population-based data-sets (Perinatal Data Collection, Admitted Patient Data Collection, Notifiable Conditions Information Management System) from 2001-2016. Logistic regression was used to examine the impact of influenza and pertussis on maternal and infant outcomes.

Results: We identified 2,850 pertussis and 925 influenza cases diagnosed during the antenatal period for 1,453,386 singleton births. Mothers with laboratory-confirmed influenza during pregnancy were significantly more likely than those without an influenza diagnosis to require induction of labour (aOR 1.21, 95% CI 1.05-1.39), have an infant born pre-term (aOR 1.18, 95% CI 1.02-1.37), or an infant requiring admission to neonatal intensive care (aOR 1.18, 95% CI 1.05-1.32). Among mothers with pertussis during pregnancy, the only adverse outcome was higher likelihood of induction of labour (aOR 1.19, 95% CI 1.09-1.29) compared to women without pertussis.

Conclusions: These findings add to our understanding of maternal and infant outcomes from influenza and provide the first population-wide examination of maternal and infant outcomes following pertussis during pregnancy. These data support the importance of maternal immunisation.

A novel approach to hepatitis A post-exposure prophylaxis in a childcare setting

Authors: Deborah Judd, Erin Ebert, Dr Bhakti Vasant

Affiliations: 1Metro South Public Health Unit, Brisbane, Australia

Abstract:
Background and methods: Hepatitis A outbreaks have been linked to childcare centres (CCC). Contacts of Hepatitis A cases in CCC have increased risk of infection, due to asymptomatic illness and rudimentary hygiene practices in children. The Metro South Public Health Unit (MSPHU) followed up two cases of asymptomatic hepatitis A infection in children attending a CCC located in an area in the lowest SEIFA Index of Disadvantage quintile. For follow up at the CCC, MSPHU developed a screening questionnaire and an infographic to assist with communication with families from culturally and linguistically diverse (CALD) backgrounds.

Hepatitis A vaccines were offered to CCC contacts over a two-day period. Prior to vaccination, education was delivered to parents using the infographic developed by MSPHU, and the screening questionnaire was administered to identify family members with symptoms suggestive of hepatitis A infection. GP referral letters and stool specimen collection jars were provided for symptomatic family members.

Results and conclusions: Of eligible children and staff, 97% (N=87/90) received a hepatitis A vaccine at the clinics. Ten people were referred to their GP and no further cases of hepatitis A associated with the CCC were identified. The infographic, screening and education were well received by the CCC and families. This tailored public health response and collaboration with the CCC may have supported high vaccine uptake in a childcare centre with a large CALD population.

Impact of a geo-targeted digital media campaign on childhood immunisation coverage.

Authors: Ms Celeste Marsh, Professor Ross M Andrews, Mr Darius Everett, Dr Masha Somi

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Abstract:
Background: The Australian Government Department of Health (DoH)’s multi-phase “Get the facts about immunisation” campaign aims to positively support parent’s vaccination decision-making by distributing evidence-based information. Residents of SA3s (Statistical Area 3) with low childhood immunisation rates received a higher frequency of digital advertisements through geo-targeting; this study assesses the impact of geo-targeting on coverage amongst 12-month-old children.
Methods: Interrupted time-series (ITS) analyses using quarterly coverage estimates published by DoH between September, 2015 and December, 2018 assessed coverage before and after campaign phases in geo-targeted zones compared with controls matched on pre-intervention trends. Regions with unreliable rates (eligible children<25, data-points with <0.8 the starting population) were excluded. Pending covariate data, multivariable linear regression will assess the influence of population-level factors on campaign effect.

Results: Of the 27 SA3s geo-targeted, four with unreliable rates were excluded. The remaining geo-targeted SA3s overall experienced a greater immediate post-campaign coverage increase (1% point) compared with 16 matched controls (0.2% point, p= 0.18). However, rapid gains in geo-targeted areas were followed by an overall gradual decline. Trend changes between individual geo-targeted SA3s varied widely.

Conclusions: ITS analysis is a robust method capable of detecting time-related nuances in community responses to population-level interventions. The campaign effect in geo-targeted zones overall was not significant, however this was not the case in all targeted SA3s; forthcoming multivariable analyses may explain the variation. The observed erosion of gains in coverage overtime in geo-targeted areas suggests sustained rather than intermittent interventions are more likely to be effective in maintaining improvements.

The impact of the pneumococcal immunisation program on adult Invasive Pneumococcal Disease epidemiology in Australia

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Abstract:
Background: Since the introduction of pneumococcal conjugate vaccines (PCV) for infants and the 23-valent polysaccharide vaccine (23v) for older adults, invasive pneumococcal disease (IPD) in non-Indigenous adults has declined. However, rates in Indigenous adults continue to rise. This study examined serotype-specific IPD epidemiology to try to ascertain reasons for these apparent differences.

Methods: Analyses were performed on IPD notifications collected through the National Notifiable Diseases Surveillance System from 2002 to 2017.

Results: There were 8,876 notifications in ≥65 year-old non-Indigenous adults (including unknown indigenous status) and 727 in ≥50 year-old Indigenous adults. Decreases in PCV serotypes excluding 3 and increases in non-PCV serotypes and serotype 3 were seen in ≥65 year-old non-Indigenous adults following the introduction of the PCV vaccines, indicating herd immunity with replacement impact consequent to the infant program. The increase in non-vaccine serotypes was significantly greater than in serotypes contained only in 23v vaccine, indicating direct impact of the 23v program. Overall, total IPD decreased by 19% (95% CI 12-26%) over this period. Similar patterns were seen in ≥50 year-old Indigenous adults, but point estimates for increases were higher while decreases were lower, resulting in an increase in total IPD of 103% (41-197). The point estimate for increase in exclusive 23v serotypes was again less than for non-vaccine serotypes, suggestive of 23v program impact, but not statistically significant.

Conclusion: Similar herd immunity and replacement impacts from infant vaccination, and direct impacts from adult vaccination, are seen in both Indigenous and non-Indigenous older adults.

Use of Normal Human Immunoglobulin prophylaxis in infants following measles exposure

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Abstract:
Background: Passive immunisation through use of Normal Human Immunoglobulin (NHIg) is recommended in national guidelines within 144 hours of measles exposure to prevent severe illness in vulnerable individuals. Current studies report the risk for non-immune people who receive passive immunisation is 83% less than if no prophylaxis were provided. However, there is no consistent evidence regarding efficacy of immunoglobulin provided four to six days after exposure. However, with reported declining seroprevalence of measles antibodies within the Australian population, effectiveness of passive immunisation might be questioned.

In early 2019, a ten-month-old infant developed measles. Whilst infectious, they attended childcare for two days exposing eight children under twelve months old and a playgroup exposing 31 children under twelve months old.

Methods: Intensive contact tracing identified 38 at-risk children. NHIg was offered to all exposed children within 144 hours of exposure. Thirty-one playgroup contacts were offered NHIg at an emergency measles prophylaxis clinic coordinated by the Department of Health at a tertiary paediatric hospital. Seven unvaccinated childcare contacts were offered NHIg via their general practitioners.
Vaccination program for invasive Meningococcal C cluster among MSM in Victoria

Authors: Janet Strachan1, Lucinda Franklin1, Stephen Pellissier1, Dr Brett Sutton1, Jay Healy1, Dr Mark Tang1, Mathilda Wilmot1, Jason Kwong2, Kerrie Stevens2

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Abstract:
Context: Between May and November 2017, eight cases of invasive meningococcal disease (IMD) were notified to the Victorian Department of Health and Human Services (DHHS). Seven of the eight cases identified as men who have sex with men (MSM). There were no known links between the cases, and no reports of similar clusters in other jurisdictions. The eighth case was an international traveller who had been in Australia for one week. All eight infections were caused by Neisseria meningitidis serogroup C (MenC) of finetype P1.5-1,10-8:F3-6:ST11(cc11), which had previously been associated with international IMD outbreaks among MSM. Whole genome sequencing of the first five isolates indicated phylogenetic relatedness of the Victorian strains, distinct from historical and international isolates.

Process: Following consultation with key community groups, sexual health clinics and other DHHS agencies, a six-month MenACWY (Menactra ®) vaccination program was implemented from December 2017 – May 2018 targeting MSM. It tied in with concurrent MSM vaccine programs (Hep A, Hep B and HPV) and a MenACWY program for 15-19 year olds. The MSM meningococcal program was later extended for an additional six months, with over 26,000 vaccine doses distributed over the twelve-month period.

Analysis: Final whole genome sequencing showed several, but not all, of the 2017 MSM isolates clustered phylogenetically, suggesting multiple import events with local strain evolution.

Outcome: Since the commencement of the MSM MenACWY campaign, there has been only one further MenC notified to DHHS. This was in early 2018 in an MSM who had not yet received MenACWY.

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Abstract:

Background: Surveillance of vaccine preventable diseases (VPDs) is important to monitor impact of immunisation programs and emergent trends. We aimed to assess VPD burden in Australia for the four-year period 2012-2015 and compare that to previous years.

Methods: We analysed national notification, hospitalisation and death data from 2012-2015 for 16 VPDs, calculating rates per 100,000 population by age group, sex, vaccination status, Indigenous status and jurisdiction. Long term trends were also assessed.

Results: Influenza, pertussis and invasive pneumococcal disease were the most commonly notified conditions during 2012-2015, whereas influenza, zoster and pneumococcal disease were the most common causes of hospitalisation.

Influenza notification rates more than doubled during 2012-2015 compared to 2008-2011 (259.1 versus 124.7 per 100,000 population), however, pertussis notifications rates declined by 44% across the same two periods (76.1 versus 135.2 per 100,000 population).

There were seven notifications of diphtheria in Australia in the four years 2012–2015, following none in the nine years 2002–2010. Also, there were localised outbreaks of mumps in Aboriginal communities and measles outbreaks in some jurisdictions, mostly linked to travellers from high endemicity regions. Overall, rates declined for hepatitis B, hepatitis A, meningococcal disease, varicella, rotavirus and rubella.

Conclusion: Declines in disease rates for numerous VPDs (hepatitis B, hepatitis A, rotavirus, varicella and rubella) likely reflect the ongoing impact of vaccination programs. The influence of improved and more available diagnostic testing (e.g. for influenza), and changes in case definitions (e.g. for diphtheria) are important considerations when interpreting trends over time.

One Health perceptions of Q fever among South Australian livestock farmers

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Abstract:

Background: Livestock farmers are at risk of Q fever, transmissible from animals such as cattle, sheep and goats to humans. Australia bears substantial Q fever burden, particularly among farmers. A One Health approach engages cross-sectoral collaboration between animal, human and the environmental health sectors and is the preferred framework to prevent Q fever.

Methods: Members of Livestock SA, representing cattle, sheep and goat farmers were invited to participate in an online survey to gauge perceptions about Q fever and its prevention. Participants were recruited via Livestock SA, newsletters, and email. Descriptive analysis was performed.

Results: A total of 351 farmers completed the survey. Most respondents (80%) had been farming for more than 20 years, with sheep and beef cattle their primary stock. Over 70% reported at least some knowledge of Q fever, and 79% identified that disease transmission through contaminated dust inhalation was highly likely. The majority of respondents (97%) were aware of Q fever vaccine, and 92.5% agreed it was effective in preventing disease, yet 42% remained unvaccinated. Reported barriers to vaccination included poor access, time, and cost. Most believed subsidised vaccination and improved awareness would promote higher vaccination rates.

Conclusion: While Q fever knowledge among respondents was good, their practices, particularly those related to airborne transmission prevention, were poor. Farmers would benefit from adherence to dust and aerosol transmission prevention practices. One Health partnerships between the government and industry are needed to promote Q fever awareness and address low vaccination rates among livestock workers by funded vaccination programs.
Early indication of live, attenuated varicella-zoster virus vaccine effectiveness in Australia

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Abstract:

Background: The live, attenuated varicella-zoster virus vaccine (ZVL) was funded on the National Immunisation Program (NIP) for all eligible adults aged 70 years with a catch-up cohort aged 71–79 in November 2016. Use of antiviral drugs specific for the treatment of herpes zoster is representative of incident zoster cases.

Methods: Monthly age-specific data on antiviral prescriptions for zoster supplied to a 10% sample of the Australian population between 1 January 2006 and 31 December 2018 was provided by the Commonwealth Department of Human Services. Age-specific trends over time were explored in the populations aged 60-69, 70-79 and 80+ years, using Poisson regression. Estimates and 95% prediction intervals were calculated using quarterly data up to the introduction of the ZVL NIP in Q4 2016, and extrapolating to the 8 subsequent quarters.

Results: Analyses showed long-term increasing trends in zoster antiviral prescriptions prior to implementation of the ZVL NIP. Thereafter for the eligible population aged 70-79 the number of antiviral prescriptions fell below the lower limit of the prediction interval for all 7 quarters from and including Q2 2017. Similar reductions were not observed in the 60-69 age group and were inconsistently observed in the 80+ group, which included some eligible subjects.

Conclusions: The reduction in zoster antiviral prescriptions observed in the eligible 70-79 population since the introduction of the vaccine may be an early indicator of the effectiveness of the ZVL NIP. Longer term follow-up data is required to confirm this interpretation.
Invasive Group A Streptococcus disease in Australian children: A descriptive epidemiological analysis

Authors: Dr Jane Oliver*, Dr Elise Thielemans*, Ms Alissa McMinn*, Ms Ciara Baker*, Dr Phillip Britton*, A. Prof Julia Clark*, Prof Helen Marshall*, Dr Christopher Blyth*, Dr Josh Frances*, Dr Jim Buttery*, Prof Andrew Steer*, Dr Nigel Crawford*

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Abstract:

Background: Invasive group A Streptococcus (iGAS) disease is serious and sometimes life-threatening. The Paediatric Active Enhanced Disease Surveillance (PAEDS) Network collects notifications on iGAS patients treated at seven major Australian paediatric hospitals. Our aims were to: 1) Describe the epidemiological distribution of paediatric iGAS disease in Australia and correlate this with influenza, 2) Identify GAS strains commonly associated with iGAS disease in children.

Methods: Notification data on iGAS patients were obtained from the PAEDS Network from 1 July 2016 to 30 June 2018. Influenza notification data was obtained from the Australia Institute of Health and Welfare. Data were described according to selected clinical and demographic characteristics, and incidence rates calculated. The proportion of iGAS patients’ household contacts were offered prophylactic antibiotic treatment was reported. The prevalence of commonly identified GAS emm-types from patient isolates was reported.

Results: A total of 181 iGAS patients were identified, with most (115, 63.5%) <5 years old. The estimated mean annual incidence was 1.6/100,000 children. A correlation with the seasonal burden of influenza was noted. Prophylaxis was reportedly offered to 85 patients’ contacts (47.0%). Of 81 patients with emm-typing results, 18 different strains were identified; 61 (75.3%) were emm-1, -4 or -12.

Conclusion: Robust surveillance systems are needed to inform iGAS disease control and prevention. Making iGAS disease nationally notifiable would help facilitate this. Influenza vaccination may minimise the risk of iGAS and co-infection, prior to iGAS vaccines being developed. Greater consistency in contact prophylaxis could mitigate household contacts’ increased risk of infection.
Clinical description and outcomes for children with invasive group A Streptococcal disease

Authors: Dr Elise Thielemans1,2, Dr Jane Oliver3, Alissa McMinn1, Clara Baker1, Dr Philip Britton2, Julia Clark4, Dr Helen Marshall5, Dr Christopher Blyth6, Joshua Francis1, Jim Buttery6, Prof Pierre Smeesters1,5, Dr Nigel Crawford, Prof Andrew Steer1

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Abstract:
Background: Invasive group A Streptococcus disease is a severe infection with a high case fatality rate, estimated to cause more than 150,000 deaths per year worldwide. There is limited data on its short and longer term outcomes, especially for children. The clinical presentation is variable and early diagnosis can be challenging. The aim of this study was to assess the clinical presentation, management and the short and longer term outcomes of children with invasive group A streptococcal disease in Australia.

Method: The Paediatric Active Enhanced Disease Surveillance network collected data on children with laboratory confirmed invasive GAS disease who were admitted to seven Australian tertiary children’s hospitals between July 2016 and June 2018. Retrospective and prospective collection of data occurred. We contacted patients six months after discharge to assess longer term outcomes.

Results: We enrolled 181 children, aged from seven days to 16 years. The principal site of invasion was blood (126 children, 69.7%). The most frequent clinical presentation was pneumonia (46 children, 25.4%). Twenty-six children developed streptococcal toxic shock syndrome (14.4%). Seventy-four children had severe disease (40.9%) including 71 admitted to the intensive care unit. Five children died (2.8%). At discharge, 29.3% of the children (53/181) had persisting health problems. This proportion had declined to 15.2% children (15/99) at six months post-discharge.

Conclusion: Invasive group A streptococcal infection in Australian children is frequently severe and has a high long term morbidity burden, highlighting the need for strengthened clinical care pathways, enhanced epidemiological surveillance and improved prevention strategies.

Genome-wide analysis of Group B Streptococcus associated with neonatal invasive disease in Australia

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Abstract:
Introduction: Group B streptococci or Streptococcus agalactiae (GBS) is a leading cause of life-threatening disease in neonates associated with sepsis, pneumonia and meningitis. It is often transmitted from mother to baby during birth. Worldwide estimates of GBS infection in neonates vary between 0.3 to 1.16 per 1000 live births, with early onset disease (EOD) incidence of 0.41 and late onset disease (LOD) 0.26. This study describes genomic characteristics of GBS strains associated with EOD and LOD in Australia.

Methods: 31 GBS isolates from the Australian Paediatric Surveillance Unit study and 11 isolates recovered from patients in New South Wales neonatal intensive care units (NICU) and their mothers included. All isolates were sequenced using Illumina NextSeq 500 platform and their genomes were examined.

Results: All these GBS isolates were responsible for sporadic EOD and LOD cases, three clusters of GBS in different NICUs, and known mother-to-child transmission events. 11 distinct multi-locus sequence types (MLST) and 6 serotypes were identified. Hypervirulent sequence type (ST) 17 and ST19 were two most common types. Phylogenetic analysis highlighted three outbreaks of ST17 each with less than 5 SNPs difference between core genomes. A previously uncharacterised transmission of cases of ST19 was also documented. The utility of genome-wide analysis in public health surveillance and investigation into outbreaks of hospital-acquired GBS will be discussed.

Conclusions: The diversity of co-circulating clones of invasive GBS in Australia requires high-resolution based surveillance. The genome-wide analysis enables characterisation of isolates associated with invasive disease, maternal and infant colonisation and hospital transmissions.
Staphylococcus aureus transmission among mothers and infants in first four weeks postpartum

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Abstract:

Aim: Investigate S. aureus transmission between first-time mothers and infants.

Methods: 360 nulliparous women participated in the Candida and Staphylococcus Transmission Longitudinal Evaluation study, Melbourne, Australia (2009 to 2011). They provided nasal, nipple and vaginal swabs at recruitment, then nasal, nipple and breast milk samples in the postnatal ward and weekly for one month. Infant oral and nasal swabs were collected weekly. Typing included spa for all MRSA, PFGE for the first S. aureus per person and all S. aureus from milk, and MLST/SCCmec for all unique PFGEs. We modelled infant S. aureus colonisation status during hospitalisation, at four weeks postpartum and any time in the four weeks, with maternal characteristics using logistic regression.

Results: The majority (90.5%) of 346 mother-infant dyads were colonised with S. aureus at least once (95%CI: 86.9-93.3), and 10.6% with MRSA (95%CI: 7.5-14.4), predominantly community-acquired. Both mother and infant were colonised with S. aureus in 67.6% of dyads (95% CI: 62.4-72.5) and 11.1% shared the same strain (95%CI: 7.4%-15.9%). For MRSA, both mother and infant were colonised in 7 dyads, with 6 sharing the same strain (85.7%, 95%CI: 42.1-99.6). Three infants were colonised before their mothers. Infants from colonised mothers were more likely to be colonised before discharge (OR: 6.2 95%CI: 2.3-16.3, p<0.001) or at any time (OR: 2.8 95%CI: 1.3-6.0, p=0.007).

Conclusion: Mothers’ prior S. aureus colonisation predicts infant colonisation, but the direction may not always be mother to infant. Peak infant S. aureus colonisation appeared earlier than the one month as commonly reported.

Sustained outbreak of community-associated methicillin-resistant staphylococcus aureus Western Australia

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Abstract:

Introduction: There is an increasing burden of CA-MRSA across Australia, particularly in Aboriginal people living in remote regions. This study describes the changing epidemiology of CA-MRSA in WA using notification data between 2004 and 2018.

Methods: Notification data, including strain type and presence of Panton-Valentine leucocidin (PVL) genes, were obtained from the PathWest Laboratory Medicine – WA Gram-positive typing laboratory. Comparisons between regional incidence rates were calculated and compared. Patient factors associated with PVL+ status were assessed.

Results: A total of 63,057 CA-MRSA cases were reported. The annual incidence in WA increased from 88 per 100,000 in 2004 to 283 per 100,000 in 2018 (IRR=3.2, 95% CI 3.0 – 3.4). The proportion of PVL+ isolates increased from 3.3% to 58.8% (p<0.0001). A marked divergence in incidence rates between regions occurred in 2009, driven primarily by an increase in PVL+ isolates in remote regions. Two strains predominated; ST393-IV (‘Queensland CA-MRSA’) and ST5-IV (‘WA 121’) which when combined, accounted for 49% of all CA-MRSA in 2018. The rate of CA-MRSA in the Kimberley is 9 times higher than that of metropolitan Perth, and significantly higher than all other regions.

Conclusion: There has been a significant increase in CA-MRSA in WA, particularly in remote regions with higher proportions of Aboriginal residents. It has been suggested that PVL+ strains have a propensity to cause more severe skin and soft tissue infections, which would increase burden on health services. A better understanding of the drivers of this outbreak is crucial.

Getting the all clear: STI testing facility at a WA music festival

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Abstract:

Context: In Western Australia (WA) chlamydia and gonorrhoea are the most notified sexually transmitted infections (STIs) among people aged 18 to 35.

In 2019 WA Health implemented WA’s first onsite STI testing facility at Falls Downtown Fremantle, a music festival. This was a convenient opportunity for chlamydia and gonorrhoea testing and aimed to increase awareness around the ease of STI testing and treatment, normalise STI testing discussions and promote safer sex messages.
Process: WA Health partnered with Falls Downtown, non-government organisations, a sexual health clinic, PathWest Laboratories, and an event management organisation to deliver the facility with the messaging “Get the All Clear”. It was supported by peer educators who facilitated the registration and specimen collection process, provided STI testing and treatment education, and provided incentives.

Analysis: 458 participants were tested, with 96 per cent aged 18 to 35. Fourteen cases of chlamydia and no cases of gonorrhoea were detected. All positives were contacted and treated at the sexual health clinic or by their GPs.

Participants provided informal feedback that the facility was easy to use, and peer educators reported high levels of participant engagement.

Outcomes: The facility sparked conversations about sexual health between participants and peer educators, and in the media. The high level of participant engagement and testing indicates the facility helped to normalise testing on the day and provided a safe space for STI and safer sex discussions. Options for future initiatives of this kind will be explored.

Antimicrobial resistance in N. gonorrhoea in Australia: systematic review and meta-analysis

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Affiliations: 1South Western Sydney Local Health District, Public Health Unit, Liverpool BC, Australia, 2Nepean Blue Mountains Local Health District, Public Health Unit, Penrith, Australia, 3Communicable Diseases Branch, NSW Health Protection, St Leonards, Australia

Abstract:

Background: Surveillance systems around the world have confirmed that Neisseria gonorrhoeae has developed resistance to all classes of antibiotics used for empirical treatment and clinical treatment failure caused by extensively resistant strains has been reported from many well-resourced settings globally.

Methods: We conducted a systematic review, meta-analysis and meta-regression to describe the changes in antimicrobial susceptibility patterns among the main classes of antibiotics used for empirical treatment and captured by the Australian Gonococcal Surveillance Program (AGSP) from 1981-2017. Annual reports by AGSP and additional papers identified from the reference list of articles published in English, including data on N. gonorrhoea isolated from >=100 human isolates, from any State or Territory in Australia were included.

Results: There is decreasing susceptibility of gonococcal isolates in Australia, to selected antimicrobials over time. In Australia, azithromycin (OR: 0.73; 95%CI 0.64-0.82) and ceftriaxone (OR: 0.69; 95%CI 0.59-0.80) shows decreasing levels of susceptibility each year. Susceptibility to azithromycin in NSW (OR: 0.57; 95%CI 0.50-0.64) and South Australia (OR: 0.50; 95%CI 0.33-0.75) shows greater decreases in susceptibility compared with the Australian average annually. Western Australia and Victoria also have decreasing levels of susceptibility to ceftriaxone over time compared to other States and Territories. All isolates remain viable to spectinomycin over the period.

Conclusion: Improved antimicrobial stewardship, enhanced surveillance and contact tracing are needed to identify and respond to changes in antibiotic resistance in a timely manner. Increasing awareness and continued public health follow-up of cases will interrupt the cycle of infection.

A syphilis outbreak preparedness plan for New South Wales, Australia

Authors: Ms Tove-Lysa Fitzgerald1, Dr Christopher Bourne2, Dr Christine Selvey1, Ms Heather McCormack1, Dr Megan Campbell2, Dr Kate Armstrong1, Ms Rose Mason2, Dr Vicky Sheppeard1

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Abstract:

Background: An ongoing infectious syphilis outbreak among Aboriginal people has affected Queensland, the Northern Territory, Western Australia and South Australia with potential to spread to NSW. NSW Ministry of Health (MOH) identified that a coordinated and comprehensive syphilis preparedness plan including prevention activities, support to the Aboriginal Controlled Community Health Service (ACCHS) sector, in addition to outbreak response preparation, was required to prevent an outbreak developing in NSW.

Methods: Key syphilis outbreak response and prevention activities were identified and documented into a plan by NSW MOH including activities being undertaken and identified by Aboriginal Health Medical Research Council (AHMRC) to support the syphilis outbreak preparedness needs of ACCHS. A working group was established to co-ordinate activities between MOH, local health districts (LHD) and AHMRC.

Results: The ‘NSW Aboriginal syphilis prevention and outbreak response plan’ includes: enhanced infectious syphilis surveillance focusing on Aboriginal identification for notifications and regions adjacent to outbreak areas; additional syphilis screening for pregnant women whose infant will be identified as Aboriginal; awareness raising among health service providers and community; support for ACCHS to undertake sexually transmissible infection (STI) screening; resource development to optimize and scale up STI/blood borne virus (BBV) testing; strengthening local clinical systems; Aboriginal sexual health workforce capacity building through education and training; syphilis outbreak response preparation.
Conclusion: The syphilis outbreak response plan raises awareness of the multijurisdictional syphilis outbreak and provides a multi-disciplinary, proactive approach for the early detection of, and response to any spread of the outbreak to NSW.

HIV epidemiology in the Australian Capital Territory, 2008 to 2017

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Abstract:
Background: There is a need, nationally, to strengthen and realign efforts in response to emerging changes in HIV incidence within priority populations and changing risk exposures. The aim of this study was to analyse the epidemiology of HIV in the ACT over a 10-year period to inform future local policy in this area.

Methods: A cross-sectional descriptive analysis of HIV cases notified to ACT Health with a diagnosis date from 01/01/2008 to 31/12/2017. This report focuses on new diagnoses only.

Results: ACT Health received 133 notifications of new diagnoses with a diagnosis date between 2008 and 2017. The median age of new diagnoses was 35 years (range 16 to 72 years). The majority of cases were male (84%) and born in Australia (62%). Male-to-male sex was the predominant sexual exposure reported (66%) followed by heterosexual sex (HS) (29%). Cases with a male-to-male sex exposure were mainly born in Australia (73%). Of cases with a HS exposure, half (51%) were male; 38% were born in Australia and 38% were born in a high-prevalence country (HPC).

Over a third (35%) of all new diagnoses were late or advanced. This proportion was higher in cases with a HS exposure (59%). In cases with a HS exposure who had a late or advanced diagnosis, 57% were born in a HPC.

Conclusions: These findings provide awareness of the local HIV epidemiology in the ACT, including the subpopulations for which consideration should be given to focusing efforts to diagnose HIV earlier.

Investigating HIV Antenatal Testing within the Tasmanian Health Service

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Background: The Australasian Society for HIV Medicine (ASHM) National HIV Testing Policy and The Royal Australian and New Zealand College of Obstetricians and Gynaecologists (RANZCOG) guidelines recommends women in antenatal care are offered routine HIV testing. HIV testing rates in the public antenatal sector of Tasmania were previously unreported but thought to be low.

The study aims to determine antenatal HIV testing rates in Tasmania and whether certain clinical interventions can improve testing. The study will also provide a better understanding of barriers and motivators of antenatal HIV testing.

Methods: This mixed method study uses quantitative data from ObstetrixTM data base to report the current and historical rate of antenatal HIV testing in Tasmania and determine if practices have changed post the implementation of the improved referral process. Qualitative semi-structured interviews with clinicians are used to explore the perceived barriers and motivators for HIV antenatal testing.

Results: Data from 2016 showed very low antenatal HIV testing rates ranging from 24-55% across geographical regions. These increased up to 48% in some areas following the intervention to 72-79% in 2018, across the same regions. Analysis of the qualitative data is underway and we will present preliminary findings.

Conclusion: Improved referral templates and raising awareness about testing appears to have improved antenatal HIV testing across Tasmania. A collaboration between Sexual health Services, General Practice and Hospital clinicians has enabled this improvement. By identifying the barriers and reasons behind the variations in HIV antenatal HIV testing practices strategies can be recommended to support clinicians.
HIV trends in Western Australia (WA) in the modern ART era.

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Background: In 2014, a record number of new HIV cases were notified in WA (n=109). In the years that followed, prevention strategies focusing on ‘treatment as prevention’ (TasP) and pre-exposure prophylaxis (PrEP) were implemented. This research describes the epidemiology of HIV and treatment uptake in WA following the implementation of these strategies.

Methods: HIV notifications and testing data from 2009 to 2018 were sourced from the WA HIV Database and pathology laboratories, respectively, and analysed to determine HIV notification and positivity rates. Antiretroviral therapy (ART) data provided by the Pharmaceutical Benefits Scheme (PBS) from 2015 to 2017 were analysed to describe trends in treatment uptake. Key policy measures in HIV prevention over this period were also reviewed.

Results: From 2009 to 2014, the number of new HIV cases in WA increased 60% to 109 cases before decreasing 48% to 57 cases between 2014 and 2018. HIV test positivity also decreased by 54%. These declines followed the implementation of several key initiatives, including the removal of the CD4+ requirement from the PBS restrictions for initiation of ART; an integrated outreach model of care to support people living with HIV with complex needs; commencement of the WA PrEP trial; and a PBS listing for PrEP. In 2017, estimated treatment coverage among people diagnosed with HIV increased to just under 90% (n=1,760).

Conclusion: TasP and PrEP-based strategies have likely contributed to a decrease in HIV transmission within WA and continue to play an important role in the state’s public health response to HIV.
3C – Respiratory and enteric infections
Murrumbidgee Room

Characterising healthcare-seeking behaviour amongst the Flutracking cohort, 2012-2017

Authors: Dr Belinda Jones1, Mr Zachary Howard2, Mrs Sandra Carlson1, Professor Robyn Lucas1, Dr Tony Merritt1, Professor David Durrheim1,2, Associate Professor Craig Dalton1,3

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Abstract:
Background: Influenza is an important public health problem, with seasonal influenza resulting in considerable annual morbidity and mortality. As the Flutracking survey collects data on community influenza-like-illness rates and healthcare seeking, it can provide useful insights into factors that may be associated with healthcare-seeking behaviour.

Methods: We undertook a retrospective analysis of all episodes of influenza-like-illness reported to Flutracking from 2012 to 2017. We used mixed effects logistic regression models to explore the relationship between reported healthcare-seeking behaviour and variables of interest. Separate models using “any type of healthcare”, “GP-only care” or “emergency department care” as the outcome measure were performed.

Results: The factors most strongly associated with seeking any type of healthcare were: being in the extremes of age (OR 2.0 for <1-year-olds and OR 1.4 for 75-year-olds, compared to the median age of 43), and time off from work/normal duties (OR 3.5 for 2 days absence from duties, doubling to OR 7.0 for 4 days absence). Remoteness was associated with higher odds of emergency department care (OR 5.62), and lower odds of GP care (OR 0.58) in comparison with participants living in metropolitan area. Identifying as being of Aboriginal and/or Torres Strait Islander origin was associated with higher odds of emergency department care (OR 2.74).

Conclusion: We identified several factors associated with healthcare-seeking behaviour amongst the Flutracking cohort. This information can be used to inform influenza modelling, pandemic planning, and to help target public health strategies.

Redefining influenza seasonality and selection of optimal immunisation period

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Abstract:
Introduction: Influenza vaccine manufacturing cycles align with temperate country seasonality in each hemisphere, yet influenza seasonality is poorly defined for many countries. The study introduces a novel and universal approach to defining and classifying seasonality.

Methods: Countries reporting to the World Health Organization’s FluNet influenza virology database in 90% of weeks during 2011 through 2017 were included. A smoothed, standardised, average proportion of influenza occurring in each week of the year was used to determine degree of seasonality based on the range of average weekly variation. The proportion of activity occurring May through October was used to align influenza activity with a hemisphere’s vaccine manufacturing cycle.

Results: From 84 included countries, there were 2,239,208 positive influenza results, of which 26% were influenza type B. Degree of seasonality was moderately positively correlated with absolute value of latitude (r = 0.69, p < 0.0001). Latitude was strongly negatively correlated with the proportion of influenza occurring during May through October (r = -0.83, p < 0.0001). Thirteen countries (12% of the included global population), mainly in tropical zones, had influenza occurrence aligned with the opposite hemisphere’s influenza vaccine manufacturing cycle. In tropical zones, concordance in the degree of seasonality and vaccine cycle alignment within regions and between adjacent countries was limited. In temperate zones, on average, influenza B peaked four weeks later than A.

Conclusions: The study provides evidence for different population dynamics of influenza B compared with A. These findings highlight the challenge of optimising influenza vaccine recommendations for tropical zones.

Pandemic influenza: what outcomes are achievable with a limited vaccine supply?

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Abstract:
Background: In an influenza pandemic, there will be many sources of uncertainty, such as which population groups have the greatest risk of severe disease. While vaccines are our primary form of protection, a suitable vaccine is unlikely to become available before the first pandemic wave. This study aimed to identify (a) what objectives may be achieved with a limited supply of pandemic vaccine; and (b) which groups should be prioritised to receive vaccination in pursuit of these objectives.

Methods: We used a published SEIR model of the Australian population to simulate various pandemic scenarios, and to evaluate the relative merits of prioritising: (1) high-risk groups (“direct protection”); versus (2) primary-school children (“indirect protection”). We assessed reductions in overall harm and health inequality gaps, and how these outcomes were affected by dose requirements and vaccine availability.

Results: With low transmission, indirect-protection was more effective at reducing harm and both strategies meaningfully reduced inequities in disease burden. In other transmission scenarios both strategies were comparable and had minimal impact on health inequality. With a 2-dose requirement, offering only 1 dose (increasing coverage at the expense of protection) reduced the intervention impact.

Conclusion: The indirect-protection strategy equalled, or exceeded, the impact of the direct-protection strategy in all scenarios. Whether the population will support a vaccination strategy focused on high-transmitting groups is the topic of further work in which community juries have been asked to consider the relative importance of competing ethical values.

Effectiveness of Oseltamivir Prophylaxis for Influenza Outbreaks in Aged Care Facilities

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Affiliations: 1Liverpool Public Health Unit, Sydney, Australia

Abstract:
Influenza outbreaks in aged care homes lead to hospitalisations and deaths. Influenza spreads rapidly through aged care homes if precautionary measures are not taken. Oseltamivir may be effective in reducing the attack rate of Influenza.

Methods: Administrative data from Sydney South West Local Health District with enhanced surveillance of Aged Care Home influenza outbreaks was used to investigate the effectiveness of oseltamivir prophylaxis. The key outcome variable was the rate of seroconversion (new cases) after receiving oseltamivir. Subgroups and various predictors of oseltamivir seroconversion were investigated including, presence of a dementia ward, high care ward, strain of influenza, vaccination rates (staff and patients) and days to PHU notification.

Results: 86 outbreaks were reported, which involved 10064 patients from 2015 to 2018 of aged care homes in the South West Sydney Local Health District. Oseltamivir prevented 90% of influenza cases in influenza outbreaks. (0.18 (95%CI: 0.084 – 0.1248; P<0.0001)). ACFs with dementias wards had a 44% (0.56RR (95%CI: 0.34-0.93);P<0.05) lower oseltamivir seroconversion rate ACFs with high level care had an 86% (0.13RR (95%CI: 0.05-0.38);P<0.05) lower oseltamivir seroconversion rate. Also, outbreak duration was increased by 0.42 days ((95%CI: 0.16-0.68 days);P<0.05) for every extra day in delay in notifying the Public Health Unit.

Conclusion: Oseltamivir prophylaxis is highly effective in preventing new cases of influenza in outbreaks at ACFs, especially in ACFs with dementia or high care wards. It is recommended that Public Health Units be notified immediately when an outbreak of influenza is suspected to decrease the duration of the outbreak.

Influenza infection in children with special risk medical conditions: a systematic review

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Abstract:
Background: Children with special risk medical conditions (SRMC) are over-represented in influenza hospitalizations. This systematic review sought to determine whether children with SRMCs experience greater complications or severity following influenza infection.

Methods: Electronic searches of MEDLINE and EMBASE (1990 - March 2018) were conducted, hand searching of reference lists undertaken and contact made with the investigators of studies containing relevant data. Studies of children (aged <18 years) with a SRMC hospitalized with influenza were included. Outcomes were pneumonia, intensive care unit (ICU) admission, mechanical ventilation, neurological outcomes (seizures, encephalopathy), death and length of stay (LOS) in hospital or ICU.

Results: 22 studies met inclusion criteria. Compared to healthy peers, children with SRMC had higher odds of ICU admission (pooled odds ratio [OR] 1.66 (95% confidence interval [CI]: 1.25-2.21), for mechanical ventilation (pooled OR 1.53 [95%CI 0.93-2.52) and death (pooled OR 1.34 [95%CI 0.74-2.41]). Additionally, children with SRMC were more likely to develop bacterial pneumonia (OR 1.7; 95% CI 1.1-2.6) or experience prolonged hospital LOS [adjusted rate ratio (aRR) 1.75 (95%CI 1.44-2.11)].
Conclusions: While there was evidence that ICU management and bacterial pneumonia increases in children with SRMC, evidence showing an increase in the probability of death or need for mechanical ventilation was inconsistent. Further research using large data sets should evaluate the impact of complications and associated morbidity from influenza in SRMC children. The level of GRADE evidence was low for all outcomes considered in this review.

Association between nasopharyngeal density of respiratory pathogens and pneumonia in Western Australia

Authors: Dr Mejbah Bhuiyan1, Dr Thomas Snelling2, Dr Chisha Sikazwe3, Ms Tasmina Rahman4, Ms Caitlyn Granland5, Ms Camilla de Gier6, Dr Lea-Ann Kirkham5, Dr Peter Richmond5, Dr David Smith2, Dr Christopher Blyth1

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Abstract:

Background: Respiratory viruses and bacteria are frequently detected in the nasopharynx of asymptomatic children, making it difficult to understand their actual contribution to pneumonia. We aimed to determine and compare the nasopharyngeal density of respiratory pathogens between children with and without pneumonia to understand if pathogen density could be used to define pneumonia.

Methods: Nasopharyngeal swabs (NPS) were collected from hospitalized pneumonia cases at Princess Margaret Hospital (PMH) and contemporaneous age-matched controls at PMH outpatient clinics and a local immunization clinic in Perth, Australia. The density (copies/mL) of eight respiratory viruses and bacteria in NPS were determined using quantitative polymerase-chain-reaction. The association between pathogen density and disease status was examined using logistic regression. Area under receiver-operating-characteristic (AUROC) curves were assessed to determine optimal discriminatory pathogen density cutoffs.

Results: Through May’15 – October’17, 230 pneumonia cases and 230 controls were enrolled. Median nasopharyngeal density for any respiratory pathogens was not significantly higher in cases than controls. After adjusting for demographics and densities of other pathogens, the odds of being a case increased by 6, 3 and 2 times for every log10 copies/mL density increase for respiratory syncytial virus, human metapneumovirus and influenza A virus, respectively. The AUROC curves were <0.70 for each pathogen, suggesting poor case-control discrimination using pathogen density.

Conclusions: The nasopharyngeal density of respiratory pathogens was not substantially higher in pneumonia cases than controls, however, the odds of being a case increases with increased density for some viruses. The utility of pathogen density, alone, in defining pneumonia was limited.

LTBI in Under 2 Year Old Refugees: Should We Be Screening?

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Abstract:

Refugees are at increased risk of tuberculosis compared to other migrants due to time spent in crowded camps, poor nutrition and moving from countries where TB control systems have been disturbed by civil war or strife.

Active TB diagnosis is vital, but Latent Tuberculosis Infection (LTBI) diagnosis remains important due to the lifetime risk of developing active TB - making it a focus in low incidence countries. In NSW, LTBI is screened for refugees aged 11-34, and for those aged 2-10 arriving from high burden countries. The focus of this study is to determine whether these children aged below two years should be screened in NSW.

Method: A systematic literature review and meta-regression were carried out of studies screened for tuberculosis of children under 18 years of age. 136 Studies were extracted from MEDLINE, EMBASE, PUBMED and Google Scholar using keywords. Studies with systematised screening using either TST or QuantiFERON (IGRA). Fifteen studies met the search criteria. Predictors for meta-regression were age, test type (TST or IGRA) and general screening or screening at a referral centre.

Results: The prevalence found was approximately 6% using IGRA and 15% using TST for screening. Meta-regression revealed that prevalence increased with age (1.12OR;95%CI:1.06-1.(169,614),(227,629)) a year cumulatively and decreased where IGRA was used for screening compared to TST (0.38OR;95%CI:0.25-0.58). There was no difference between general and referral screening centre.

Conclusion: A prevalence of 15% for LTBI using TST in the under two years of this group would support them being included in screening programs.
Whole genome sequencing (WGS) to identify local transmission of tuberculosis in NSW

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Abstract: Context: WGS provides higher resolution than traditional typing methods and reveals relationships between isolates.

Process: All Mycobacterium tuberculosis isolates referred to the NSW Mycobacterium Reference Laboratory (MRL) are sequenced. We identified clusters of cases, less than 5 single nucleotide polymorphisms apart, and collected epidemiological information. We classified cases as confirmed locally acquired where epidemiological investigations identified links between cases, or likely locally acquired where the timing deemed transmission within NSW was plausible.

Analysis: In 2017 and 2018, MRL sequenced 740 TB cases. We found 87 (12%) cases were related in 32 clusters. Most clusters involved two cases (n=25, 78%), three clusters had three cases (9%), one cluster had four cases (3%), two clusters had seven cases (6%) and one cluster of ten cases (3%).

Epidemiological links for all cases were identified in 17 clusters (53%), for some cases in 5 clusters (16%), and no links were found in 10 clusters (31%).

For clusters with no known links, possible explanations include a common source case occurring prior to routine WGS or outside of NSW, insufficient patient recall, or our investigations were not comprehensive enough to discover the link.

Three per cent (n=25) of cases sequenced in 2017 and 2018 were confirmed to be locally acquired. A further 4% (n=28) were likely locally acquired. The remaining clustered cases appear to be acquired overseas (n=34).

Outcomes: WGS cluster investigations are proving that there may be more local transmission of TB in NSW, particularly in overseas born people, than has previously been recognised.

Detection of Enteroinvasive Escherichia coli in the Era of Culture-Independent Direct Testing

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Abstract: Background: Enteroinvasive Escherichia coli (EIEC) is one of the causes of food- or water-born gastroenteritis, closely related to Shigella species. The growing uptake of the culture-independent direct testing (CIDT) of diarrheal samples has highlighted the lack of reliable protocols for EIEC detection as CIDT nucleic acid amplification assays rely on the target which is shared by Shigella species and EIEC. This project evaluated the protocol for detecting EIEC in CIDT Shigella positive but Shigella culture negative samples.

Methods: An in-house PCR has been implemented using EIEC specific markers that classify EIEC into subtypes that were consistent with phylogeny. Whole genome sequencing using Illumina NextSeq500 platform was employed to characterise EIEC.

Results: The protocol has been evaluated since mid-2018. The laboratory protocol can assist in characterisation of Shigella species and allowed us to recognise EIEC among Escherichia coli strains recovered from CIDT positive samples. Demographics, travel history of the patients and subtypes and multi-locus sequence types of EIEC will be discussed. All of them possess virulence genes ipgD and mxiA. Two isolates had mphA gene indicating macrolide resistance and, separately, two other isolates had D87G mutation in gyrA gene indicating fluoroquinolone resistance. No clusters of EIEC disease have been detected.

Conclusion: The implementation of this laboratory protocol enabled reliable detection of patients with EIEC in cases classified as probable shigellosis by CIDT assays.

Increase in Shigella-Campylobacter coinfections in Victoria: 2016-2019

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Abstract: Background: In early 2019, several coinfections with Shigella and Campylobacter were notified to the Victorian Department of Health and Human Services. To better understand the significance of these cases, we reviewed past notification data to determine the burden of coinfections over time.

Methods: Notifications of shigellosis and campylobacteriosis in Victorian residents from 1st January 2016 to 31st March 2019 were examined. A coinfection was defined as one person having both a shigellosis and campylobacteriosis notification with specimen collection dates within seven days of each other. Demographic and risk factors for coinfections and mono-infections were investigated.
Communicable Diseases Control Conference 2019 – Tuesday 19 to Thursday 21 November 2019

Results: The number of coinfections has increased over time, from 35 in 2016, to 59 in 2018, and 22 in the first quarter of 2019. The proportion of notifications that were coinfections increased from 6% to 11% for shigellosis and 0.4% to 1.2% for campylobacteriosis. Coinfections were more likely to be male (70%) than either Shigella or Campylobacter cases (58% and 55% respectively) and cases tended to be younger (median 29 years vs 33 and 36). Coinfection cases were slightly more likely to report overseas travel during their exposure period (68% vs 60%) than Shigella only cases, though the proportion reporting male-to-male sexual contact as a risk factor was similar (22% vs 20%). Trends in these factors over time were similar in both groups.

Conclusion: Notifications of coinfections with Shigella and Campylobacter are increasing in Victoria, but there is no strong evidence to suggest these cases represent a different population than single infections.

Multi-state outbreak of Salmonella Typhimurium caused by a novel MLVA type, 2018-2019.

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Abstract:
Context: 235 people across the ACT, NSW and QLD were affected by a Salmonella Typhimurium (STm) outbreak between 10 October 2018 and 26 June 2019. The multi-locus variable number tandem repeat analysis type (MLVA) profile for this outbreak (5-17-9-13-490) had not been identified in humans since MLVA typing was introduced in NSW in 2010.

Process: On 14 December 2018, investigation commenced between NSW Health and the NSW Department of Primary Industries Biosecurity and Food Safety (DPI-BFS). NSW Health interviewed cases using a national questionnaire and suspected point sources were investigated by DPI-BFS. We used whole genome sequencing (WGS) to characterise a sample of cases in the outbreak.

Analysis: Since its emergence, this MLVA accounted for 27% of all STm cases and >7% of all Salmonella infections in NSW. 188/235 (80%) cases were interviewed. 133 (71%) cases reported egg consumption, and a further 38 (total 171, 91%) reported potential consumption of egg products. 26% were children <10 years of age. 77 (33%) cases were linked to point source clusters. Five deaths of people with this MLVA occurred in the outbreak period. 81/82 (99%) WGS isolates were highly related, indicating a single originating source for all infections.

Outcomes: This is the first increase of STm incidence in NSW since the NSW Foodborne Illness Reduction Strategy launched by the DPI-BFS in 2015. Point source outbreaks were linked to one egg farm through complex distribution channels. The impact on illness of extensive control measures on the farm are being monitored.

Epidemiology and genetic distribution of Giardia duodenalis in humans in Metropolitan Sydney.

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Abstract:
Background: Giardia is an important non-viral cause of human gastroenteritis; yet, its epidemiology in developed countries is poorly understood. This study describes the epidemiology of giardiasis in south western Sydney and the distribution of G. duodenalis genotypes in Metropolitan Sydney.

Methods: A 1:2 matched case-control study of 190 confirmed giardiasis cases, notified to the South-Western Local Health District Public Health Unit from January to December 2016, was employed to explore the epidemiology, including risk factors for giardiasis in Sydney. Two groups of controls were selected to increase response rate; Pertussis cases and neighbourhood (NBH) controls. Giardia cysts in 105 human faecal samples collected from various tertiary hospitals and private (community) laboratories in Sydney, Australia, were genotyped by sequence analysis of the triosephosphate isomerase gene.

Results: Significant risk factors for giardiasis include age under 5 years, a household member diagnosed with a gastrointestinal illness, swimming in swimming pools and contact with farm or domestic animals or wildlife. Cases that travelled overseas had an increased risk of infection when compared with locally acquired pertussis cases (controls). Preliminary genotyping results revealed the majority of samples belong to assemblage A (including potentially zoonotic sub-groups), and only a small percentage (4%) belonged to assemblage B. Surprisingly, mixtures of genotypes A and B in individual cases were relatively common. Co-infections (39%) especially with Blastocystis species and Dientamoeba fragilis was common.

Conclusion: Enhanced surveillance and prevention strategies are recommended, particularly with the circulation of potentially zoonotic Giardia genotypes in metropolitan Sydney.
3D – Emerging, re-emerging and resistant infections
Federation Ballroom Sth

Spatio-temporal identification of target areas for prevention of Australian bat lyssavirus exposure

Authors: Dr Fiona May¹, Dr Kay Mann¹, Mr Daniel Francis¹, Dr Megan Young¹

Affiliations: ¹Metro North Hospital And Health Service, Windsor, Australia

Abstract:
Background: Due to the severity of Australian bat lyssavirus infection (ABLV), all cases of potential exposure are treated as though the person is infected. Follow-up and treatment of these cases is expensive and time consuming. Many of these exposures are intentional and therefore preventable.

Methods: We analysed the epidemiology of cases of preventable potential ABLV in the Metro North Hospital and Health Service region of Queensland between 1 January 2007 and 31 December 2017. To find areas for targeted response, we geocoded the case addresses and produced maps showing case counts and rates by statistical area. To identify areas with higher numbers of cases regardless of population, we counted cases in a grid of equal sized squares. We also used SaTScan software to identify statistical areas and years with clusters of higher than expected numbers of cases.

Results: Of the 144 people reporting an intentional bat encounter, 93% were adults, 60% were male and the most common reason for touching the bat was to rescue a trapped or injured bat (72%). Reports of preventable potential ABLV exposures have increased since 2013 and are more common during bat breeding and nursing seasons. Spatio-temporal clusters of higher than expected numbers of cases were identified in the northern less populated areas though cases were denser in a band stretching north from the inner city through the northern metro suburbs.

Conclusion: Targeted prevention messaging will provide the largest impact if directed to those who rescue bats through the urban corridor north of Brisbane city.

New and old hotspots for rickettsial spotted fever acquired in Tasmania, 2012-2017

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Affiliations: ¹Communicable Diseases Prevention Unit, Tasmanian Department Of Health, Hobart, Australia, ²National Centre for Epidemiology and Population Health, Australian National University, Canberra, Australia, ³Department of Microbiology and Infectious Diseases, The Royal Hobart Hospital, Hobart, Australia

Abstract:
Background: Flinders Island spotted fever, a rickettsial infection caused by Rickettsia honei, was first described on Flinders Island, Tasmania. Although not nationally notifiable, rickettsial infection is notifiable in three Australian jurisdictions, including Tasmania. We describe the epidemiology and clinical characteristics of rickettsial disease notified to the public health unit in Tasmania during 2012-17.

Method: Confirmed, probable and possible rickettsiosis cases acquired and notified in Tasmania between 1 January 2012 and 31 December 2017 were analysed descriptively.

Results: Eighteen cases of rickettsial infection were notified and likely acquired in Tasmania during 2012-17: 12 confirmed (67%), 4 probable (22%), and 2 possible (11%). The mean number of cases per year was 3.0 (population rate 0.6 per 100,000 population/year). Sixty percent of cases occurred in November and December. Cases were more commonly older males. Fever, lethargy, and rash were commonly reported symptoms. Thirteen cases were likely acquired on Flinders Island, and 5 on mainland Tasmania (3 around Great Oyster Bay, 2 in the Midlands).

Conclusions: This review of surveillance data extends our knowledge of the epidemiology of rickettsial infection in Tasmania. This is the first account including confirmed cases in the Midlands of Tasmania. We are using these findings to engage with local clinicians and other stakeholders including Parks and Wildlife and Environmental Health Officers. Increased knowledge and awareness of the epidemiology of rickettsial infection in Tasmania is likely to improve the timely diagnosis and appropriate treatment of cases, thus reducing burden of disease.
Computational Monitoring of Tweets for Early Detection of the 2014 Ebola Epidemic

Authors: Dr. Aditya Joshi¹, Dr. Ross Sparks¹, Dr. Sarvnaz Karimi¹, Dr. Cecile Paris¹, Dr. C Raina MacIntyre²

Affiliations: ¹Commonwealth Scientific & Industrial Research Organisation, Sydney, Australia, ²Kirby Institute, UNSW, Sydney, Australia

Abstract:
Background: First reported in March 2014, the Ebola epidemic impacted West Africa, most notably Liberia, Guinea and Sierra Leone. This epidemic is regarded as one of the deadliest epidemics in recent times, that resulted in a high loss of life and severe stress to medical services in the countries impacted.

Method: In this work, we create a dataset of tweets posted from the affected region from 2011 to 2014, that report fever and rash. Using this dataset, we apply computational techniques based on natural language processing and statistical time series monitoring to obtain alerts for the epidemic. Our techniques are computational in that they use artificial intelligence-based algorithms to perform the linguistic as well as time series analysis.

Results: Our results show that we obtain alerts in December 2013, i.e., three months prior to the official announcement of the epidemic.

Conclusion: Social media-based surveillance for large-scale epidemics like Ebola is a viable opportunity for public health surveillance.

Changing epidemiology and risk profile of arboviral infections in Tasmania

Authors: Beth Reszke¹, Kerryn Lodo¹

Affiliations: ¹Department Of Health, Hobart, Australia

Abstract:
Background: Recent changes in the epidemiology of arboviral infections in Tasmania include the first locally-acquired cluster of Barmah Forest virus infection (BFv), and new places of acquisition of Ross River virus infection (RRV). These prompted a review of the public health surveillance and communication strategy for arboviruses in Tasmania. We describe the changing epidemiology of arbovirus notifications over 21 years in Tasmania, and our recent public health response.

Methods: We did a 21 year retrospective descriptive analysis of arboviral cases notified in Tasmania (1998 to mid-June 2019). Following the BFv cluster in 2019, mosquito trapping was undertaken to identify species involved in transmission.

Results: From 1998 to mid-June 2019, 1090 arboviral infections were notified in Tasmania. There were 19 notifications of BFv between1998 and 2018 (annual notifications ranged from 0 to 3). In 2019 there have been 10 notifications. Mosquito trapping identified Aedes notoscriptus in urban areas. In the 2017-18 season, a major change in distribution was seen along the East Coast in Tasmania.

Conclusions: Changes to the epidemiology and potential vectors of arboviral diseases in Tasmania has required Public Health to respond to these new risks. An arboviral disease communications strategy was developed with messaging to residents and tourists, and partnerships developed with the University of Tasmania, local councils and Parks and Wildlife Service. Further research on the effect of climate change on disease transmission, vector habitat and modelled risk assessment in Tasmania would provide evidence to inform public health intervention.

Epidemiology of a re-emerging STI: lymphogranuloma venereum in New South Wales, 2010-2018

Authors: Ms Jana Sisnowski¹, Ms Tove Fitzgerald¹, Dr Christine Selvey¹, Mr Phillip Keen¹, Dr Vicky Sheppeard¹

Affiliations: ¹Communicable Diseases Branch, Health Protection NSW, NSW Health, St Leonards, Australia, ²Kirby Institute, University of New South Wales, Kensington, Australia

Abstract:
Background: Lymphogranuloma venereum (LGV) is a sexually transmitted infection (STI) caused by Chlamydia trachomatis serovars L1-3. Since 2003, LGV cases have increased in high-income countries, primarily among gay and other men-who-have-sex-with-men (GMSM) presenting with proctitis. LGV is laboratory-notifiable in New South Wales (NSW).

Methods: We analysed LGV and other STI notifications with calculated onset dates in 2010-2018. LGV was confirmed by detection of LGV serovar-specific DNA by polymerase chain reaction. Concurrent STIs were defined as gonorrhoea and/or syphilis within four weeks before/after LGV onset.

Results: In 2010-2018, 391 LGV notifications were received, ranging from 16 notifications in 2014 to 80 notifications in 2018. All but one case occurred in males. The median age was 38 years (range 18-75). Rectal infections accounted for >94% of notifications; three specimens were buboes; the remaining sites were unclear. Among NSW residents (n=385), 21% had concurrent STIs; 50% had ≥1 other STI notification in the same calendar year; 83% had ≥1 other STI notification in 2010-2018. Residents of postcodes where >5% of males are estimated to be gay accounted for 76% of LGV notifications in 2010, 54%-69% in 2011-2017, and 48% in 2018.
Increasing gonococcal notifications and changing antibiotic susceptibility trends in the ACT, 2009-2018

Authors: Mr Callum Thirkell1,2, Associate Professor Vanessa Johnston1,2, Dr Ben Polkinghorne3, Dr Marlena Kaczmarek4

Affiliations: 1ACT Health, Canberra, Australia, 2Australian National University, Canberra, Australia

Abstract: Background: There is increasing public health concern about rising numbers of gonococcal infections and emerging antimicrobial resistance globally and in Australia.

Methods: Descriptive epidemiological review of all gonococcal notifications in the ACT from 1 January 2009 to 31 December 2018. Data sources included ACT notifications, enhanced surveillance data and antibiotic susceptibility test results.

Results: There were 1,478 gonococcal notifications from 2009 to 2018. Notifications increased year-on-year, with notifications in 2018, five times greater than in 2009. Infections were predominantly in males (74% were MSM) and highest in the 25-29 age-group. Notifications among women aged 20-29 have also increased since 2015.

Low-level azithromycin resistance (MIC value ≥ 1.0 - <256mg/L) was detected in 60 isolates, 95% of which were male; 92% reported some same-sex exposure; and predominantly isolated from pharyngeal and rectal specimens. Between 2009-2017, there was a median of 4 (range 0-12) notified per year. In 2018 there were 19 resistant isolates notified.

By contrast, the number of isolates with decreased-susceptibility to ceftriaxone has decreased, with only one notified since 2014.

Almost two thirds of infections diagnosed by sexual health clinicians (62%) included culture, compared to less than a third of infections diagnosed by GPs (29%).

Conclusion: Culture of N. gonorrhoeae is critical for detecting antimicrobial resistance. All clinicians, but particularly GPs, should be encouraged to take swabs from all potentially infected sites for culture prior to treatment and undertake a test of cure. MSM and young adults are priority populations for sexual health promotion and routine screening.

Molecular epidemiology of gonorrhoea in Western Australia.

Authors: Carolien Giele1, Julie Pearson1, Donna Mak1, Charlene Kahler1, David Whiley4

Affiliations: 1Communicable Disease Control Directorate, Department of Health, Perth, Australia, 2PathWest Laboratory Medicine, Fiona Stanley Hospital, Perth, Australia, 3Infection and Immunity Division, University of Western Australia, Perth, Australia, 4UQ Centre for Clinical Research, University of Queensland, Brisbane, Australia

Abstract: Background: Historically in Western Australia (WA), gonorrhoea affected Aboriginal people from remote areas, men who have sex with men (MSM) from metropolitan areas and recently heterosexual people from metropolitan areas. Using molecular typing, we explore the relationship of gonorrhoea strains between these groups.

Methods: Gonorrhoea isolates from WA residents in 2017 were characterised using the iPLEX method and assigned a ‘WA type’.

These were analysed with corresponding demographic and behavioural notification data.

Results: Molecular characterisation was available for 710 isolates (21%). Behavioural data were available for 78% of these. Of 76 WA types were identified, 10 types accounted for 519 cases (73%). Type WA-10 was most prevalent (157 cases, 22%).

Of the 10 most common WA-types, eight (WA-3, 6, 10, 14, 24, 32, 51 and 52) were predominantly in non-Aboriginal people (83-99% per type) in the metropolitan area (81-96%) of which five (3, 6, 10, 51, 52) comprised mostly heterosexual people (85-100%), and three (WA-14, 24 and 32) comprised higher proportions of MSM (53%, 23% and 82%, respectively). The remaining two common types, comprised mostly Aboriginal people (WA-29:76%, WA-63: 93%) accounting for 55% of Aboriginal isolates; all were heterosexual with >65% from remote areas.

Additionally, one type (WA-56, 15 cases) was exclusively associated with Aboriginal people from remote regions.

Conclusion: Molecular typing of gonococcal isolates revealed strains that were associated with sexual orientation, Aboriginal status and geographical regions. Understanding transmission dynamics between sexual networks will enhance the ability to target interventions.
Cholera risk in Australian travellers, 1991-2018

Authors: Miss Malinda Vibol Chea¹, Prof Martyn Kirk², Dr Luis Furuya-Kanamori³, Ms Rhonda Owen³

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

Abstract:
Background: Cholera has been reported to the National Notifiable Diseases Surveillance System (NNDSS) in Australia since 1991. The majority of cases in Australia are travel-associated. We describe cholera risk importation from return travellers to Australia, and provide risk estimates by country/region of travel.

Methods: We used cholera notifications from NNDSS from 1991-2018. We excluded cases of cholera acquired in Australia. We used descriptive analysis to summarise the data and calculated traveller rates of infection using returned traveller data from the Australian Bureau of Statistics as the denominator.

Results: There were 92 cholera notifications in the 27-year period (2-6 per year), 4 locally acquired and excluded from analysis. Of all cases, 54% were male and 46% female, with a median of 41 years (IQR= 25-54). 71% of cases were Serogroup O1 (equally distributed between Classical and El Tor), O139 (1%), and untyped (28%). Only 34% of all notifications had information on country/region of acquisition, however, in the last 10 years this improved to 86%. The highest proportion of cases were from South-East Asia (33%) and Southern and Central Asia (33%), and Oceania (23%). Overall, Papua New Guinea had the highest number of notifications with infection rate of 3.9 per 100,000 travellers in 2011.

Conclusion: The risk of cholera importation to Australia is low. Most infections were acquired from travel to Asia and Oceania. Despite the low risk, travellers should take precautions while travelling to cholera endemic areas. There is a need to improve data quality within NNDSS, particularly for earlier years.

Acquisition Rate and the Effect of Dukoral on Multidrug-Resistance Enterobacteriaceae among Travellers

Authors: Dr Luis Furuya-Kanamori¹, Dr Deborah Mills¹, Dr Jenny Robson¹, A/Prof Colleen Lau¹,²,³

Affiliations: ¹Australian National University, Acton, Australia, ²Deb The Travel Doctor, Brisbane, Australia, ³Travel Medicine Alliance, Brisbane, Australia, ⁴Sullivan Nicolaides Pathology, Bowen Hills, Australia

Abstract:
Background: Recent studies have shown that a high proportion of international travellers to developing countries become colonised by multidrug resistant enterobacteriaceae (MRE). The acquisition rate and risk factors associated with MRE colonisation among Australian travellers were investigated.

Method: Travellers aged ≥18 years, not colonised by MRE, and attending the clinic prior to travel to Asia were invited to join the study. Questionnaires were used to collect demographic, clinical, and travel information. Pre- and post-travel rectal swabs were collected from study participants and cultured.

Results: Fifty three participants (75.6% females; mean age 49.2 [SD 14.3] year) were enrolled in the study. The most common destinations were India (39.6%) and Thailand (15.1%). One third of the participants had comorbid conditions and two thirds received Dukoral before their travel. Thirty participants (56.6%) were colonised by MRE (ESBL E.coli [n=21] and AmpC type beta-lactamase E.coli [n=9]). Baseline characteristics were similar among MRE colonised and non-colonised participants, except for India as the travel destination, presence of comorbidities, and Dukoral vaccination (higher proportion in the MRE colonised group). When the analysis was adjusted for travel destination and comorbidities, the relative risk of MRE colonisation with Dukoral compared to non-Dukoral was 0.91 (95%CI 0.40-2.09).

Conclusion: The majority of participants acquired MRE while travelling in Asia. The study revealed a lower risk of MRE colonisation in travellers vaccinated with Dukoral, but did not have enough power to assess statistical significance. A randomised controlled trial is needed to confirm whether Dukoral significantly reduces MRE colonisation.

Travel factors and antibiotic susceptibilities among enteric fevers cases notified in NSW

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Affiliations: ¹Westmead Hospital - ICPMR, Westmead, Australia, ²Ministry of Health, St Leonards, Australia

Abstract:
Background: Typhoid and paratyphoid fever in Australia is predominantly an infection that is acquired overseas. Following an increase in enteric fever in returning travelers, we evaluated the risk factors and antimicrobial susceptibilities of all notified cases in New South Wales.

Methods: Patient characteristics, travel history, and antibiotic susceptibilities for all enteric fever cases notified to NSW Health between 1 Jan to 30 April 2019 were analysed.
Results: A total of 53 infections (20% higher than the 5-year average) were notified. Serotyping of the isolates revealed slightly higher S.Typhi than S.Paratyphi A at 52% and 45 % respectively. The mean age was 22 years, and 28% of infections were among children under ten years. 41% of patients were born in India and 34% in Australia. 66% reported travel to India, where they likely acquired the infection. Two infections (3.7%) were acquired locally. Among all travelers from India, 30 of 35 traveled to North-western states (Gujarat, Punjab, Delhi, and Rajasthan). Antibiotic susceptibilities (MIC) to ceftriaxone, ciprofloxacin, and azithromycin were available in 50/53 isolates. The rates of resistance to ceftriaxone, ciprofloxacin (Etest MIC>0.06 µg/ml) and azithromycin (Etest MIC>16 µg/ml) amongst travelers from India was 0%, 100%, and 12% respectively, with ciprofloxacin resistance significantly higher in travelers from India compared to other destinations (p=0.03).

Conclusion: Travel to India was related to a higher chance of acquiring enteric fever with fluoroquinolone resistant strains. Patients with severe disease should empirically be treated with parenteral ceftriaxone and switched to azithromycin when susceptibilities available

An outbreak of Shigella flexneri with potential for antimicrobial resistance

Authors: Dr Lea Merone¹, Ms Sally Rubenach², Ms Ann Richards³, Ms Sandyl Kyriazis³, Ms Juliet Esmonde², Ms Carlie Thirlwell², Dr Richard Gair²

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Abstract:
Background: Globally, Shigella spp. are a leading cause of diarrhoea and dysentery. In Australia, S. sonnei and S. flexneri are the prevailing strains.

In North Queensland, cases of shigellosis have been increasing since 2014, with a notable increase in notifications of S. flexneri for Aboriginal and Torres Strait Islander residents observed since 2017.

In early 2019, an outbreak of S. flexneri in a remote town in north Queensland was characterised by extended periods of illness and repeated presentations to health services. The outbreak subsequently spread to other socially connected towns in the region.

This paper describes the microbiological and epidemiological features of the outbreak and its subsequent management.

Methods: Epidemiological analysis involved a descriptive, cross-sectional study of the outbreak.

Microbiological investigation included whole genome sequencing and cluster analysis to determine genetic relatedness and presence of antimicrobial resistance (AMR) markers.

Results: Microbiological investigation revealed the clone of S. flexneri 2b endemic to Northern Australia has recently acquired mobile genetic elements associated with increased potential for antimicrobial resistance to standard treatments including Azithromycin, Bactrim, and Quinolones.

Conclusions: Notifications of S. flexneri are increasing in North Queensland, particularly in Aboriginal and Torres Strait Islander people. Mobility between communities and the challenges associated with outbreak responses in remote towns contribute to the spread of outbreaks, and the incursion of potentially multi-drug resistant strains into this population has significant implications for future public health responses.
Antibiotic use associated with confirmed influenza, pertussis and non-typhoidal salmonella infections

Authors: Dr Wen-Qiang He¹, Prof Martyn Kirk², Prof Vitali Sintchenko³, Prof John Hall¹, A/Prof Bette Liu¹

Affiliations: ¹University Of New South Wales, Sydney, Australia, ²National Centre for Epidemiology and Population Health, Australian National University, Canberra, Australia, ³Centre for Infectious Disease and Microbiology-Public Health, Westmead Hospital, Sydney, Australia

Abstract:
Background: Antibiotics are not recommended treatment for uncomplicated influenza or non-typhoidal salmonella infections whereas they are for pertussis infection. We investigated adherence to these recommendations in a population of older community-dwelling adults.

Methods: Population-based prospective cohort study of Australian adults aged 45 years and older followed by record-linkage to laboratory-confirmed influenza, pertussis and non-typhoidal salmonella notifications, hospitalisation records and antibiotic dispensing data from 1st Jan 2009 to 31 December 2015. We estimated the proportions of adults with each infection dispensed antibiotics according to various characteristics and examined the specific antibiotics dispensed.

Results: There were 1056 influenza, 151 pertussis, and 334 non-typhoidal salmonella cases in the cohort eligible for analysis. Among cases, 56.2% (594/1056) of influenza, 78.8% (119/151) of pertussis, and 39.5% (132/334) of non-typhoidal salmonella cases were dispensed antibiotics in the +/-10 day window around the infection onset date. The likelihood of antibiotic dispensing did not differ according to most participants characteristics examined including whether cases had an associated hospitalisation, their age, and co-morbidities. As for types of antibiotics, macrolides were the predominant antibiotic dispensed (79%) for pertussis which is according to guideline whilst for influenza both beta-lactams (36.3%) and macrolides (35.4%) were used neither of which is indicated by guideline. There was no dominant antibiotic class dispensed among those with non-typhoidal salmonella.

Conclusion: Given concerns regarding increasing antibiotic resistance, the high proportion of adults with influenza and non-typhoidal salmonella dispensed antibiotics suggests that antimicrobial stewardship need to include better education and awareness around treatment guidelines for such infections.
4A – Public health genomics
Towards an optimised model for the national genomic surveillance of Listeria monocytogenes

Authors: Dr Patiyan Andersson1, Dr Amy Jennison2, Professor Vitali Sintchenko3, Dr Qinning Wang4, Dr Louise Cooley5, Dr Ivan Bastian6, Dr Lex Leong7, Dr David Speers6, Dr Avram Levy8, Dr Karina Kennedy6, Dr Ella Meumann9, Dr Susan Ballard1, Associate Professor Deborah Williamson1, Professor Benjamin Howden1

Affiliations: 1Microbiological Diagnostic Unit Public Health Laboratory at The Peter Doherty Institute, University of Melbourne, Melbourne, Australia, 2Queensland Health Forensic and Scientific Services Public Health Microbiology Laboratory, Brisbane, Australia, 3Centre for Infectious Diseases and Microbiology - Public Health, University of Sydney, Sydney, Australia, 4Department of Pathology, The Royal Hobart Hospital, Hobart, Australia, 5SA Pathology, Adelaide, Australia, 6PathWest Laboratory Medicine WA, Perth, Australia, 7Microbiology and Infectious Diseases Department, ACT Pathology, Canberra, Australia, 8Royal Darwin Hospital, Darwin, Australia

Abstract:

Background: Since 2012, all Listeria monocytogenes samples (specimen, isolates or sequences) in Australia are forwarded to the Microbiological Diagnostic Unit Public Health Laboratory (MDU PHL) for whole genome sequencing (WGS). This nationally coordinated high-resolution analysis allows for more precise detection of outbreaks, generation of internationally compatible typing data and improved source attribution. While WGS provides an opportunity to reduce turn-around times, a critical aspect for effective public health action, this has yet to be investigated.

Methods: Using temporal data (2016-2018) on date of collection, notification, sequencing, and receipt at jurisdictional reference laboratories (JRL) and at MDU PHL, an analysis of turn-around times was performed. Analysis was stratified by jurisdiction, collection year, sample-type and source.

Results: During 2016-2018, there were 361 samples received by MDU PHL. Data showed reductions in overall median transfer-times between 2016 to 2018 (10, 13, 7 days, respectively), but that ranges remained wide (0-92, 0-44, 0-49 days, respectively). For some jurisdictions the delays were observed before submission to a JRL, while for others the delays were mainly seen between a JRL and MDU PHL. There was a reduction in primary specimens submitted (10, 14, 2, respectively), with more confirmatory work conducted in jurisdictions. One jurisdiction submitted enough genome sequences to allow assessment of this aspect, and encouragingly only a 2.5-day increase in median transfer-time compared with isolates was observed.

Conclusions: While the project is aimed at optimising quality and timeliness of Listeria surveillance, the findings and the subsequent improvements identified are likely highly applicable to other pathogens.

The genomic landscape of Legionella pneumophila in New South Wales

Authors: Dr Verlaine Timms1,2, Dr Rosemarie Sadsad1,2, Peter Howard3, Anna Smith4, A/Prof Sharon Chen1,3,5, Professor Vitali Sintchenko1,3,5

Affiliations: 1Centre For Infectious Diseases And Microbiology - Public Health, Westmead Hospital, Westmead, Australia, 2Sydney Informatics Hub, University of Sydney, Sydney, Australia, 3Centre for Infectious Diseases and Microbiology Laboratory Services, NSW Health Pathology, Westmead, Australia, 4Forensic and Analytical Science Services, NSW Health Pathology, Sydney, Australia, 5Marie Bashir Institute and Sydney Medical School-Westmead, The University of Sydney, Westmead, Australia

Abstract:

Background: Legionella pneumophila is ubiquitous and sporadically infects humans causing legionnaires disease. Globally, the number of reported cases of Legionnaire’s disease has risen four-fold from 2000-2014 raising concerns about future surveillance and control. In 2016, Sydney was the epicentre of an outbreak caused by L. pneumophila serogroup 1 (Lp1). This outbreak has triggered the interest in utilising whole genome sequencing (WGS) for laboratory surveillance of Lp1. This report describes the experience of WGS-based surveillance of Lp1 in New South Wales.

Methods: WGS was therefore employed to investigate historical Lp1 from clinical and environmental samples to determine the major outbreak clones in Sydney. WGS of clinical and environmental Lp1 isolates collected since 1990 (n= 224) was performed using Illumina NextSeq500. The genomes were typed using the L. pneumophila sequence based typing (SBT) Scheme and clustered using BAPS software.

Results: The large outbreak of Lp1 in Sydney was caused by (ST) 211, a rare ST only reported in Canada. As SBT cannot resolve all clusters, given many strains are non-typable, this clone may cause unnoticed outbreaks. ST211 was found in clinical and environmental samples since 1994. A further common outbreak strain, ST37 was also found and both of these STs had highly related pangenomes. BAPS clustering placed all outbreak strains together including ST211 and ST37 strains plus other related strains that could not be typed with the SBT method.

Conclusions: Genomic surveillance of Lp1 has important public health implications and indicates the dominance of highly successful clones in NSW and worldwide.
Impacts of carbapenemase producing-Enterobacteriales surveillance: Increased screening, stabilising infections and defined transmissions

Authors: Courtney R Lane1,2, Siobhan St George1, Judy Brett1, Mark Schultz1,3, Kerrie Stevens1, Donna R M Cameron1,4, Annaleise van Diemen1, Susan A Ballard1, Norelle L Sherry1,2,3, Deborah A Williamson1,2, Anders Goncalves da Silva1,2, Nicola Stephens4,5, Benjamin P Howden1,2,3

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Abstract: Background: Carbapenemase-producing Enterobacteriales (CPE) are multi-resistant organisms (MRO), posing a major threat to public health and hospital safety. Following a multi-facility outbreak of Klebsiella pneumoniae carbapenemase (KPC)-producing Enterobacteriales, Victoria implemented a state-wide public health surveillance program for CPE in December 2015.

Methods: Using a ‘search and destroy’ approach, state-wide standardised active screening, laboratory testing and carrier isolation practices were implemented. Isolates and epidemiological data, including travel and hospitalisation history were collated centrally. Combined analysis of phylogenetic and epidemiological data was undertaken to identify the time and place(s) of CPE transmission, and targeted interventions deployed.

Results: The occurrence of CPE in Victoria remains low but increased over the surveillance period to 1.42 cases/100,000 population. Despite this, rates of active clinical infection have remained steady since 2017 (0.45-0.60/infections/100,000 population, p=0.640), while the proportion of cases with an unknown source of acquisition halved from 30% to 15% in the second-half of 2018 (p=0.033). This indicates an increase in case ascertainment and better resolution of transmission networks. Notably, the occurrence of KPC-2 clinical infection decreased from 0.29 infections/100,000 population prior to program implementation to 0.03 infections/100,000 population in 2018 (p=0.003). Centralised combined genomic and epidemiological analysis has enabled identification of intra-facility, inter-facility and propagated outbreaks.

Conclusion: Through multi-sector cooperation Victoria has successfully implemented one of the first centralised combined genomic and epidemiological surveillance systems for a primarily hospital-associated MRO globally. This system has contributed to the maintenance of Victoria’s low incidence of CPE. The structure of this system may be transferrable to other settings, and other emerging MROs.

Using genomics to distinguish relapse of recurrent invasive pneumococcal disease from reinfection

Authors: Dr Rebecca Rockett1,3, Dr Shahin Oftedah1,3, Ms Karen-Ann Gray1, Prof Gwendolyn Gilbert2, Professor Vitali Sintchenko1

Affiliations: 1University Of Sydney, Westmead, Australia, 2Institute of Clinical Pathology and Medical Research, NSW Health Pathology, Westmead, Australia, 3Centre for Infectious Diseases and Microbiology - Public Health, Westmead Hospital, Westmead, Australia

Abstract: Introduction: Invasive pneumococcal disease (IPD) is a major cause of morbidity and mortality worldwide, particularly in children and elderly. Recurrent IPD (rIPD) remains uncommon but can be difficult to manage as it is often unclear if the infection persists through treatment failure or acquisition of a new strain of Streptococcus pneumoniae. This study aimed to characterise rIPD and identify markers that can be used to identify relapse over new infections.

Methods: A total of 46 rIPD episodes (94 isolates of S. pneumoniae) where investigated. rIPD were defined as episodes diagnosed >31 days apart. All isolates were serotyped and subjected to whole genome sequencing and their genomes compared to differentiate re-infection from relapse.

Results: The same causal serotype occurred in 26 episodes. Almost all cases of rIPD (24/26), with the same serotype had high homology (<20 SNPs) between core genes and the resistome indicating a relapse of the original infection. Genomes from rIPD caused by a different serovar had low homology (>9000 SNPs) indicative of a new pneumococcal infection. Cases of relapsed disease occurred within 12 months (median 10 months (range 1-161)). Whereas new IPD infections occurred >12 months after the primary IPD (median 17 months (2-108)).

Conclusions: Genomic comparison of pneumococci associated with rIPD showed a higher resolution than serotyping and indicated that 52% of events were due to relapse caused by the same strain. High core and resistome homology were detected in relapse cases suggesting that the development of antibiotic resistance did not play a major role in rIPD.
Economic outcomes of whole genome sequencing availability on containing a nosocomial outbreak

Authors: Mr Thomas Elliott¹, Dr Xing J Lee², Dr Patrick N.A Harris²,³, Mr Joel Douglas⁵, Mrs Belinda Henderson⁶, Ms Catherine Watson⁷, Prof David L Paterson⁷, Prof Deborah S Schofield⁷, Prof Nicholas Graves¹, A/Prof Louisa G Gordon¹,²,³

Affiliations: ¹Qimr Berghofer, Brisbane, Australia, ²Australian Centre for Health Services Innovation, Institute of Health and Biomedical Innovations, School of Public Health and Social Work, Faculty of Health, Queensland University of Technology, Kelvin Grove, Australia, ³Pathology Queensland, Herston, Australia, ⁴University of Queensland Centre for Clinical Research, Herston, Australia, ⁵Infection Management Services, Princess Alexandra Hospital, Woolloongabba, Australia, ⁶Macquarie University, Macquarie Park, Australia, ⁷School of Nursing, Faculty of Health, Queensland University of Technology, Kelvin Grove, Australia, ³School of Population Health, The University of Queensland, Herston, Australia

Abstract: A key infection control measure is the timely detection and identification of the particular organism, and their antimicrobial susceptibility. Whole genome sequencing (WGS) is a new avenue of investigation with substantially greater discrimination power compared with conventional typing methods. We evaluated the clinical and economic impact of WGS availability in containing a large-scale hospital outbreak of E.coli (OXA-181).

Methods: We built a hybrid simulation model to assess hospital ward dynamics, pathogen transmission and pathogen detection in a tertiary care hospital during a five-month outbreak. Model inputs were determined using microbiology and WGS data, hospital admission databases and local clinical knowledge. The model was calibrated to mirror the actual pathogen detections within each hospital ward affected. We assessed outbreak size and hospital cost for early, late or no WGS and additional scenarios where there was environmental contamination or increased virulence. Sensitivity analyses were performed to address input uncertainty.

Results: An estimated 197 patients were colonised during the outbreak with 75 patients detected. The total outbreak cost was $460,137 with 6.1% spent on sequencing. Without WGS, the outbreak was estimated to result in 352 colonised patients costing $766,921. With earlier use of WGS, the outbreak size was three patients, one detection and a cost of $65,374. Microbiology tests were the largest cost component across all scenarios.

Conclusion: We showed WGS on a potentially serious pathogen to be associated with a smaller outbreak and lower hospital costs. Sequencing costs accounted for a small fraction of total hospital outbreak costs.

Using Genomics to ensure the robustness of Salmonella culture-independent testing

Authors: Dr Rebecca Rockett¹,³, Dr Alicia Arnott¹,³, Dr Nathan Bachmann³, Dr Qinning Wang³, Mr Peter Howard³, Prof Vitali Sintchenko¹,³²

Affiliations: ¹University Of Sydney, Westmead, Australia, ²Centre for Infectious Diseases and Microbiology - Public Health, Westmead Hospital, , Westmead, Australia, ³Institute of Clinical Pathology and Medical Research, NSW Health Pathology, Westmead, Australia

Abstract: Nontyphoidal Salmonella causes an estimated 129 million gastrointestinal illnesses annually. Salmonella is a highly diverse genus of zoonotic organisms, characterised by over 2600 serovars. The high incidence of salmonellosis and the need for rapid and cheap diagnostics has driven the development of culture-independent diagnostic tests (CIDT). A range of fully-automated gastrointestinal CIDT systems are rapidly replacing routine culture to diagnose Salmonella infections.

Sensitivity of PCR-based CIDT systems is reliant on a highly conserved gene target. Single nucleotide polymorphisms (SNPs), indels and genomic rearrangements within primer and probe sequences can reduce the sensitivity of CIDT and lead to false negative results. If PCR systems are to become the sole diagnostic tool to detect Salmonella, ongoing monitoring of the diversity in PCR target regions is needed.

A total of 3299 Salmonella isolates were prospectively sequenced, representing 53 serovars and 79 MLST types. The sequence of PCR gene targets, ttrA (Roche LightMix), spaO (BD Max) and invA (inhouse Salmonella PCR target) were interrogated to measure the nucleotide dissimilarity of each PCR target. We demonstrated dissimilarity between PCR gene targets employed by CIDTs ranging between 0 – 81.3 SNP/Kbp (0 and 141 SNPs). The lowest average dissimilarity was 2.11 SNP/Kbp [range 0 - 51.3]) was detected in the spaO gene target.

The debate continues over the benefits and pitfalls of replacing bacterial culture with molecular assays, however, local validation and ongoing monitoring of CIDT targets is imperative and can be readily performed with the wealth of genomic surveillance data available.
4B – Vaccine preventable diseases

Mount Ainslie Room, 1:30pm – 3:00pm

Burden of vaccine-preventable disease in Australia

Authors: Mr Lucas Mills¹, Dr Patyian Andersson², Ms Nancy Stace-Winkles¹, Ms Tracy Dixon¹

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Abstract:

Background: Burden of disease analysis measures the combined effect of the fatal and non-fatal impacts of diseases on a population.

Methods: This study used an incidence-based modelling approach to estimate the burden of 17 vaccine-preventable diseases in Australia using DALYs. This approach reflects the burden of new cases of disease occurring in the reference year and the immediate and future consequences (including death) of those cases.

A model was developed for each disease incorporating the acute phase of infection, possible long-term disability and death. Disability weights were applied to reflect the severity of health loss associated with a disease and an Australian life table was used to calculate the burden due to premature death.

Results: The 17 vaccine-preventable diseases were responsible for 15,781 DALY in 2015.

Influenza had the largest overall burden, accounting for over one-third (5,674 DALY, 36%) of the total burden, followed by pneumococcal disease (3,793 DALY, 24%) and HPV (3,710 DALY, 24%). Shingles contributed a further 7% to the total and meningococcal disease just over 4%. Together these 5 diseases accounted for around 94% of the total burden. The overall rate of burden decreased by 31% between 2005 and 2015.

Conclusion: This study estimated the burden of 17 diseases covered under the National Immunisation Program. The use of an incidence-based approach allowed estimation of future disability arising from infections acquired in the reference year, including the cancer-related outcomes following HPV infection and long-term disability from bacterial meningitis. The results demonstrate the positive impact of Australia’s vaccination program.

Long-term pneumococcal disease trends in Australians in conjugate pneumococcal vaccine era (2002-2016)

Authors: Kelley Meder¹,², Dr Sanjay Jayasinghe¹,³, Dr Frank Beard¹,³, Dr Aditi Dey¹,³, Dr Martyn Kirk², Heather Cook⁴, Janet Strachan³, Prof Vitali Sintchenko⁶, Helen Smith⁷, Carolien Giele⁸, Benjamin Howden⁹, Dr Vicki Krause⁴, Prof Peter McIntyre¹,³

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Abstract:

Background: Universal 7-valent pneumococcal conjugate vaccine (7vPCV) programs began in Indigenous Australian children in 2001 and all children in 2005, changing to 13vPCV in 2011 with 10vPCV use in Northern Territory only in 2009-11. We used laboratory data for invasive pneumococcal disease (IPD) and coded hospitalisations for non-invasive pneumococcal community acquired pneumonia (PnCAP) to evaluate long-term vaccine impact.

Methods: Annual incidence (per 100,000 population) was calculated for age-specific total IPD, 13-non7v serotypes and PnCAP by Indigenous status. Incidence in pre-universal 7vPCV (2002-2004), early-7vPCV (2005-2007), pre-13vPCV (2008-mid 2011) and post-13vPCV (mid 2011-2016) periods was used to calculate incidence rate ratios (IRR) to assess changes over time.

Results: In the total population, all-age IPD incidence declined from 11.8 pre-7vPCV to 7.1 post-13vPCV (IRR 0.61, 95% CI 0.59-0.63). PnCAP incidence declined only in children aged <1 year (IRR 0.34, 95% CI 0.25-0.45) and 1-4 years (IRR 0.50, 95% CI 0.43-0.57) and increased significantly in age ≥5 years (IRR 1.08 to 1.14). In Indigenous people, baseline 13-non7v IPD incidence was 3-fold higher, amplified by a serotype 1 epidemic in 2009-12. In recent post-13vPCV period (2015/2016) IPD and PnCAP incidences were three to seven-fold higher in Indigenous Australians than others.

Conclusions: Direct and indirect impact of 7 years of post-7vPCV/10vPCV and 5 years post-13vPCV on IPD and PnCAP differed by age and between Indigenous and non-Indigenous people. Recent change to 13vPCV schedule is expected to improve pneumococcal disease control further but review of recommendations for Indigenous Australians with measures to optimize uptake are needed.
Changing epidemiology of invasive pneumococcal disease following introduction of PCV13, Victoria, 2008-2018

Authors: Dr Sophia Bowman-Derrick1,2,3, Ms Marion Easton3, Ms Janet Strachan3, Dr Emma Field4, Professor Benjamin Howden2

Affiliations: 1National Centre for Epidemiology and Population Health, Australian National University, Canberra, Australia, 2Victorian Department of Health and Human Services, Melbourne, Australia, 3Microbiological Diagnostic Unit Public Health Laboratory, Melbourne, Australia

Abstract:

Introduction: The 13-valent pneumococcal conjugate vaccine (PCV13) replaced the 7-valent vaccine (PCV7) on the National Immunisation Program in July 2011. We assessed changes in pneumococcal serotypes and antimicrobial resistance (AMR) profiles for invasive pneumococcal disease (IPD) in Victoria in the period following PCV13 introduction.

Methods: IPD data for 1 January 2008 to 30 June 2018 were extracted from the Victorian Hospital Pathogen Surveillance Scheme, a voluntary laboratory-based system for invasive isolates. Cases were divided into three equal periods (Pre-PCV13: 1 January 2008-30 June 2011; Transition: 1 July 2011-31 December 2014; Post-PCV13: 1 January 2015-30 June 2018).

Antimicrobial susceptibility data were assessed using clinical breakpoints as interpreted by diagnostic laboratories. Using poisson regression, the incidence of serotypes and penicillin and third-generation cephalosporins (3GC) susceptibilities were compared between periods.

Results: There were 3865 IPD cases with available serotype data. The pre-PCV13 period included 1215 cases; of which 99% had penicillin susceptibilities and 95% had 3GC susceptibilities. The post-PCV13 period included 1277 cases; of which 100% had penicillin susceptibilities and 91% had 3GC susceptibilities. Univariate regression found that the incidence risk ratio (IRR) for PCV13 serotypes decreased (IRR 0.54, p<0.001), notably serotype 19A (IRR 0.23, p<0.001), after the PCV13 was introduced. Levels of penicillin non-susceptibility decreased (IRR 0.75 p=0.02) while 3GC non-susceptibility did not change (IRR 1.1, p=0.8).

Conclusion: There was a significant decrease in the incidence of vaccine serotypes following introduction of PCV13. Levels of AMR did not increase however ongoing surveillance is essential to identify emerging changes.

Rotavirus epidemiology and Rotarix vaccine effectiveness in New South Wales, 2010–2017

Authors: Ms Julia Maguire1,2, Ms Keira Glasgow1, Associate Professor Kathryn Glass2, Ms Susie Rocco-Farkas4, Professor Julie Bines4,5,6, Dr Vicky Shepheard3, Professor Kristine Macartney1,7, Dr Helen Quinn1,7

Affiliations: 1National Centre for Immunisation Research and Surveillance, Westmead, Australia, 2National Centre for Epidemiology and Public Health, College of Health and Medicine, Australian National University, Canberra, Australia, 3Communicable Diseases Branch, Health Protection New South Wales, Sydney, Australia, 4Enteric Diseases Group, Murdoch Children’s Research Institute, Parkville, Australia, 5Department of Paediatrics, The University of Melbourne, Parkville, Australia, 6Department of Gastroenterology and Clinical Nutrition, Royal Children’s Hospital, Parkville, Australia, 7Discipline of Child and Adolescent Health, The University of Sydney Children’s Hospital at Westmead Clinical School, Westmead, Australia

Abstract:

Background: Rotavirus vaccine has been funded for infants under the National Immunisation Program since 2007, with Rotarix vaccine (RV1) used exclusively in New South Wales (NSW) from that time. In 2017, NSW experienced a large outbreak of rotavirus gastroenteritis. We examined the epidemiology, genotypic profile and vaccine effectiveness (VE) of outbreak cases.

Methods: Notified laboratory test-positive rotavirus cases in NSW between 1 January 2010 and 31 December 2017 were analysed. VE estimates were calculated in children via a case-control analysis. Specimens from a sample of hospitalised cases were genotyped and analysed.

Results: In 2017, 2,319 rotavirus cases were reported, representing a 3.1-fold increase on the 2016 notification rate. The highest notification rate was among children aged <2 years. For notified cases in 2017, two-dose VE was estimated as 88.4%, 83.7% and 78.7% in those aged 6–11 months, 1–3 years and 4–9 years, respectively. VE was significantly reduced from 89.5% within 1 year of vaccination to 77.0% at 5–10 years post-vaccination. Genotype analysis identified equine-like G3P[8] (48%) and G8P[8] (23%) as the most common genotypes in cases aged 26 months.

Conclusion: RV1 is highly effective at preventing laboratory-confirmed rotavirus in Australia, especially in infants. Reduced VE in older age groups and over time suggests waning of protection, possibly related to the absence of subclinical immune boosting from continuously circulating virus. G8 genotypes have not previously been common in Australia and their emergence, along with equine-like G3P[8], could be the result of vaccine-related selective pressure.
Sparse data bias in influenza vaccine effectiveness estimates for the elderly

Authors: Olivia Price1, Febbie Tambala2, Sheena Sullivan1,3

Affiliations: 1WHO Collaborating Centre For Reference And Research On Influenza at the Peter Doherty Institute, Melbourne, Australia, 2School of Global and Population Health, University of Melbourne, Melbourne, Australia

Abstract:

Background: Sparse data bias (SDB) occurs when there are inadequate participant numbers for important combinations of exposure, outcome and covariates, and may lead to bias towards the null and unhelpfully wide confidence intervals. We reviewed studies of influenza vaccine effectiveness (VE) to assess their vulnerability to SDB and its potential impact on estimates. We focused on the elderly because their high vaccine uptake may make data collected more vulnerable to SDB and this group is frequently a target vaccination group, so their VE estimates may influence policy.

Methods: We searched for studies that published VE estimates for the elderly stratified by influenza season and subtype and included 45 studies containing 101 estimates. We diagnosed SDB by calculating events per variable (number of cases divided by number of model parameters) and considering cell numbers in 2x2 tables and prevalence of vaccination. We pooled estimates by subtype and, in sensitivity analyses, estimates at serious risk of SDB were excluded to ascertain the impact of sparse data on pooled estimates.

Results: Of 101 estimates, 65.3% (n=66) were at serious risk of SDB. Excluding these estimates did not affect pooled estimates. Only two studies used statistical methods to mitigate sparse data, while five referred to it as a limitation.

Conclusions: Sparse data is a prevalent yet generally unacknowledged source of bias in studies estimating VE. While pooled estimates were little influenced by SDB, the interpretation of individual studies, particularly those at high risk of bias due to sparse data should be done with caution.

Adverse events following HPV vaccination: 11 years of surveillance in Australia

Authors: Dr Anastasia Phillips1, Mr James Trotterdell2, Dr Richard Hill2, A/Prof Julia Brotherton3, Dr Megan Hickie4, Dr Aditi Dey4, Ms Han Wang5, Dr Frank Beard3, Dr Tom Snelling3, Prof Kristine Macartney4

Affiliations: 1University Of Sydney & National Centre for Immunisation Research and Surveillance & Wesfarmers Centre of Vaccines & Infectious Diseases, Telethon Kids Institute, Perth, Australia, 2University Of Sydney & National Centre for Immunisation Research and Surveillance, Sydney, Australia, 3Wesfarmers Centre of Vaccines & Infectious Diseases, Telethon Kids Institute, Perth, Australia, 4Pharmacovigilance and Special Access Branch, Therapeutic Goods Administration, Canberra, Australia, 5National HPV Vaccination Program Register, Melbourne, Australia, 6National Centre for Immunisation Research and Surveillance, Sydney, Australia

Abstract:

Background: Australia was the first country to implement a fully funded vaccination program with quadrivalent Human Papillomavirus vaccine (4vHPV) in April 2007. We examined adverse events following immunisation (AEFI) from 11 years of surveillance with a focus on adverse events of special interest (AESI) including did not identify any new or unexpected safety concerns.

Methods: We analysed AEFI following 4vHPV doses administered between April 2007 and December 2017 and reported by number of model parameters) and considering cell numbers in 2x2 tables and prevalence of vaccination. We pooled estimates by subtype and, in sensitivity analyses, estimates at serious risk of SDB were excluded to ascertain the impact of sparse data on pooled estimates.

Results: 4551 reports of AEFI were identified after administration of over nine million doses of 4vHPV vaccine. The reported AEFI rate within the target cohorts varied from 30.5 per 100 000 doses administered in women over 18 during the catch-up program (2007 to 2009) to 93.1 per 100 000 in younger females during an enhanced surveillance period (2013 to 2014). The most commonly coded MedDRA preferred term was headache for females (n= 550) and syncope for males (n=362). Detailed analysis of pre-specified AESI including did not identify any new or unexpected safety concerns.

Conclusion: Reported rates were consistent with those in the literature; analysis of AESI did not demonstrate any new or unexpected safety signals. AEFI reports do not demonstrate causality, but rather reflect temporal associations that can be used to guide signal investigation.
**4C – One Health**
Murrumbidgee Room, 1:30pm – 3:00pm

**Hendra, habits and hierarchy: drivers of infection control practices in equine workers.**

**Authors:** Dr Kathryn Taylor¹, Dr Susan Thomas², Dr Diana Mendez³, Dr Jane Heller⁴, Dr Catherine Chicken⁵, Dr Joan Carrick⁶

**Affiliations:** ¹Hunter New England Population Health, Wallsend, Australia, ²University of Newcastle, Callaghan, Australia, ³James Cook University, Townsville, Australia, ⁴School of Animal and Veterinary Sciences, Charles Sturt University, Wagga Wagga, Australia, ⁵Scone Equine Hospital, Scone, Australia, ⁶Equine Specialist Consulting, Scone, Australia

**Abstract:**

**Background:** Employees in the equine industry are at risk of zoonoses such as Hendra virus and equine chlamydiosis through exposure to infected materials. This study aimed to gain a deeper understanding of the views and experiences of employees, and the key drivers of infection control and biosecurity practices in the equine breeding industry.

**Methods:** A qualitative study was conducted in 2018 in New South Wales using interviews (9) and focus groups (7). The 29 participants included veterinarians, veterinary nurses, foaling staff, stud managers and laboratory personnel working in a range of equine medicine settings. Interviews and focus groups were recorded, transcribed and analysed manually by at least two members of the research team. An iterative approach was used to derive themes.

**Results:** Emergent themes included; i) Personal experience with illness or injury in the equine industry encouraged use of Personal Protective Equipment (PPE), ii) Greater awareness of current and emerging biosecurity risks will promote use of PPE, iii) Strong leadership from the top down is required to implement sustainable change, iv) A systematic approach to infection control and use of PPE reduces risk of exposure to infectious materials v) current PPE is not comfortable, practical or suited to Australia’s hot climate.

**Conclusion:** Study results can inform change within the equine industry to ensure staff are protected from zoonotic disease. There is an opportunity for Public Health services and industry partners to collaborate and implement strategies most likely to be effective in ensuring infection control is used by everyone, every time.

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**“Biblical” bat mortality owing to climate change; surprising public health challenges!**

**Authors:** Dr Lea Merone¹, Ms Carlie Thirlwell², Ms Juliet Esmonde²

**Affiliations:** ¹Apunipima / James Cook University, Cairns, Australia, ²Queensland Health, Cairns, Australia

**Abstract:**

**Background:** The association between climate disruption and extreme heat events is irrefutable; heatwave events will inevitably become increasingly frequent and intense. Mass-mortality of insectivorous bats has been documented during previous heatwaves; Cambodia (2016) and India (2010). Far North Queensland experienced a record-breaking summer in 2018-19, including the hottest day for the region on record. Extreme heat decimated the local flying bat population by almost a third. Management of mass-bat mortality posed new challenges for the local public health team, from increased exposure to bat-scratches and subsequent risk of Australian Bat Lyssavirus, to large-scale disposal of decaying bodies from residential areas.

**Methods:** Public health teams from communicable disease control and environmental health were deployed to sites of mass-bat mortality to assess the public health implications. Amongst the multiple noted issues were increased bat exposures and requirement for post-exposure prophylaxis, lack of a co-ordinated clean-up plan, multiple emergency department presentations for “free” pre-exposure prophylaxis and an overwhelming odour from rotting carcasses.

**Results:** Co-ordinated response from the Tropical Public Health Service and local council included: a public health media campaign regarding bat exposure, a co-ordinated clean-up effort for residential areas and mass-education surrounding the handling of injured/dead bats.

**Conclusion:** Whilst the crisis was handled effectively by the team, there are many lessons to be learnt for future events. Climate change will bring foreseen and unforeseen challenges. It is the unforeseen challenges that will pose potentially the greatest threat. It is imperative that we develop flexible responses, expect and prepare for the unexpected.
Initial Lyssavirus post-exposure prophylaxis via Emergency Department: QE2 Hospital pilot project

Authors: Dr Kari Jarvinen1, Dr Alison Ryan2

Affiliations: 1Metro South Public Health Unit, Coopers Plains, Australia, 2Queen Elizabeth 2 Hospital, Coopers Plains, Australia

Abstract:
Context: Potential Lyssavirus post-exposure prophylaxis (PEP) is coordinated in Queensland through local Public Health Units. This entails case-by-case training of treating doctors and stock ordering, without detailed follow-up of required human rabies immunoglobulin (HRIG) infiltration, which is strictly body weight dependent (WHO recommendation 20 IU/Kg).

Process: A pilot project was initiated collaboratively by the greater Brisbane Metro South Public Health Unit (MSPHU) and Queen Elizabeth 2 Hospital Emergency Department (ED) to concentrate initial PEP through the one centre. In addition to summarising presentations, we describe the training, operational and monitoring systems that were set up.

Analysis: During the initial 25 months of the pilot project (up to 1.3.2018) a total of 141 cases were seen through the ED with a median waiting time of 1 hr. The majority (66%) were for overseas rabies exposures. Most exposures were to monkeys and bats (41% and 34% respectively of 133 cases with information). Hand and upper limb were commonest exposures sites. HRIG dosing accuracy was acceptable or varied slightly in 94% of 121 cases (dose range 17.4 to 29.0 IU/Kg). Top-up HRIG was offered where inadequate HRIG was administered, and additional rabies vaccine with serological follow-up recommended for HRIG overdosing.

Outcomes: Case audit demonstrated that initial PEP was managed well overall by ED staff, with simplified processes and close monitoring in contrast to what was possible with previous practice. Vaccination documentation, non-prompted form return and form completeness were most common concerns. The successful collaborative model continues as standard practice in Metro South.

Investigation of the role of domestic pets in Q fever epidemiology

Authors: Dr Gemma Ma1,2, Karen O Mathews1, Katrina L Bosward1, Michael P Ward1, Jacqueline M Norris1

Affiliations: 1The University Of Sydney, Sydney, Australia, 2RSPCA NSW, Sydney, Australia

Abstract:
Background: Q fever is one of the most common and serious zoonotic diseases in Australia. Whilst most cases are attributed to contact with livestock, cases are increasingly reported in individuals without traditional occupational exposures. In addition, Aboriginal people are disproportionately affected. Q fever can occur following contact with companion animals, however their role in Q fever epidemiology is incompletely understood.

Methods: Sample were collected from pet dogs and cats participating in RSPCA Indigenous Community Companion Animal Health Programs in communities across western NSW, a region with high Q fever incidence. Coxiella burnetii antibody titres were determined using an immunofluorescence assay. Quantitative PCR was performed on DNA extracted from whole blood, reproductive tissues and reproductive tract swabs targeting C. burnetii genes com1 and IS1111. Potential risk factors where explored using a pet owner questionnaire.

Results: The seroprevalence was high in both dogs (26.1%) and cats (11.0%). Seroprevalence varied significantly between communities and was correlated with human Q fever incidence. Feeding raw kangaroo was identified as a risk factor. No C. burnetii DNA was detected from dog or cat samples using PCR.

Conclusions: Serocconversion to C. burnetii in dogs and cats correlates with human Q fever incidence making pets valuable sentinels. Variation in seroprevalence in pets likely reflects variation in environmental factors – including dust levels and exposure to major reservoir species – with important implications for public health interventions. The absence of C. burnetii DNA from pet samples suggests the risk posed by pets to the public is low.

South Australian veterinary students’ One Health perspectives on Q fever prevention

Authors: Mr Md Rezanur Rahaman1, Dr Adriana Milazzo1, Prof Helen Marshall2, Dr Anne-Lise Chaber3, Prof Peng Bi4

Affiliations: 1School of Public Health, The University of Adelaide, Adelaide, Australia, 2Adelaide Medical School and Robinson Research Institute, The University of Adelaide, Adelaide, Australia, 3School of Animal and Veterinary Sciences, The University of Adelaide, Roseworthy, Australia

Abstract:
Background: Animal science and veterinary studies may place students at risk of Q fever, transmissible from animals to humans, particularly when unvaccinated. A One Health approach that combines animal, human and the environmental health sectors is a suitable framework to prevent Q fever.

Methods: All animal science and veterinary students enrolled at the University of Adelaide in 2019 were invited to participate in an online survey using SurveyMonkey to gauge their perceptions about Q fever and its prevention strategies. Descriptive analysis was performed.
Results: Of the 694 invited students, 255 completed the survey (response rate 36.7%). Forty-eight percent of students had no/negligible knowledge about Q fever. The majority (66%) were unsure about disease transmission. Most (89%) students reported some contact with beef cattle and sheep during their studies. Seventy-seven percent of students rarely/never used a facemask during their contact with animals, despite 87% believing it is effective in preventing airborne transmission. Twenty-five percent of students reported they were unvaccinated against Q fever. Identified challenges for vaccination included cost (85%), time (73%), and poor access (60%). Most (90%) students suggested that subsidized vaccination, improving healthcare access, and improving workers’ and health practitioners’ knowledge are likely to be effective in improving vaccination uptake.

Conclusion: Knowledge on One Health approach, and Q fever among the surveyed students, particularly about disease transmission is less-than-optimal. Students’ adherence to biosecurity guidelines, particularly those related to airborne transmission prevention e.g. using a facemask could potentially reduce Q fever infection. Unvaccinated students need urgent vaccination for adequate protection.

Citizen science and mosquito surveillance – an approach to track infectious diseases

Authors: Miss Larissa Braz Sousa, Associate Professor, School of Pharmacy and Medical Sciences Craig Williams, Associate Professor, School of Health Sciences Katherine Baldock, Dr Cameron Webb

Affiliations: 1University Of South Australia, Adelaide, Australia, 2The University of Sydney, Sydney, Australia

Background: Citizen science consists of community members’ involvement in scientific research, whereby they contribute to scientific discoveries while learning about their local environment. This research presents an opportunity to investigate a citizen science approach to track vector mosquitoes and assess the impacts on participants’ public health awareness.

Methods: This research is divided into 4 complementary studies:

1) Assessment of data utility for mosquito and disease management;
2) Comparison of different citizen science mosquito surveillance methods;
3) Education and public health literacy benefits of citizen science;
4) Citizen science methods applied in different contexts.

Study 1 explored the reliability and utility of the data collected by the participants in the establishment year of the program. Studies 2 and 3 will focus on collecting data on mosquito surveillance with participants using traps and smartphone apps to track mosquitoes, besides assessing their learning outcomes. Study 4 focuses on a more impoverished, higher disease risk community.

Results: With more than 9,000 mosquitoes collected in one year, this program proved to be successful in yielding increased information about mosquito populations in South Australia, with a possibility to be upscaled to different social and environmental contexts. As a next step, different local communities will be assessed for their contributions to citizen science mosquito surveillance, and their health literacy gains.

Conclusion: The four studies can assess the value of a citizen science mosquito surveillance program in different communities holistically. It also enables participants to bring into science their local contextual knowledge on mosquito diversity and infectious diseases.
4D – Surveillance and information systems
Federation Ballroom Sth, 1:30pm – 3:00pm

Strengthening communicable disease surveillance in Timor-Leste.

Authors: Mr Anthony Draper1,2, Mrs Maria Varela Niha3, Dr Merita Armindo Monteiro3, Dr Nicholas Fancourt4, Ms Rowena Boyd1, Dr Vicki Krause1, Dr Peter Markey4, Ms Karen Champlin4, Dr Joshua Francis4,5

Affiliations: 1Northern Territory Centre For Disease Control, Darwin, Australia, 2Department of Surveillance and Epidemiology, Ministry of Health, Caicoli, Timor-Leste, 3Department of Communicable Disease Control, Ministry of Health, Lahane, Timor-Leste, 4Menzies School of Health Research, Darwin, Australia, 5Royal Darwin Hospital, Tiwi, Australia

Abstract:
Context: Timor-Leste is a low middle-income country 600km north of Australia that has a high burden of infectious diseases. Health infrastructure is weak as a result of the Indonesian Occupation (1975-1999), the post-referendum violence (1999) and the political crisis of 2006-2008.

Process: STRONG TL (Surveillance, Training, Research Opportunities, National Guidelines for Timor-Leste) commenced in July 2018. STRONG TL is a 3-year project funded by the Australian Government Department of Foreign Affairs and Trade (DFAT), through the Indo-Pacific Centre for Health Security and is administered by the Menzies School of Health Research. The project aims to improve the capacity of Timorese ministries to conduct surveillance and response to communicable diseases by: improving clinical and laboratory based communicable disease identification; implementing national guidelines for public health and clinical responses to communicable diseases; conducting operational research on priority communicable diseases; and promoting collaboration between Timor-Leste and Northern Australia.

Analysis: We report on qualitative aspects of the project as well as summarise key outputs such as changes in notification data, training conducted, guidelines developed and outbreaks investigated.

Outcomes: STRONG TL has provided side-by-side mentorship to laboratory, surveillance and clinical staff, improved the quality of notifications, increased the accuracy and number of laboratory and clinical detections of communicable diseases and contributed to the development of the Integrated Disease Surveillance and Response (IDSR) guideline. Our experience is useful for further capacity building in Timor-Leste and other countries in the region.

Web-based applications for communicable disease surveillance and response: a systematic narrative review.

Authors: Dr Isis Maitland-Scott4, Dr Kai Hsiao1, Dr Emma Quinn4

Affiliations: 1Sydney Local Health District, Camperdown, Australia

Abstract:
Background: Early public health intervention can reduce the duration, spread and health impacts of communicable disease (CD) outbreaks. Applications for CD surveillance have evolved rapidly and have been effective in early detection of CD outbreaks in diverse healthcare settings. We conducted a systematic narrative synthesis of the literature to describe studies reporting the barriers/enablers of development, implementation and evaluation of web-based applications that support not only detection of but also response to acute CD outbreaks.

Methods: MEDLINE, Web of Science and Proquest databases were searched (1998 – 2018) for peer-reviewed original research articles in English. Article abstracts were screened using exclusion criteria (n=5) and remaining articles were thematically analysed to identify features, barriers and enablers in the design, implementation as well as evaluation of these applications.

Results: A total of 4001 articles were extracted, reviewed by exclusion criteria and seventeen articles remained for analysis. There was significant variability in type and number of technical features. All noted improvement in detection of outbreaks in terms of timeliness and sensitivity, with incomplete surveillance data the most noted issue. Ease-of-use was identified as the greatest enabler for implementation and uptake. No articles reported efficacy evaluations of these applications.

Conclusion: Web-based applications for CD outbreak response have great potential to improve timeliness and sensitivity of outbreak detection. More research is needed to identify factors that support the effective implementation and use of these applications to directly support CD outbreak response. Evaluation studies are needed to determine the cost-benefit of these applications.
FluCARE: an innovative web-based application supporting influenza outbreak response in aged-care facilities

Authors: Mr Travers Johnstone1, Dr Emma Quinn1, Mr Arun Parasaruman1, Dr Zeina Najjar1, Dr Leena Gupta1

Affiliations: 1Sydney Local Health District Public Health Unit, Camperdown, Australia

Abstract: Influenza outbreaks have significant impacts on residential aged care facilities (RACFs), both on the health of their residents and the workload on their staff. Early outbreak recognition, notification and response are critical in minimising outbreak spread and impact. However, this can be challenged by difficult-to-remember outbreak definitions, time-consuming notifications and communications with multiple stakeholders, and cumbersome daily line listing completion and submissions.

The Sydney Local Health District (SLHD) Public Health Unit (PHU) has developed an innovative web-based application, FluCARE, to address some of these challenges. FluCARE allows RACF staff to report their line listing data online, automatically analyse this data to detect an outbreak, send email notifications to the PHU and relevant responders, and deliver web-based instructions to the RACF for immediate outbreak response actions.

A pilot evaluation with roughly 25 RACFs is being undertaken within SLHD during 2019. The primary objective of the pilot study will evaluate the user acceptability and user satisfaction of the implementation of FluCARE to help RACFs recognise, notify and control influenza outbreaks. The secondary objective is to identify any perceived barriers or facilitators to the implementation and use of FluCARE from a RACF perspective. The pilot study will be followed by an effectiveness study during 2020.

We will showcase the key features of the application as well as present findings from the pilot study highlighting the user experience and key outcome and evaluation measures including; reductions in time to notification, outbreak attack rate, outbreak duration, hospitalisation rates and mortality rates.

Use of REDCap to investigate a gastroenteritis outbreak at a large function

Authors: Dr Belinda Jones1,2, Mrs Kim Lilly1, Ms Julie Collins1, Mr James Flint1, Professor David Durrheim1,3

Affiliations: 1Hunter New England Health, Wallsend, Australia, 2National Centre for Epidemiology and Population Health, Australian National University, Canberra, Australia, 3University of Newcastle, Callaghan, Australia

Abstract: Introduction: In August 2017, the Hunter New England public health unit was notified of several cases of gastroenteritis amongst guests who had attended function ‘X’. An outbreak investigation was commenced with the objectives of identifying the source.

Methods: A cohort study was undertaken. An event-specific online questionnaire was created using Research Electronic Data Capture (REDCap) and emailed to 227 of the 240 function attendees on the same day as notification. Univariable analysis of exposures was conducted to identify the potential source of the outbreak.

Results: A total of 180 attendees (79%) completed the online questionnaire, with 32 attendees meeting the event-specific case definition. Within 3 hours of sending out the questionnaire, 92 attendees (51%) had responded, allowing for rapid epidemiological analysis and assessment of the situation. Two stool specimens were submitted and tested positive for norovirus, confirming this as the causative agent.

Conclusion: Use of the REDCap software to develop and rapidly disseminate an event-specific questionnaire to function attendees allowed a large number of attendees to be reached in a short period of time with rapid collation of data that would be unachievable using conventional phone interviewing techniques. REDCap software proved to be a highly useful tool in this outbreak setting.

Using data linkage to quantify mortality burden of communicable diseases in Victoria

Authors: Stacey L Rowe1,2, Lawrie Jock1, Rebecca Schack1, Nicola Stephens4, Benjamin C Cowie5, Terry Nolan6,7, Leder Karin2, Allen C Cheng2

Affiliations: 1Health Protection Branch, Department Of Health And Human Services, Melbourne, Australia, 2School of Public Health and Preventive Medicine, Monash University, Melbourne, Australia, 3School of Public Health, University of Tasmania, Hobart, Australia, 4Healthcare Resources Optimization, Melbourne, Australia, 5University of Melbourne, Melbourne, Australia, 6WHO Collaborating Centre for Viral Hepatitis, Melbourne, Australia, 7Melbourne School of Population and Global Health, University of Melbourne, Melbourne, Australia, 8Murdoch Children’s Research Institute, Melbourne, Australia

Abstract: Background: Data linkage involves bringing together information about individuals from disparate sources and is useful for monitoring population-wide health outcomes. We describe the establishment of an enduring linkage system to quantify the mortality burden of communicable diseases in Victoria, Australia.

Methods: People notified to the Victorian Department of Health and Human Services between January 1991 and April 2019 with a notifiable condition and captured on the Public Health Events Surveillance System (PHESS) were linked with the Victorian Death Index (VDI) capturing death registrations. Time between illness onset and death were described. Seven- and 30-day case fatality rates for each notifiable condition pre- and post-linkage were calculated.
Results: There were 712,253 people notified with 780,037 conditions (cases), and 47,862 (6.7%) people had a corresponding death registration. Of the 780,037 cases captured in PHESS, 2,805 (0.4%) were recorded as having died, and in 140,749 (18.0%) cases this data item was missing or unknown. Following linkage, 3,998 (0.5%) were identified as having died within 30-days of illness onset. Increases in 30-day case fatality rates were observed for most conditions, notably varicella zoster virus (unspecified: 98%, shingles: 90%), hepatitis B (unspecified: 79%), influenza (79%) and pertussis (77%).

Conclusions: Mortality status is a mandatory data element in the National Notifiable Disease Surveillance System. We developed an enduring data linkage process to improve completeness of this data item and to more accurately quantify mortality burden of notifiable conditions in Victoria. This approach will be used prospectively to enhance existing surveillance and control practices.

Adult vaccine uptake in the Australian Immunisation Register: a first look

Authors: Dr Frank Beard1,2, Mr Brynley Hull1, Dr Alexandra Hendry1, Dr Aditi Dey1,2, Prof Peter McIntyre1,2, Prof Kristine Macartney1,2

Affiliations: 1National Centre For Immunisation Research And Surveillance, Westmead, Australia, 2The University of Sydney, Sydney, Australia

Abstract:
Background: The Australian Immunisation Register (AIR) expanded to whole-of-life on 1/10/2016. Limited data were previously available on adult vaccine uptake. Vaccines recently introduced onto the National Immunisation Program (NIP) include zoster (at 70 with catch up to 79 years) and enhanced immunogenicity trivalent influenza vaccine (TIV) for ≥65 years. We analysed first two years of adult AIR data.

Methods: Analysis of AIR data from 1/10/2016-30/9/2018, focusing on zoster, influenza and 23-valent pneumococcal polysaccharide (23vPPV) vaccines, by year, age and Indigenous status. AIR data were also compared with vaccine dose distribution and survey data.

Results/Discussion: Influenza vaccine uptake was highest in ≥65 year age group (46.3% in 2018). Uptake in Indigenous adults was substantially higher – 64.9% in ≥65 and threefold higher in 18-<65 years in 2018. These figures substantially underestimate true uptake, given uptake in ≥65 years from previous surveys has been ≥70%, and number of enhanced TIV doses in AIR was 44% lower than number distributed under NIP.

For zoster vaccine, 31.2% of adults 70–<80 years were recorded as vaccinated during 1/10/2016-30/9/2018, higher for Indigenous (36.7%) than non-Indigenous (31.1%). True uptake is likely considerably higher, as number of doses in AIR was half that distributed under NIP.

Zoster and 23vPPV doses given peaked in May in both 2017 and 2018, suggesting seasonal influenza vaccination prompts concomitant zoster and pneumococcal vaccination.

Conclusion: Adult vaccination data in AIR substantially underestimate true uptake. It is important to engage with immunisation providers to optimise reporting, and to monitor adult vaccination data over time.
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