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VETERINARY EPIDEMIOLOGY

CHAPTER SCIENTIFIC

ABSTRACTS

Scoping review; African swine fever virus spread between domestic and free-living pigs

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African swine fever virus (ASFV) spread in the South-East Asian region, including to Indonesia, Timor-Leste and Papua New Guinea, increases the threat to the Australian pork industry. ASFV spread has been partially attributed to the free-living—domestic pig interface. This scoping review identified primary research in which authors made statements to support ASFV spread between free-living and domestic pigs, and assessed the circumstances in which such spread occurred.

Five bibliographic databases and the grey literature were searched. Records were screened and data were charted to identify the demographics of the pig populations, their husbandry (domestic pigs) and habitat (free-living pigs), the occurrence of ASF in the populations, and whether ticks were present in the geographic range of the pig populations. Data synthesis included descriptive statistics and a narrative summary. From 1349 records screened, data were charted from 46 individual studies published from 1985 to 2020.

Outbreak investigations revealed that whilst poor biosecurity of domestic pigs was often reported, direct contact resulting in transmission between free-living and domestic pigs was rarely reported. Studies in which quantitative associations were made generally found that spread within populations was more important than spread between populations, although this was not always the case, particularly when husbandry practices included free-ranging domestic pigs.

The limited evidence of transmission of ASFV between free-living and domestic pigs is an important consideration and can be used to inform strategies for ASF preparedness in Australia. Biosecurity strategies that compartmentalise free-living and domestic pigs could maintain trade of domestic pigs.

Using genomics to fill knowledge gaps in an elimination programme

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Elimination of *Mycoplasma bovis* from cattle in New Zealand (NZ) largely depends on three criteria holding true: ¹ infection established from a single source ² the primary case was infected relatively recently, and ³ all infected properties are connected by an identified and confined network of cattle movements. We present how genomics are incorporated into the rationale for continued efforts towards elimination.

Where possible, a minimum of two whole genome sequences (WGS) are generated for each Confirmed Property (CP). These are analysed using ancestral state reconstruction and transmission models: BEAST¹, SCOTTI² and Lau.³ Regular meetings are held between the Programme's Disease Control team and mEpiLab to ensure outputs are interpreted appropriately.

At 17 February 2020, a total of 492 WGS from 91 CPs are available for analysis. Sequences obtained through tracing and background surveillance are represented. Phylogenetic analyses support the introduction of a single strain and the absence of subsequent introductions. Recent common ancestor estimates place the time of introduction of the circulating strain to between August 2016 and April 2017 (95% HPD intervals). SCOTTI and Lau modelling support transmission through a complex network of animal movements between CPs.

Genomic analyses substantiate that the *M. bovis* Programme is tracing the evolution of a single introduced bacterial strain over a confined network of cattle movements. Paired with a likely date of introduction that falls close to the time of identification of the index case and a low herd-level prevalence, elimination of *M. bovis* from NZ cattle currently is assessed as being technically feasible.

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Modelling the effects of bovine viral diarrhoea virus on Australian beef production

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Bovine viral diarrhoea virus (BVDV) is responsible for significant economic losses in the Australian beef industry.¹ Farm-level biosecurity can reduce the impact of endemic disease but implementation is dependent on individual producer values. Simulation models have been used by many countries to justify BVDV control at both a national and farm level; however, most of these models represent disease transmission in intensive dairy or semi-intensive beef cattle systems. We hypothesise that the effects of BVDV on production will differ in the extensive Australian beef farm.

An individual-based, stochastic simulation model is being developed to predict and assess the effects of BVDV on a herd that represents a typical extensive beef production system in south-eastern New South Wales (NSW). The model will be used to predict the effects of BVDV on production parameters such as pregnancy rate, calf mortality rate, live weight of sale animals, purchased replacements and culling rate. The outputs will be collected from simulations that run for a 10-year period. Three scenarios will be simulated: no disease, point-infection of a naïve herd and infection in an endemic herd.

Currently, we are collecting and analysing model outputs. Following this, sensitivity analysis will be conducted to identify parameters that influence outputs. We describe the modelling process, and present preliminary results. Planned future studies will use this model to examine the influence of biosecurity practices on the predicted impacts of BVDV for different producer typologies in south-east NSW, to determine the role of producer values for decisions regarding on-farm biosecurity.

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Descriptive Epidemiology of *Salmonella Enteritidis* outbreak in New South Wales

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Historically, the Australian egg industry has been free of *Salmonella Enteritidis* (SE)¹. In September 2018, traceback from a human SE cluster not attributable to overseas travel led to the detection of SE in a New South Wales (NSW) poultry flock.

There have been 17 premises detected with SE within NSW since September 2018, one of which is solely an egg grading facility. Of the 16 premises with poultry, six (38%) had an onsite grading facility and the remaining 10 (62%) premises had their eggs graded off site.

All infected premises link through movements of eggs, egg packaging, people, vehicles or machinery. The time lag between potential introduction of the SE agent and establishment and subsequent detection on farm was on average 8 - 14 weeks, and up to five months. At this stage rodents have not played a significant role in transmission.

Clinical disease was present in aged birds (70 - 100 weeks) in three (19%) of flocks. There was no clinical disease or increased mortalities in younger birds.

Within NSW SE has expressed itself as a disease with a slow and insidious spread both within and between premises. With minimal clinical signs in poultry flocks and spread via fomites, SE may spread undetected until contaminated eggs enter the food chain.

A Control Order under the Biosecurity Act 2015 has been implemented for all licenced poultry businesses in NSW to increase biosecurity both on farm and at the farm gate.

References

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Improving the detection of African Trypanosomiasis in cattle under field conditions

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The study investigated the impact and performance of PCR and LAMP against microscopy in determining prevalence of trypanosomes in cattle under field conditions. In a cross-sectional survey, blood was collected from 227 cattle from Mambwe district of eastern Zambia. Examination and detection of trypanosomes from blood samples was undertaken using: buffy coat (detected 17 cases), thin smears (detected 26 cases), thick smears (detected 28 cases), combined microscopy (detected 40 cases), PCR-FP (detected 47 cases), PCR-FTA (detected 83 cases) and LAMP-FTA (detected 18 cases; n = 131).

Using microscopy as gold standard, sensitivity and specificity of diagnostic tests were compared. LAMP-FTA was highly specific (88-96%) but lacked sensitivity (36-65%) in detecting trypanosomes as compared to PCR-FP (specificity 82-88%, sensitivity 53-78%) while PCR-FTA had the best sensitivity (specificity 67-72%, sensitivity 73-86%).

The study concluded that PCR remain a better diagnostic test for detecting trypanosomes than LAMP when compared to microscopy. However, the practicality in the use of PCR for field diagnosing of trypanosomes in Africa remains a challenge. Therefore, the study recommends the use of combined microscopy in order to reduce under estimation of trypanosome prevalence resulting from single microscopy methods. In terms of blood sample collection and storage in remote areas where collection and storage of whole blood samples is not feasible, the study recommends the use of FTA cards instead of normal filter paper for improved trypanosome case detection using molecular techniques.

Using a co-creation process to develop extension materials for smallholders

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This study explored the benefits of using a co-creation process in the development of a glovebox guide to animal health and welfare standards and guidelines for smallholders. Co-creation is a process of bringing together expert and non-expert stakeholders; using their experience, knowledge and insights to achieve an outcome.¹ By actively engaging a range of stakeholders in its development, the guide was considered more likely to reflect end-user needs.

Using the framework of an acceptability study, features such as utility, usability and likeability were considered, all of which can determine the extent to which an intervention will meet the needs of a target population.² To obtain in-depth information on the guide, semi-structured interviews were conducted with nine smallholders. Participants were provided with a draft guide and asked to consider acceptability factors over a two-week period, followed by a telephone interview. Draft guides were sent to ten stakeholders representing industry, government and welfare groups to confirm the accuracy of the technical content.

The results demonstrate that within the smallholder population there are diverse opinions and preferences that need to be balanced. Common areas of priority were highlighted, along with areas that were not considered to be useful. Different opinions on whether using a regulatory versus an awareness raising approach would be more effective were expressed.

One of the clear advantages of using a co creation process was the ability to understand and communicate the different needs of both experts and end-users throughout the development process, resulting in a well-considered final product.

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The racing pigeon (*Columba livia domestica*) industry in Victoria, Australia, and epidemiology of a novel Group A rotavirus outbreak

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A novel Group A rotavirus, first identified clinically in racing, feral and fancy pigeons in Western Australia, had spread throughout Australia by March 2017. In December 2016, the putative index case of rotavirus in racing pigeons in the state of Victoria was confirmed at a regional bird sale, with rapid spread to peri-urban Melbourne, the capital city. A survey sent to approximately 400 Victorian pigeon fanciers identified eight (of 85 respondents) with a confirmed rotavirus infection in their loft(s). If a fancier had purchased live birds, either from the regional sale or from another source, there was a 13% to 38% increased likelihood of the loft subsequently being confirmed rotavirus-positive. An increased loft-level risk of rotavirus was also positively associated with the number of neighbouring lofts within a five-kilometre radius of a home loft.

It was concluded that rotavirus was primarily transmitted beyond the Victorian index case through the movement of live birds into a loft, either deliberately through bird purchase and/or inadvertently through the entry of pigeons from neighbouring lofts. As pigeon racing inherently requires consistent contact between birds from different lofts, vaccination was recommended as a primary method of rotavirus control in this unique industry.

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Classical swine fever in Victorian domestic pigs: Evidence of disease freedom

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Australia is currently regarded as free of classical swine fever (CSF), a highly contagious disease of pigs caused by a pestivirus. To provide additional evidence that the Victorian domestic pig population is free of CSF, 391 pigs from 23 holdings were sampled at the time of slaughter between March 2016 and October 2017. All samples were negative for CSF virus Ab on ELISA. Because of uncertainty in the sensitivity of the CSF Ab ELISA, estimates of the true prevalence of CSF were calculated using Bayesian methods. The median and upper bound of the 95% credible intervals for the true prevalence of CSF was zero when the diagnostic sensitivity of the CSF Ab ELISA was assumed to range from 0.75 to 0.95. These results provide evidence that the population of domestic pigs in Victoria in 2016-2017 was free of CSF.

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A review of social impacts of emergency animal diseases

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Emergency animal diseases (EADs) have human consequences which are often overlooked. This review summarises the current literature covering producer tendency to report, communication between producers and authorities during EAD outbreaks and the role that veterinarians play in each of these areas.

After overviews of three selected recent EAD outbreaks, we describe factors contributing to the timeliness of reporting suspicious clinical cases in passive surveillance systems. These issues are not only financial in nature, but also technical and social. Understanding and modifying the drivers behind these factors is likely to promote enhanced case reporting and, as a result, improved emerging infectious disease (EID) management and control.

Communication is an integral factor of outbreak management where situations and solutions are rapidly evolving and coordination between stakeholders and disease control authorities are imperative. Miscommunication is stated by producers to be a source of distress as well as a barrier to timeliness of reporting of suspicious cases. Based on recent, large EID outbreaks private practice veterinarians feel unprepared to play a role as communication mediator between producers and disease control authorities.

From our findings, we synthesise the literature to identify factors that contribute to effective communication and the timeliness of disease reporting and provide recommendations for the future.

We conclude that the human impact of EAD outbreaks must be recognised as an integral influencer of EAD surveillance and management.

Mycoplasma bovis infection dynamics in a New Zealand large beef finishing operation

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A large beef finishing operation in New Zealand is persistently infected with *Mycoplasma bovis*. With a continuous supply of naïve animals, we can monitor *M. bovis* infection dynamics at the animal and group levels.

Serum samples from seven groups of 30 cattle were collected at monthly intervals until slaughter at 104-202 days post-arrival. Serum samples were tested for *M. bovis* antibodies using the *M. bovis* IDVet ELISA. Individual and group-level ELISA test thresholds and cut-points were used to determine seroprevalence and group-level infection status.

At slaughter, paired tonsil swabs and tonsil samples were taken and tested for the presence of *M. bovis* by RT-PCR.

After 27-28 days post-arrival, group-level seroprevalence ranged from 0% to 33% and six of seven groups were deemed infected. At the time of slaughter group-level seroprevalence ranged from 96% to 100% demonstrating high rates of animal-to-animal transmission.

Of the tonsil swabs collected, 33.1% (53/160) tested positive for *M. bovis* with RT-PCR and 87.3% (117/134) of tonsil samples tested positive.

The serology results demonstrate that most naïve groups of cattle will seroconvert to *M. bovis* by 27-28 days post exposure. Work is underway to determine the serostatus of animals at induction and the persistent sources of infection and modes of *M. bovis* transmission within this large beef finishing operation.

RT-PCR testing of tonsil tissue is more sensitive than RT-PCR of tonsil swabs at the individual animal level. This finding is informing a trial to test the practicality of collecting tonsil tissue at slaughter to increase sensitivity of RT-PCR.

Avian influenza in Denmark: Passive surveillance bias and future monitoring

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Continuous incursions of avian influenza (AI) in Northern Europe is a potential zoonotic threat and causes economic losses to poultry farmers. Passive surveillance programs for AI may aid in pinpointing high-risk AI areas but often suffer from submission bias. We investigated the importance of potential bias types.

In Denmark, several incursions of low pathogenic avian influenza (LPAI) and high pathogenic avian influenza (HPAI) have been discovered, resulting in both a passive and an active surveillance program¹. We here assessed data from the passive surveillance program (2006–2020) with reports of dead wild birds found by the public at 882 reporting sites. To assess potential submission bias, we compared the submission locations to random locations in Denmark considering human population density, distance to nearest city, distance to coastline, and distance to the nearest road.

The passive AI surveillance data significantly differed from random locations within Denmark for all four parameters investigated (all $P < 0.001$). Reported birds were generally found in areas with low population densities, but closer to cities and closer to roads. A majority of the records were found closer to the coast.

Our results showed that AI passive surveillance suffer from submission bias - thus, there is room for improvement of the passive AI surveillance program. A risk assessment framework is missing, which could include simulation modeling to predict possible outbreak zones. However, knowledge gaps include bird migration routes, bird density estimates and interactions of the different bird species. We will address this in future work.

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Emergency preparedness in Fiji: Animal Biosecurity Emergency Response Plan

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Emergency preparedness is essential for a rapid and effective response following a disease incursion. Fiji is an island nation in the South Pacific, free of many significant animal diseases. The development of an Animal Biosecurity Emergency Response Plan for Fiji is presented.

In collaboration with the Biosecurity Authority of Fiji, stakeholder consultations were conducted with over 20 different agencies from key ministries and animal and veterinary industries during April 2019. Site visits to smallholder and commercial farms and cargo terminals were also conducted. Discussions focused on current disease surveillance activities, decision-making and existing disaster management arrangements, feasible disease control activities, legislation including the Biosecurity Act 2008, and methods of communication, among other relevant topics. A simulation exercise was conducted to test and further refine the plan.

Fiji and other Pacific Islands have a unique setting, requiring consideration of factors such as: geography and environment, farming systems, transport and accessibility, communications, carcass disposal, common on-farm practices that may contribute to disease spread (such as swill feeding) and limited veterinary services including diagnostics. Practical and feasible approaches to field response activities were identified, taking into consideration Fiji's biosecurity and disaster management structures and legislation.

A response plan is one of numerous elements required for preparedness in the face of exotic diseases. Operational planning arrangements, formal stakeholder agreements, legislation, community engagement and ongoing training are also imperative to enhance capacity for a rapid and effective response.

Risk factors of gastric dilatation-volvulus in shepherd dogs: case-control study

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Shepherds are widely used as police dog and are predisposed to gastric dilatation-volvulus (GDV), a life-threatening condition common in large, deep-chested dogs.¹ This study investigates risk factors of GDV and compares between police and pet shepherd dogs.

Shepherd dogs, including German and Belgian, were categorized into case (dogs with GDV) and control (dogs without GDV) groups. A total of 1335 dogs were included, with 1002 dogs in case group and 333 in control group, including 1285 household pet dogs and 50 police working dogs. Bivariable and multivariable logistic regression were employed to assess the relationship between independent factors (demographics and diseases history) and GDV.

Compared to Belgian Shepherd, German Shepherds are at higher risk of GDV development ($p=0.01$). Significant risk factors to GDV were being male ($p<0.001$) and being of older age ($p=0.026$). There was no significant difference in risk of GDV between police working shepherd dogs and pet shepherd dogs ($p=0.313$). Weight and gastrointestinal disease history were also not significant.

Risk factors of GDV in shepherd dogs include breed, gender and age. Police working dogs do not possess higher chances of GDV development compared to pet dogs.

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Survey of biosecurity risks on New Zealand commercial pig farms

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A survey was conducted to describe the occurrence and frequency of activities on New Zealand commercial pig farms that related to biosecurity.¹ Reference values for the prevalence and frequency of behaviours related to disease entry and opportunities for improvements in biosecurity and systemic deficiencies that can be managed through whole-of-industry action were identified.

The survey was distributed by email link to 116 pig farming sites in New Zealand during January/February 2020. The 102 questions considered activities related to staffing, pig movement on/off the farm, AI, feed and water supply, removal of manure and dead pigs, visitors, receiving farm supplies, and rodent and bird control over the previous 12-month period.

A 57% response rate represented 83.8% (sows) and 98.4% (pigs) of the industry. All farms required clean boots and coveralls be worn by visitors as a minimum requirement, but only a limited number of farms required more detailed procedures (bench entry system, shower-in/shower-out).

Contract haulers transporting pigs was common and was associated with controllable risks (truck cleaning / disinfection, off-site lairage and quarantine areas, and cross-contamination between farms). On-farm composting was the most prevalent (60%) means of managing pig mortalities.

Areas for improvement included pig transportation processes and visitor entry.

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An epidemiological overview of *Mycoplasma bovis* in New Zealand

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On 21st July 2017 samples were collected from cattle experiencing clinical signs consistent with *Mycoplasma bovis* (*M. bovis*) infection. Its presence was subsequently confirmed on a dairy farm in the South Island of New Zealand. Prior to this date, ongoing passive surveillance and various surveys failed to identify *M. bovis* in New Zealand¹. A national response commenced and on 28th May 2018 New Zealand's *M. bovis* Eradication Programme was announced.

Descriptive analyses were conducted to describe the outbreak. Time from infection to movement restrictions and estimated dissemination rates were calculated to track progress towards eradication.

As of 31st December 2019, overall prevalence among places containing cattle was less than one percent (0.585 %; 95% CI 0.513 - 0.668 %). A total of 2339 places completed sampling and testing as part of Programme surveillance and were deemed not infected. The number of newly infected places peaked in the latter half of 2017 and has since been declining. On average, compared to other farm types infected cattle dairies put a greater number of places at risk of infection, with a higher proportion of those places found to be infected. Phylogenetic analyses combined with tracing information suggest incursion of a single strain during the latter half of 2015. Estimated dissemination rates and time from infection to movement restrictions have improved overall since detection of the index case. The estimated dissemination rate is now less than one, which must be sustained for the outbreak to remain in decline and to ensure successful eradication².

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Primary photosensitisation in Thoroughbred horses grazing aphid infested lucerne

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Primary photosensitisation is uncommon in horses. We describe twenty-three cases in thoroughbreds grazing aphid infested Lucerne. There are few reports of this association in cattle and horses, however another local stud grazing infested Lucerne found cases at the same time.

Distal limb oedema was the earliest sign. Tissue disruption with serum leakage, extensive ulcer formation with crusting, scaling and lameness was observed in the worst cases. Eighty-five percent of susceptible horses with unpigmented skin and white hair showed clinical signs on the face and distal limbs. Most were pregnant broodmares. In severe cases crusting persisted for several months.

Diet, pasture and drug administration were investigated. Haematological and biochemical parameters were unremarkable ruling out secondary (hepatogenic) photosensitisation. Lucerne pastures were heavily infested with cow pea aphids, with ladybird beetles also present. Similar skin lesions were observed in cross-grazing lambs. The unaffected susceptible horses grazed grass pasture. Primary photosensitivity was confirmed by deep skin biopsy in three cases.

Management was directed toward eliminating access to the photodynamic agent, decreasing exposure to sunlight and symptomatic treatment of secondary dermal lesions. However, further studies are required to identify the photoactive agent in this case.

Differentiation between types of photosensitivity is important as clinical signs mimic several conditions between which the prognosis and management differs significantly.



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