



Australian and New Zealand College of Veterinary Scientists

**2018 College Science Week Scientific
Conference**

5–7 July 2018

QT Gold Coast, Surfers Paradise

Epidemiology Chapter proceedings

**Australian and New Zealand College of Veterinary Scientists Science Week 2018
Epidemiology Chapter Conference Proceedings**

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| 10:50 AM | Exploring pet ownership as a risk factor for extended spectrum β-lactamase (ESBL) infection in humans Leah Toombs-Ruane | 26 |
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Current animal disease surveillance systems in Australian livestock industries: where to from here?

Y T Maru¹, M Hernández-Jover², B Loechel¹, **J Manyweathers²**, A Mankad¹, H Kruger³, L Hayes², R Woodgate²

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³Australian Bureau of Agricultural and Resource Economics

To inform the development of a model of farmer-led partnerships for improved animal health surveillance, a review of Australia's current surveillance systems was undertaken. This review was part of a broader research project on "Improved surveillance, preparedness and return to trade for emergency animal disease incursions using foot-and-mouth disease as a model" (FMD Ready).

Data from literature reviews examined surveillance in relation to current on-farm practices and behaviours, the influence of institutions and the role of technology and extension approaches. Interviews and focus groups were carried out with both government and industry representatives involved in the development of policy for, communication around, and adoption of regulations from, the surveillance system.

Key findings include the multifaceted nature of the surveillance system, with major variations between jurisdictions and industries; significant improvements in general surveillance are thought to be possible and necessary. Interacting structural and behavioural issues were also identified, needing institutional attention and behaviour change considerations. The importance of clear program focus, compelling drivers, transparent incentives and effective relationships were also identified as crucial to establishing effective partnerships in the surveillance arena.

Future approaches to improving animal disease surveillance must consider facilitating trust and transparency, as well as understanding core drivers and optimal outcomes for all stakeholders.

Cross-sectional study among Australian livestock producers to investigate the risk of emergency animal disease introduction and spread

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As part of a project to improve animal health surveillance, a cross-sectional study was undertaken to characterise the vulnerability of Australian livestock producers to harm from exposure to, and spread of

an emergency animal disease. This paper explores current levels of trust around animal health monitoring and reporting within the beef and sheep industries. An online survey was developed and distributed through government and industry groups nationally. Data were analysed descriptively and logistic regression analysis was used to characterise producers. A total of 234 beef and 194 sheep producers completed the survey. The majority of these producers identified themselves as being responsible for observing their animals (93%) and reporting unusual signs of disease in their animals (92.5%). Self-responsibility was lower for disease detection, with 20% producers identifying others as responsible. No significant differences were observed between beef and sheep producers. Of a total of 915 beef cattle health problems recalled in the last 12 months (average 5 per respondent), 33.9% (average 2 per respondent) were reported to a private or government veterinarian. When asked about actions in the event of unusual signs of disease, 90% of beef and 82% of sheep producers, ranked contacting private veterinarians in their top five activities. The majority of beef and sheep producers reported high levels of trust in private veterinarians (85%), with 65% producers reporting high trust in their government veterinarians. This study indicates that producers perceive a high level of self-responsibility for observing their animals and reporting diseases. However, their perceived responsibility in detecting diseases is lower. In addition, the level of reporting of animal health problems is low. Findings from this study suggest that producer practices in relation to passive surveillance could be improved and there is potential for enhancing surveillance with more effective producer – veterinarian relationships.

Can Agricultural Innovation systems assist with assessing and reducing Emergency Animal Disease (EAD) risk?

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Australia's strong livestock export and domestic markets are reliant on freedom from many emergency animal diseases (EADs). However, the risk of introduction and spread of exotic, emerging or re-emerging animal diseases, such as foot and mouth disease is rising primarily due to global, regional and national drivers. These include increased trade and movement of people (tourism, migration), animals and animal products, and changes in land use and climate as well as bioterrorism threats. This requires vigilance and continuous improvement of Australia's current animal health biosecurity and surveillance system, in the context of static or declining public sector personnel and resources for managing these risks.

Continuously improving on-farm biosecurity and passive surveillance can play a significant part in reducing the risk of introduction and spread of EADs. Studies have established that improved surveillance

can reduce the time between initial infection and first disease detection which in turn can lead to significant reduction in the number and extent of disease outbreaks and their economic and social impact.

As part of the project FMD Ready project, the authors of this paper are involved in ongoing research to develop a farmer-led partnership model for improved animal health surveillance' in Australia. This research so far a) has developed a synthesised understanding of the constraints and opportunities for improving surveillance based on interview and focus group discussions with representatives from industry and government, b) is undertaking a vulnerability based risk characterisation or typology of producers to the introduction of, and surveillance for, EADs and c) is in the process of establishing innovation pilots informed by the AIS approach.

Our synthesis work found that interacting structural and behavioral factors constrain improvement in passive surveillance. These include low trust, strained relationships, low risk perception, low priority and motivation, and concern about potential economic and social costs from movement restrictions; while quarantine is often considered as punitive.

These complex factors working are not responsive to conventional top-down provision of more information or more regulative actions to persuade behavioral change and/or adoption of improved practices. Neither is research or technology development alone a solution to the trust, relationship and institutional issues. Instead, we are using the AIS approach to develop partnership among surveillance stakeholders: producers, veterinarians, regulatory authorities, livestock agents, rural suppliers, and researchers. We propose that this approach may have a better chance than conventional approaches to enhance trust and build relationship from the ground up and come up with innovations fit for local contexts. We are in the process of establishing five pilots groups consisting of farmers and other relevant stakeholders in the pig, dairy, beef, sheep and goat industries, distributed across five states. The outcome we are expecting from this change in approach is that farmers are motivated to increase monitoring and early reporting of suspected animal health problems, and have easy access to rapid diagnostics and response feedback. Improved partnerships are not only important for 'peace' time but also crucial if and when outbreaks happen, to facilitate an effective response to EADS.

Prioritisation of animal diseases for Australia's emergency preparedness

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¹Biosecurity Animal Division, Australian Government Department of Agriculture and Water Resources

A structured method of prioritising emergency and emerging animal diseases ensures that governmental resources can be appropriately allocated to preparedness activities to address the threat these diseases pose in a systematic way. This is a global issue for both human and animal health, and a wide variety of different methodologies and criteria are being used for prioritisation worldwide.

This presentation outlines a prioritisation project for terrestrial emerging and emergency animal diseases. An initial disease target list was created using criteria such as inclusion on Australia's nationally notifiable disease lists (animal or human), listing by the World Organisation for Animal Health (OIE) or evidence that they were a new and emerging disease. The disease agents were then further evaluated using a semi-quantitative scoring process to determine their rank of importance. The intended outcome is to help prioritise emergency animal disease preparedness activities within the Department of Agriculture and Water Resources.

The veterinary profession's contribution to animal health surveillance in Australia

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Animal health surveillance is key to detecting and controlling animal disease, by creating data to demonstrate disease freedom for trade and to enable domestic disease management. The sensitivity of passive surveillance is influenced by the clinical effects of disease, rate of transmission, population structure (e.g. herd size, production system), disease awareness of animal owners and veterinarians, and their preparedness to report.

Veterinarians are important in surveillance systems. In Australian states and territories the diagnosis of animal disease is a legislated Act of Veterinary Science. Previous studies have shown that veterinarians are key in biosecurity systems as they have been identified as the trusted advisors of farmers to provide advice on topics such as farm biosecurity. However, one study identified that in some instances veterinarians did not see themselves as significant providers of biosecurity information to farmers. This study will investigate the perceived and actual capacity of veterinarians to contribute to surveillance in the Australian context.

This study will involve a quantitative component (Phase 1) and a qualitative component (Phase 2). Phase 1, a cross-sectional observational study using an online questionnaire, will be conducted among the veterinary profession in Australia. The questionnaire gathers data on demographics, work type, current surveillance activities and perceptions on the potential additional contribution of veterinarians to biosecurity and surveillance and Emergency Animal Disease risk management. Phase 2 will involve semi-structured interviews with a cohort of veterinarians participating in Phase 1 conducted over the phone or face-to-face, to gather in-depth information on the veterinary contribution to surveillance systems in Australia, including motivators and barriers to this contribution. The expected outcomes are to characterise key components of veterinarians' relationship with disease surveillance activities to identify any significant relationships.

Preliminary data from Phase 1 will be presented at this conference.

Insights into the knowledge, practices and training needs of veterinarians working with smallholder livestock producers in Australia

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The location of properties holding livestock is fluid; edging towards the boundaries of urban Australia, increasing the likelihood that veterinarians will be exposed to livestock as part of the provision of routine veterinary services. This study was conducted to ascertain the challenges, knowledge level and training needs of veterinarians working within this landscape, with the ultimate aim of informing the development of resources and training to better equip them in this capacity. For this purpose, a cross-sectional study, using a self-administered questionnaire was conducted among Australian veterinarians. The questionnaire comprised a mixture of 47 short closed, semi-closed and open-ended questions and was available for electronic distribution. Complete responses were obtained from 91 veterinarians. Data was analysed descriptively and logistic regression analysis was used to identify potential factors associated with knowledge and practices of veterinarians in relation to smallholders. The main livestock species kept by smallholder clients were sheep, goats, and cattle; with over 90% of respondents reporting mixed species. On-farm visits were reported as the most frequent interaction type, and responding to emergency situations the most frequently performed activity. Over 95% of respondents provided some level of biosecurity advice and zoonotic disease information as part of their routine veterinary service. Although veterinarians provide advice and support to smallholders, only 14.5% considered themselves to be highly influential on smallholder practices. Confidence level in investigating disease differed by livestock species, with lower confidence reported in pigs, poultry and alpaca. The challenges experienced by veterinarians when working with smallholders were mostly related to external factors such as; lack of facilities, lack of client knowledge on animal health management and client's financial constraints. Respondents were open to receiving assistance to support smallholders on matters related to disease, welfare or biosecurity, with other veterinarians (government and private), reported as the most frequently utilised resource. Having access to materials that could be distributed to smallholders was considered to be an effective way in which to provide information. While the risk of zoonotic disease was considered a challenge associated with working with smallholders, respondent's use of personal protective equipment (PPE), whilst performing common veterinary activities, was in many instances inadequate. Similarly, vaccination levels among veterinarians and other workers within the veterinary practice to prevent zoonotic diseases were variable. This study provides an insight into the way in which veterinarians

engage with smallholders, highlighting the importance of providing both groups with the tools necessary to manage the livestock to which are exposed.

Hayes, L., Britton, S., Weerasinghe, G., Woodgate, R., Hernandez-Jover, M., 2018. Insights into the knowledge, practices and training needs of veterinarians working with smallholder livestock producers in Australia. *Preventive Veterinary Medicine* 154, 54-62.

Use of regulatory surveillance data for industry sanitary improvement: a case study of Chilean salmonid data and SRS risk factors

Brendan D. Cowled¹, Emma Zalcmán¹, Jonathan Happold¹, Anne Meyer¹, Amy Burroughs¹, Alison Hillman¹, Ben Madin¹, Angus Cameron¹, Michael P. Ward², Mark A. Stevenson³, and Alicia L. Gallardo Lagno⁴

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Background and objective: The Chilean National Fisheries Service (SERNAPESCA) collects regulatory data from salmon producers on diseases such as Salmon Rickettsial Septicaemia (SRS), a major disease of salmon in Chile and globally. This work concentrated on identifying risk factors for SRS to enable enhancement of SRS management in Chile.

Method: Regulatory data were extracted from 2010-2018. These environmental and disease data were combined using SQL and spatial queries to provide a holistic epidemiological database with ~ 87 000 weekly production records.

Biologically plausible *a priori* hypotheses about what factors drive disease were developed.

Zero inflated mixed negative binomial spatial models were implemented to represent each of the hypotheses. The most supported models were selected using information theory.

Coefficients of the most supported models and other models generated *post hoc* were examined to understand which factors modulated the incidence rate of SRS.

Results and discussion: Several important risk factors for SRS were identified. Species of salmonid, co-infection with sea lice, sea vaccination for SRS, infection pressure in a local waterway, site fish density and indicators of smolt quality were key risk factors associated with SRS mortality. Many of these have the potential to be manipulated to reduce SRS (e.g. coordinated stocking/fallowing).

Accumulating cumulative degree days were closely negatively associated with the likelihood that a site would remain un-infected in the zero-inflated part of the model. Coho and rainbow trout were less likely to be infected by SRS (excess of zero's), but once infected rainbow trout suffered high mortality rates compared with Atlantic salmon.

These results indicate that regulatory data maybe inexpensively used a second time to advance the industry wide management of severe production and trade limiting diseases, thereby enhancing the sanitary status of a national industry.

Using lung scoring as a tool to evaluate thoracic lesions in pigs from selected slaughterhouses in the provinces of Batangas and Bicol, Philippines

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¹²Bureau of Animal Industry, Diliman, Quezon City, Philippines.

Respiratory disease is one of the most important disease syndromes of pigs in the Philippines. Lung scoring is a widely accepted technique to evaluate thoracic lesions and can be used for respiratory disease surveillance. This study aimed to estimate the prevalence of thoracic lesions in slaughter-age pigs in two provinces in the Philippines (Batangas and Albay) and identify patterns of co-occurrence of lesions in these populations.

A total of 260 pigs from five slaughterhouses in Batangas and 300 pigs from four slaughterhouses in Albay were included in the study. Farm type (commercial or smallholder) was recorded for each pig. Lungs were scored for cranio-ventral pneumonia using a scale of 0 to 55 and for pleurisy from 0 to 3. Presence or absence of pericarditis and lesions consistent with *Actinobacillus pleuropneumoniae* (APP-like lesions) were recorded. Lung scores were categorised as zero: 0, mild: 1-6, moderate: 7-20, and severe: 21-55. Latent class analyses considering four indicator variables (categorised lung score, pleurisy, pericarditis and APP-like lesions) and two covariates (province and farm type) were used to explore different patterns of thoracic lesions across the study populations.

The median lung score was 7 in Batangas and 0 in Albay with interquartile ranges 2-19 and 0-2, respectively. Using a threshold of ≥ 7 , 51.9% and 13.7% pigs had a high lung score from Batangas and Albay. Similarly, 56.9% and 5.0% had a pleurisy score of ≥ 1 , 24.6% and 1.7% had pericarditis and 7.7% and 0% had APP-like lesions, Latent class analysis identified four classes based on thoracic lesions: 1)

“healthy pigs” unlikely to have any thoracic lesion, 2) “multi-lesion pigs” likely to have a moderate-severe lung score, pleurisy score of ≥ 1 and much more likely than any other class to have pericarditis and two intermediate classes, 3) one likely to have a zero-mild lung score a 0-1 pleurisy score and unlikely to have pericarditis, and 4) the other a mild-severe lung score but unlikely to have pleurisy or pericarditis. The relative frequency of these classes differed between the two provinces and between smallholder and commercially raised pigs within provinces. Most pigs from Albay were “healthy pigs”, whereas most pigs from commercial farms in Batangas were “multi-lesion pigs”.

This study has provided baseline data for these provinces and identified patterns of co-occurrence of lesions. Targeting areas where “multi-lesion pigs” are most common should maximize impact of future control measures.

This work is supported by ACIAR and PCAARRD.

Analysis of animal health data using text processing methods

Barbara Moloney¹

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Free-text information is commonly stored in medical and veterinary databases in addition to structured information such as owner/patient names, age, species, diagnosis codes, laboratory test results etc. In NSW Department of Primary Industries (DPI) and Local Lands Services (LLS) biosecurity information is collected from veterinary property contacts and visits, and laboratory investigations.

This presentation aims to explore text processing methods to analyse animal health data in free-text form which cannot be done using standard modelling methods such as logistic regression. Specifically, by analysing free-text in animal health records, this could enable additional insights for biosecurity decision making.

The clinical Text Analysis and Knowledge Extraction System (cTAKES)¹ is an open source Apache1 project developed specifically for the analysis of electronic medical records. It is based on the Unstructured Information Management Architecture (UIMA)² framework. cTAKES can run various annotation procedures over free text to enable output of a more structured form of the data to which more standard analysis methods and Natural Language Processing (NLP) can be applied.

¹ The Apache Software Foundation <http://www.apache.org>

² Apache UIMA <https://uima.apache.org>

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Use cases for cTAKES and NLP include in the human medical domain: syndromic surveillance², smoking status³ and clinical document feature engineering⁴ using dictionaries such as the Unified Medical Language System (UMLS)³.

Veterinary use cases for NLP include VetCompass Australia⁵ for surveillance analysis of companion animal clinical records, identification of cases and controls for risk factor studies of myiasis in rabbits⁶ and laminitis in horses⁷. There is also a veterinary extension for the UMLS dictionary⁴.

This work will explore, as a pilot, the application of text processing to gain further insights from NSW Biosecurity data.

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1. Savova GK, Masanz JJ, Ogren PV et al. Mayo clinical Text Analysis and Knowledge Extraction System (cTAKES): architecture, component evaluation and applications. *J Am Med Inform Assoc* 2010;17:507-513.
 2. Lu HM, Zeng D, Chen H. Ontology-Based Automatic Chief Complaints Classification for Syndromic Surveillance. 8-11 Oct. 2006 2006.
 3. Savova GK, Ogren PV, Duffy PH, Buntrock JD, Chute CG. Mayo Clinic NLP System for Patient Smoking Status Identification. *Journal of the American Medical Informatics Association : JAMIA* 2008;15:25-28.
 4. Garla VN, Brandt C. Ontology-guided feature engineering for clinical text classification. *J Biomed Inf* 2012;45:992-998.
 5. McGreevy P, Thomson P, Dhand N et al. VetCompass Australia: A National Big Data Collection System for Veterinary Science. *Animals* 2017;7:74.
 6. Turner R, Arsevska E, Brant B et al. Risk factors for cutaneous myiasis (blowfly strike) in pet rabbits in Great Britain based on text-mining veterinary electronic health records. *Prev Vet Med* 2018;153:77-83.
 7. Welsh CE, Duz M, Parkin TDH, Marshall JF. Disease and pharmacologic risk factors for first and subsequent episodes of equine laminitis: A cohort study of free-text electronic medical records. *Prev Vet Med* 2017;136:11-18.

Beyond the proximate risk factors

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In the context of emerging infectious diseases, many epidemiologists are recognising the need to balance empirical and predictive research. This interest has grown as proximal disease causation models fail to adequately inform the anticipation of disease events at relevant spatial scales. This thinking is also pushed by the view that epidemiology should not be essentially reactive. So although factors leading to the emergence are often identified in retrospect, there is a need to better anticipate areas of higher risk of emergence, to better inform broad ranging policy and risk based surveillance. This work requires more anticipatory and scenario based research, which is in addition to the more traditional risk factor type

³ UMLS <https://www.nlm.nih.gov/research/umls/>

⁴ Veterinary extension SNOMED CT <http://vtsi.vetmed.vt.edu/>

epidemiological research and models. Globally, interest in these approaches was initially stimulated by avian influenza, but more recently the Ebola virus emergence and outbreaks in West Africa has added further impetus to this thinking. This presentation will provide an overview of work that captures various elements of the drivers of disease emergence and how these can be considered and incorporated in such anticipatory and scenario based epidemiological approaches. Drivers covered will include issues such as trade flows of animal and animal products within countries or across country borders, the development of demographic and urbanization projections quantifying changes in demand patterns, intensification of farming systems and changes in land use. This work is intended to assist in better assessing the policy implications of economic development (including new infrastructure developments) in advance, so that unintended consequences are more likely to be avoided.

The prevalence of dairy goats shedding *Coxiella burnetii* at the time of parturition in an endemically infected herd and associated milk yield losses

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Introduction: This was a panel study of the prevalence of *Coxiella burnetii* in goats in a Q-fever endemic dairy enterprise in Victoria, Australia. Our objectives were: i) to determine the prevalence of does shedding *C. burnetii* at the time of parturition; ii) to select a subset of does identified as *C. burnetii* positive and to resample them at their subsequent kidding event to determine the proportion that were persistent shedders; and iii) to quantify the association between *C. burnetii* qPCR status at the time of kidding and daily milk yields produced during the subsequent lactation.

Materials and methods: Vaginal swabs ($n = 490$) were collected from does on three herds and analysed using qPCR targeting *com1* and *IS1111*. Does were classified as qPCR-negative ($n = 392$), qPCR-positive low ($n = 56$) and qPCR-positive high ($n = 14$) based on the estimated number of genome equivalents (GE) from the qPCR *com1* analyses. A mixed effects regression model was developed to compare daily milk yields among the three *C. burnetii* qPCR *com1* status groups.

Results: Across the three study herds there were 15 (95% CI 12 to 18) *com1* qPCR-positive does per 100 does at risk. The number of GE in positive qPCR *com1* samples was highly skewed, with a small number of animals shedding extremely large quantities of *C. burnetii* (super-shedders). Persistent shedding was detected when using the more sensitive *IS1111* qPCR in 8 (20%; 95% CI 10% to 35%) out of 40 does resampled. Does within the qPCR-positive high group produced 0.536 (95% CI 0.086 to 0.986) liters less per day compared to qPCR negative does ($p = 0.019$).

Conclusion: Q-fever control strategies for dairy goat herds should aim at identifying and removing super-shedder does before they kid to reduce disease transmission. An additional benefit of this strategy is the removal of low producer does.

Socioeconomic impacts and risk factors analysis of foot and mouth disease in livestock in central Myanmar

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Foot-and-Mouth Disease (FMD) is a highly infectious disease that affects livestock holders in South East Asia including Myanmar. Control of FMD in this region is challenging due to low awareness by farmers, frequent illegal animal movements across border, limited veterinary infrastructure and resources. A questionnaire survey was conducted in late 2016 to understand the socioeconomic impacts and risk factors of FMD in typical households in Mandalay and Sagaing regions in central Myanmar. Face-to-face questionnaire interviews with animal owners were conducted in 816 randomly selected households in 136 villages of 24 townships. The questionnaire was designed to obtain information about human demographics, livestock population dynamics, general farm practices, vaccination history, farm income/expenditure, livestock husbandry and livestock disease management, particularly related to FMD. More than half of the households (52%) reported at least one observation of clinical FMD between 2012 and 2016. Households with a recent occurrence of clinical FMD in 2015/16 tended to have a lower income from rice (-26%) presumably due to lower efficiency in cultivation and harvesting. In addition, small draft cattle herds (≤ 3 cattle) with FMD had a higher sales rate (+23%) and a higher purchase rate (+63%) for draft cattle, resulting in a net loss of USD 100 per year for a typical small herd. Households with FMD spent USD 4 per animal on treatment (88% of households), USD 11 on renting another animal (16% of households), USD 0.7 on vaccination (10% of households), or USD 572 per animal on buying additional animals (4% of households). The estimated average financial cost due to FMD in draft cattle herds was USD 57 per household. Moreover, reduction in milk by 72% for 2 or more months due to FMD was reported by the majority (95%) of the dairy farmers. The average cost of the milk loss due to FMD in lactating cows was estimated at USD 89 per cow. Clinical FMD was less frequently observed in households using vaccination (OR=0.38, $p=0.008$) or selling cattle/buffaloes (OR=0.37, $p=0.002$). The risk of FMD increased when animals were grazed on communal pasture (OR=2.02, $p=0.016$) and in households with pigs (OR=2.54, $p=0.002$). The role of herd size was marginal (OR=0.96, $p=0.001$) and

the role of purchasing animals was unclear. The findings indicated that FMD was widespread in Central Myanmar and that was associated with socio-economic loss.

Cross-sectional serological survey, risk factors and financial impacts of foot and mouth disease in Southern Lao PDR: a baseline study

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Foot-and-Mouth Disease (FMD) is a highly infectious disease that affects livestock holders in South East Asia and is endemic in Lao PDR. A serological and baseline survey was conducted in late 2016 to understand the prevalence, risk factors and socioeconomic impacts of FMD in typical households in two provinces of Southern Lao PDR (Champasak, Savannakhet). Blood samples (n=1,769) were collected from cattle and buffaloes and face-to-face questionnaire interviews with animal owners were conducted in randomly selected households (n=456) of 100 villages in 19 districts. The questionnaire was designed to obtain information about human demographics, livestock population dynamics, general farm practices, vaccination history, farm income/expenditure, livestock husbandry and livestock disease management, particularly related to FMD. The serosurvey revealed that 47.4% (817/1725) of the large ruminant population had been exposed to FMD virus with an estimate of 21.1% incidence occurring in the previous 12 months. Aggregating tested animals at household level, 76% households had at least one animal testing sero-positive. FMD prevalence was increasing with age ranging from approximately 22.4% in calves (<18 months), 43.3% in young (18-36 months) and 61.5% in adult animals (>36 months). Questionnaire respondents of 59% of the households reported at least one observation of clinical FMD between 2012 and 2016. A recent occurrence of FMD in a household did not affect the household income, the sales rate or the sales price of cattle or buffaloes, but was associated with a lower calving rate (-30%) and a higher death rate (+125%) of cattle or buffaloes. The majority of households (>70%) with a history of clinical FMD spent USD 8 per animal on treatment of infected animals. These findings indicated that FMD might reduce net household income due to extra expenditure or reduced livestock productivity. Factors associated with reduced clinical FMD in a household were vaccination status (OR=0.23, p=0.02) and keeping livestock as the main agricultural activity (OR=0.26, p=0.003). Moderate herd size (OR=3.25, p=0.037) increased the risk of clinical FMD. Moderate village-level livestock population size was a risk factor (OR=2.06, p=0.018) for high seroprevalence in the household. While spurious effects and common causes could not be ruled out, the survey demonstrated a high incidence of

FMD in the two provinces with likely negative socio-economic impact on household income and livestock productivity.

The relationship between rainfall and the geographic distribution and prevalence of sparganosis in wild boar

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Sparganosis is a zoonotic disease caused by the cestode *Spirometra erinacei*. Wild boar (*Sus scrofa*) are secondary intermediate hosts and the presence of the plerocercoid larvae or spargana in meat is a cause of condemnation at post mortem inspection.

Wild boar are harvested for export in Queensland and New South Wales. Prior to 2010, the endemic area for sparganosis in wild boar was confined to Cape York Peninsula and the Gulf Country (south of the Gulf of Carpentaria). In 2010, low levels of infection were detected from wild boar from across Qld and northern NSW. In 2013, the condemnation rate, due to sparganosis, of processed boar from the two states reached 2.4% before declining to 0.5% currently.

Given the first intermediate host is a crustacean (cyclopod or water flea), a putative cause of this epidemic is the very high rainfall that occurred across the two states in 2010 and 2011. The possible mechanisms for the rapid expansion of the geographic distribution are discussed by the authors but remain a mystery.

The seroprevalence and risk factors associated with selected flaviviral infections of horses in North Queensland

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In the last 10 years, little work has been done on flaviviral infection of horses in the tropical regions of Australia despite the widespread distribution of two major Australian mosquito-borne flaviviruses, namely Murray Valley encephalitis virus (MVEV) and Kunjin virus (KUNV). A study of the seroprevalence of MVEV, KUNV and Edge Hill virus (EHV) in horses of North Queensland (NQ) was therefore undertaken from March 2014 until May 2015. Furthermore, the associations between potential risk factors and the seroprevalence of these viruses were evaluated by completion of a questionnaire and using univariable analysis and multivariable logistic regression models. A total of 267 horse samples originating from the Far North, Northern, Mackay and North West regions of NQ were collected from regional veterinary

clinics, horse competitions and shows. The samples were tested using the serum neutralisation test and samples reacting to specific flaviviruses at dilution of 1:10 or greater were considered positive.

The apparent prevalence of antibody to MVEV, KUNV and EHV in NQ was 17%, 31% and 25% respectively. The true prevalence was calculated, taking into account the clustering effect of the survey design, and was found to be 8-26% for MVEV, 27-36% for KUNV, and 19-31% for EHV. The most frequent titre recorded for all selected flaviviruses was 10. No difference in the seroprevalence of KUNV between the Far North, Northern and Mackay regions was observed ($\chi^2=5.0$, $df=2$, $p=0.08$). However, the seroprevalence of MVEV ($\chi^2=9.8$, $df=2$, $p<0.01$) and EHV ($\chi^2=7.9$, $df=2$, $p=0.02$) in the northern region was significantly higher than that in Mackay and Far North regions.

The seroprevalence of MVEV was higher in the areas with below average rainfall levels compared to above-average rainfall areas ($P_{Wald}=0.01$, $OR=2.3$). Moreover, horses in the above average temperature areas are at higher risk of being positive for MVEV than those in the below average temperature areas ($P_{Wald}=0.04$, $OR=0.1$). The presence of cattle was associated with the seroprevalence of EHV in horses ($P_{Wald}=0.01$, $OR=2.4$).

The present study shows that a high proportion of horses in NQ are exposed to the selected flaviviruses with low titre antibodies. It also describes for the first time the seroprevalence of EHV in horses in Australia.

“Operation Bluestorm”: surveillance for bluetongue virus exposure in herds surrounding an index property in northern Victoria, October 2017

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Bluetongue is an arthropod-borne, viral (arboviral) disease of ruminants, caused by a member of the genus *Orivirus* (family: *Reoviridae*), with 24 serotypes identified globally. Within Australia, bluetongue virus (BTV) is transmitted by biting midges or haematophagous flies belonging to the genus *Culicoides* (Diptera: Ceratopogonidae). Although Australia remains free from clinical disease due to bluetongue virus infection, significant livestock mortalities have been recorded internationally and the disease poses a significant threat to agricultural economies worldwide.

Since 1993, the geographic distribution of BTV across Australia has been monitored using sentinel cattle herds. Transmission and surveillance zones for BTV have typically involved the northern Australian states of Queensland, Northern Territory, New South Wales and Western Australia, with regular zone updates. Historically, the state of Victoria has been categorised as free of BTV and this status underpins a significant dairy heifer export trade to numerous destinations, including China, Israel and Mexico.

In early October 2017, seven dairy heifers from a northern Victorian property that were undergoing routine testing prior to export to China were identified as BTV cELISA positive, with four heifers confirmed with exposure to serotypes 1 and/or 21 using the serum neutralisation test (SNT). All seven heifers were negative on qPCR and none showed clinical signs of bluetongue. Four of the heifers (including three that were SNT-positive) were sourced from a property in northern New South Wales (within the BTV transmission/surveillance zone) while two (both SNT-negative) were confirmed as Victorian born and bred ('home-bred'). One SNT-positive heifer (BTV-1) was confirmed, based on available evidence, as Victorian home-bred.

This represents the first recorded case of a verifiably Victorian home-bred animal with serological evidence of exposure to BTV (of any serotype).

In response to this detection, a temporary 50 kilometre potential BTV 'transmission' zone and an additional 50 kilometre 'buffer' zone was placed around the index premises on 13 October 2017. A cross-sectional study of 2,531 Victorian home-bred cattle within a five kilometre radius of the index premises ('surveillance zone') identified a further twenty-three cELISA-positive animals; a prevalence of 0.9 (95% CI 0.6 to 1.4) cELISA-positive animals per 100 animals at risk. Two of this group were positive on SNT for serotype 21. All animals were clinically normal and were negative on qPCR. All diagnostic testing was undertaken at the Australian Animal Health Laboratory (AAHL; Geelong; Victoria).

On review of the results, the Animal Health Committee (AHC) concluded that, while there was no evidence of virus circulation within the temporary surveillance zone at the time of sampling, a small number of Victorian home-bred cattle may have been exposed to BTV. On the basis of these conclusions, the temporary transmission and buffer zones were lifted on 6 December 2017 and a program of enhanced BTV surveillance has been implemented in the region.

This event, the results of enhanced monitoring and possible scenarios in northern Victoria, will be discussed.

Anthrax in Swan Hill, 2017; the story of an outbreak

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Anthrax is a zoonotic disease caused by *Bacillus anthracis*, an aerobic, gram-positive spore-forming bacterium. The spore form of *B. anthracis* is extremely resilient to heat, desiccation and chemicals and can remain dormant in soil for decades. Grazing herbivores become infected through ingesting spores present in contaminated soils. The bacteria produce potent toxins that cause the clinical signs of anthrax, typically sudden death with blood-stained exudate visible at the nose, mouth and/or anus.

The first recorded case of anthrax in Australian livestock occurred in 1847 in New South Wales following the importation of meat and bone meal fertilizer believed to be contaminated with the organism. Subsequently, there have been sporadic but consistent reports of clinical anthrax in sheep and cattle in Victoria and New South Wales. Prior to 2017, the last major outbreaks of anthrax in Victoria occurred in 1997 (83 farms and a total of 220 cattle and 4 sheep) and 2007 (10 farms and a total of 37 cattle), both located in the Goulburn Valley. Since 1950, the majority of cases of anthrax in sheep have occurred in central New South Wales. Prior to 2017, there had been one recorded case of anthrax in the Swan Hill district (north-west Victoria), specifically a single bovine in 2002.

Anthrax was diagnosed in a sheep at Swan Hill on 3 March 2017. The disease was controlled but revealed itself again in March 2018 in another, closely associated property. Across March and April 2017 and March 2018, 172 sheep carcasses were incinerated from a total of six individual parcels of land across the Swan Hill district, with 49 carcasses confirmed as infected with anthrax using an immunochromatographic test (ICT), culture and qPCR. Over 9,000 sheep and a small number of cattle, goats, pigs and horses were vaccinated for anthrax in 2017 or 2018, representing a significant resource allocation by Agriculture Victoria and the cattle and sheep industries that co-fund anthrax vaccination. Although the cases were geographically located across an area with a radius of approximately 20 kilometres to the west and north-west of Swan Hill, all were associated with one of two management groups who managed numerous parcels of land across the district.

Historically, within Victoria, anthrax had typically been observed in cattle and an outbreak of this disease in sheep, was unexpected. The unique story of the 2017 and 2018 anthrax outbreaks in Swan Hill will be described, including an evaluation of caching behavior by red foxes, the risk of anthrax transmission in wool, re-vaccination and whether you can vaccinate alpaca for anthrax.

Searching for anthrax in the clouds: an anthrax early notification system

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Anthrax is a world-wide disease caused by *Bacillus anthracis*, a resilient, spore-forming bacterium that primarily affects herbivores although is infamously zoonotic. Anthrax was first recorded in livestock in Australia in 1847; reportedly introduced in contaminated fishmeal fertilizer. It spread south following historic stock routes with recent major Australian outbreaks in 1997 (83 farms) and 2007 (10 farms) in the Goulburn-Valley district and 2017 (5 farms) in Swan Hill, Victoria. Today, many Victorian farmers resist prevention measures (primarily vaccination) as they are believed to decrease herd production and fertility. Profound social and media stigma associated with the infection also affects willingness to report suspect cases. If, as anecdotal evidence purports, disease incidence is associated with climatic conditions,

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meteorological data could predict the periods of greater risk offering more effective and efficient application of control measures and promote targeted compliance, especially if delivered through a trusted communication route.

This project modelled historic daily meteorological data from each shire in Victoria and New South Wales to predict high risk periods based on all confirmed regional diagnoses from 1958. The model parameters were then applied to current daily weather data in each shire to predict the odds of a case over the coming 30 days. Concurrent to the building of the model, the social impact of anthrax and farmer engagement with disease prediction was assessed. This was then used to guide the design of an optimal tool to best demonstrate the daily risk and improve outcomes.

Predictive model

Cumulative rainfall and mean maximum and minimum daily temperature data from each shire were summarised in incremental durations from 10, to 100 days preceding both the start of the shire-year risk period or the case-date respectively. Absolute values, deviations from the annual mean value and transformed values were tested in a generalised linear mixed effect model where shire was fitted as a random effect to account for climatic differences between shires. Model selection was led by the need to maximize the predictive performance of the model and was quantified using the area under a receiver operating characteristic (ROC) curve. Shires were given a spatial weighting based on frequency of previous cases and previously modelled geological risk.

Greater odds of disease were found in shires-years that had cooler, wetter springs (OR = 0.56 (95%CI 0.37-0.81) and OR = 0.99 (0.99-1.00) respectively) and warmer minimum temperatures in early summer as well as following 30-day periods of warmer than average minimum temperatures (OR = 1.55 (95% CI 1.27-1.91) and OR = 1.64 (95% CI 1.25-2.18) respectively).

Communication route

To determine the most effective platform to demonstrate the outcome of this predictive model, a sample of Victorian dairy farmers volunteered to participate in a Design Thinking process that included in-depth interviews and structured post-interview interpretation. Distinct themes that reflected findings from the composite interviews included geographically distinct perceptions of risk, a profound sense of social isolation following a diagnosis and an implied resistance to report fallen stock due to previous management of infected premises. Farmers cited public perceptions of bioterrorism coupled with a sense of powerlessness to control the disease as primary reasons for its elevated profile. Highest engagement with disease predictions was reported if information was received from more than one of their farm network and not simply through a web application. However, key farm network representatives preferred visual cues delivered through a web application hosted by official State Departments.

Preliminary release of the Anthrax Early Notification System web application to farm network representatives provides timely coverage of an overlooked issue in the industry, especially following the

recent outbreak in Swan Hill, Victoria. It heralds a refocus by Victoria on how it engages with farming communities regarding anthrax in livestock and can inform the department of the future viability of lightweight, targeted disease forecasting models.

Seroprevalence of *Coxiella burnetii* in North Australian beef cattle using an indirect Immunofluorescence assay (IFA)

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Coxiella burnetii is a zoonotic bacterium able to infect multiple species; it is the causative agent of Q fever in humans and coxiellosis in animals. Ruminants, including cattle, sheep and goats are considered to be an important source of human Q fever. While Q fever in humans is a notifiable disease in Australia, the infection in animals is not, and knowledge of the true prevalence and distribution of coxiellosis in cattle populations across Australia is limited. The aim of this study was to estimate the prevalence of detectable IgG antibodies against *C. burnetii* in thawed frozen serum samples collected from breeding cattle across Queensland and the Northern Territory. An indirect immunofluorescence assay (IFA), previously validated for use in cattle, was used to test the sera from 2013 breeding cattle from 62 properties. Results from serological testing will be presented at the animal, mob and regional level. Test sensitivity and specificity of the IFA, will be used to estimate the true prevalence of *C. burnetii* exposure in cattle populations tested. Seroprevalence results will provide baseline data necessary to further investigate associations between serostatus and environmental and farm management factors to provide insights into potential risk factors and implications of coxiellosis in the northern Australian beef industry.

Antibiotics in the environment: sources and consequences

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The production of antibiotic chemicals and resistance to these chemicals are ancient survival strategies of bacterial species living in complex and competitive natural environments. However anthropogenic activities such the release of active and partially metabolized antibiotics into the natural environment may contribute significantly to the current global health crisis of antibiotic resistance. Every year thousands of tonnes of antibiotics are administered to humans and animals, 70- 90% of which are released unchanged in waste. Whilst manure and waste water treatments are effective in removing pathogens they are

generally ineffective at removing antibiotic residues. In addition waste products contain antibiotic resistant bacteria and antibiotic resistance genes selected for in the gastrointestinal tracts of humans and animals treated with antibiotics. Treated and in many countries untreated waste products are used as crop and pasture fertilizer or may simply be disposed of in waterways. Antibiotics have been detected in most environmental media including soil and surface, underground and coastal water and sediment. Even at sub therapeutic concentrations antibiotic residues promote antibiotic resistance as bacterial populations evolve by mutations and/ or horizontal gene transfer. Identical antibiotic resistance genes and insertion sequences have been found in environmental bacteria and clinical isolates implicating the environment as a source of antibiotic resistance in pathogenic bacteria. Humans and animals are exposed to antibiotic resistant bacteria and antibiotic resistant genes in water, pastures, forage crops and vegetables.

The aim of this review is to provide an overview of the literature on the topic of anthropogenic antibiotic contamination in the environment and the causes and consequences of this contamination.

Antimicrobial use and resistance in plant based agriculture

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Bactericides, fungicides and other plant protection products play an important role in the management of plant diseases. However, their use can result in residues on plants and in the environment with detrimental consequences. Use of streptomycin and oxytetracycline is correlated with increased resistance among these plant pathogens to these agents. Resistance to copper compounds and other fungicides is also frequently observed. Importantly genes can be exchanged among a variety of bacteria in the plant production environment and in the food chain. Through co-resistance, cross resistance and gene up-regulation, resistance to one compound may confer resistance and multi-drug resistance to other similar or even very dissimilar compounds. Given the alarming and global rise in antimicrobial resistant organisms worldwide and their effects on plant, animal and human health, the prudent use of plant protection products is required to maintain their effectiveness and limit the emergence and transmission of AMR microorganisms from horticultural sources.

Biocide and disinfectant use driving antimicrobial resistance

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Biocides are chemicals with antimicrobial properties that are used as antiseptics, disinfectants or preservatives in healthcare, industry and consumer products. They play an essential role in limiting the spread of infectious diseases. The food industry is dependent on these chemicals, and their increasing use is a matter for concern due to their potential to promote emergence of resistant microbial strains. Specifically, the emergence of bacteria demonstrating increased tolerance to biocides, coupled with the potential for the development of a phenotype of cross-resistance to clinically important antimicrobial compounds is of public health relevance.

The aim of this study was to summarize the current state of knowledge on biocide use as a driver of antimicrobial resistance and to identify knowledge gaps.

The role of biocides as selectors of resistant strains, or as inducers of mechanisms involved in antimicrobial resistance has been described in numerous genetic and bacteriological experiments. Studies reporting cross-resistance in clinically important antibiotics are conflicting. However, data establishing risks in the food processing environment as well as data linking the cross-resistance with antibiotics in clinical and food isolates is lacking. Upon the synthesis of the available evidence, prudent use of biocides might be recommended in order to maintain their effectiveness and to limit release in the environment. However, additional research including epidemiologic investigation and analysis of the data from commercial settings is required to better assess the implications of biocide resistance in possible monitoring recommendations for food industry.

Understanding antibiotic prescribing practices: a comparative study of doctors, dentists and veterinarians

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Antibiotic resistance (AbR) is a threat to human and animal health. Contributing factors are diverse, as are stakeholders. A One Health approach is advocated to address the AbR crisis

(<http://www.who.int/antimicrobial-resistance/publications/global-action-plan/en/>), and a key strategy is to improve antibiotic prescribing practices. To achieve this, prescribing attitudes and perceptions need to be understood. A comparison of doctors, dentists and veterinarians – the only prescribers of antibiotics in the Australian context – can provide critical information for the design and adoption of policies to improve prescribing practices. This study was undertaken to collect such data.

A survey of doctors, dentists and veterinarians practicing in primary, secondary or tertiary care in Australia was conducted online. A sampling frame was created by integrating a range of professional lists. Demographic information was collected. Questions – generally using a Likert scale – sought information on prescribers' knowledge, attitudes and perceptions of AbR. Significant ($P < 0.05$) differences in responses between prescriber groups were identified using Kruskal-Wallis tests.

A total of 547 doctors, 380 dentists and 403 veterinarians completed the survey. Key attitudes and perceptions were noted. Veterinarians were less likely to rate unnecessary use of broad-spectrum agents, prescribing with uncertain benefit, and longer antibiotic courses as “significant”, but more likely to rate low doses of antibiotics as “significant” contributors to ABR; dentists, were more likely to rate failure to remove the source of infection as “significant”; and doctors were less likely to consider patients not taking a full course or using leftover antibiotics as “significant”.

Doctors and dentists were more likely to perceive antibiotic use in livestock and companion animals as “significant” and “moderate”, respectively, whereas veterinarians rated these as making “moderate” and “minimal” contributions to AbR, respectively. Doctors generally rated current levels of antibiotic use in “my principal place of practice” as making a “moderate” contribution to AbR; dentists and veterinarians rated this as “minimal”.

Veterinarians generally rated AbR as a “moderate” problem for health of the livestock and food animal industry, but a “minor” problem in other veterinary patients. Doctors and dentists were more likely to rate their own roles as “very important” in preventing or managing AbR.

The majority of respondents across all prescriber groups were aware of the current and increasing problem of AbR, which is an encouraging foundation towards achieving a One Health approach. However, characterisations of AbR more as a human health problem than an animal health problem, and externalisation of responsibility of AbR on to others (by all prescriber groups), represents a challenge to achieving a One Health approach, as individuals may be less critical of their own actions in relation to others.

Exploring pet ownership as a risk factor for extended spectrum β -lactamase (ESBL) infection in humans

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Companion animals often live within homes and share living space with people. In New Zealand, 60% of households have a pet, with 44% having at least one cat and 28% having at least one dog. As multidrug resistant infections become more common in the community, especially those involving extended spectrum beta-lactamase- (ESBL) producing *E. coli*, the role that companion animals play in these human community-acquired infections warrants investigation.

A prospective case-control study was conducted between August 2015 and September 2017. Cases were defined as people with community-acquired urinary tract infection (UTI) caused by newly acquired ESBL- or AmpC beta-lactamase- (AMPCBL) producing Enterobacteriaceae. Both cases and controls were recruited from the Auckland and Northland regions of New Zealand, with randomised dialling selection of controls. A telephone questionnaire was administered to 141 cases and 525 controls. Putative risk factors were assessed using regression analyses and included pet ownership and any other animal contact. Faecal samples from both people and companion animals were submitted from 27 case households. The whole genomes of ESBL- or AMPCBL-producing isolates collected from urine and faecal samples were sequenced and analysed through a bioinformatics pipeline.

In both univariate and multivariate regression, pet ownership did not constitute a risk for human ESBL- or AMPCBL-producing Enterobacteriaceae UTI. Of the 27 case households where at least one pet was sampled, three case households had a dog carrying ESBL-producing *E. coli*. The isolates recovered from the dogs in two of these households were the same MLST-type (ST-131 and ST-38) as those cultured from people in the home, and clustered with those human isolates on whole-genome MLST.

The results of this study suggest that companion animals do not constitute a risk for acquisition of ESBL- or AMPCBL- producing Enterobacteriaceae urinary tract infection in the community. However, animals living with people who carry ESBL-producing *E. coli* may also be carriers; in these cases, pets may play a role in community transmission of ESBL *E. coli*.

Bayesian latent hierarchical model for detecting MIC creep

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Public health officials seek to properly interpret the volumes of data generated by surveillance programs such as the US National Antimicrobial Resistance Monitoring Scheme (NARMS), there is a critical need to develop new/alternative approaches to the statistical analysis of antimicrobial resistance (AMR) data that will detect development of resistance in a timely manner and enable the quick implementation of mitigation measures. AMR data are collected through surveillance programs and describe the concentration of an antibiotic at which an organism ceases to grow and proliferate i.e. a minimum inhibitory concentration (MIC). For statistical analysis, proportion of bacteria in the resistant category is used as an indicator of changes in resistance. The central hypothesis of our project is that statistical analysis based on MIC breakpoints, while simple to conduct, does not facilitate timely detection of changes in resistance. The major issue with statistical analysis based on proportion in the breakpoint categories, is that the average MIC can be increasing long before changes in the proportion above the threshold are statistically detectable i.e. MIC creep. The objective with the project was to develop the statistical methods that facilitate timely detection of MIC creep. We developed a statistical model to detect MIC creep and test the hypothesis that the number of years required to detect MIC creep using a Bayesian latent class hierarchical model is less than an analysis based on the MIC breakpoint-based categories analysis. For this project we demonstrated the method using NARMS human data for Salmonella. We found that MIC values for non-resistant category were statistically significant increasing from 1996 to 2014 for Typhimurium serotype tested on chloramphenicol antibiotic, while no significance was detected on the proportion of non-resistant category. Also our proposed pair-wise comparison for MIC values between consecutive years could mimic the observed MIC trend reasonably well. This analysis enables more timely detection of emerging resistance. The impact will be, that public health officials can implement targeted antimicrobial stewardship programs sooner.

Design of dosage regimens that least select for resistance

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Optimisation of antimicrobial treatment is a cornerstone in the fight against antimicrobial resistance. Various national and international authorities and professional veterinary and farming associations have released generic guidelines on prudent antimicrobial use in animals. However, these generic guidelines need to be translated into a set of animal species- and disease-specific practice recommendations. This presentation focuses on prevention of antimicrobial resistance and its complex relationship with treatment efficacy, highlighting key situations where the current antimicrobial drug products, treatment recommendations, and practices may be insufficient to minimize antimicrobial selection. The topic requires a multidisciplinary approach, involving microbiology, pharmacology, clinical medicine, and animal husbandry. Four key targets for implementing the concept of optimal antimicrobial treatment in veterinary

practice need to be considered: (i) reduction of overall antimicrobial consumption, (ii) improved use of diagnostic testing, (iii) prudent use of second-line, critically important antimicrobials, and (iv) optimisation of dosage regimens. Important examples of practice recommendations for achieving these four targets will be selected from specific conditions that account for most antimicrobial use in pigs (intestinal and respiratory disease), cattle (respiratory disease and mastitis), dogs and cats (skin, intestinal, genitourinary, and respiratory disease), and horses (upper respiratory disease, neonatal foal care, and surgical infections). Finally, the importance of education and research needs for improving antimicrobial use in the future, including key elements of precision medicine, will be highlighted.

Guardabassi L, Apley M, Olsen JE, Toutain P-L, Weese JS. 2018. Optimization of Antimicrobial Treatment to Minimize Resistance Selection. *Microbiology Spectrum Article in Press.*

Antimicrobial resistance (AMR): the New Zealand perspective

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When measured in terms of antimicrobial use per kilogram of biomass, New Zealand is considered to be a relatively low user in livestock production but a relatively high user in human medicine. Although there are limited data on antimicrobial resistance (AMR) in animals in New Zealand, evidence indicates AMR in animals is generally low compared to other countries. However, the recent emergence of a resistant strain of *Campylobacter jejuni* associated with the poultry supply in North Island showed how rapidly this situation can change. This underlines the need to continue to reduce unnecessary use of antimicrobial use in humans and animals and seek alternative ways of preventing infection without compromising health and welfare.

In this talk I will report the results of recent estimates of antimicrobial use in animals and people in New Zealand, compared to other countries, and provide examples of ongoing research using genome sequencing and modelling to explore the zoonotic transmission of AMR pathogens between animals (livestock and companion animals) and people. I will also address the question: what will happen to AMR in humans if we successfully reduce antimicrobial use in animals?

Antimicrobial resistance (AMR): the Australian perspective

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Antimicrobial resistance (AMR) is a global issue of increasing importance. Australia's engagement with the issue of AMR has been broad and spans both human and animal populations, industries and governing bodies. Indeed, the government's approach to the issue could be considered the first example of a cross-disciplinary One Health response to an issue that spans species in Australia.

Australia's history with respect to AMR is chequered. An early proactive approach, taken in the late 1990's with a report tabled by the Joint Expert Technical Advisory Committee on Antimicrobial Resistance (JETACAR) made strong recommendations for oversight and intervention, but this was followed by 13 years of almost complete inaction. However, the development of the Antimicrobial Resistance Standing Committee (AMRSC) in 2012 with the aim of oversight of AMR in Australia and the Australian Antimicrobial Resistance Prevention and Containment (AMRPC) Steering Group, chaired jointly by the Commonwealth Chief Veterinary and Medical Officers, signalled the start of a structured cross-disciplinary response. Reports were commissioned and tabled on surveillance and reporting of antimicrobial resistance and usage for human health (2013) and animal health (2014) and in 2015 a national AMR strategy (2015 – 2019) was released and an implementation plan followed in 2016.

In addition, and likely as a response, to these initiatives at the level of government, in recent years many other stakeholders in Australia have moved forward in this space. There is now increased engagement of state government, industry, peak and regulatory bodies in the area of AMR. Each of these stakeholders are engaged in differing (and often multiple) strategies to address AMR, inclusive but not limited to: collection of surveillance data, development of consistent testing and reporting strategies, publication of biosecurity, infection prevention and prescribing guidelines, and development of teaching material. Numerous research streams have been developed within a One Health framework and are gaining funding across a number of disciplinary areas, where previously they may not have been looked upon favourably. Furthermore and, in my opinion, most excitingly, it is obvious that the defensive attitudes that may have played a role in limiting progression in the early 2000's are now rarely encountered across any stakeholder or contributor within this space. This marked cultural shift signals the potential for continuation and enhancement of the collegiate and beneficial collaborative processes that have been seen in recent years, paving the way for value adding within the One Health framework.

While Australia still has a long way to go before we can be fully comfortable with our knowledge and response surrounding AMR, we certainly appear to be moving, at speed, in the right direction.

Bayesian two-part model to correct both herd and animal level misclassification errors

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The model we present is aimed at reporting the true associations between herd and animal level prevalence and herd level predictors. The model requires two tests: the one is non-individual specific test

such as bulk tank milk ELISA/culture or pooled faecal culture to investigate whether or not infection is present in the herd; the other can be a cost-effective animal level test (test on individual animal) to find out the numbers of visible cases. Both tests are considered imperfect.

The model is built based on the following structure (Figure 1).

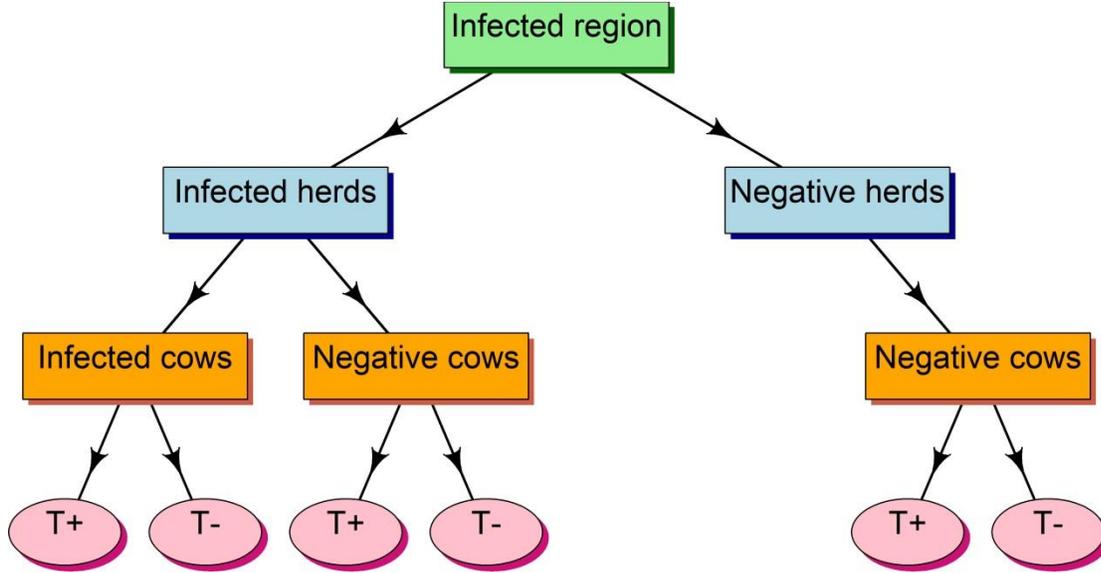


Figure 1 Scenario on which the model is based

The numbers of cases of a disease of interest (y_{ij}) within i^{th} herd in j^{th} region followed a Gamma-Poisson distribution:

$$y_{ij} \sim \text{Poisson}(\lambda_{ij})$$

$$\lambda_{ij} = \mu_{ij} * \pi_{ij}$$

$$\pi_{ij} \sim \text{Gamma}(\alpha, \alpha)$$

$$\alpha = e^{\theta}$$

$$\theta \sim \text{Normal}(0, \sigma_{\theta}^2)$$

The mean (μ_{ij}) was dependent on the true herd level infection status (t_{ij}):

$$\mu_{ij} = t_{ij} * [n_{ij} * v_{ij} * se + n_{ij} * (1 - v_{ij}) * (1 - sp)] + (1 - t_{ij}) * n_{ij} * (1 - sp)$$

$$se \sim \text{Beta}(a_{se}, b_{se})$$

$$sp \sim \text{Beta}(a_{sp}, b_{sp})$$

where n_{ij} , v_{ij} , se and sp were herd size, true within herd prevalence and animal level test sensitivity and specificity, respectively.

The predictors could be modelled as:

$$\log(v_{ij}) = \beta X_{ij} + U_j$$

$$\beta \sim \text{Normal}(0, \sigma_{\beta}^2)$$

where β is the regression coefficients vector, X_{ij} is the predictor vector and U_j is the normally distributed region level random effect.

The true herd level infection status (t_{ij}) can be linked to the non-individual specific test results (z_{ij}) as following:

$$\begin{aligned} z_{ij} &\sim \text{Bernoulli}(q_{ij}) \\ q_{ij} &= t_{ij} * SE + (1 - t_{ij}) * (1 - SP) \\ SE &\sim \text{Beta}(a_{SE}, b_{SE}) \\ SP &\sim \text{Beta}(a_{SP}, b_{SP}) \end{aligned}$$

where SE and SP are the non-individual specific test's sensitivity and specificity; q_{ij} is the probability that the non-individual specific test returning to a positive result.

The true herd level infection status also follows a Bernoulli distribution with the true probability that the herd is infected (τ_{ij}). And this can be modelled as:

$$\begin{aligned} t_{ij} &\sim \text{Bernoulli}(\tau_{ij}) \\ \text{logit}(\tau_{ij}) &= \gamma X_{ij} + V_j \\ \gamma &\sim \text{Normal}(0, \sigma_\gamma^2) \end{aligned}$$

where γ and V_j are the regression coefficients vector and normally distributed random effect at region level. It is also plausible to assume V_j and U_j are correlated:

$$\begin{aligned} \begin{pmatrix} V_j \\ U_j \end{pmatrix} &\sim \text{Normal}(0, \Sigma), \\ \Sigma &= \begin{pmatrix} \sigma_V^2 & \rho\sigma_V\sigma_U \\ \rho\sigma_V\sigma_U & \sigma_U^2 \end{pmatrix} \\ \sigma_V^2 &= \eta_V^2 \\ \sigma_U^2 &= \kappa^2\eta_V^2 + \eta_U^2 \\ \rho &= \frac{\kappa\eta_V^2}{\sqrt{\eta_V^2(\kappa^2\eta_V^2 + \eta_U^2)}} \\ V_j &\sim \text{Normal}(0, \eta_V^2) \\ V_j|U_j &\sim \text{Normal}(\kappa V_j, \eta_U^2) \\ \kappa &\sim \text{Normal}(0, \sigma_\kappa^2) \\ \eta_V^2 &\sim \text{Inv} - \text{Gamma}(c, d) \\ \eta_U^2 &\sim \text{Inv} - \text{Gamma}(l, m) \end{aligned}$$

Time to consider livestock movement as a temporal network.

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In social network analysis of livestock movement data, the connections (edges) in the network are explicitly temporal; an animal movement connecting two farms links them only at a single time point, which is important for the temporal aspect of infectious disease transmission. Standard static network measures cannot account sufficiently for network temporality. In this paper, we review and demonstrate analytical methods that incorporate the temporality of network edges, which offer new insights into network data available in many countries worldwide. Temporal network measures are demonstrated using sheep movement data from Victoria, Australia in 2015, aiming to identify high-risk farms for targeted surveillance. Farm values for the temporally explicit incoming and outgoing contact chain values are compared to static network measures such as betweenness. We also compare network 'small world' and 'slow world' properties, illustrating how accounting for temporality can reduce the perceived connectedness of the network, and therefore its potential for rapid infectious disease spread. In the Victorian sheep movement network, farm betweenness showed strong correlation with farm incoming contact chain (Spearman's rho 0.68, $p < 0.001$) and very weak correlation with farm outgoing contact chain (Spearman's rho 0.16, $p < 0.001$). Despite correlation, the subset of farms with betweenness values in the top 1% of the state only captured 12% (17/141) of farms with top 1% incoming contact chain values, demonstrating that influential farms in the network may not be identified using static measures alone. Temporal network measures can improve network analyses to better reflect the true disease transmission risks associated with livestock movement. By reviewing and demonstrating temporal network measures, we aim to encourage uptake and continuing development of temporal approaches to livestock movement network analysis.

We thank Agriculture Victoria for providing access to anonymised NLIS sheep movement data.

The hokey pokey model of Q fever on farm transmission dynamics

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Q fever is a zoonotic disease with major impacts on public health within populations working in the livestock industry. In Victoria, Australia 2012-2014 an intensively managed dairy goat farm was the centre of a Q fever outbreak that resulted in 24 people infected. Ensuing long-term monitoring of *C. burnetii* shedding by does at the time of kidding have shown that the disease has established at relatively high endemic levels. Further, long-term monitoring has identified the presence does shedding relatively large

quantities of *C. burnetii* at the time of kidding. In absence of a Q fever vaccine licenced for use in animals in Australia, efforts are currently underway to develop an autogenous vaccine for use on this farm. Mathematical models of disease transmission have been used to assess the efficacy of vaccination as well as changes in reproductive management as methods for controlling Q fever in intensively managed dairy goat herds following the large outbreak of Q fever that occurred in The Netherlands in 2007-2010. Differences in management practices in dairy goat production systems between Europe and Australia, particularly the local use of four kidding seasons per year, mean that models developed for European conditions need to be redeveloped and fit to Australian conditions. Moreover, existing within-farm Q fever transmission models do not account for the occurrence of heterogenous shedding intensity by individuals, a feature that could have a major impact on model predictions. Also, to the best of our knowledge, no formal fitting statistical procedures have been used to parameterise these models. The purpose of this study was to develop a mathematical model of Q fever within farm transmission adapted to local management practices and capable of accounting-for differences in shedding by individual. Approximate Bayesian Computation was used to fit model parameters to data obtained from long term infection monitoring studies carried out on the farm. The model was then used to assess different control strategy scenarios and compare times to disease eradication under different control scenarios.

Using causal loop diagrams to facilitate the understanding of the complex set of factors influencing calf wastage and identify possible leverage points for interventions

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Calf wastage (foetal and calf losses between confirmed pregnancy and weaning) has been identified as a major cause of income loss by beef producers in northern Australia. It is a complex problem for which proximate risk factors are most readily identified. While such findings are useful, a deeper understanding requires looking further back in time at more distal factors. This can be done using the systems thinking methodology of causal loop diagrams. These diagrams allow visualisation of processes that are not necessarily linear and sequential and may involve feedback with the latter being represented by reinforcing (positive feedback) and balancing (stabilising) loops. The aims of this study were to develop causal loop diagrams to facilitate the understanding of the complex set of factors influencing calf wastage and to use these diagrams to identify possible leverage points for interventions.

An expert opinion workshop was held and a group model building process was used to develop a series of causal loop diagrams focussing on three key outcomes: born dead (loss of foetus or calf between confirmed pregnancy and the day of parturition), loss around calving (death of calf within 14 days of live

birth) and heifer/cow mortality (death of heifer or cow following confirmed pregnancy). After the workshop, each diagram was recreated electronically using Vensim®. As many of the variables were common to two or more of the webs and linkages existed between outcomes, a single diagram was created.

The causal loop diagram incorporating all three outcomes of interest included 76 variables. Although quite complex, the diagram showed that many of the variables can act through multiple pathways and affect more than one of the three outcomes, and that several pathways can lead from one variable to one of the outcomes. There were three groups of balancing loops including the following variables (i) pasture quality/availability, soil quality and animal density in utilisable area (ii) cow phosphorus reserve, body condition and level of cow milk production (iii) a range of infectious diseases and heifer/cow/calf immunity. There were also two reinforcing loops (i) between calf vigour and milk intake and (ii) between separation of cow and calf and predation.

The variables involved in the loops can be prioritised as leverage points to reduce calf wastage. While it is recognised that the diagrams cannot realistically incorporate all direct and indirect causes of calf wastage and associated linkages they have provided strong support for holistic management interventions such as “manage the feed-base”, “manage lactation” and “manage cattle health and stress”.

Social network analysis in the molecular era: unravelling the relationship between New Zealand’s commercial poultry contact structures and campylobacter transmission

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Study objectives: This study aimed to integrate whole-genome-based phylogeny with data from social network analysis (SNA) to identify the relative contribution of different transmission pathways to the spread of an antibiotic-resistant lineage of the foodborne pathogen *Campylobacter jejuni* Sequence Type (ST) 6964 and identify strategies for improved food-production biosecurity.

Materials and methods: This study used whole-genome sequencing (WGS) data from 167 *C. jejuni* isolates, originating from the emergence of a new antimicrobial resistant strain in New Zealand’s commercial poultry sector, to estimate phylogenetic ancestries using maximum-likelihood methods. Questionnaire data was collected concerning the movement of (1) live birds, (2) feed, (3) waste and litter, (4) personnel and, (5) poultry products. Responses were used to differentiate contacts patterns between each contact network, calculate pairwise Euclidean and road network distances, and build network models to identify hierarchical community structures. Tanglegrams were used to make visual comparisons before using multiple statistical approaches including permutational analysis of variance

(PERMANOVA) and quadratic assignment procedures (QAP) to investigate the association between the genetic relatedness of isolates with network characteristics and pairwise geographical and contact network distance matrices.

Results: Preliminary findings provide additional evidence for intra-company transmission whilst also identifying further spread between poultry enterprises located within the same geographical region but belonging to different parent companies. These findings alongside the ongoing burden of human campylobacteriosis cases linked to the consumption of poultry products, highlights a clear gap in biosecurity and a strong need to identify cost-effective strategies for reducing disease transmission along the entire poultry supply chain.

Conclusion: Future work aims to identify which of these contact networks were facilitating this local spread, focusing on using the reconstructed evolutionary history alongside SNA to gain insight into where this resistant lineage had come from, the extent to which it had spread and how to prevent further transmission.

Human behaviour and livestock disease spread: challenges and opportunities in modelling dynamic feedback loop in disease simulation model

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Over the past several decades, infectious disease modelling has become an essential tool for creating counterfactual scenarios that allow the effectiveness of different disease control policies to be evaluated prior to implementation in the real world. However, there are still many limitations in how we currently model animal disease dynamics. Critical among these is that many models make the assumption that human behaviours remain constant over time. As many studies have shown, livestock owners change their behaviours around trading, on-farm biosecurity, and disease management in response to complex factors such as increased awareness of disease risks, pressure to conform with social expectations, and the direct imposition of new national animal health regulations; all of which may significantly influence how a disease spreads within and between farms. Failing to account for these dynamics may produce a substantial layer of bias in infectious disease models, yet surprisingly little is currently known about the effects on model inferences. In this talk, we summarise the current knowledge about farmers' behavioural change in on-farm biosecurity and livestock trading practices and highlight the knowledge gaps that prohibit these behavioural changes from being incorporated into disease modelling frameworks.

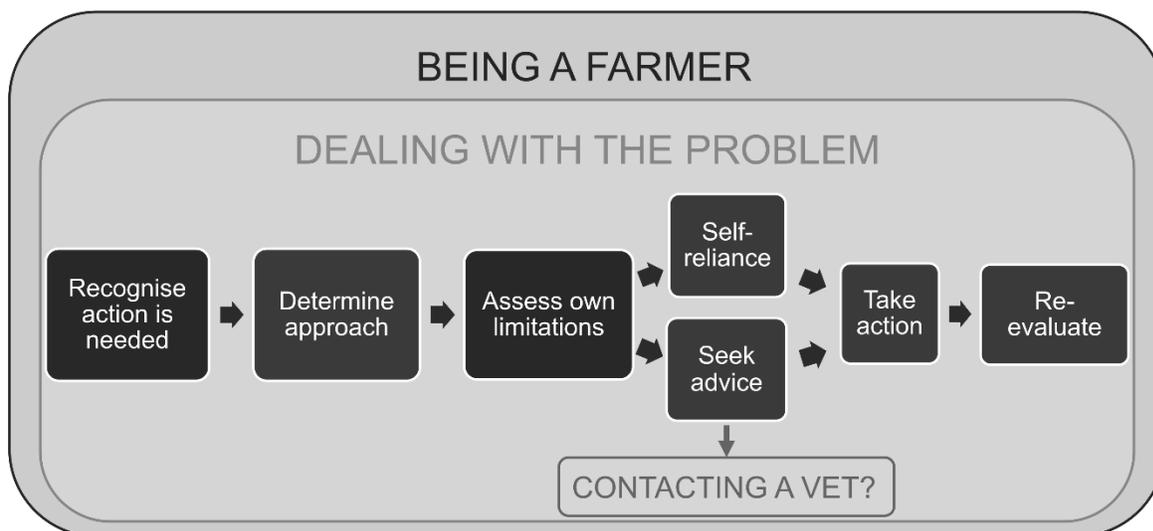
Detecting disease on sheep farms: the effect of farmer behaviour

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Effective passive surveillance depends on those in regular contact with livestock to report unusual or important disease signs to animal health authorities or veterinarians. Farmers' observations are a rich source of passive surveillance data, if they are captured by a surveillance system. In Australia as in many countries, veterinary contact by farmers is infrequent, limiting the sensitivity of passive surveillance. This study aimed to understand why Australian sheep farmers chose not to contact veterinarians when their animals showed signs of disease. We used established qualitative methods to investigate farmers' decision-making process when facing unusual endemic disease situations. Data were collected during three focus group discussions with sheep farmers in Victoria, Australia. Transcripts of those discussions were analysed using a modified grounded theory approach. From this analysis, we present a preliminary theory of Australian sheep farmers' disease response behaviour (Figure). Within the contextual identity of 'being a farmer', when 'dealing with the problem', the farmer must recognise action is needed, and then determine what that action will be. The farmers reported self-assessment to determine whether their experience was sufficient act independently, or whether advice was needed. Veterinarians played a small but important role as potential advisors. Self-reliance in Australian farmers' responses to endemic diseases has not received sufficient previous attention. Rather than being seen as a barrier to effective passive surveillance, farmers' self-reliance needs to be acknowledged when designing novel surveillance approaches.



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To be neutered or not? Reasons why farmers don't neuter their working dogs

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A survey of New Zealand veterinary clinics found that reproductive and gastrointestinal conditions were the most common non-trauma related reason that farm dogs were presented ¹. Further, unpublished data suggest that more working dog puppies than are needed are born and subsequently killed. Many of the health conditions and wastage of puppies could be prevented if the dogs were neutered, however, most farm dogs are not neutered. At present there are opinions and anecdotes as to why farmers do not neuter their working dogs but there has never been an attempt to catalogue the reasons behind farmers neutering decisions. The aim of this study is to describe the beliefs and attitudes farmers have around neutering of working farm dogs using qualitative research methods. Pairs of undergraduate veterinary science students conducted semi-structured interviews with six farmers in the Manawatu region of North Island. During the interview farmers were asked to discuss their views around neutering of male and female dogs separately. The interviews were recorded and students reviewed the interviews to identify themes. Reasons for not neutering male and female dogs included wanting to preserve the option to breed from dogs and deeming it unnecessary as they ran single-sex teams of dogs. When dogs had been neutered, health reasons were often cited. The one respondent who did neuter all of her female dogs, did so to avoid costly health conditions. Interestingly, cost was not given specifically as a reason for not neutering but two of the six did add that the 'cost was unnecessary because...'. Preliminary analysis of the data suggests we have not reached saturation of themes and as such additional interviews will be conducted later this year. The ideas and themes identified in the interviews will be used to construct a questionnaire that will be used to determine the relative importance of these reasons in the farming community. The results of the interviews and the survey will be used to develop an education campaign to encourage neutering of farm dogs.

1 Cave, N., Bridges, J., Cogger, N. & Farman, R. A survey of diseases of working farm dogs in New Zealand. *New Zealand Veterinary Journal* **57**, 305-312 (2009).

Update on the Indo-Pacific Centre for Health Security, the roles of epidemiology and surveillance, and how to engage

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The Australian Government's Health Security Initiative (the Initiative) for the Indo-Pacific region was launched in October 2017 and is being implemented by a new part of the Australian Department of Foreign Affairs and Trade (DFAT) – the Indo-Pacific Centre for Health Security (CHS). Funded with \$300 million over 5 years, the Initiative aims to strengthen country and regional capacity for prevention, preparedness, early detection and response to new and emerging infectious diseases (EID) such as Zika virus and new forms of influenza, existing infectious diseases currently impacting the Indo-Pacific region such as dengue, malaria and TB, as well as drug-resistant infections. The Initiative is taking a One Health approach due to regional risk factors for EIDs such as high human and animal population densities (especially in South East Asia), shared land borders, frequent human and livestock cross-border traffic, the developing nature of regional human and animal health systems and the high percentage of EIDs originating in animals. As such, capacity building in epidemiology and surveillance in both human and animal health will play a key part in the CHS's work over the next four years.

Applying animal health economics to improve companion animal care

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Animal health economics (AHE) has been used in veterinary medicine for many decades to help farmers make better decisions around livestock management. AHE is based on the principle that owners have limited resources to invest in animal health care and provides a framework for comparing the relative costs and benefits of different interventions. Although financial limitations are also important in companion animal medicine, there has been little research to date determining whether the same AHE principles can be used to improve individual patient care. In this article, we provide a basic overview of AHE for veterinarians and highlight several key areas where AHE can be potentially be applied to companion animal medicine including preventative care, chronic disease management, animal welfare, public health, shelter medicine, and national companion animal health policy. We then discuss some of the unique challenges in companion AHE particularly around developing a strong evidence base to support economic models, link between companion animal care recommendations and practice finances, getting small animal veterinarians to adopt a population medicine mind set, legalities of managing diseases with public health implications, assigning an economic value to the human-animal bond, and the political sensitivities attached to many companion animal health issues. To progress companion AHE as new discipline, the methodologies need to reflect the different role of companion animals in society and conduct more research to determine whether presenting clinical scenarios in an economic framework is effective in motivating owner behavioural change.

Wildlife reservoirs for *Mycobacterium bovis* in Fiji: could these be important for BTB control? And if so, What? Where? When?

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The presence of a wildlife reservoir for *Mycobacterium bovis* significantly complicates eradication of bovine tuberculosis (BTB) from domestic cattle populations. This has been shown in relation to the European badger (*Meles meles*) and brushtail possum (*Trichosurus vulpecula*) in the United Kingdom and New Zealand, respectively. For the BTB eradication program in Fiji, there is concern about potential reservoir species and the role they may play in maintenance of infection. This paper will outline the status of BTB in Fiji and considerations about potential reservoir species, including a pilot investigation of the small Indian mongoose (*Herpestes auropunctatus*). Mongoose are an introduced species, established in high numbers, and living in contact with cattle.

The pilot investigation was conducted in partnership with the Ministry of Agriculture in Fiji, and comprised the small research activity requirement for a Year 3 Doctor of Veterinary Medicine student at the University of Sydney.

Reproductive outcome impacts on live weight production of beef cows in northern Australia

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Live weight production (LWP) is a primary measure of beef business income. The annual LWP of a cow is the sum of the weight of its calf at weaning and of its own annual live weight change since the previous year's weaning muster. The aims of this study were to describe typical LWP for breeding cattle in northern Australia and identify factors, particularly those relating to reproductive outcomes, which are associated with its variation.

An existing dataset from a longitudinal study following 2,118 tropically-adapted cows for six mating cycles at four sites representing the major land types in northern Australia was used. Causal diagrams were used to identify models to estimate total and direct effects for risk factors of interest. Separate analyses were conducted for first, second and third to sixth mating cycles. Generalised estimating equation models using site x year as the clustering variable with robust standard errors and an exchangeable working

correlation matrix were used for the main analyses. Variance components were assessed by fitting null and full random effects models with site and year fitted as nested random effects.

Average annual LWP was 175kg (s.d. 71kg, range -150 to 429 kg). Mating outcome had the greatest impact on LWP. Cows weaning a calf had the highest LWP, followed by non-pregnant cows; cows that lost a calf between pregnancy diagnosis and weaning had the lowest LWP. This was consistent across the mating cycles with the average difference between weaning and losing a calf greatest in the third to sixth mating cycle group (144kg 95% confidence interval: 133-156kg). The mating outcome from the previous cycle was also associated with LWP. Cows weaning a calf in that cycle had a higher LWP in the subsequent cycle compared to non-pregnant cows and those losing a calf. LWP was higher in tropical composite compared to Brahman cattle. This was due to combination of a higher probability of weaning a calf and greater weaner weight among tropical composite cattle. Based on the null models, the majority of the variance in LWP was at the cow-year level, but with 26-31% at the year-within-site level. There was almost no variance at the site level. Full models explained 42-53% of the variance and the majority of the unexplained variance was at the year-within-site level.

The findings from this study can be used to benchmark achievable LWP in northern Australia beef businesses and to quantify the financial impact of calf loss and pregnancy failure.

Blowing in the wind: decision support tools for vector-borne animal diseases

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Introduction: Effective decision making in emergency animal disease outbreaks requires an understanding of the potential for disease transmission appropriate for local conditions. Disease models are tools to prepare for such risks. The Australian Animal Disease (AADIS) model has been developed to support foot-and-mouth disease preparedness and response. In this study the capability of AADIS has been extended to simulate the spread of the vector-borne disease bluetongue. The objective of this study was to model the spatial distribution of *Culicoides brevitarsis*, the main competent vector for bluetongue virus in Australia.

Materials and methods: We used a raster approach to adapt Kelso and Milne's 2014 model to estimate the spread of *C. brevitarsis* across Australia as a function of calendar time. Growth and spread of *C. brevitarsis* within each raster cell was dependent on three factors: average daily temperature, short range diffusion and wind-borne dispersal. Wind-borne dispersal was simulated using the Hybrid Single Particle Lagrangian Integrated Trajectory Model. Partial validation of the model was carried out by comparing *C.*

brevitarsis counts at locations throughout Australia, as recorded by the National Arbovirus Monitoring Program (NAMP) with the simulated *C. brevitarsis* counts at the same location.

Results: Our model provided biologically plausible estimates of the spatial distribution of *C. brevitarsis* across Australia as a function of time. While *C. brevitarsis* were not present further south than northern coastal New South Wales during the cooler winter months of the year they re-emerged in more southerly coastal regions of New South Wales as temperatures increased and midges were re-introduced from wind-borne spread.

Conclusion: Our model provides a credible estimate of the distribution of *C. brevitarsis* across Australia in response to temperature and wind. This model provides a basis for simulating the dispersion and control of bluetongue in Australia.

Effect of season and climate on bovine digital dermatitis in spring-calving pasture-based dairy farms in Taranaki, New Zealand

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To investigate the temporal pattern and the effect of climate on bovine digital dermatitis in spring-calving farms in Taranaki, New Zealand, whole herd assessments of bovine digital dermatitis (BDD) were made on 57 farms which had been previously identified as having cows with BDD. Assessments were made on five occasions between early lactation (September 2015) and drying-off (May 2016) (at ~6-week intervals). The raw temporal pattern was analysed using a generalised estimating equation (GEE) method, followed by a mixed effects negative binomial model which modelled prevalence and time. Climate data, i.e. soil temperature, air temperature and rainfall, were then used instead of date in the negative binomial model to model the effect of climate on the prevalence of BDD after accounting for farm level management practices.

The highest farm level and cow level prevalences were seen on the second visit (27/Oct/2015-11/Dec/2015) and were lowest on the fourth visit (29/Jan/2016-10/Mar/2016). Farms with a higher proportion of infected cows at the first visit tended to have a higher proportion of infected cows at later visits, even though the affected individuals were often different. There was thus a strong correlation (0.94) between prevalence (proportion of cows infected at each time point) and incidence (proportion of cows with new infections at each time point). Two climate measurements were found to have an association with BDD prevalence. Firstly, increased rainfall in the previous month was associated with decreased cow level prevalence; secondly, there was a quadratic relationship between prevalence and soil temperature, with prevalence increasing as soil temperature increased from 11.8°C to ~18°C and then decreasing as soil temperature increased from ~18°C to 23.9°C. In addition to the effect of climate, using outside staff to

perform hoof trimming was found to increase the risk of BDD infection (risk ratio [RR]: 2.06, 95% confidence interval [CI]: 1.05-4.06).

Impact of climate on livestock diseases in New Zealand: a review

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Changes to climate have resulted in the changes in the distribution of animal's disease (e.g. West Nile in North America and bluetongue in Europe) and there is growing evidence that this trend will continue for other diseases. The resources to mitigate the risk of climate change on animal disease are limited and policy makers, farmers and veterinarians need to decided how best to allocate resources.

We systematically reviewed the effect of climate of 41 diseases or adverse health events affecting cattle and sheep and known to be endemic or emerging in New Zealand. Abstracts were scored (0 to 3) to identify research articles quantifying the relationship between disease occurrence and climatic variables. Tuberculosis and haemonchosis returned the highest number of results, ergotism and ovine brucellosis the lowest. Between 0 and 25 articles per disease presented a direct quantitative association between disease and climate.

The results of this review will be used to prioritise diseases and to inform modelling in a effort to improved preparedness for climate change.

Impacts of climate change on facial eczema for New Zealand: how big a problem?

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Facial eczema (FE) is a disease of grazing livestock caused by spores of the fungus *Pithomyces chartarum*. FE is a concern for New Zealand (NZ) farmers, when and where the local climate conditions support growth and sporulation of the fungus. Higher temperatures and a change in rainfall patterns are projected as part of climate change in NZ. The objective of this study was to assess the likely impact of climate change on the risk of FE in NZ.

A systematic literature review was conducted to identify key climate variables associated with FE risk. Paddock spore count data from 131 North Island farms for up to 7 seasons (2011 – 2017) were collated with the local climate data, and analysed to describe seasonality and the relationship between spore counts and the climate variables.

We found over 30 studies quantifying the sensitivity of FE risk to climate variables, mainly seasonality, rainfall, moisture, and temperature. There was a high variability in spore count by season and area, which was in part explained by variations in the key climate variables.

Our findings suggested importance of the impact of climate change on FE risk. We demonstrated an approach to combine multidisciplinary knowledge to address the problem. The need of animal health data was highlighted to improve our understanding and enhance resilience of farming communities to climate change.

Investigation of climate change perceptions among Maasai pastoralists in Northern Tanzania and its impacts on cattle production

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This study examined pastoralists' perception on climate change and impacts on cattle production across ten villages of Monduli District in Tanzania during 2015. This study analysed data from a survey of 130 cattle owners and focus group discussions in the study villages. Findings from this study indicate that The pastoralists are well aware of the general climate trends in their location, its variability and the impacts of extreme weather events on cattle production. More erratic and reduced amounts of rainfall, rise in temperature, and prolonged and more frequent periods of drought were reported. The pastoralists viewed population pressure and tree cutting as contributors to the changes in climate they are experiencing. Negative impacts on cattle production discussed were severe recurrent drought periods leading to forage and water shortage and subsequent cattle starvation and malnutrition. Pastoralists reported cattle deaths and outbreaks of diseases such as contagious bovine pleuropneumonia and tick-borne diseases. Further, reduction in milk production and poor livestock market prices were also considered to be negative impacts on cattle production. Given the range of negative impacts of current climate change and extreme weather events on cattle production, the implications of climate change must be taken into account to ensure longer-term survival and sustainability of pastoralist communities through strengthening of climate risk awareness programs and early warning systems across the district, that were virtually non-existent at the time of this study.

Are New Zealand pet owners ready and would they get through a natural disaster?

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People risk their lives during disasters to protect their pets and are less likely to evacuate in a disaster. When they do evacuate without their pets, are likely to return for their animals¹ endangering their lives and others including family, friends and relief personnel. The aim of this project was to determine New Zealand pet owners' current level of preparedness in relation to themselves and their dogs and cats. An online survey was created in Qualtrics and links to the survey promoted through social media accounts of individuals and organizations such as the New Zealand Association of Veterinary Nurses and the New Zealand Companion Animal Council. The survey will remain open until 30th June 2018 and as of the 15 June 2018 1,658 people have responded. Sixty-eight percent of respondents were cat owners; half owned only one cat. Of those with only one cat 73% reported that the cat was microchipped but only 13% of cats were wearing a collar with the owner's contact phone number. Similar values were reported when people owned multiple cats. Dog ownership was reported by 68% of respondents with 58% owning one dog. Collars were on 80% of dogs and 40% had council registration tags on the collar. The majority of respondents had more than five days food on hand for their dogs and 95% had space to take their pets in their vehicle if they had to evacuate. However only 30% of respondents had a grab bag packed and 72% did not have contact details for a place they could house their pet in the event that an evacuation center did not allow pets. While the numbers of pets with identification is high a substantial number of pets had no identification, meaning that it would be difficult to reunite them with their owners if they were separated. Furthermore, the majority of owners do not have basic planning in place for themselves in the event of a disaster. Given that research has shown that people expect to take their pets with them in an evacuation, these results highlight the importance of civil defense planning that explicitly considers how to manage large numbers of pets in disasters.

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Never happens? How prepared are New Zealand farmers for a natural disaster?

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Bushfire preparedness research in Australia has shown that livestock producers often do not have formal emergency plans nor do they have adequate insurance for livestock¹. However, many of the routine practices they engage in as part of farming do contribute to increased preparedness. This project aims to explore how prepared New Zealand livestock owners are for natural disasters. An online survey was created in Qualtrics and links to the survey promoted through social media accounts of individuals and

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organizations such as the New Zealand Farming, Beef and Lamb New Zealand and Ministry for Primary Industries. The survey launched on May 28th 2018 approximately 30 minutes before the New Zealand government announced its plans to attempt an eradication of *M.bovis*, and the survey lost visibility.. Consequently, responses to this survey have been slow and so we have run a second social media campaign to increase participation. On the 15 June 2018 we have had 94 respondents Of the respondents 61% identified as lifestyle block owners, 90% had a generator on the farm and 95% had at least one chain saw. If a disaster occurred at the time of responding (May/June) majority of respondents (95%) had supplementary feed on the farm and for 77% of these it would last one or more weeks. While the respondent pool is small, the results do support Australian research that suggests livestock producers do have an increased preparedness due to standard operating practices. Consequently, they are likely to cope with the initial recovery phase of response. However, as the 2016 Kaikoura (NZ) earthquake has shown some vulnerabilities in farm infrastructure. Therefore, farmers will need still require assistance and there can be significant challenges in rural areas when road access is blocked.

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