

AVTRW

The Association for Veterinary
Teaching and Research Work



CONFERENCE 2019

16-17th September
Moredun Research Institute,
Edinburgh

AVTRW Annual Meeting 2019

The Association for Veterinary Teaching and Research Work
Moredun Research Institute, Edinburgh

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Meeting Programme

Monday 16th September

10:00 - 11:00 Registration

11:00 - 11:15 Welcome address

Scientific session 1:

Chair: Matt Denwood

11:15 - 12:00 **Keynote 1: Dominic Mellor (EPIC): x Deep y Wide? Coherent evidence synthesis for disease control**

12:00 - 12:15 O1: An evaluation of the risk of bovine tuberculosis posed by standard inconclusive reactor animals identified at the single intradermal comparative cervical tuberculin (SICCT) test but not removed at backward check tests. A cohort study.

Anastasia Georgaki Veterinary Epidemiology unit, VSAHG, Northern Ireland.

12:15 - 12:30 O2: Transmission Dynamics of Highly Pathogenic Avian Influenza Among Multiple Waterfowl species and Poultry: the impact of migration timing

Dylan Yaffy, Royal Veterinary College

12:30 - 12:45 O3: Canine Infectious respiratory disease (CIRD) prevalence in UK rehoming shelters and associated within-shelter risk factors.

Ulrike Mauchle, Royal Veterinary College

12:45 - 13:00 O4: Prevalence and risk factors associated with failure of passive transfer (FPT) in beef calves

Rachel Bragg, Royal (Dick) School of Veterinary Studies

13:00 - 14:00 Lunch

Scientific Session 2:

Chair: Valentina Busin

14:00 - 14:45 **Keynote 2: Lee Innes (Moredun Research Institute): It's good to talk. How knowledge exchange can drive collaboration and innovation.**

- 14:45 - 15:00 O5: A multi-disciplinary approach to knowledge exchange using research data to improve livestock health, water quality and public health.
Beth Wells, Moredun Research Institute/University of Glasgow
- 15:00 - 15:15 O6: Effective engagement: Pathology and the public.
Lucy Eckersley, Royal Veterinary College
- 15:15 - 15:30 O7: How does the utilisation of different information sources affect antibiotic prescription habits of veterinarians in Nigeria?
Isabella Endacott, University of Surrey
- 15:30 - 15:45 O8: Knowledge of antimicrobial resistance and antibiotic use habits of veterinarians in Nigeria
Erika Galipo, University of Surrey
- 15:45-16:00 O9: Investigating Ovine Abomasal Tuft cells following a gastro-intestinal nematode infection
Kate Hildersley, University of Glasgow/ Moredun Research Institute
- 16:00 - 16:15 Tea and Coffee

Poster session:

16:15 Flash Poster presentations followed by Poster Session.

17:30 Coach to drinks reception at Summerhall.

Tuesday 17th September

08:30 - 09:15 AVTRW annual general meeting (open to all conference attendees)

Scientific Session 3:

Chair: Dr Tom McNeilly

09:30 - 10:15 Keynote 3: Henny Martineau (Royal Veterinary College): Foxed by the Croydon Cat Killer?

10:15 - 10:30 O10: Identification of suitable T-cell associated transcripts for the development of veterinary diagnostic testing for T-cell lymphoma
Honor Brown, University of Cambridge

10:30 - 10:45 O11: Avian Papilloma and squamous cell carcinoma: A histopathological, Immunohistochemical and virological study.

Alwyn Jones, The Royal Veterinary College

10:45 – 11.00 O12: Understanding Chronic Wasting Disease in Europe

Amy Robinson, Division of Infection and Immunity, The Roslin Institute

11.00 – 11.30 Tea and Coffee

Scientific Session 4:

Chair: Dr Henny Martineau

11:30 - 12:15 Keynote 4: Mandy Nevel (AHDB): African Swine Fever. The UK and global perspectives

12:15 - 12:30 O13: Naturally occurring pneumolysin and autolysin negative equine *Streptococcus pneumoniae* induce less pattern recognition receptor activation than pneumolysin and autolysin competent human strains.
Hannah Wong, University of Cambridge.

12:30 - 12:45 O14: Application of next generation phage display technology to develop new serology diagnostics for Louping ill virus.
Anitha Varghese, University of Nottingham

12:45 – 13.00 O15: The application of deep amplicon sequencing to study gastrointestinal nematode species diversity and isotype-1 β -tubulin SNPs on a UK sheep farm
Mike Evans, Royal (Dick) School of Veterinary Studies

13:00 - 13:10 Conference close

13:10 - 14:00 Lunch and depart



AVTRW Joining Instructions

Do I have to be a vet to join?

No. Members may be either veterinarians or other graduates who have a major interest in either Veterinary Research or Teaching. Currently, members range through:

- Academic staff in many veterinary and non-veterinary faculties
- Research workers in both universities and research institutions
- Medical researchers with particular interests in the veterinary field
- Veterinary investigation officers
- Individuals in commerce and diagnostic laboratories

How do I join?

Please download and complete the application forms either from our website at:

<http://www.avtrw.co.uk/membership/>

or from the following direct download link (full instructions and an overview of the procedure are provided on the first page of the document) at:

http://www.avtrw.co.uk/index.php/download_file/view/45/125/

Once your membership application is received and processed, you will begin to receive Association correspondence and notice of future meetings and will be eligible for all benefits and discounts that are available to AVTRW members. Your membership will be classified as provisional until it is either ratified or declined at the next Annual General Meeting of the full Association following your application. Should your application be declined, your membership joining fee will be refunded.

How much does it cost?

- Annual membership is currently £25 sterling when paid by standing order from a UK bank, or £26 when paid by PayPal.
- Applicants that are registered as a student (undergraduate or postgraduate) at the time of application will receive three years membership for the price of the membership joining fee. Thereafter the annual fee is as above.
- Note that conference costs are kept low to encourage attendance, and participation from students is actively encouraged.

Sponsorship

The AVTRW is grateful to the following sponsors:

The Agriculture and Horticulture Development Board (AHDB) have generously sponsored the presentation prizes and contributed towards student travel bursaries for the 2019 conference.

The Royal Veterinary College (RVC) have generously sponsored the poster prizes for the 2019 conference.

Bioinformatics and Statistics Scotland run a programme of training courses targeted at scientists working in the biological and agricultural sciences, many of which may be relevant to conference delegates. For more details see <http://www.bioss.ac.uk/training.html>

Keynote Speaker Biographies

Professor Dominic Mellor

Dom has a veterinary degree and PhD in veterinary epidemiology from the University of Glasgow. His research interests are in the applied epidemiology of diseases of all animal species and of humans. Of particular interest are the circumstances that conspire to bring people into contact with animals and/or their products in ways that alter their risk of zoonotic disease. Dom is currently Professor of Epidemiology and Veterinary Public Health at the University of Glasgow, and director of EPIC - The Scottish Government's Centre of Expertise on Animal Disease Outbreaks.



Professor Elisabeth Innes

Elisabeth has an honours degree in Immunology from the University of Glasgow and a PhD in Tropical Animal Health from the University of Edinburgh. She has conducted research in the area of infectious diseases of livestock, developing solutions to control diseases caused by protozoan parasites. Following a sabbatical year spent in Hong Kong in 2002-03, she became more interested in science communication, knowledge exchange and education. Elisabeth is currently the Director of Communications at Moredun and she was recently awarded Honorary Professorships from Heriot Watt University and the University of Edinburgh.



Dr Henny Martineau

Henny Martineau currently works as faculty pathologist at the Royal Veterinary College, where she holds the position of Head of Veterinary Forensic Pathology. She qualified as a Veterinary Surgeon from Glasgow Veterinary School in 1998. Following time as an assistant veterinary surgeon in mixed practice in Wales, she spent three years working in a training position in Veterinary Pathology at the Faculty of Veterinary Medicine of the University of Glasgow, where she gained a Master's degree in Veterinary Medicine, investigating the pathogenesis of gastric ulceration in the horse. She then worked as a research pathologist for Astrazeneca in Cheshire, as a large animal diagnostic pathologist for the Scottish Agricultural College in Edinburgh, and in 2010, she gained a PhD from the University of Glasgow. The title of her thesis was "Early events of Jaagsiekte retrovirus infection in the ovine lung". During her time at the RVC, she has gained a certificate in Post Graduate Education and has become a Fellow of the Higher Education Authority and a Fellow of the Royal College of Pathologists.



Dr Mandy Nevel

Mandy Nevel is currently the Head of the Animal Health and Welfare team at AHDB. She graduated as a veterinary surgeon in 1992 after completing a BSc in Animal Physiology and Nutrition. After a period of some years in farm animal practice she obtained her PhD in Physiology of the Sow, from the Royal Veterinary College. She spent a year as a post-doctoral worker at the University of Saskatoon and returned to the UK in 1999 to take up a position with Pfizer Global Animal Health in vaccine development for pigs and cattle. She returned to the RVC in 2003 to pursue her research interests of pathology of livestock, infectious diseases and welfare of pigs and still undertakes undergraduate and postgraduate teaching in these areas. She is Honorary Secretary of the Pig Veterinary Society and Chair of the education sub-committee and co-ordinates the Pig Health and Welfare Council and its sub-groups. She is also a member of the BVA CPD committee. She has a certificate in Post Graduate education and is a Fellow of the Higher Education Authority.



Oral Abstracts

Scientific session 1:

O1: An evaluation of the risk of bovine tuberculosis posed by standard inconclusive reactor animals identified at the single intradermal comparative cervical tuberculin (SICCT) test but not removed at backward check tests. A cohort study.

Anastasia Georgaki^a, Alan W. Gordon^b, Liam P. Doyle^a, Fraser D. Menzies^a

^a Veterinary Epidemiology Unit, Veterinary Service Animal Health Group, Department of Agriculture, Environment and Rural Affairs, Dundonald House, Belfast BT4 3SB, Northern Ireland, UK.

^b Biometrics Division, AgriFood and Biotechnology Institute, Newforge Lane, Belfast BT9 5XF, Northern Ireland, UK.

This retrospective cohort study on bovine tuberculosis (bTB) compared a cohort of animals that were standard inconclusive reactors (ICs) to the bTB skin test at a backward check test (BCT) (exposed group), to a matched cohort of animals that were negative at the same herd test (unexposed group). The aim was to quantify the risk of standard ICs having bTB relative to the risk of negative animals having bTB.

When the two cohorts were matched for sex, age group, herd test and follow up period the incidence of bTB in standard ICs was 24% (95% CI 18 - 30) and that in negative cattle at the same test was 5% (95% CI 4 - 7), giving a relative risk of 4.5 (95% CI 3.13 - 6.48, $p < 0.0001$). The interpretation of this result was that the risk of bTB infection in cattle previously disclosed as ICs at a BCT was four and a half times greater relative to the risk of bTB in cattle found negative at the same BCTs.

The effects of breed, testing veterinary surgeon and herd size were investigated with logistic regression models. The models indicated that there is no statistically significant association between these factors and the exposure factor and the outcome of interest.

This result is significant to herd owners, veterinary surgeons and policy makers who are working towards identification of potential bTB sources and elimination of the infection.

O2: Transmission Dynamics of Highly Pathogenic Avian Influenza Among Multiple Waterfowl Species and Poultry: The Impact of Migration Timing.

Marina Pavlak¹, Dylan Yaffy^{2,3}, Rachel Jennings³, Wendy Beauvais³, Renata Ivanek³

¹Veterinary Faculty, University of Zagreb, Croatia

²Royal Veterinary College, London, United Kingdom

³Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY

Outbreaks of highly pathogenic avian influenza (HPAI) among wild birds and poultry pose a risk to human health and increase concern about the likelihood of another epidemic comparable to that of the 2016/17 H5N8, European epidemic. With a focus on the overlap between stop-over period of different migratory species, we have modelled the transmission of HPAI between wild birds and domestic poultry at wetland regions in Croatia. Under a simplifying assumption of homogenous mixing, we developed a deterministic SIR compartmental model that can account for the direct mode of pathogen transmission among 4 bird species. The model includes compartments for backyard poultry farms and compartments for Mute Swans (*Cygnus olor*), a sentinel species for HPAI outbreaks.

Additionally, we modeled Mallards (*Anas platyrhynchos*), an asymptomatic carrier of HPAI, represented with two groups of compartments corresponding to the migratory and non-migratory (resident) birds. The uncertainty and variability in model predictions is being analyzed using Monte Carlo simulations. The preliminary results support that migration timing and the duration of overlap between Mute Swans and Mallards strongly and positively affect the HPAI-induced mortality in wild birds and number of infected poultry farms. In future years, we hope our model can use real-time migration dates to predict the risk of an HPAI outbreak occurring. Future work will evaluate the role of indirect transmission in the epidemiology of HPAI in the area.

O3: Canine infectious respiratory disease (CIRD) prevalence in UK rehoming shelters and associated within-shelter risk factors.

Ulrike Mauchle¹, Simon Priestnall¹, Judy Mitchell¹, and Jacqueline M Cardwell¹

¹Department of Pathobiology and Population Sciences, The Royal Veterinary College

Objectives - To estimate the prevalence of Canine Infectious Respiratory Disease (CIRD) in the UK shelter dog population and to identify shelter-level risk factors for CIRD occurrence.

Design – Questionnaire-based cross-sectional survey of UK rehoming shelters.

Sample – A sampling frame of rehoming shelters in the UK and Republic of Ireland was compiled from dog rehoming websites and all 454 rehoming shelters identified were invited to participate.

Procedures - Standard descriptive and univariable analyses were performed. Shelters were categorised as large or small based on the median number of animals entering shelters annually.

Results – Of 141 returned questionnaires, 82 (58%) provided information on CIRD prevalence and were included in the analysis. CIRD was present in all regions of the UK. The median estimated prevalence of CIRD in UK rehoming shelters was 5.7 % (range: 0 – 82.5%) with a low mortality rate. A median of 2.6% (range: 0 – 82.5%) of dogs in shelters were examined by a veterinarian for suspected CIRD. CIRD prevalence was associated with shelter size with a median prevalence of 10% (95% CI: 7.4 – 22.7%) in large shelters and 0.7% (95% CI: 0 – 2.7%) in small shelters ($P < 0.0001$). Just over half of respondents (55%; $n = 80$) indicated that CIRD had a negative impact on the welfare of dogs in their establishment. Analysis of further shelter-level risk factors is ongoing and will be presented.

Significance of results – CIRD is widespread in UK dog shelters. Identification of modifiable risk factors would help to improve shelter dog welfare.

O4: Prevalence and risk factors associated with failure of passive transfer (FPT) in beef calves.

Rachel Bragg, Alexander Corbishley, Alastair Macrae, Samantha Lycett

Royal (Dick) School of Veterinary Studies and the Roslin Institute, University of Edinburgh

Failure of passive transfer (FPT) of colostral antibodies is well documented in dairy calves, with prevalence estimates varying from 19.2% to 33.1% worldwide. However knowledge of the rate of FPT in beef calves remains limited with very few published studies.

The objectives of this study were to 1) investigate the current prevalence of FPT in UK spring calving beef herds, 2) identify associated risk factors for the development of FPT in spring born suckled calves at the calf, cow and herd level and 3) to develop models to predict the occurrence of FPT in beef calves.

1171 individual calf blood samples were collected in the first week of life from 86 farms across Scotland and England in spring 2018 (mean 13.5 calves per farm). Calf blood samples were analysed for serum IgG by Radial Immuno-Diffusion (RID). 15% of calves sampled had under 10 g/l serum IgG, indicating complete FPT. 37% of calves sampled had under 24 g/l serum IgG results, indicating either partial or complete FPT. On 25 farms, greater than 20% of the calves sampled had complete FPT.

Calves requiring feeding assistance for colostrum had an increased risk of complete FPT (Odds Ratio [OR] 2.35 [95% CI: 1.09 – 5.05] when fed artificial colostrum). Being a twin increased the risk of partial FPT (OR 3.34 [95% CI: 1.65 – 6.76]). Overall prevalence of FPT in spring born suckled beef calves was similar to dairy calves, with significant risk factors including dam parity, twins, assistance at calving and assistance for feeding colostrum.

Scientific session 2:

O5: A multi-disciplinary approach to knowledge exchange using research data to improve livestock health, water quality and public health.

Beth Wells¹, Hannah Shaw¹, Emily Hotchkiss⁴, Janice Gilray¹, James Green², Frank Katzer¹, Andrew Wells³ and Elisabeth Innes¹

¹Moredun Research Institute, Pentlands Science Park, Penicuik, Midlothian. EH26 0PZ

²Scottish Water, Juniper House, Heriot Watt Research Centre, Edinburgh. EH14 4AP

³The Crown Estate, 6 Bells Brae, Edinburgh. EH4 3BJ

⁴School of Veterinary Medicine, University of Glasgow, Bearsden Road, Glasgow G61 1QH

Cryptosporidium parvum is a ubiquitous, zoonotic parasite responsible for high economic losses in beef and dairy herds, water contamination and consequent public health risk. This study was based in a catchment with a history of frequent contamination events of the public water supply with *C. parvum*, leading to strained relations between water providers and local livestock farmers, who had reported problems in their calves due to cryptosporidiosis.

The aim of the project was to investigate parasite transmission within the catchment and devise management strategies for control with farmers, vets, landowners and the water industry, through a coordinated knowledge exchange (KE) programme.

Faecal samples were collected from four participating farms from adult cattle, calves, ewes, lambs, red and roe deer and water samples were collected at three points in the catchment.

Cryptosporidium prevalence and speciation results revealed a very high prevalence of *C. parvum* within the catchment and genotyping suggested that all of the species tested, including cattle, sheep and deer, were contributing to *C. parvum* loading in the catchment waters.

KE events and information, tailored for farmers and vets, was designed to help reduce cryptosporidiosis on farms and hence reduce parasite output in to the environment, whereas KE designed for water industry catchment officers aimed to increase knowledge of parasite control on farms, including the difficulties this involved. Due to an increased understanding between stakeholders, grazing and land management changes were implemented and the subsequent improvement in water quality and public health will be discussed.

O6: Effective engagement: Pathology and the public.

Lucy Eckersley, Outreach Officer.

The Royal Veterinary College

The RVC's Outreach Team organises events to disseminate the pathology and epidemiology research undertaken at the RVC, we will present two collaborative events at the Royal Institution and Royal Society. Both aimed to inform the public of recent developments in these fields, but also to provide opportunity for discussion where we can showcase our diverse cohort of experts, and to encourage future applicants into scientific study. Firstly, Animal CSI: Predator built on an initial pathology event with the Ri the previous year. It included interactive science stalls with topics ranging from *T.gondii* infection, prion diseases, and parasites, to post mortem analysis of predated wildlife. These were hosted by our staff and members of the Royal College of Pathologists, who also sponsored the event during Biology Week.

The main event was a live-streamed dissection carried out by Mr Andrew Crook MBE, of a white tiger from a UK Zoological collection. The audience watched the full dissection in real time, and asked questions of Mr. Crook at the end. This was followed by a panel of 5 pathologists of different specialisations, with an audience Q&A where visitors learnt more about their motivations behind pathological research, and the scientist's lives. We will discuss the process of collaboration between pathologists and outreach staff, how our goals and funding shaped the event, and feedback from visitors. Finally we will discuss the planning and implementation of our stall showcasing *Tuberculosis* gene knockout research using an innovative Nerf gun game, at the recent Royal Society Summer Exhibition.

O7: How does the utilisation of different information sources affect antibiotic prescription habits of veterinarians in Nigeria.

Isabella Endacott¹, Adah Ogwuche², Abel Ekiri¹, Beatty-Viv Maikai³, Enokela Idoga⁴, Ruth Alafiatayo¹, Alasdair Cook¹

¹Department of Veterinary Epidemiology and Public Health, Faculty of Health and Medical Sciences, University of Surrey Veterinary School, Guildford, Surrey, United Kingdom

²Zoetis-ALPHA Initiative, Zoetis, Zaventem, Belgium

³Department of Veterinary Public Health and Preventative Medicine, Ahmadu Bello University, Zaria, Kaduna, Nigeria

⁴Department of Veterinary Physiology, Biochemistry and Pharmacology, University of Jos, Jos, Plateau, Nigeria

Antimicrobial resistance (AMR) is recognised as a global One Health issue, with AMR driven by the overuse and misuse of antibiotics. In Nigeria veterinarians and para-veterinarians are responsible for antibiotic prescription in both production and companion animals, and decisions on antibiotic treatment are influenced by the sources of information that are available and actively used. This study investigated the sources of information utilised by veterinarians and para-veterinarians to guide antibiotic prescription habits and the implications for appropriate antibiotic use in Nigeria.

The antibiotic prescription habits of 413 veterinarians and para-veterinarians in Nigeria was assessed using an online survey. The most frequently used sources of guidance were manufacturer labels on products and personal experience, with colleague advice secondarily. Over 55% were not aware of government-issued guidelines on antibiotic use in animals though of those aware 70% utilised this resource. The use of laboratory test results to aid diagnosis prior to antibiotic treatment was used only 1-2 times annually or never by over half of respondents and almost a third did not undertake sensitivity testing before treatment.

The study highlights potential inadequacies in the breadth and reliability of information sources utilised to guide antibiotic decisions and insufficient use of laboratory diagnostics and antimicrobial sensitivity testing in Nigeria. The development of reliable information sources on antibiotic use and greater dissemination of formal guidelines, increased awareness of the

value of antimicrobial sensitivity testing, and enhanced information sharing between laboratories and animal health practitioners could help promote antimicrobial stewardship in Nigeria.

O8: Knowledge of antimicrobial resistance and antibiotic use habits of veterinarians in Nigeria.

Usman Adekanye¹, Abubakar Bala Muhammed², Roberto La Ragione³, Ana Mateus⁴, Aliyu Wakawa⁵, Erika Galipó³, Ruth Alafiatayo³, Abel Ekiri³, Alasdair Cook³

¹Nigeria Ministry of Defence Health Implementation Programme

²LMS

³vHive, University of Surrey

⁴Royal Veterinary College

⁵Ahmadu Bello University

Antibiotic resistance (ABR) is a global issue that requires urgent attention from both the human and veterinary health sectors. In Nigeria, little is known about the knowledge and attitudes of veterinarians towards antibiotic use. The present study investigated the knowledge and attitudes of Nigerian Veterinarians towards antibiotic use and antibiotic stewardship.

A total of 241 participants responded to the survey and most respondents were male (79.7%), aged less than 45 years (83.4%), and worked in mixed practice (40.2%) and poultry practice (39.0%).

Only 36.9% of respondents had previously heard the term antimicrobial stewardship and from these, only 69% correctly defined it. Most of the respondents (83.8%) agreed that the excessive use of antibiotics in livestock is a contributor to ABR. Of concern was the finding that almost half of the respondents (46%) indicated that prophylactic antibiotics are an appropriate alternative to protect animal health when there is poor biosecurity. Only 20.3% of the respondents reported performing Antimicrobial susceptibility testing (AST) more than 3 times a month before starting an antibiotic treatment. The main barriers to AST use reported included the lack of laboratories and the owners' inability to pay.

The study findings highlighted important knowledge gaps and practices for which interventions may be designed to increase veterinarian knowledge on antimicrobial resistance and practices that can help promote antibiotic stewardship in Nigeria.

O9: Investigating Ovine Abomasal Tuft cells following a Gastro-intestinal Nematode Infection.

Katie A. Hildersley^{1, 2}, Collette Britton¹, Eileen Devaney¹, Stewart T. G. Burgess², Yolanda Corripio-Miyar², Victoria Gillan¹, Jeanie Finlayson², David Frew², Tom N. McNeilly²

¹University of Glasgow, ²Moredun Research Institute

Tuft cells (TCs) are of major interest in mucosal immunology due to their proposed function in sensing changes in the gut lumen environment and initiating the Type-2 T-helper immune responses to gastro-intestinal nematodes (GIN). This study aimed to determine whether orthologs of known murine TCs markers could identify the presence and expansion of ovine TCs in the abomasal epithelium following infection with GIN, *Teladorsagia circumcincta*. Expression of the murine tuft cell markers; POU2F3, Gfi1b, TRPM5 and DCLK-1, in ovine abomasum was first evaluated using immunohistochemistry. Anti-POU2F3 and anti-Gfi1b antibodies were both found to give a strong specific signal on putative ovine TCs within the abomasum, and POU2F3+ cells increased over the course of a *T. circumcincta* infection, but no labelling with anti-DCLK-1 or anti-TRPM5 antibodies was

detected. To investigate gene expression profiles of ovine TCs, RNA-Seq was performed on purified abomasal epithelial cells from *T. circumcincta* infected and uninfected sheep. This revealed a significant up-regulation of *trpm5* expression in infected sheep; however, *dclk-1* transcripts were not detected. Tissue and RNA samples from a previous *T. circumcincta* project provided further insight into ovine tuft cell dynamics over the course of an infection. Using RT-qPCR, the upregulation of *trpm5*, *pou2f3* and *gfi1b* expression was confirmed in infected sheep, and for the first time *dclk-1* expression has been detected in the ovine abomasum. This project has taken the first steps in identifying markers of putative ovine TCs, and demonstrated the expansion dynamics over the course of an experimental GIN infection.

Scientific session 3:

O10: Identification of suitable T-cell associated transcripts for the development of veterinary diagnostic testing for T-cell lymphoma

Honorina Brown, University of Cambridge

O11: Avian Papilloma and squamous cell carcinoma: A histopathological, Immunohistochemical and virological study.

Alwyn Llewelyn Jones, Alejandro Suárez-Bonnet, Judy Mitchell, Gustavo Ramirez, Mark Stidworthy and Simon Priestnall.

The Royal Veterinary College.

We describe the histopathological findings in 7 papillomas and 45 squamous cell carcinomas (SCCs) from psittacine birds, raptors and domestic fowl. The majority of tumours were located on the skin (24/52, 46.2%) or uropygial gland (10/52, 19.2%). Of the SCCs, 30 (66.7%) were well differentiated and 15 (33.3%) were poorly differentiated. SCCs exhibited a significantly higher degree of nuclear pleomorphism ($P=0.005$) and a greater proportion exhibited surface ulceration ($P=0.001$) compared to papillomas. The expression of Cox-2 and E-cadherin was investigated by immunohistochemistry. Tumours were assigned a Cox-2 total score (TS) based on the intensity multiplied by the distribution of labelling. The Cox-2 TS was significantly higher in SCC compared to papillomas ($P=0.002$). Cox-2 labelling was predominantly cytoplasmic but some tumours exhibited concurrent membranous and/or perinuclear labelling. SCCs exhibiting membranous labelling had a significantly higher mitotic count ($P=0.028$). Tumours were determined to be negative for E-cadherin if there was loss of membranous expression in $\geq 65\%$ of neoplastic cells. A significantly higher proportion of SCCs were negative for E-cadherin compared to papillomas ($P=0.042$). Fourteen papillomas and SCC from psittacine birds were also tested by PCR for the presence of Psittacus erithacus papillomavirus 1 (PePV1) and Psittacid herpesvirus 1 (PsHV1), however all samples tested negative. We demonstrate for the first time the expression of Cox-2 and E-cadherin in avian tissues, and suggest that these markers may be useful in differentiating papillomas from SCCs. We also propose that selective Cox-2 inhibitors may have therapeutic value in the treatment of SCCs in birds.

O12: Understanding Chronic Wasting Disease in Europe.

Amy L Robinson¹, Wilfred Goldmann¹, Khalid Salamat¹, Debbie Mckenzie², Abigail Diack¹, Fiona Houston¹

Division of Infection and Immunity, The Roslin Institute and The Royal Dick School of Veterinary Studies, University of Edinburgh, Midlothian, EH259RG, UK

University of Alberta, Edmonton, Canada

Chronic wasting disease (CWD) is an important and highly transmissible prion disease of both wild and farmed deer, present in at least 25 US states, 3 Canadian provinces and South Korea. The recent identification of CWD in Norwegian reindeer, with further cases in moose in Norway, Sweden and Finland, make it vital to understand CWD in the European context.

We aim to investigate how susceptible wild British deer species would be to CWD, if it were identified in the UK. As susceptibility to prion diseases is strongly associated with polymorphisms of the prion protein gene (*PRNP*), we performed a large-scale genetic survey of *PRNP* sequence variation between and within deer species in the UK. We have identified novel variants in British deer species not common to any North American deer species. Our objective is to predict the effects of these *PRNP* genotypes on susceptibility to CWD, using *in-vitro* models of prion conversion to assess their effects on prion replication. It is also important to understand the diversity of CWD strains found in Scandinavian cases. Biochemical analysis of material from the Norwegian cases has demonstrated that they are different from CWD cases in North America. We are undertaking transmissions of infected material into well-established panels of wild-type mice, to characterize the prion strains present in Norway and provide a comparison to North American isolates. Our results will aid in understanding the nature of CWD strains present in Europe, and how susceptible wild British deer species may be.

Scientific Session 4:

O13: Naturally-occurring pneumolysin- and autolysin-negative equine *Streptococcus pneumoniae* induce less pattern recognition receptor activation than pneumolysin- and autolysin-competent human strains.

Hannah Elizabeth Wong, Panagiotis Tourlomousis, Gavin K Paterson, Clare E Bryant.

University of Cambridge, Department of Veterinary Medicine, Cambridge UK (Wong, Tourlomousis, Bryant). University of Edinburgh, Roslin Institute, Edinburgh UK (Paterson).

Streptococcus pneumoniae causes pneumonia in humans and horses.

S. pneumoniae produces the toxins autolysin and pneumolysin that contribute to host damage. These toxins, combined with the host immune system, drive a protective immune response, but can cause immunopathology. Equine strains of *S. pneumoniae* do not produce autolysin or pneumolysin. My hypothesis was that equine *S. pneumoniae* would induce less pattern recognition receptor (PRR) driven inflammation than pathogenic human strains. The project aims were to determine the contribution of PRRs to the host response to human and equine *S. pneumoniae* isolates and then to compare the inflammatory response induced by these strains *in vivo*.

The equine strain induces TNF α -release from mouse macrophages comparably to the human strain *in vitro* at early time points, but that the equine strain is deficient in TNF α production at late time points and IL-1 β production throughout the infection. The human strain induces TNF α predominantly through TLR2 and MyD88 whilst the equine strain is solely dependent on MyD88.

In a mouse model of acute pneumonia, infection with the equine strain resulted in reduced bacterial counts and lung pathology in comparison to the human strain. The equine strain retained the ability induce IL-1 α within lung tissue, but was deficient in the induction of IFN- γ , IL-6, RANTES and TNF α . These data support the *in vitro* data suggesting less activation of PRRs by equine pneumococci. These data also suggest a role for IL-1 α in mediating an inflammatory response to equine pneumococcal strains, and that this response is sufficient to control bacterial numbers without inducing immunopathology.

O14: Application of next generation phage display technology to develop new serology diagnostics for Louping ill virus.

Anitha Varghese^{1,2}, Janet Daly¹, Kevin Gough¹, Mara Rocchi²

¹School of Veterinary Medicine and Science, University of Nottingham ;

² Moredun Research Institute, Scotland

Louping ill virus is a UK endemic flavivirus vectored by *Ixodes ricinus* ticks. LIV mainly affects sheep and red grouse usually with a fatal outcome in the latter. The disease in sheep was controlled by a vaccine that has recently become unavailable. This is likely to lead to a rise in new cases and economical loss, especially in lambs who would have been protected by maternal antibodies. There is a need for a rapid diagnostic test as current serology diagnostics require CL3 facilities and are time consuming.

Next Generation Phage Display is a technique that combines classic phage display with next generation sequencing. The main advantage of phage display is the linking of the phenotype (peptide binding properties) with genotype (the peptide gene displayed by the phagemid). Serum antibodies can be used to select specifically binding phage.

Serum from LIV infected and uninfected sheep have been biopanned against P8 linear random peptide phage library to generate a phage sub-library specific for LIV antibodies. The phage genomes will be sequenced using Ion Torrent sequencing and antigenic peptide regions ranked using Z-score analysis. The most antigenically potent peptides will be used to create a rapid diagnostic assay such as an ELISA.

O15: The application of deep amplicon sequencing to study gastrointestinal nematode species diversity and the isotype-1 β -tubulin SNPs on a UK sheep farm.

Mike Evans¹, Umer N. Chaudhry², Kim Hamer^{1,3}, Jenifer McIntyre³, Neil D. Sargison^{1,2}

¹Royal (Dick) School of Veterinary Studies, University of Edinburgh

²Roslin Institute, University of Edinburgh

³University of Glasgow

Current recommendations for reducing the development and spread of anthelmintic resistance are largely based on modelling exercises. These recommendations have been shown to be efficacious in the field; however improved methods of studying parasite epidemiology are required to refine models. This presentation describes the application of deep amplicon sequencing to study gastrointestinal nematode species diversity and the prevalence of benzimidazole resistance SNPs on a UK sheep farm across 3 years, as a proof of concept for future studies into the epidemiology of anthelmintic resistance.

Faecal egg counts and pooled coprocultures were performed from 10 ewes and 10 lambs, approximately every 3 weeks from spring to autumn in 2016-2018. Deep amplicon sequencing was performed on lysates of the pooled L₃ using conserved primers for the ITS2 region to produce a 'nemabiome' for each sample pool, and with *Teladorsagia circumcincta* specific primers for the isotype-1 β -tubulin locus.

The nemabiome data illustrate marked variation in the relative abundance of different strongylid species (particularly *Teladorsagia circumcincta*) within and between years. These data also illustrate variations in species composition between ewes and lambs, and alterations after some anthelmintic treatment but not others.

The β -tubulin SNP data show a lack of variation between ewes and lambs and across the three years, with the F200Y resistant polymorphism predominating at almost all time points, suggesting that this polymorphism is approaching genetic fixation within the *T. circumcincta* population on the farm. Analysis of β -tubulin haplotype diversity is on-going but preliminary results suggesting temporal variation in diversity will be presented.

Poster Abstracts

P1: Optimisation of methods for Influenza D virus detection in bovine and porcine clinical samples.

Benjamin C Mollett¹, Alexander MP Byrne¹, Pauline M van Diemen¹, Vanessa Ceeraz¹, Chiara Chiapponi², Emanuela Foni², Sharon M Brookes¹ and Ian H Brown¹ and Helen E. Everett^{1*}

¹Virology Department, Animal and Plant Health Agency (APHA Weybridge), Addlestone, Surrey KT15 3NB, United Kingdom.

²Istituto Zooprofilattico Sperimentale della Lombardia ed Emilia Romagna, Brescia, 25124, Italy.

Influenza D virus was first detected and isolated in the USA in 2011. This novel virus has been isolated from swine and cattle and has been associated with respiratory disease in some cases. Within Great Britain, only a limited survey has been conducted to assess the circulation of influenza D virus in livestock. By optimising the viral culture and detection methods for influenza D viruses, we aim to assess possible influenza D virus circulation in swine and cattle in the UK.

Representative strains of influenza D virus from Europe, (D/swine/Italy/199724-3/2015) and the USA (D/swine/Oklahoma/1334/2011) were found to replicate efficiently in embryonated chicken eggs and two cell lines, Caco2 and MDCK. Control swine serum raised against influenza D virus successfully detected the virus by haemagglutination inhibition (HI) and viral RNA is detected by an established RRT-PCR assay, targeting the PB1 gene.

The limited numbers of bovine and porcine samples submitted from animals with respiratory signs have been negative for viral RNA. The newly developed, specific HI assay will allow retrospective screening of archived serum samples. Field samples from animals with respiratory signs will be screened by HI (serum) or RRT-PCR (swabs or tissues). Virus isolation will be conducted with any positive samples using the viral culture methods developed.

This enhanced screening capability will facilitate influenza D virus investigation and promote greater understanding of this newly emergent pathogen.

P2: Exploring FPT and colostrum quality in Scottish dairy calves.

Alexandra Haggerty, Katharine Denholm.

The University of Glasgow

The Stewartry Veterinary Centre

Ruminants are born immunologically naïve and are reliant on passive transfer of colostral antibodies to protect against disease until their own immune system becomes fully functional. Calves that fail to absorb sufficient concentrations of immunoglobulins are said to suffer from failure of passive transfer (FPT). FPT is associated with an increased risk of calfhood morbidity and mortality.

Study Objectives:

- To measure the prevalence of FPT in Scottish dairy calves.
- Validate a cost-effective method of directly measuring IgG using radial immunodiffusion (RID) agarose plates (Triple J test kits).
- To assess agreement between serum testing using RID, Zinc Sulphate Turbidity Test, Total Protein and Brix refractometry.
- To measure IgG and bacterial loads of colostrum at point of feeding

Preliminary results from the current work show that the mean proportion of calves with FPT is 30%. Furthermore, while mean Brix percentages of colostrum are adequate (mean 22%), colostrum is highly contaminated with mean total bacterial counts of 4.57×10^6 CFU/ml and mean coliform counts of 6.80×10^4 CFU/ml.

The Scottish data from this study indicates the prevalence of FPT at 30%. This fits with data from surveys of dairy calves in the USA, Australia and New Zealand which report the prevalence of FPT between 19 and 38%.

Achieving adequate passive transfer is a function of colostrum quality, quantity fed and feeding in a timely fashion. Preliminary results from this study indicate colostrum bacterial contamination is high and therefore practitioners should not fail to focus on hygiene when investigating FPT on Scottish dairy farms.

P3: Newcastle disease virus diversity in the Middle East: food security threat.

James Seekings¹, Nabil Wali², Scott M. Reid¹, Rowena Hansen, Steve Essen¹, Ian H. Brown¹

¹Department of Virology, Animal and Plant Health Agency - Weybridge, Woodham Lane, New Haw, Addlestone, Surrey, KT15 3NB, United Kingdom

² Kurdistan Ministry of Agriculture - Sulaimania Veterinary Department.

Newcastle disease (ND) is endemic in Iraq and Kurdistan and is the most significant disease facing the poultry industry in the Middle East. Regional control efforts for ND incorporate the use of two vaccines, B1 and LaSota, but mitigation activities are hindered by lack of biosecurity and modern diagnostic methods such as real-time reverse transcription polymerase chain reaction. Data on the genetic characterization of ND virus (NDV), which is the virulent form of avian avulavirus type 1 (AAvV-1, formerly avian paramyxovirus type 1) is limited considering the importance of this pathogen in the Middle East. The objectives of this study were a) to carry out molecular virological investigation and downstream genomic analyses of AAvV-1 strains circulating since 2003 in Kurdistan, elsewhere in the Middle East and in Eastern Europe; b) to provide a more detailed understanding of the characteristics of circulating viruses, their epidemiology in these regions and c) to evaluate the fitness of current molecular techniques in the identification of these viruses. Samples were sequenced using the Illumina platform followed by an in-house pipeline to determine the consensus sequence of the whole genome. Phylogenetic analysis and genotyping, using maximum likelihood trees of the full fusion gene, showed that AAvV-1 genotype VII was the dominant circulating infectious virus in the Middle East and Eastern Europe. Identification of the circulating strains will help to develop better prophylactic measures and diagnostic tools to prevent outbreaks of ND in the Middle East.

P4: A study on Homology and Heterology among different isolates of Foot and Mouth Disease Virus type "O".

Hafza Zahira Manzoor, Dr. Imran Altaf

Quality Operation Laboratories, University of Veterinary and Animal Sciences, Lahore.

Background: Foot-and-mouth disease (FMD) is one of the trans-boundary and economically devastating diseases among livestock animals. Although having a little mortality figure, FMD has high morbidity rate and its contagiousness can result in massive economic consequences. Vaccination is still applied policy against the virus in many of developing countries e.g. in Pakistan in purpose to control the disease because still no treatment is available for the disease and ultimately mortality rate is very high. The causative agent of FMD virus belongs to genus Aphthovirus, family *picornavaridae*, are non-enveloped, single stranded RNA molecule with positive polarity, 30nm in diameter and genome 82kb in length, having seven serotypes.

Objectives: To study the homology and heterology among different isolates of FMD type O Viruses (PAK-98 and Pan-Asia-2 clusters) and to select a suitable field strain to be used as vaccinal seed against FMD type O Viruses

Methodology: Antigenic relationship among different isolates of FMDV type “O” was calculated by using serological tests (ELISA & Virus Neutralization Test). The isolation of virus, culturing of virus by reviving BHK-21 cell line were performed. Previously identified and molecularly characterized eight virus isolates five belongs to (Pan-Asia-2) and three from (PAK-98) were processed and propagated on selected cell line. TCID₅₀/100ul of virus dose was calculated. Total 40 animals were challenged with each virus and booster was given at 7, 14 & 21 day, in order to obtain antisera raised against each virus. Antibody detection ELISA was performed to obtain antibody titre from samples. To calculate antigenic relationship between and among virus isolates of Pan-Asia-2 and PAK-98 in term of their Homology and Heterology were checked by using Virus Neutralization Test.

Results: TCID₅₀ values of five virus isolates of Pan-Asia-2 were 10^{4.7}, 10^{4.8}, 10^{4.6}, 10^{4.3}, 10^{4.3} and for PAK-98 were 10^{4.8}, 10^{4.6}, 10^{4.3} along with percentage of inhibition calculated from antibody titre of serum samples were 70%, 72%, 70%, 73%, 71% and 70%, 72%, 71% at 1/30 dilution of neat sera of both clusters. Combination results of Homology and Heterology was determined by calculating the neutralization titre and virus dose according to SOP No.8 of Pirbright Institute. The VNT data was run to find out relationship between combination of challenges of PAK-98 and Pan-Asia-2 within the clusters and between clusters showed that r₁-values 0.3-0.7 exhibiting similarity among strains within the cluster but between clusters viral strains were antigenically different provided r₁-values 0.07-0.2.

Conclusion: The result shows heterologous combination of PAK-98 and Pan-Asia-2 isolates were antigenically different and upon challenges will not confer the immunity, while all strains from both clusters with homological and heterological combinations were antigenically similar within clusters and can provide protective titre during in-vivo challenges. Overall all strains between clusters but not across the cluster provide broad spectrum immunity and can be used as vaccinal candidate in order to control outbreak caused by FMD.

P5: Making a move: Do NGF inhibitors alter microvesicle production to induce cell migration?

Beth Kraines, Emily Mills, Lauren Powell, Imelda McGonnell.

Dept. Comparative Biomedical Sciences, Royal Veterinary College, London

Funded by BBSRC STARS

Background: Malignant Peripheral Nerve Sheath Tumours (MPNSTs) occur in humans and canines. Its metastatic mechanisms are poorly understood. Nerve Growth Factor (NGF) signalling is involved in cancer metastasis in MPNSTs. NGF inhibitors can reduce metastasis, however resistance to inhibition can develop. NGF may alter microvesicle (MV) production which could contribute to this phenomenon. MVs transport and deliver cargo to target tissues. They can induce beneficial and deleterious changes and contribute to cancer pathogenesis. Little is known about how exogenous signalling inhibitors modify MV production and function in MPNSTs, and how these MVs might change cell behaviours.

Objectives: We hypothesised that altering NGF signalling changes MV production and function, investigating:

- a) How NGF activation and inhibition alters MV production and characteristics in MPNST
- b) Whether MVs from NGF treated or inhibited cells influence migration of naïve MPNST cells

Methods: MPNST cells (ST88-14) were treated with Pro-NGF, NGF, and NGF-receptor inhibitor CEP-701. MVs were extracted from harvested media by centrifugation, labelled with Annexin-V and analysed by flow cytometry to quantify size and number. Naïve cells were treated with these MVs and cell migration assessed in scratch assays over 28hours

Results: There were no statistically significant differences in number of MVs produced compared to controls. Naïve cells exposed to MVs from cells treated with 50ng/ml Pro-NGF or NGF and 100ng/ml NGF had significantly increased migration at 4hours ($P=0.0076$, $P=0.0015$, $P=0.0476$). MVs from 1 μ M CEP-701 treated cells significantly decreased migration after 8hours ($P<0.0001$).

Conclusion: NGF activation and inhibition does not affect MV production. However, NGF and Pro-NGF cause MPNST cells to release migration-promoting MVs, confirming this pathway's potential role in metastasis. Treating MPNST cells with a higher CEP-701 concentration causes cells to release migration-repressing MVs, suggesting potential benefits of inhibitor use against MPNST metastasis.

P6: Elucidating the role of *Toxoplasma gondii* on wild fox (*Vulpes vulpes*) behaviour: a novel study of stress levels in foxes using cortisol as a biomarker.

Harry J. Peters, Henny Martineau and Joanne P. Webster.

Department of Pathobiology and Population Science, Royal Veterinary College.

The parasite *Toxoplasma gondii* (*T. gondii*) has been showed to induce behavioural changes in its intermediary hosts in a rodent model. These changes have been partly associated with changes in intermediate host anxiety and risk behaviours. The aim of this study was to identify a decrease in chronic cortisol levels (indicative of decreased anxiety) in foxes, a secondary host, infected with *T. gondii*. Post mortems were performed on foxes during which fur and brain samples were taken. The presence of infection was determined via nested PCR on brain samples before cortisol levels were assessed from fur samples using a commercially available assay kit. Results showed that there was no difference between age, sex and body condition score matched positive and negative samples. Histological analysis of the amygdalae and nucleus accumbens of infected foxes showed no identifiable lesions nor cysts. There was a trend for higher cortisol levels in 3 out of 4 matched infected versus uninfected foxes, although this was not significant due to a small sample size. However, the changes seen in this study could be a basis for future research, with a larger sample size, into how *T. gondii* influences its intermediate host's behaviour and anxiety levels.

P7: AMRSim: A Microbial Reality Simulator.

Shona Noble, Alastair Macdonald, Mark Chambers, Roberto La Ragione, Matthieu Poyade, Kayleigh Wyles, Tom Kupfer, Andy Wales, Fraje Watson, Filbert Musau.

This research is being conducted by The Glasgow School of Art and the University of Surrey and is funded by AMR/AHRC grant number: AH/R002088/1.

Introduction: Insights into human perception and behaviour can help with managing antimicrobial resistance (AMR) in clinical practice. 'AMRSim', engages veterinary staff in visualising bacterial cross-contamination. The aims of the project are to develop a 3D graphical simulation tool, deploy it among veterinary staff, and quantify its effects upon their perceptions of contamination and infection risk.

Methods: Intervention and control groups of staff were formed within a clinical partner's small animal veterinary practice. Risk assessments for bacterial cross-contamination were conducted using videos of full orthopaedic surgical procedures to inform the design of a short pre-operative sequence for the simulation tool. This was evaluated by volunteer clinical staff from Surrey University at various stages of its development. Pre- and post-intervention data

on attitudes and perceptions relating to infection prevention and control (IPC) measures and infection risk was collected. The tool is being used as part of 30-minute trainer-led, structured, interactive small-group seminar sessions (the intervention).

Results: The tool renders a preparation area: three veterinary staff and a canine patient in monochrome; IPC measures in green; and surface bacterial contamination in pink. The cross-contamination behaviour of the bacterial layer can be modified by the IPC elements. Participants in the developmental workshops indicated they valued the visual, interactive approach.

Conclusion: A multi-disciplinary approach has produced a novel contribution to the ever-present challenge of IPC in veterinary practice. The graphical simulation 'makes visible the invisible' and provides an accessible and potentially flexible tool for training and reflection by staff performing any role in practice.

P8: Does Antimicrobial Therapy in Dogs Increase the Risk of Antimicrobial Resistance in Owners? Quantifying *mecA* Abundance in Faecal Samples.

Georgina L Gallow.

Clinical Science and Services (CSS) Department, Royal Veterinary College.

Background-Staphylococci are commensal and opportunistic bacteria on the skin of humans and dogs. The use of antimicrobials causes a selective pressure which promotes the exchange of *mecA* between bacteria and bacteria between hosts, therefore resistant pathogens can spread between hosts.

Aims–1) How does faecal *mecA* abundance in dogs and their in-contact owners relate to known nasal methicillin-resistant staphylococci (MRS) carrier status? 2) How do dogs on antimicrobial therapy affect the *mecA* abundance in faecal samples from dogs and their owners?

Method–DNA was extracted directly from faeces. Faecal *mecA* abundance was measured in individual MRS carriers (5 dog, 4 human) and non-carriers (11 dog, 20 human) using an optimised quantitative PCR (qPCR) method. Faecal *mecA* abundance was measured over time from 10 dogs on antimicrobial therapy and their in-contact humans (18 humans) using qPCR.

Results–16S rRNA was detected in 77/85 (32 dog, 45 human) faecal DNA extractions. The qPCR method was optimised to successfully detect *mecA* from faecal DNA. Faecal *mecA* abundance did not significantly relate to nasal MRS carriage ($P = 0.3659$). Dogs on antimicrobial therapy did not significantly affect their own or owners faecal *mecA* abundance ($P = 1.000$).

Conclusion–This study indicates that dogs on antimicrobial therapy did not increase their owners' risk of antimicrobial resistance. Despite the low sample size and discrepancy in extracting DNA from faeces, the successful detection of *mecA* in some faecal samples confirms that the qPCR method works, but in the future a larger sample size would obtain significant results.

P9: A colostrum-substituted model for the study of atypical porcine pestivirus (APPV).

Holly Hill^{1,5}, Mara Rocchi¹, Madeleine Maley¹, George Russell¹, Susanna Williamson², David Reddick³, Andrew Peters⁴, Francesca Chianini¹, Tanja Opriessnig^{4,5}, Tom McNeilly¹

¹Moredun Research Institute

²Animal and Plant Health Agency

³Moredun Scientific Ltd

⁴The Roslin Institute

⁵The University of Edinburgh

Atypical Porcine Pestivirus (APPV) has recently been associated with clinical cases of Congenital Tremors in piglets in Europe, Asia and America. Despite being infrequent, the welfare and economical implication of APPV outbreaks can be substantial. Maternally-derived antibodies can confound results during APPV challenge infections, however rearing of colostrum-deprived piglet without SPF accommodation has proven challenging. We have developed a colostrum-substituted model which allows piglet challenge, monitoring of clinical and virological responses and easier sample collection. To test this, three colostrum-substituted Landrace piglets were challenged at 14 days of age with tissue homogenates of UK clinical cases of APPV and followed for 11 days. Viremia was monitored by RT-qPCR and clinical data and samples collected during the challenge and at post-mortem. APPV was detected in oropharyngeal and rectal swabs from 7 days post infection (DPI), in nasal swabs from day 9 and peak serum viremia was between 7 and 9 DPI. All of the 21 tissue types tested resulted APPV positive with titres ranging between 1×10^6 and 3×10^{11} copies/gram of tissue. This new model will prove useful in further investigations of APPV and other porcine pathogens in which the presence of maternal antibody interference is significant.

P10: Dog Owner Perceptions on Raw Meat-Based Diets.

Alysia Empert-Gallegos, Sarah Poole, Philippa Yam.

University of Glasgow School of Veterinary Medicine

Feeding a raw meat-based diet (RMBD) to dogs is a practice of increasing interest to owners and veterinarians alike; the commercial market for such products is expanding rapidly even while health professionals raise concerns over the risks inherent in such diets. While many studies have looked into the pathogenic risks of RMBDs, scant research has been conducted on owner perceptions of raw diets. The objective of this study was to survey dog owners about the motivations behind their chosen feeding method, their opinions on RMBDs, and their awareness of the zoonotic risks of such diets. An anonymised web-based survey has been distributed asking dog owners about their feeding habits and opinions and to compare RMBDs with traditional kibble diets in terms of nutritional value and riskiness to human and dog health. We hypothesise that raw feeders believe RMBDs to be equally or more nutritious than traditional kibble with no more risk in terms of human or animal health. The results of this study will provide insight into owner perceptions of raw feeding which will aid both veterinarians and public health officials with owner education. Data collection is ongoing and will be completed by the end of August 2019.

P11: Characterisation of red fox scavenging patterns on cat carcasses

Kita Hull ¹, Sonja Jeckel¹, Lucy Webster², Sherryn Ciavaglia², Ruby Chang², Ella Fitzgerald², Henny Martineau¹

1. Royal Veterinary College, Hertfordshire, UK
2. SASA, Scottish Government, UK Royal Veterinary College

Introduction

29 mutilated cat carcasses were submitted to the police by distressed members of the public over a three year period. Objectives of this study were to determine the causes of death and mutilation, and assess whether there had been any human involvement.

Methods

Swabs for DNA analysis were taken from eight mutilated carcasses and eight live outdoor cats, and analysed for dog, fox, and badger DNA. A full postmortem examination including CT scan, carcase dissection, microscopic examination and bone photography was performed on all 29 carcasses.

Results

All swabs from mutilated carcasses tested positive for fox DNA but not badger or dog. One of eight swabs taken from live cats tested positive for fox DNA, and three tested positive for dog (all three lived in a dog household).

Carcasses had varied portions of body absent, with 72% missing heads and/or necks, 59% missing tails, 34% missing forelimbs, 18% missing abdomen/thorax, and 7% hindlimbs. Mutilation wound edges showed a combination of ragged and smooth contours, and shortened or normal length hair. All carcasses had multiple puncture wounds in the skin both adjacent to and away from mutilation sites. Underlying musculature had higher numbers of puncture wounds than skin, with/without tissue bridging. Bony damage was present in long, flat, short and irregular bones.

Causes of death were determined in 25/29 cats and included road traffic accidents, heart/lung failure, toxicity and predation.

Conclusion

There were variable causes of death, and no evidence of non-accidental injury by human. It was proposed that all mutilations occurred as predation and/or scavenging injury by a red fox.

AVTRW Annual Meeting 2020

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