

AVTRW

The Association for Veterinary
Teaching and Research Work



17-18 September
University of Nottingham

CONFERENCE 2018

AVTRW Annual Meeting 2018

Association for Veterinary Teaching and Research Work
School of Veterinary Medicine and Science, University of Nottingham



Contents

Welcome	3
Conference Programme	4
AVTRW Joining Instructions	6
Speaker Biographies.....	7
Invited Oral Presentations	9
Submitted Oral Abstracts.....	15
Poster Abstracts.....	25
Conference General Information.....	32
Travel to Sutton Bonington Campus.....	32
Conference Venue	32
Accommodation.....	32
Breakfasts.....	32
Parking	32
Oral Presentations	32
Poster Presentations.....	33
Conference Meal.....	33
Wifi.....	33
Taxi Hire	33

Welcome

Welcome to the School of Veterinary Medicine here at the University of Nottingham for the 72nd AVTRW Annual Conference. Although the conference is smaller in size than the meetings which some of us remember (hazily) from the 1990's, the programme remains as diverse as ever, highlighting the range of veterinary research that continues throughout the UK and overseas, this year extending as far as Senegal and Ethiopia!

We hope that you find the meeting both enjoyable and educational giving you an opportunity to discuss your work in front of a friendly audience.

Attendees who have been granted a bursary, please remember to pick up a claim form on Tuesday. We would welcome feedback after the event and will circulate an online link to enable this.

A very special thank you to our sponsors the Agriculture and Horticulture Development Board, the Royal Veterinary College and Somni Scientific.

Steve Dunham

AVTRW President

Conference Programme

Monday 17th September

09:00 - 09:30 Registration

09:30 - 09:45 Welcome address (Steve Dunham, AVTRW President)

09:45 - 10:30 Keynote 1: Adelle Bowden (University of Nottingham): From PhD to Public engagement: Getting Equine colic research into practice.

10:30 - 10:50 O1: Smartphones to teach examination of the equine optic fundus. Marco Duz.

10:50 - 11:10 O2: Junior and Teen Vet Club- Programming activities for under-represented young people. Alexander Hall.

11:10 - 11:30 Tea and Coffee

11:30 - 12:15 Keynote 2: Amy Jackson (University of Nottingham, AHDB Sponsored Invited Speaker): Are we getting science communication right?

12:15 - 12:35 O3: Characterising dairy farms and milk supply chain to consumers to explore the risks of milk-borne diseases, control options and related challenges: A case study of E coli O157:H7 and Staphylococcus aureus from Senegal. Bhagyalakshmi Chengat Prakashbabu.

12:35 - 12:55 O4: The reduction of antibiotic use in the UK pig herd from 2015-2017. Luchia Gregson.

12:55 - 13:15 O5: Genetic diversity of Mycobacterium bovis and its zoonotic potential in Ethiopia: A systematic review. Begna Tulu.

13:15 - 14:00 Lunch

14:00 - 14:45 Keynote 3: Adrian Philbey (University of Edinburgh): Veterinary pathology: Where have we come from and where are we going?

14:45 - 15:05 O6: Development of a protocol in domestic sheep (Ovis aries) and alpaca (Vicugna pacos) for identification and characterisation of tonsillar tissue in wild saiga antelope (Saiga tatarica tatarica). Thomas Bunn.

15:05 - 15:25 O7: Modelling the Ovine Lung: Development and Validation of 3D Models of Sheep Lungs for Veterinary Public Health Teaching. Jessica Simmonds.

15:25 - 15:45 O8: Animal CSI - Veterinary Pathology and the Public. Grace Mackintosh Sim.

15:45 - 16:15 Tea and Coffee

- 16:15 Flash Poster presentations followed by Poster Session.
- 19:00 Head to local eatery for Conference Meal. Delegates required to pay for own meals and drinks.

Tuesday 18th September

09:00 - 09:30 Registration

09:30 - 10:15 Keynote 4: Sabine Totemeyer (University of Nottingham): Towards a better understanding of footrot in sheep: Is *Dichelobacter nodosus* the primary instigator or setting the scene for opportunists?

10:15 - 10:35 O9: Limited transmission of H5N6 (2017) HPAIV from infected waterfowl to terrestrial poultry: An investigation of species tropism and pathogenesis. Sahar Mahmood.

10:35 - 10:55 O10: Validation of real-time RT-PCR protocols for subtyping European swine influenza A viruses. Alexander Byrne.

10:55 -11:30 Tea and Coffee

11:30 - 12:15 Keynote 2: Janet Daly (University of Nottingham): Cross-species transmission in companion animals.

12:15 - 12:35 O11: Impact of Hepacivirus A (NPHV) infection in racehorses in Newmarket. Terry Nnaemeka Akagha.

12:35 - 12:55 O12: Generation of Vesicular Stomatitis Virus (VSV) pseudotypes for serological studies of Zika virus (ZIKV). Ge Wu.

12:55 - 13:15 O13: Epidemiology of Tick Borne Pathogens of Dogs in Nigerian Communities. Ternenge Thaddaeus Apaa.

13:15 - 14:15 Lunch

14:15 - 15:00 Keynote 3: Damer Blake (Royal Veterinary College): Eimeria interactions with the enteric microbiota – saints or sinners?

15:00 - 16:00 Workshop: Planning your next experiment.

16:00 - 16:30 Tea and Coffee

16:00 - 17:00 **AVTRW annual general meeting, open to all conference attendees**

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 from our website - full instructions and an overview of the procedure are provided on the first page of the document:

- Download Word Version
http://www.avtrw.co.uk/index.php/download_file/view/45/125/
- Download PDF Version
http://www.avtrw.co.uk/index.php/download_file/view/42/125/
- 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.

Speaker Biographies

Adelle Bowden

Adelle graduated from the University of Nottingham Veterinary School in 2013 before undertaking her PhD titled “Maximising the impact of evidence-based medicine on equine health and welfare” which she graduated in 2018. Alongside her studies, she also spent some time working as an equine first opinion practitioner at a local private practice. Adelle has worked at the University of Nottingham as a teaching associate in clinical and professional skills since September 2016 and has recently been appointed as a senior tutor.

Amy Jackson

Amy graduated with an MSc from University of Aberdeen in Farm and Rural Business Management and is currently studying for a PhD at the University of Nottingham School of Veterinary Medicine and Science in “Consumer perceptions and cultural values around the housing and management of dairy cows”. Amy is an Accredited PR Practitioner with the Chartered Institute of Public Relations, and an Accredited Animal Technologist with the British Society of Animal Science.

Adrian W. Philbey

Adrian was born in New Zealand, then moved to Australia, where he attended an agricultural high school and completed his veterinary degree at the University of Sydney. In Australia, he has worked as a field veterinary officer, a veterinary pathologist and a veterinary virologist for the New South Wales Department of Agriculture, with interests also in microbiology and parasitology. In the United Kingdom, Adrian has worked as a veterinary pathologist and virologist at the University of Glasgow and as a research virologist at Moredun Research Institute. Currently, Adrian works at the University of Edinburgh as a veterinary pathologist, with continued interests in virology and microbiology. He is Co-Editor-in-Chief of *The Veterinary Journal*. His interests include the pathology of infectious diseases of domestic animals and wildlife, including emerging infectious diseases, zoonotic diseases and oncogenic viruses.

Sabine Totemeyer

Sabine has been interested in host pathogen interactions since postdoc positions at the Christian de Duve Institute for Medical Sciences, Université Catholique de Louvain in Brussels on *Yersinia enterocolitica* interactions with primary human endothelial cells and at the University of Cambridge on *Salmonella enterocolitica* and murine TLRs. Sabine moved to the School of Veterinary Medicine at the University of Nottingham four weeks before the first students started and had the privilege to help shaping new vet school. She is now Associate

Professor in Cellular Microbiology. Her current research focusses on footrot in sheep with an interest in both, the complex bacterial interactions of this multi-bacterial infection and the host response and preventative approaches to this disease. To make microbiology more accessible for the general public, Sabine combines her love of science with that for crafts and making giant knitted microbes and sponge based tissue culture models.

Janet Daly

Janet is an Associate Professor in Emergent Viruses at the University of Nottingham's School of Veterinary Medicine and Research. The focus of her research is on RNA viruses, in particular, the epidemiology and evolution of viruses and the development and testing of vaccines and diagnostic tests for influenza A viruses. However, her expertise extends to Flaviviridae, and members of the family Bunyaviridae including Schmallenberg virus. She has extensive experience of strain surveillance of equine influenza A viruses gained while a PhD student at the Animal Health Trust. In collaboration with mathematical modellers, she has been involved in the development of models to predict the likelihood of vaccine breakdown and occurrence of outbreaks in equine populations. In the field of human influenza, she studied the genetic and immunological safety of DNA vaccines (using influenza as a model system in mouse studies) at the National Institute for Biological Standards and Control. While working for GlaxoSmithKline, she was involved in studying neuraminidase inhibitors of influenza. Recent studies of influenza A viruses at the University of Nottingham have focused on understanding molecular and cellular pathogenesis, host range restrictions and transmissibility.

Damer Blake

Following a PhD focused on bacterial genetics from the University of Aberdeen, Damer began working with *Eimeria* species parasites in 2001 at the Institute for Animal Health (IAH, UK). During his time at IAH he carried out fundamental and applied genetics-led research, contributing to the *Eimeria* genome sequencing consortium, developing reverse-genetics strategies for use with *Eimeria* and using genetic mapping as a step towards new cost-effective anticoccidial vaccines. Damer joined the Royal Veterinary College in 2010, becoming Professor of Parasite Genetics in 2016. Current research strands include population genetic analyses of recognised and cryptic *Eimeria* species, development of novel vaccine delivery strategies, understanding the genetic basis of host resistance to coccidiosis and interactions of *Eimeria* with bacterial microbiota of poultry. Work with other parasites includes *Cryptosporidium*, *Toxoplasma gondii*, and the poultry red mite *Dermanyssus gallinae*. In 2017 Damer became Editor-in-Chief of the journal Avian Pathology.

Invited Oral Presentations

Keynote 1: Development of a research-based owner educational campaign on the recognition and assessment of equine colic.

Adelle Bowden

School of Veterinary Medicine and Science, University of Nottingham, College Road, Sutton Bonington, Loughborough, Leicestershire, LE12 5RD.

The role of the owner is pivotal in the early recognition of horses with colic. We therefore aimed to develop a research-based educational campaign for owners to assist the early recognition of colic. An online survey of 1,564 owners evaluated gaps in knowledge of colic, and opinions on different resources; outcomes were used to identify which educational materials should be created. Common signs of colic were identified through a Delphi process, consisting of two multi-stakeholder workshops (88 participants) and an online Delphi survey (436 owners with experience of colic). Statements generated in the workshops were circulated online through 1-3 rounds (with amendments as required). Statements with the highest consensus were used to develop an acronym on recognition of colic. Key knowledge gaps were identified: 'what is colic', 'recognising colic', 'preventing colic', 'emergency decision making', 'normal parameters', 'waiting for the vet', 'what the vet will do', 'rectal examination', 'nasogastric intubation' and 'referral hospital procedures'. Corresponding resources were produced as hard copy and online educational leaflets. The common signs of colic were developed into an acronym "REACT" representing 'Restlessness', 'Eating less or droppings reduced', 'Abdominal pain', 'Clinical changes', 'Tired or lethargic'. Each category had 3-5 descriptors according to their Delphi ranking. The campaign was launched through The British Horse Society through a variety of media, including a dedicated webpage, social media, magazine articles and representation at key equine events. This is the first study to generate an educational campaign to assist horse owners recognise colic based on a research approach.

Keynote 2: Are we getting science communication right?

Amy Jackson: AHDB Sponsored Speaker

School of Veterinary Medicine and Science, University of Nottingham,
College Road, Sutton Bonington, Loughborough, Leicestershire, LE12
5RD.



Two-plus decades back when I graduated from agricultural college, pharmaceutical and agrochemical companies guest-lectured on the wonders of rBST in boosting feed conversion efficiency and milk yields in dairy cows, and the benefits of glyphosate-tolerant plants in revolutionising crop management regimes. It was a brave and exciting new world and any public outrage at these developments baffled scientists and agriculturalists alike. Fast forward to 2018 and where are we now? Recognition of the benefits of good communication – driven partly by the disruptive challenges laid down by social media – means we are a whole lot better at using the right words and the right arguments in the right way. But we're still not getting it quite right. Recent efforts to turn around negativity about use of antibiotics in UK farm animals almost happened too late. The European Court of Justice may have just killed any opportunity to use gene editing to eradicate a wide range of debilitating animal conditions and reduce pressure on antibiotic use. And by the time I finish my PhD studying why people don't accept intensive farming systems, those systems may be a thing of the past. We have more to do if we want to generate true sense and excitement about animal science. We must start engaging, not 'educating'; have conversations about the benefits at the inception of the project, not the end; and anticipate and deal with barriers before they happen not sweep up afterwards. Considering communication as an integral part of any scientific development from the start can only improve its long term chances of delivering beneficial change.

Keynote 3: Veterinary pathology: Where have we come from and where are we going?

Adrian W. Philbey

Easter Bush Pathology, Royal (Dick) School of Veterinary Studies and The Roslin Institute, University of Edinburgh, Easter Bush, Edinburgh EH25 9RG, Scotland.

Veterinary pathology has evolved as a discipline based on observations of natural and experimental disease in animals, underpinned by advances in understanding the pathogenesis of disease. Many of these advances have been made in parallel with progress in medical pathology. Pathologists have constructed a complex portfolio of terminology to describe disease, which has strengthened the discipline, but sometimes has imposed constraints on the way in which concepts of disease are communicated. Ongoing developments in technology, in fields including digital pathology, image analysis, immunohistochemistry and molecular biology, will continue to bring new opportunities to pathologists, supported by automation of laboratory procedures and development of laboratory information platforms. Appropriate collection of specimens remains the cornerstone of diagnostic pathology, no matter how sophisticated their subsequent analysis. A multidisciplinary approach to diagnosis and research will allow veterinary pathologists to contribute to advances in many fields, including infectious disease, immunology, tumour biology, neurobiology, genetic diseases, toxicology and degenerative diseases.

Keynote 4: Towards a better understanding of footrot in sheep: Is *Dichelobacter nodosus* the primary instigator or setting the scene for opportunists?

Sabine Totemeyer

School of Veterinary Medicine and Science, University of Nottingham, College Road, Sutton Bonington, Loughborough, Leicestershire, LE12 5RD.

Dichelobacter nodosus is the causative agent of footrot in sheep. Ovine underrunning footrot is a two-stage disease characterised by interdigital dermatitis (ID) that in the presence of virulent *D. nodosus* progresses to the separation of skin and hoof horn. The role of the innate immune system in footrot is not well understood.

We developed an MLST scheme to investigate the diversity of currently circulating *D. nodosus* isolates in the Midlands. We used post slaughter biopsies of the interdigital space from footrot affected and matched healthy feet to investigate the bacterial communities on the skin surface and within skin and the host response. Using metatranscriptomics enabled quantification of the transcriptional differences of the host during a natural footrot infection and identify the bacterial species present within the tissue. As expected, the causative agent of footrot, *Dichelobacter nodosus* was significantly more abundant in footrot samples. In addition, in footrot affected samples, the abundance of other bacterial species were significantly increased, suggesting a role for these bacteria in the infection. Most differentially expressed genes in footrot affected feet are associated with an increase in transcripts associated with the wound healing and/or chronic wounds and inflammation.

We also developed an *ex vivo* explant model of the interdigital skin that allows study of the initial stages of infection with *D. nodosus* and the host response. To understand the early stages of infection is a fundamental step that in the long term will underpin the design of an efficacious and affordable vaccine.

Keynote 5: Cross-species transmission of viruses in companion animals

Janet Daly

School of Veterinary Medicine and Science, University of Nottingham, College Road, Sutton Bonington, Loughborough, Leicestershire, LE12 5RD.

Influenza A viruses (IAVs) occur as different subtypes (e.g. H3N8) named according to the proteins that project from their surface (haemagglutinin, H, and neuraminidase, N). The traditional view of the ecology of influenza A viruses was that ducks and shorebirds are the reservoir hosts; all known subtypes were found in these species and infection usually results in no or mild clinical signs. Occasionally, certain subtypes have 'spilled over' and, more rarely, become established in other hosts, including horses. What allows certain subtypes to jump to a new host is not fully understood.

Early studies established that specific recognition of host cell receptors plays a role. However, viruses that are more pathogenic may overcome the barrier posed by lack of relevant receptors. In 2005, the first evidence for transmission of equine influenza virus to dogs (greyhounds in the USA) was reported. The virus subsequently became endemic in the USA. It was demonstrated retrospectively that equine influenza virus had also jumped from horses to foxhounds in the UK in 2002, but did not become established. Experimental infection of ponies with an equine influenza virus strain isolated in 2003 confirmed the more severe clinical signs reported from the field than with earlier isolates. This was associated with greater induction of pro-inflammatory cytokines. Genome sequencing of the 2003 equine influenza virus strain revealed a truncation in the viral NS1 protein, which modulates the host cytokine response. Understanding factors involved in species jumps may help predict the significance of emerging variant viruses.

Keynote 6: *Eimeria* interactions with the enteric microbiota – saints or sinners?

Damer Blake

Pathobiology and Population Sciences, Royal Veterinary College, Hawkshead Lane, North Mymms, AL9 7TA, UK.

Eimeria species are parasites that can cause the enteric disease coccidiosis, most notably in poultry, where they have a huge impact on health and welfare. When combined with *Clostridium perfringens*, *Eimeria* also contributes to necrotic enteritis but there is a paucity of information regarding the impact of infection on the broader enteric microbiome. Parasite-associated microbiome variation may exacerbate the outcome of infection, or predispose towards secondary infections. However, the global impact on microbiome complexity and structure might also be beneficial as a consequence of variation in commensal or symbiotic sub-populations, contributing to the compensatory growth commonly seen following sub-clinical coccidiosis. Consideration of specific interactions between *Eimeria tenella* and *Campylobacter jejuni* has revealed a contradictory relationship, where parasite infection significantly increases caecal *C. jejuni* load but decreases extra-intestinal colonisation in the liver and spleen (all $p < 0.05$). Increased faecal *C. jejuni* shedding poses a risk to public health through surface contamination of poultry products. However, decreased colonisation of the liver reduces public health risk from sources such as pâté. Broader assessment of caecal 16S rRNA microbiome variation associated with the occurrence and severity of *E. tenella* infection (quantified by lesion scoring) revealed surprising stability in alpha diversity (bacterial occurrence), but significant variation in beta diversity (bacterial abundance). The greatest changes were observed in samples collected from infected chickens displaying the most severe caecal pathology, but also the least. Following *E. tenella* infection taxa belonging to the order Enterobacteriaceae were commonly found to be increased, while *Bacteroides* almost disappeared in infected birds which exhibited no pathological signs of disease. Many taxa belonging to the orders Clostridiales and Lactobacillales were identified, with some species increasing and others decreasing in abundance. A greater understanding of caecal microbiome dysbiosis associated with *E. tenella* infection could aid in the development of in-feed probiotics with the ultimate aim of reducing the most severe effects of this ubiquitous parasite. Exploring the positive outcomes that associate with parasite infection could increase the value of live parasite vaccines.

Submitted Oral Abstracts

O1: Smartphones to teach examination of the equine optic fundus

Dr Duz Marco, Emma Shipman, Dr John Burford, Prof Mark Bowen

School of Veterinary Medicine and Science, University of Nottingham

Veterinary students often find learning to visualise the equine optic fundus challenging. Smartphones allow simultaneous optic fundus visualisation by students and teacher and may aid teaching the procedure.

The objectives were to evaluate if teaching the equine fundus examination using smartphones: i) is useful for students learning ii) affects students confidence.

After traditional teaching of direct ophthalmoscopy on a live horse the teacher used a smartphone to visualise the optic fundus with the student, who then repeated the procedure with the ophthalmoscope. Students then completed a questionnaire using a visual analogue scores (VAS) to investigate if smartphones had assisted learning and students self-assessed confidence had improved. VAS scores were compared using the Wilcoxon Signed Rank Test (significance set for $p < 0.05$).

Thirty year-4 students participating in an optional practical session were enrolled. The confidence in performing the equine fundus examination was significantly higher after the practical (confidence after the practical $65.3(\pm 19.8)\%$ compared to before the practical when confidence was $20.1(\pm 15.6)\%$ - $p < 0.001$). The perceived usefulness of traditional teaching was $62.3(\pm 23.8)\%$. The perceived usefulness of the teaching with the smartphone was $91.1(\pm 8.6)\%$. While students found both methods useful, they perceived the use of the smartphone to be significantly more useful ($p < 0.001$). Free-text comments on the use of the smartphone were all positive and included “useful”, “fun” and “good teaching tool”.

The results of this study show that the use of the smartphone was positively received by the students and these findings support its use in teaching the equine fundic examination.

O2: Junior and Teen Vet Club- Programming activities for under-represented young people

Dr Grace Mackintosh Sim and **Alexander Hall**

Royal Veterinary College

The Royal Veterinary College has run Junior and Teen Vet Clubs, free newsletters and events for 7-18 year olds, for over a year. These meet the goals of encouraging young people from backgrounds which are currently under-represented in the profession, to enjoy fun activities which allow them to find out more about career options. We will present research showing the demographics of our audience, and how we have collaborated with institutions such as local councils, pharmaceutical companies, and even the Royal Institution to widen our reach. This

will be viewed in the light of the new Office for Students' guidance on Access and Participation plans, and the implications for Widening Participation, which is applicable to all universities. In particular, we will show how we have reconciled increasing requirements for reporting longitudinal progression of prospective students, with GDPR regulations.

O3: Characterising dairy farms and milk supply chain to consumers to explore the risks of milk-borne diseases, control options and related challenges: A case study of *E coli* O157:H7 and *Staphylococcus aureus* from Senegal.

Bhagyalakshmi Chengat Prakashbabu B¹, Matteo. Crotta M¹, Andre Prisca Ndour², Laura Craighead L¹, Imadiden Musallam¹, Ruffine Yempabou², Rianatour Alambédji Bada², Ayayi Justin Akakpo², Javier Guitian¹

¹Royal Veterinary College, London, United Kingdom. ²Ecole Inter-Etats des Sciences et Médecine Vétérinaires de Dakar, Sénégal.

The objective of the study is to demonstrate how farm typology, milk flow and hazard characteristics are combined to assess the risk of exposure to milk-borne hazards to support interventions in limited data settings. Data gathered through cross-sectional survey of dairy farms was analysed using multiple correspondence analysis and hierarchical cluster analysis to identify farm typologies. Qualitative risk assessment was conducted for *Escherichia coli* O157:H7 and *Staphylococcus aureus* to assess the exposure risk to raw milk consumers in Senegal. Key informant interviews to plot milk flow and systematic literature search was used to identify hazard characteristics. We identified three different farm types: Type I- subsistence farms with multiple species, small herds sharing milk with neighbours, Type II- transhumant herds with indigenous breeds, selling milk in markets and to collectors and Type III - intensive farms keeping crossbred and exotic animals selling milk in markets. For *E. coli* O 157:H7 and *S. aureus* exposure Type I farm had "low" and "medium" risk and Type II had "medium" and "medium" risk respectively. However, Type III had "high" risk of exposure to all the considered hazards. Table 1 lists best control strategy based on farm type. By considering the milk supply chain in its entirety, on-farm harvest practices and post-harvest marketing channels, we were able to identify heterogeneities in the risk associated with specific hazards by farm typology. Our results highlight the potential for risk-based food safety measures particularly important in rapidly growing dairy sectors of many developing countries.

Table 1: Different farm typologies identified through multiple correspondence analysis and hierarchical cluster analysis and the best control strategy for *Escherichia coli* O157:H7 and *Staphylococcus aureus*.

Farm type	Potential control options to ensure consumer safety
Type I	- Boiling at consumer level - Pasteurisation or boiling at milk collector level
Type II	- Boiling at consumer level - Pasteurisation at milk collector level - Establishment of mini-diaries
Type III	Pasteurisation at farm level

O4: The reduction of antibiotic use in the UK pig herd from 2015-2017.

Luchia Gregson, Jennifer Newman and Amanda Nevel.

Agriculture and Horticulture Development Board (AHDB)

Antibiotic use per se drives antibiotic resistance. This means that resistance can develop whether antibiotics are used according to recommendations or inappropriately. The risk of AMR emerging in livestock and spreading to humans is often used as justification for reducing use in livestock. Evidence for such spread is uncommon, nevertheless, prudent use of antibiotics in the livestock sector is a priority.

Aim: Develop a data collation mechanism for antibiotic use in pigs and to drive a move to more responsible use of antibiotics

Objectives:

- 1) Establish a mechanism for collation of use data
- 2) Determine the level of use on an annual basis
- 3) Use benchmarking of use on farms as a tool to drive responsible use.

Material and methods: An electronic medicines book (eMB) to collate data was established. Pig producers on the Red Tractor assurance scheme were required to enter antibiotic use data on the eMB on a quarterly basis. National antibiotic use was calculated using the European (ESVAC) calculation. In brief, data were extracted from the eMB and the PCU calculation applied: $\text{mg active ingredient} \div \text{standardised average pig weight at time of treatment (kg)} = \text{mg/PCU}$.

Results: Increased data were collated in 2015, 2016 and 2017 and represented 61, 70 and 87 % of pigs slaughtered in the UK respectively. Antibiotic use was reduced from 278mg/PCU in 2015, 183 in 2016 and 131mg/PCU in 2017.

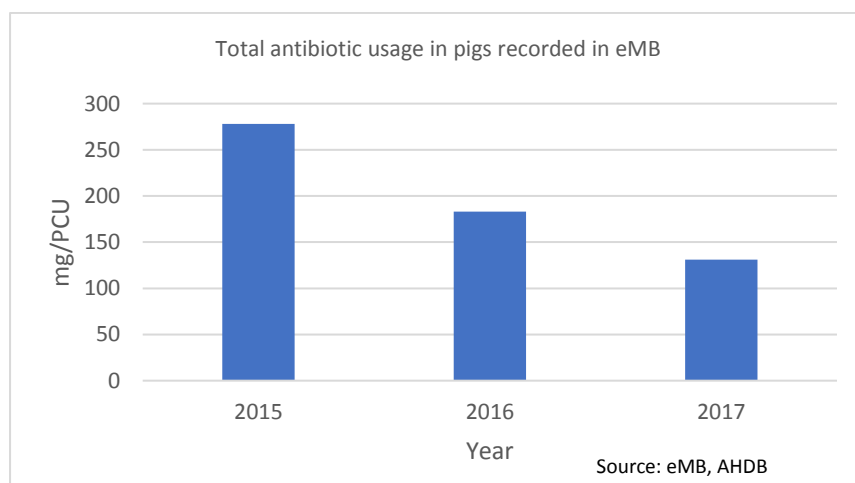


Figure 1. Year on year reduction in antibiotic use recorded on eMB.

Discussion: Producers are reducing their antibiotic usage and on the way to achieving the industry set target of 99mg/PCU by 2020. Uptake of the database was facilitated by making its use a RT requirement. Continued reductions are encouraged to enable the industry to

achieve targets set by RUMA. However, reduction will hit a nadir at which point further reductions could compromise animal welfare.

Conclusions: Antibiotics are an essential tool to ensure animal welfare. Reductions in use have been evidenced but this reduction will not continue indefinitely if animal welfare is not to be compromised. Many vets and farmers have changed their approach to antibiotic use but further work is required to ensure all within the sector are using antibiotics responsibly. Antibiotic use per se drives antibiotic resistance. This means that resistance can develop whether antibiotics are used according to recommendations or inappropriately. The risk of AMR emerging in livestock and spreading to humans is often used as justification for reducing use in livestock. Evidence for such spread is uncommon, nevertheless, prudent use of antibiotics in the livestock sector is a priority.

O5: Genetic diversity of *Mycobacterium bovis* and its zoonotic potential in Ethiopia: A systematic review

Begna Tulu^{1,2}, Gobena Ameni¹

¹Aklilu Lemma Institute of Pathobiology, Addis Ababa University, Ethiopia, ²Medical Laboratory Sciences Department, Bahir Dar University, Ethiopia

Background: Understanding the types of *Mycobacterium bovis* (*M. bovis*) strains circulating in a country and exploring its zoonotic potential has significant contribution in the effort to design control strategies. The main aim of this study was to review and compile the results of studies conducted on *M. bovis* genotyping and its zoonotic potential of *M. bovis* in Ethiopia.

Methods: A systematic search and review of articles published on *M. bovis* strains in Ethiopia were made. PubMed and Google Scholar databases were considered for the search while the keywords used were "*Mycobacteria*," "*Mycobacterium bovis*," "Bovine Tuberculosis" and "Ethiopia."

Result: Fourteen studies were considered in this review and a total of 31 distinct strains of *M. bovis* (N=211) were obtained; the most dominant strains were SB0133 (N=62, 29.4%), SB1176 (N=61, 28.9%), and followed by SB0134 and SB1476 each (N=18, 8.5%). The clustering rate of *M. bovis* strains was found to be 42.0%. On the other hand, 6 strains of *M. bovis* were reported from human namely; SB0665 (N=4), SB0303 (N=2), SB0982 (N=2), SB0133 (N=1), SB1176 (N=1), and 1 new strain. Similarly, a total of 8 strains (N=13) of *M. tuberculosis* bacteria were also identified from animal subjects; namely SIT149 (N=3), SIT1 (N=2), SIT1688 (n=2), SIT262 (N=2), SIT53 (N=1), SIT59 (N=1), and one new-Ethiopian strain.

Conclusion: The result showed that the genetic diversity of *M. bovis* strains reported from Ethiopia are less diversified. The result also underlines that there is an ongoing active transmission of *M. bovis* and *M. tuberculosis* between human and animals in Ethiopia because significant number of both *M. tuberculosis* and *M. bovis* strains were reported from both human and animals.

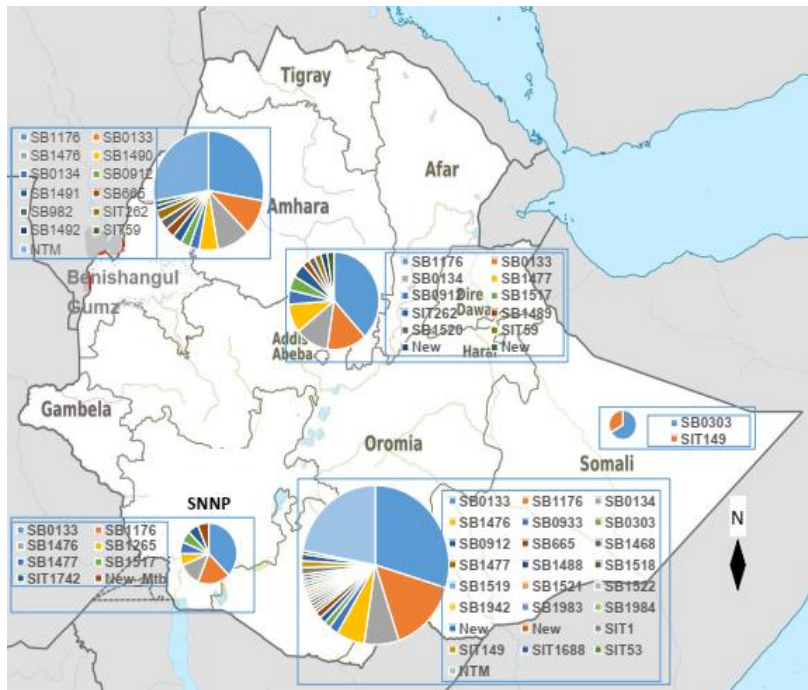


Figure 1: Geographical distribution of the *M. bovis* strains and NTM reported from animals and humans and *M. tuberculosis* from animals in Ethiopia.

O6: Development of a protocol in domestic sheep (*Ovis aries*) and alpaca (*Vicugna pacos*) for identification and characterisation of tonsillar tissue in wild saiga antelope (*Saiga tatarica tatarica*).

Thomas Bunn, Henny Martineau and Richard Kock.

Royal Veterinary College, University of London

Recent mass mortality events in the critically endangered saiga antelope (*Saiga tatarica tatarica*) have been attributed to *Pasteurella multocida*. As the tonsils are a valued sampling site for isolating *Pasteurella* species, characterisation of the tonsillar anatomy of saiga antelope is a vital step to improve screening of this species to better understand its relationship with *Pasteurella multocida*. Using literature on sheep (*Ovis aries*), a method of dissection that prioritises visualisation and extraction of all six tonsillar regions in sheep was developed, appropriate for use in field conditions. This method, using a ventral dissection approach, was compared against paramedial sectioning of the head to qualitatively assess effectiveness. The method developed was applied in sheep and five out of six described tonsils were identified. It was also applied in alpaca (*Vicugna pacos*), for which tonsillar anatomy has not been described in literature, and the palatine tonsil, tubal tonsil and tonsil of the soft palate were identified and described. Tonsillar anatomy was compared between the species and suitability of sheep as a model for saiga tonsillar anatomy discussed in relation to their phylogenetic relationship.

O7: Modelling the Ovine Lung: Development and Validation of 3D Models of Sheep Lungs for Veterinary Public Health Teaching

Jessica Simmonds

University of Glasgow School of Veterinary Medicine (GUSVM), Glasgow School of Art.

Veterinary public health teaching currently relies on labs and lectures; this means opportunities for self-study can be limited. There is also growing pressure to 'reduce, refine and replace' the use of animals for teaching purposes.

The looming threat of Brexit also increases pressure on UK veterinary schools to improve public health teaching- 90% of vets working in UK public health are non-UK European graduates; recent surveys by the RCVS and BVA show that a significant proportion of these vets are considering leaving the UK due to the current political climate.

Certainly, there is much scope for improving veterinary public health teaching. Many advances in veterinary teaching have followed the examples set by our human counterparts- many peer-reviewed papers exist that show the success of mobile applications and simulations as teaching and learning aids in the human medical curriculum.

This thesis intends to use an existing bank of images from GUSVM's Post Mortem facility and use them alongside CT scans, 3D modelling and game engine software to create anatomically accurate models of healthy and diseased sheep lungs. These will be imported into an interactive app to allow veterinary students to use the models as an adjunct to traditional public health learning.

The app is currently awaiting testing by a group of final year veterinary students; the results of this will be analysed to determine whether the models are accurate enough to be used for learning/teaching, and whether the format of a mobile app with interactive models is a useful tool for veterinary public health teaching.

O8: Animal CSI- Veterinary Pathology and the Public

Grace Mackintosh Sim and Henny Martineau

Royal Veterinary College

The Royal Veterinary College has developed our offering of public events over the past five years, including our popular Night at the Vet College events. In October 2017, we delivered 'Animal CSI' at the Royal Institution, a showcase of veterinary pathology including a live linked dissection.

We will discuss our audience research about who attends our events, and how our audience goals and funding influence content development. In addition, we will show how involvement in large scale science events such as New Scientist Live has led to productive collaborations. We will explain case studies of two forthcoming events in November 2018 and Science Week, March 2019.

O9: Limited transmission of H5N6 (2017) HPAIV from infected waterfowl to terrestrial poultry: An investigation of species tropism and pathogenesis.

Sahar Mahmood¹, Amanda H Seekings¹, Saumya S Thomas¹, Alex Nuñez², Carlo Bianco², Caroline J Warren¹, Ben C Mollett¹, Joe James¹, Marek J Slomka¹, Ian H Brown¹ and Sharon M Brookes¹

¹Avian Influenza and Mammalian Research, Virology Department and ²Pathology Department, Animal and Plant Health Agency (APHA-Weybridge), Woodham Lane, Addlestone, Surrey KT15 3NB, UK

H5N6 highly pathogenic avian influenza virus (HPAIV) first occurred in the UK in late December 2017, with wild bird incursions continuing until June 2018, but no spread from migratory waterfowl to UK poultry was reported. This H5N6-2017 strain is a reassortant derived from the H5N8 (2016) HPAIVs which differed by causing numerous UK and European wild bird and poultry cases during 2016-2017.

We investigated the waterfowl / poultry interface by infecting three groups of ducks (4-weeks age, n=9 per group) with three different doses of H5N6-2017. The ducks served as surrogates for infected waterfowl. Each dose group was divided into three separately-housed subgroups of three ducks each. At 1-day-post-infection, five ducks, chickens, or turkeys were introduced to each subgroup as recipients.

Ducks directly-infected with H5N6-2017 shed virus and transmitted infection to contact ducks, but less efficiently to contact chickens and turkeys, requiring longer exposure compared to similar H5N8-2016 trans-species investigations where transmission was much more efficient. There were two virus-related deaths among 27 infected ducks (7.4%) across all dose groups. Infected ducks exhibited evidence of pathogenicity with marked lymphoid tropism. Where H5N8-2016 did transmit to terrestrial poultry species, typical HPAIV mortality rapidly ensued. Seroconversion to H5N6 occurred in some birds (all species) which did not shed virus, indicating evidence of immunological exposure with no detectable viral replication.

Therefore, H5N6-17 is less well adapted to cross the species barrier productively from waterfowl to poultry than H5N8-16, thereby possibly explaining the absence of H5N6 UK poultry outbreaks.

O10: Validation of real-time RT-PCR protocols for subtyping European swine influenza A viruses

Sharon M. Brookes¹, Scott M. Reid¹, Christine Russell¹, Jayne L. Cooper¹, Steve Essen¹, Susan Collins¹, Helen E. Everett¹, **Alexander M. P. Byrne¹**, Susanna Williamson², Kristien Van Reeth³, Ian H. Brown¹

¹Animal and Plant Health Agency-Weybridge, Woodham Lane, New Haw, Addlestone, Surrey, KT15 3NB, United Kingdom ²Animal and Plant Health Agency-Bury St. Edmunds, Rougham Hill, Bury St. Edmunds, Suffolk, IP33 2RX, United Kingdom ³Department of Virology, Parasitology and Immunology, Faculty of Veterinary Medicine, Ghent University, Salisburyaan 133, 9820 Merelbeke, Belgium.

Objectives: Swine influenza A viruses (swIAVs) cause respiratory disease and productivity loss in pigs world-wide. Three subtypes (H1avN1, H1N1pdm09, H1huN2) including reassortants are currently found in Great Britain (GB) pigs. Real-time reverse transcription polymerase chain reaction (RRT-PCR) assays were developed to improve the sensitivity and speed of swIAV subtyping, negating the need for virus isolation (VI) prior to subtyping. Simplex RRT-PCR assays for detecting H1av and H1hu, or H3, and duplex assays targeting N1 (N1av) or N2 were assessed on influenza A PCR-positive, mostly VI-negative, field material from British pigs (2012-2018) affected by respiratory disease. Further validation was performed on isolates from Belgium (2013-2018) and GB (2012-2014).

Results: Subtyping identified H1avN1 and H1huN2 swIAVs in 35.1% of swabs/tissues (n = 128), while in 39.1% only HA or NA were detected, and in 25.8% no subtype was detected. Diagnostic sensitivity improved when testing amplified virus isolates. Of the 42 Belgian isolates, H1avN1 (n = 19), H1huN2 (n = 7), H1N1 (n=1) and H3N2 (n = 11) were fully subtyped. Four isolates provided only an HA or NA result. All 19 GB isolates fully subtyped (H1huN2 [n = 17] and H1avN1 [n = 2]). H1N1pdm09 was also active in GB pigs (n=45; 2012-2018).

Significance of the results: Subtyping of previously uncharacterized swIAVs directly from field material without VI or nucleotide sequencing was successful. Assay sensitivity requires improvement to achieve full subtyping for a greater proportion of field samples. This will provide veterinarians with more prompt subtyping, assisting control of swine influenza.

O11: Impact of Hepacivirus A (NPHV) infection in racehorses in Newmarket

University Of Nottingham:

Terry Akagha¹, Alexander Tarr¹, Barnabas King¹, Richard Urbanowicz¹, Patrick McClure¹, Janet Daly¹, Julia Kydd¹, Bithe Tegtmeier², Eike Steinmann², Thomas Krev³, Marcha Badenhurst⁴, Jessika Cavalleri⁴.

¹University of Nottingham, ²Twincore, Hannover, ³Hannover Medical School, ⁴University of Vienna.

Non primate Hepacivirus (NPHV) is the closest relation to the Hepatitis C virus (HCV). This virus infects horses and has several similarities to HCV, ranging from delayed onset of seroconversion, persistent infection and liver pathology, thereby making it the closest model to study hepacivirus infections in their natural host. We screened for the presence of NPHV RNA, E1/E2-reactive antibodies and neutralizing antibodies in serum from 66 horses sampled

at the Newmarket Equine Hospital (NEH). Of these, 27% of the samples were positive for NPHV RNA and 71% positive for antibodies. The phylogeny of these infections revealed considerable variability, highlighting the possibility of different genotypes. This study demonstrates that the prevalence of NPHV in training horses at NEH is high and transmission may be occurring during training. The influence of this infection on performance is yet to be determined. Further research includes assessing performance characteristics of infected horses and viremia over time, as well as utilizing these assays for diagnostic testing.

O12: Generation of Vesicular Stomatitis Virus (VSV) pseudotypes for serological studies of Zika virus (ZIKV)

Ge Wu¹, Barnabas King², Stephen Dunham¹, Janet Daly¹.

¹School of Veterinary Medicine and Science, University of Nottingham, ²School of Life Science, University of Nottingham

Zika virus (ZIKV) is an emerging flavivirus transmitted by mosquitoes in the tropical and sub-tropical regions. Other notorious arboviruses from the same family include Japanese encephalitis virus, West Nile virus and Dengue virus. The co-circulation of ZIKV and other members of flaviviruses in humans causes a substantial problem for accurate diagnosis due to extensive cross-reactivity between these viruses. Pseudotyped viruses (PVs) can detect virus-specific neutralising antibodies and do not require high-level biocontainment as they are unable to produce replication competent virus. The aim of this project is to generate pseudotyped ZIKV based on Vesicular Stomatitis Virus (VSV) backbone, which can then be used in a pseudotype virus neutralization assay for diagnosis of ZIKV infection.

Producer (BHK21) cells are transfected to generate recombinant VSVs with plasmids encoding structural proteins of VSV: pBS-N-ΦT, pBS-P-ΦT, pBS-G-ΦT, pBS-L-ΦT and the VSV backbone pVSV-ΔG-luc in which the glycoprotein (G) gene was deleted and replaced with luciferase reporter gene. To generate pseudotyped ZIKV, this recombinant VSV was then used to infect target cells that were transiently expressing ZIKV glycoproteins.

Transcription of the VSV proteins is under the control of T7 RNA polymerase promoter (T7 pol). when infecting producer cells with fowlpox virus expressing T7 pol prior transfection, recombinant VSVs were successfully generated. However, attempts to generate PVs using ZIKV glycoproteins have been unsuccessful to date. Glycoproteins of viruses from other viral families (e.g. Lassa virus, Lujo virus and Chikungunya virus) were used in comparison during the generation of PVs.

O13: Epidemiology of Tick Borne Pathogens of Dogs in Nigerian Communities

Ternenge Thaddaeus Apaa^{1,2}, Stephen Dunham¹, Rachael Tarlinton¹

¹University of Nottingham, UK. ²University of Agriculture Makurdi, Benue State, Nigeria.

Tick borne diseases (TBDs) have significant impact on the health and welfare of domestic animals and humans. There is extremely little data on the prevalence of tick species, TBDs or their impact in Nigeria. Nigeria's scenario is further worsened by lack of basic diagnostic facilities and treatment, compared with the average person's income. The multiple climate zones and animal husbandry practices in Nigeria also make it difficult to extrapolate studies from one zone to the other five geopolitical zones.

TBDs reported in Nigerian dogs include *Anaplasma* sp. (*A. platys*, *A. omatnenne*), *Babesia* species (*B. rossi*, *B. canis* and *B. gibsoni*), *Theileria* sp. (*T. equi*, *T. sable*), *Ehrlichia* sp. (*E. canis*, *E. ruminantum*), *Hepatozoon* species (*H. canis*) and *Candidatus Neoehrlichia mikurensis*. The prevalence of zoonotic pathogens of dogs such as *Borrelia* sp., in humans in West Africa also indicates that these are likely to present in dogs in Nigeria.

This main study aim is to identify ticks taken from dogs in Nigeria using morphological and molecular methods, determine which host species the ticks have fed on, and identify pathogens that they are carrying. It also aims to compare molecular and point of care diagnostics for TBDs in blood from Nigerian dogs. The overall objective is to provide robust data on which tick species and TBDs are present in Nigerian dogs and the potential zoonotic or epizootic risk.

Poster Abstracts

P1: Using a multi-disciplinary, One Health approach to understanding how emerging infectious diseases and antimicrobial resistance (AMR) can transfer from livestock to humans

Piyali S. Basu, Helen L. Brown, Maria Getino, Daniel L. Horton, Elizabeth Royall, Roberto M. La Ragione

School of Veterinary Medicine, Department of Pathology and Infectious Diseases, Daphne Jackson Road, University of Surrey, Guildford, Surrey, GU2 7AL.

The European Joint Programme (EJP), is a co-funded action supporting coordinated national research and innovation programmes. The University of Surrey, alongside partners across Europe, were successful in obtaining 90€ million to pool a critical mass of national resources to work on the objectives and challenges of Horizon 2020. Here we will provide an overview of the programme and its scope, highlighting the benefits of the one health, multidisciplinary approach applied.

The University of Surrey will focus primarily on an education and training work package (summer school, continuous professional development, short term missions etc.) and two complementary research areas. Emphasis will also be placed on training of scientists, in order to ensure the sustainability of the research area and collaborations.

The first project will analyse the microbiome of commercial pigs and poultry in order to determine if specific microbiota compositions are linked to the pathogen shedding status of the host. Probiotic species and nutraceuticals will also be identified and assessed for their ability to limit shedding. Interactions between the gut microflora, probiotic species and pathogens will then be modelled in order to better understand how interactions within the microbial community affect shedding.

In parallel, the main drivers and agents involved in AMR transmission and dissemination across Europe will be interrogated. A particular focus of the studies will be on mobile genetic elements and their transfer potential between hosts. It is anticipated that the outputs of the studies will result in reduced zoonotic pathogens in the food chain, reduced antimicrobial usage and AMR.

P2: Analysis of the interaction of influenza A virus with the PI3K pathway in different avian hosts

Irene Di Lauro, Janet Daly and Stephen Dunham

School of Veterinary Medicine and Science, University of Nottingham.

The PI3K/Akt signalling pathway has been identified as having a major role in influenza A virus pathogenicity. The pathway has been shown to be active in humans and chickens, but inactive in ducks. Furthermore, the p85 β catalytic subunit of PI3K was shown to bind to NS1, a non-structural protein of influenza viruses, in human lung cells (A549). This triggers a downstream effect of activating the PI3K/Akt pathway, which prolongs cell survival, thus working in favour of viral replication. Western blots of lysed infected primary embryonic quail cells, showed that the pathway is also active in infected quail cells for up to 24 hours post infection. A phylogenetic tree was constructed using the amino acid sequences of p85 β originating from different species. Further research is necessary to understand if NS1 interacts with the p85 β of avian species, to better understand the mechanisms that affect influenza A virus pathogenicity.

P3: Mathematical modelling to enhance preparedness for the emergence of midge-borne diseases

Emma Fairbanks

School of Veterinary Medicine and Science, University of Nottingham.

Exotic midge-borne viruses were once restricted to tropical geographical regions. However, due to climate change and increased globalisation, these diseases now pose a greater threat, with outbreaks of bluetongue virus (BTV), Schmallenberg virus (SBV), and African horse sickness virus (AHSV) having occurred within Europe.

Using knowledge gained from previous outbreaks we develop epidemiological models to investigate the likelihood of transmission within the UK throughout the year. The basic reproductive number, R_0 (the average number of new cases generated by one individual during their infectious period), is used to determine the risk of an outbreak. We also consider the vectorial capacity C , the contribution to R_0 due to 1 day of biting the infected host. We find that C peaks during June and is particularly high in SBV, due to its high replication rate at lower temperatures. However, BTV has a higher R_0 value due to its longer infectious period.

Future work will focus upon further understanding of midge-borne disease transmission and providing policy makers with epidemiological forecasts that will enable them to assess current and future outbreak risk, as well as quantitative assessments of the effectiveness of intervention strategies, such as vaccination. This research may also have implications for other vector-borne diseases, such as West Nile virus, which can infect humans.

P4: Primary pigeon embryo fibroblasts as an alternative to fowls eggs for propagation of pigeon avulavirus.

Paul Skinner¹, David Sutton³, Jo Mayers^{1,2}, Clive Watson¹, Sharon M. Brookes¹ and Ian H. Brown¹

¹Animal & Plant Health Agency (APHA), Woodham Lane, Addlestone, Surrey, KT15 3NB, United Kingdom, ²University of Surrey, Guildford, Surrey, GU2 7XH, United Kingdom, ³Current address: Qiagen, Skelton House, Lloyd St N, Manchester, M15 6SH.

Pigeon avulavirus 1 (PAvV-1), also known as pigeon paramyxovirus 1 (PPMV-1), is a pigeon-adapted variant of Newcastle disease virus. The hosts are primarily pigeons/doves (*Columbiformes*), but clinical disease in domestic poultry has also been observed. Current diagnostic and isolation methods require propagation in embryonated fowls eggs (EFE) or primary chicken embryonic liver cells (CEL). To eliminate any potential host-adapted mutations involved with current chicken cell/egg propagation methods, this study describes the development of primary pigeon embryonic fibroblast (PEF) cell cultures as an alternative to our existing *in vitro* diagnostic capabilities, and to provide benefits for studying the evolution of PAvV-1.

A novel protocol was developed to harvest the non-visceral tissues of 11-day-old pigeon embryos. The cells quickly formed confluent multi-layers composed primarily of fibroblasts FBS. Preliminary evaluation has demonstrated that these cells can be cryogenically stored and resuscitated, yielding four-to-five passages before losing vigour. The PEF cell cultures were subsequently inoculated with PAvV-1 that had been propagated in the allantoic fluid of embryonated pigeon eggs, and incubated for five days, or until cytopathic effect (CPE) was observed. The cell culture supernatant was tested by haemagglutination assay (HA) and real-time polymerase chain reaction (RT-PCR), yielding comparable results to that of existing methods. Therefore, the use of PEFs provides an advantageous method for propagating PAvV-1 as an alternative to EFes and CELs, and reduces the reliance on *in vivo* egg work in line with the principles of the 3Rs (replacement, reduction, & refinement).

P5: Applying Next Generation Phage Display technology to identify peptide mimotopes for use in flavivirus diagnostics

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

¹School of Veterinary Medicine and Science, University of Nottingham, ²Moredun Research Institute, Scotland.

Flaviviruses are a large family of viruses, some members of which cause human and veterinary disease and pose a potential risk of death. The transmission route is typically through the bite of arthropods such as ticks or mosquitoes and. They are a major cause of emerging and re-emerging viral infections. One of the major issues faced when carrying out serology diagnostics is the risk of cross reactive antibodies among closely related species.

Next Generation Phage Display is a molecular biology technique combines phage display with next generation sequencing. A phage library is created by inserting peptide sequences into a phagemid vector. Each phage in the resultant library displays a particular peptide on its external surface and the resultant phagemid is packaged within the phage particle. The main advantage of phage display is linking the phenotype (peptide binding properties) with genotype (the peptide gene within the phagemid)

Serum antibodies from flavivirus infected species are immobilised on a solid support and incubated with the phage library. Following washing steps to remove non-specific binding, the phage are rescued and propagated in bacteria. This process is called biopanning and is repeated up to 4 times. The phage genomes are sequenced using Ion Torrent sequencing and through analysing the sequences, the antigenic peptide regions can be identified.

The most antigenically potent sites can then be used to create a diagnostic assay such as an ELISA.

P6: *Salmonella enterica* serotype Dublin infection of bovine caruncular epithelial cells: a model for investigating abortive infection in cattle.

Jemma May Franklin¹, Christiane Pfarrer², Paul Barrow¹, Sabine Töttemeyer¹

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

²Department of Anatomy, University of Veterinary Medicine, Hannover, Germany.

Salmonella enterica serotype Dublin is an important bacterial cause of infectious abortion in cattle. Previous work has shown the systemic dissemination of *S. Dublin* in orally challenged animals to various tissues, including the liver, spleen, and the reproductive tract. Ungulate placentation involves interdigitating maternal (caruncular) and foetal (cotyledonary) tissues in “button-like” structures called placentomes. Bovine caruncular epithelial cells (BCECs) isolated from the maternal caruncular tissues have been used to model the reproductive tract in this study.

The aim of this study was to characterise the invasion and survival of *Salmonella* Dublin within BCECs, to further our understanding of the mechanisms behind infectious abortions in cattle. *S. Dublin* with insertion mutations in genes of the *Salmonella* Pathogenicity Island (SPI), a Type 3 Secretion System (T3SS), as well as wild-type *S. Dublin* were used to infect BCECs for 2 to 24 hours. SopB, SopE, SopC, SopD and SipB mutants were used to determine their importance as virulence genes in the infection of bovine placental cells, and the intracellular bacteria were quantified.

S. Dublin is able to invade and replicate within the BCEC cell line. Preliminary results suggest that SipB and SopC mutants were attenuated in their ability to infect and replicate within the cells, whilst SopD mutants were unaffected. This study was the first to characterise the invasion of bovine caruncular epithelial cells with *Salmonella* Dublin. This approach allows investigation of aspects of *S. Dublin* tissue tropisms within the bovine placenta which may lead to abortion. This study was the first to characterise the invasion of bovine caruncular epithelial cells with *Salmonella* Dublin. This approach allows investigation of aspects of *S. Dublin* tissue tropisms within the bovine placenta which may lead to abortion.

P7: Investigating the potential of phospholipids to reduce avian influenza virus infectivity

Lamyaa Al-Dalawi, Cyril Rauch, Stephen P Dunham.

School of Veterinary Medicine and Science, University of Nottingham, Sutton Bonington Campus, College Road, LE12 5RD.

Influenza virus is an enveloped, negative single standard RNA that subverts host cell factors like lipids for their own replication. Cellular lipids have been shown to play an important role in the virus lifecycle for virus entry and outward budding to produce new virions. Phospholipids have been shown to play a role in protective innate immune responses to infectious agents, including influenza virus, mediated by alveolar surfactant. The objective of this study is to determine the ability of phospholipids to reduce virus infectivity by pre-treating influenza A viruses (IAV); avian influenza H2N3, equine influenza H3N8 and pandemic influenza H1N1 with different phospholipids. 1, 2-dipalmitoyl-sn-glycero-3-phosphocholine (DPPC) had no apparent influence on virus infectivity. However, 1, 2-dipalmitoyl-Sn-glycero-3-phospho-(1'-rac-glycerol) (DPPG) had a significant impact on H2N3, H3N8 and H1N1 infectivity. Treating the influenza viruses with lyso-analogues: 1-palmitoyl-2-hydroxy-sn-glycero-3-phospho-(1'-rac-glycerol) (LPG) and 1-palmitoyl-2-hydroxy-sn-glycero-3-phosphocholine (LPC) showed a significant inhibition of influenza virus infection in both MDCK and A549 cells, that was dose-dependent. TEM images showed that influenza virus without treatment is mostly spherical for H2N3 virus and filamentous for H3N8 whereas incubation with lipids, led to the formation of liposome-virus aggregates or changes in virion morphology. Flow cytometry showed that DPPG or LPG, significantly reduced virus binding to cells. Overall, pre-treatment of IAVs with phospholipids seems to have an impact on the ability of the virus to bind and enter susceptible cells. Further investigation is needed to determine their potential role in treatment of IAV infection.

P8: Profiling AMR of Enterococci in the dairy environment.

Erin Bond¹, Dov Stekel², **Michael A. Jones**¹

¹School of Veterinary Medicine and Science, ²School of Biosciences University of Nottingham, Sutton Bonington, UK.

Background: Enterococci are nosocomial pathogens increasingly found to be multi drug resistant (MDR) in human medicine. There is interest in defining the risk of AMR selection and zoonotic transfer from agriculture. Vancomycin resistance is of particular interest as it is one the last line treatments for MDR-enterococci. While this drug is not used on dairy farms there are a range of antimicrobials and antibiotics used which may pose a risk for direct or co-selection for this or other resistances

Objective: The aim of this study was to profile the AMR of Enterococci from slurry samples. An environment where a number of antimicrobial selections co-exist, to determine if there is evidence of co-selection.

Results: Susceptibility testing identified a high proportion of isolates expressing resistance to ciprofloxacin and erythromycin, whilst the majority of isolates remained susceptible to other groups of antimicrobials. 2.8% of isolates were vancomycin resistant which is significantly lower than that of pork and poultry isolates but is in line with the low prevalence observed in dairy products. A correlation was observed between antibiotic tolerances below resistance breakpoints but not at higher concentrations. This is suggestive of general tolerance factors for low levels of antibiotics.

Conclusion: The data presented show a low prevalence of vancomycin resistance and limited evidence of antibiotic co-selection of enterococci in this environment.

P10: Formulation of a novel protocol for the retrieval of pollen grains from forensic gelatine lifters and its potential application in combating the illegal ivory trade

Sophie Claire Pulcella, Royal Veterinary College, Zoological Society of London.

Each year the illegal ivory trade places increasing pressure on populations of African elephants (*Loxodonta africana* and *L. cyclotis*), with both species listed as 'vulnerable' by the International Union for Conservation of Nature. Current conservation efforts by wildlife forensic experts include the assessment of the geographic origin of seized ivory and the use of forensic gelatine lifters in retrieving latent fingerprints. These gel lifters also show the potential for retrieving pollen grains from seized samples of ivory, the forensic palynological analysis of which could then be used to determine geographic origin through the study of endemic plant species or multiple species profiles. The current piece of research investigated this concept through the optimisation and formulation of a novel protocol for the retrieval of pollen grains from gel lifters. Protocol viability was tested across four species found in sub-Saharan Africa (*Osteospermum*, *Agapanthus*, stinging nettle and tufted hair grass), three temperatures of distilled water (8°C, 25°C, 45°C) and a range of pollen grain quantities (500, 300, 100, 50, 10, 1). Statistical analysis showed that pollen species had the most significant effect on grain retrieval success ($p = 0.002$), whereas water temperature had no significant effect ($p = 0.086$) and the sensitivity of the protocol was such that it was possible to retrieve just one pollen grain on 25% of occasions. The findings of this study indicate that gel lifters are a viable means of retrieving pollen grains from ivory and further research should involve the application of this protocol in wildlife forensics.

P11: Antibiotic resistance: Is there a link between sheep and pasture run-off?

Diana Vargas¹, Hayley Marshall¹, Katie Kelly¹, Peers Davies², Adam Blanchard³, Kim Hardie⁴, Sabine Töttemeyer¹

¹School of Veterinary Medicine and Science, University of Nottingham, ²Department of Epidemiology and Population Health, University of Liverpool, ³Department of Animal, Rural and Environmental Sciences, Nottingham Trent University, ⁴School of Life Sciences, University of Nottingham.

The misuse and overuse of antibiotics has accelerated the dissemination of resistant bacterial strains, mainly through horizontal transfer. It has been observed that antibiotics given to animals are not absorbed completely and are rapidly excreted, contaminating soil and water.

The aim of this pilot study was to investigate sheep as a vector in the transfer of antimicrobial resistance bacteria in the agricultural environment. Characterisation of antimicrobial resistance in *E. coli* from pasture run-off and ovine interdigital skin isolates was performed using disc diffusion essays with nine antibiotics important in human and commonly used in veterinary medicine.

Resistance to tetracycline, ampicillin, streptomycin, spectinomycin and sulphatriad was observed in water and ovine interdigital isolates. Some isolates were multidrug resistant, as resistance to at least three antibiotic classes was observed, including aminoglycosides and ampicillin. Resistance to aminoglycosides and penicillin represent a major problem for farmers and veterinarians, as they are widely use during lambing periods and lameness.

The results obtained suggest a possible transfer of antimicrobial resistance bacteria from ovine flocks into pasture-run off, which may act as a reservoir for resistant bacteria. The propagation and growing resistance in pathogenic bacteria not only increase the problem of treating animals against infections but is also a principal threat to human health.

Conference General Information

Travel to Sutton Bonington Campus

The University web page below has lots of information and links to route planners, whether you plan to drive or use public transport.

<https://www.nottingham.ac.uk/about/visitorinformation/mapsanddirections/suttonbonington.aspx>

Conference Venue

Conference registration and poster sessions, as well as lunch and refreshment breaks will all take place in the atrium of the Veterinary School Main Building (building 27 on map). Talks will take place in the nearby lecture room, A29.

<https://www.nottingham.ac.uk/sharedresources/documents/mapsuttonbonington.pdf>

Accommodation

For those who have booked accommodation on campus, bedrooms will be ready by 2pm on day of arrival. Keys can be collected from the Accommodation Office based in the STANFORD accommodation block (building A on the campus map above). The office is open 24 hours a day, if you are planning a late arrival on the Sunday! Check out is by 10am, please return keys to Accommodation Office.

Breakfasts

Because of the low numbers for Monday and Wednesday breakfast, it's not feasible to open up the Barn Servery for a full breakfast. We will provide residents with a voucher for the Mulberry Café where you can purchase drinks/continental items to the value of £10. The breakfast vouchers for Mulberry will be handed out during check in on Sunday by the Accommodation team.

Breakfast on Tuesday morning will be in the Barn from 8.00 – 8.45am.

Parking

As the main reception will not be open on Sunday, the accommodation team will hand out parking permits for early arrivals. Those arriving on Monday or Tuesday can collect your parking permit from the Main Reception (building 11 on campus map). You will only need one permit which will cover the duration of your stay.

Oral Presentations

Keynote speakers are requested to keep their talk to 40 minutes and allow 5 minutes for questions. Authors presenting oral presentation for submitted abstracts should allow 15 minutes for their talk and 5 minutes for questions.

Presentations will take place in lecture theatre A29 within the main Veterinary School building. Please see me at the start of the day or during coffee break, or lunch and I'll help get your presentation onto the computer IN ADVANCE of your session.

Poster Presentations

Posters should be displayed on the boards situated in the Vet School atrium, close to the registration desk. There is sufficient space to fit posters, in portrait orientation, of A0 size or smaller on the provided boards. Please put posters up following registration on day 1 and take down at the end of day 2.

Flash poster presentations will take place in A29 at 16.15 on Monday 17th September. Could authors please use a maximum of two slides and speak for no longer than 3 minutes to introduce their posters. Please see me at the start of lunch on Monday and I'll help get your presentation onto the computer IN ADVANCE of the session.

Conference Meal

We plan to head out as a group to a local pub or restaurant on the Monday evening around 7pm. In order to keep the conference as affordable as possible, the cost of this is not included in registration. If you are planning to come for a meal on the Monday please let me know and suggest whether you have a preference for pub (short walk or drive down a country lane) with a good range of food or local restaurant (drive to a local village, Kegworth where there is a choice of restaurants e.g. curry).

Wifi

Eduroam can be accessed on campus using your own login details if your institution is part of this network – please check your own institution for details of how to login as user names can be subtly different in some cases! A guest wifi network is also available – you will need to register when joining.

Taxi Hire

East Leake: East Leake Taxis, 01509 590075; EMT Private Hire, 0800 328 8442.

Gotham: Collo Cars, 0115 983 1182.

Loughborough: A2B Taxis, 01509 236444.

Shepshed: Amalgamated Cars, 07763 564752.