

The Prevention and Control of Zoonoses: From Science to Policy



Poster Abstracts

POLICY SETTING

National Centre for Zoonosis Research

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Many headline problems in public health concern infections, and of these most are either zoonoses or involve human-animal interactions of some sort. World-wide, around 75% of human emerging infectious diseases are zoonoses, yet research in the area is often piecemeal, incomplete and sometimes contradictory. At least in part, this is because zoonotic infections have traditionally spanned medical and veterinary responsibilities – and have often fallen in the divide between them. A better understanding of zoonoses requires an integrated, multidisciplinary approach, that brings together infectious disease specialists with epidemiologists, veterinary scientists, ecologists, mathematicians and statisticians, with molecular- and micro- biologists, in order to produce a gene-to-population understanding of the diseases. A national centre, of international excellence, bringing these skills together is the obvious way forward. A collaborative venture by the Universities of Liverpool and Lancaster, the HPA and the VLA, with core funding from NWSF, has established a National Centre for Zoonosis research which will:

- Undertake world-class scientific procedure, and become a focus of collaboration,
- Provide consultancy services to governments and other bodies (including industry) with scientifically sound, evidence-based and timely advice on zoonotic diseases, including risk analysis and horizon scanning.
- Deliver cross-cutting and joined-up, flexible provision of advice through active networking with existing organisations with interests in or responsibilities for zoonotic diseases.
- Develop training programmes in the prevention and control of zoonotic infections, emerging and external threats through collaborative ventures with educational institutions and others.

Poster number 16

Setting up and maintaining a local zoonoses group -

Q Syed^a, KL Morgan^b on behalf of the North West Zoonoses Group (see below*)

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There is considerable current interest in establishing and coordinating local zoonoses groups. The Northwest Zoonoses Group was established in 1996. It represents a predominantly rural geographical area, extending from Cumbria to Cheshire, in which a significant proportion of the population is concentrated into two major urban areas.

The group was established by inviting willing representatives, from key organizations, to dinner at a Liverpool restaurant. Here the reasons for setting up the group and its potential significance were set out. Individuals, who agreed to host the meeting and provide food, arranged subsequent evening meetings. Developing a focus for the group proved difficult. Establishing a co-ordinated reporting system for zoonotic disease within the region was set as a priority in 1997. Organizational and resource barriers prevented this and attendance at

meetings dwindled and eventually they stopped. They were rejuvenated by the provision of PHLS secretarial support, with responsibility for organizing the time and location of meetings. At subsequent meetings a number of valuable ideas were generated but few of these were achieved, mainly because the daily commitments of members of the group.

The next significant step was the appointment of a part-time "information officer". The aim was to facilitate the transformation of resolutions into actions. This has been effective. The group now has an active website (www.northwest-zoonoses.info), has developed and coordinated training scenarios and holds annual scientific meetings. It has focused on identifying the gaps between veterinary and medical information, policy and practice, in the control of zoonotic disease. Local outbreaks, e.g. of bat rabies have helped inform national policy, and the provision of "seedcorn" research funding has generated major projects on sporadic cryptosporidiosis and zoonotic, enteric bacteria of pet dogs. The HPA takes the lead in organizing the group and it has good links with the National Zoonosis Group and Advisory Committee. The Northwest Zoonoses Group continues to address issues of organizational and geographical representation in the co-ordination of multi-agency surveillance, active and timely sharing of information, dissemination of intelligence and development of collaborative research initiatives.

Members of the NWZG are: Chair – Qutub Syed, Vice Chair – Kenton Morgan, John Ashton, Nick Beeching, Mark Bellis, Malcolm Bennett, Eric Bolton, Steve Gee, Caroline Harcourt, Tony Hart, Robert Hogg, Mike Howard, John Kelsey, Lorraine Lighton, Dilys Morgan, John Newbold, Sarah O'Brien, Martyn Regan, John Reid, Keith Osborn, Magda Sachana, Will Sopwith, Alex Stewart, Mike Watkins-Jones, David Wild

Poster number 17

The Defra Veterinary Epidemiology Fellowship: Zoonotic enteric pathogens on Cheshire farms

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The Defra Epidemiology Fellowship Unit at Liverpool was an interdisciplinary network providing research and training in veterinary public health. The research programme comprised a number of integrated projects in statistics, applied mathematics, medical microbiology, ecology, pathology and epidemiology. Each focussed on different aspects of the epidemiology and risk assessment of food borne and environmental pathogens, both on-farm and further along the food chain.

Cross sectional and longitudinal studies were conducted in two study areas, in Wirral, and in a 100km² area of dairy farmland in Cheshire, providing information on the spatial, longitudinal and molecular epidemiology of *Campylobacter* spp. and *E. coli* O157. Excellent cooperation was achieved from farmers, allowing good coverage of contiguous areas of farmland. Sampling of livestock, wildlife and water yielded large collections of isolates of *C. jejuni*, *C. coli*, *C. lari*, *C. hyointestinalis*, verocytotoxigenic *E. coli* and *Salmonella* spp., which have been characterised by PFGE and MLST. Molecular typing, combined with epidemiological data and novel statistical models, revealed important associations of relevance to the control of these pathogens. For example, we have provided the most conclusive evidence to date of a strain of *C. jejuni* associated with cattle: MLST type ST 61.

Longitudinal studies on *E. coli* O157 also provided valuable information on the numbers of organisms shed by naturally infected cattle of all ages. The variability and uncertainty in microbial counts was characterised, and this provided essential data for the development of qualitative and quantitative microbial risk assessment models. Mathematical models of the transmission of pathogens through the multi-group structured dairy herd, were developed and

used to inform potential control strategies. The combination of analytical and simulation-based studies has shown that control measures aimed at single groups, such as post-weaned youngstock, could be an effective and efficient way of reducing contamination along food and environmental pathways.

Poster number 18

SURVEILLANCE, MODELLING AND UNCERTAINTY

WebGIS-based system to share epidemiological information about zoonoses

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Control measures have been set up by the European Community to guarantee safe food and healthy livestock. Zoonoses surveillance must be supported by an information system that can give real-time data about animals' sanitary status, food quality and diseases in the human population.

The aim of this work is to present a project on an Internet-based application to publish, on the WEB, epidemiological data concerning animal diseases and their possible connections with human health cases, with the support of a GIS based system.

The WEB interface would supply two different access levels:

- public access, providing a publication of thematic maps at municipality level and on a mid-large scale (to avoid privacy problems), regarding notifiable diseases detected in the area of interest;
- private access, showing on-fly maps with specific event data on a progressive small scale, which would permit the sharing of epidemiological data about zoonoses between human and veterinary health authorities.

This could permit a spatial characterisation of zoonoses outbreaks, and the sharing of epidemiological information, to identify and analyse the risk factors involved.

Poster number 1

Sequence typing for surveillance of environmental campylobacter

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Aim: Despite several case control studies and enhanced surveillance of both human and animal cases, there is still much unknown about the transmission of *Campylobacter* spp. A multi-agency project in North West England aims to explore the feasibility of using sequence typing of human isolates to inform surveillance and distinguish environmental sources of human infection.

Methods: Multilocus sequence typing (MLST) developed for *C. jejuni* is being applied to all human isolates from four Local Authority areas in North West England, two largely rural and two largely urban. Samples from water supplies and recreational surface waters are also being typed. Typing is planned for three consecutive seasonal cycles of *Campylobacter* and results are combined with detailed epidemiological information collected by postal questionnaire through the relevant Health Protection Units.

Results: In the first year of the study, the majority of the isolates were found to belong to clonal complexes 21 and 45, both of which may have a strong association with poultry as well as human infection. Several common and new sequence types were identified in environmental samples. We present here preliminary results for the second year and seasonal variations in sequence types of both human and environmental isolates.

Poster number 2

Elucidating the epidemiology of human campylobacter infections by Penner typing

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Penner schemes have been developed for typing campylobacter but have had only limited success in helping explain the etiology of this disease. Here we have used epidemiological information on human cases in conjunction with Penner typing data to investigate human campylobacteriosis in Grampian.

The seasonality of human campylobacter cases is one of the main conundrums associated with this zoonosis. We have found that seasonality in young children is greater in rural regions compared with their urban counterparts. In addition, we have found that the Penner types in rural areas are predominantly type O:2, whilst in urban areas this Penner type is relatively rare. This suggests that the seasonal peak in young children could be predominantly due to environmental infection pathways rather than food borne. This hypothesis is further supported by significant correlations between human incidence and farm animal densities.

We have also investigated the Penner types of human campylobacter isolates in Grampian stratified by 5 year age groups. We have found that there are significantly more rare types in the older population (>40 years). This could be explained by acquired immunity to common strains in the older population or possibly lifestyle differences in this cohort.

Although genotypic schemes such as MLST are proving increasingly useful, the information that can be obtained by Penner typing should not be ignored and is valuable when used in combination with epidemiological data.

Poster number 2a

A stochastic model for transmission of verotoxigenic *Escherichia coli* O157 within a domestic beef herd

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Given the severity of human illness of VTEC O157 infection, it would be advantageous from a public health perspective to reduce the burden of infection in the source (i.e. cattle and the environment) to negligible or low levels. To achieve this, an understanding is required of the transmission dynamics of VTEC O157 within the cattle herd in order to implement effective on-farm control measures. An increasingly common approach for gaining this understanding is to use epidemiological models; an approach that is adopted here. A stochastic simulation model is developed considering the transmission dynamics of VTEC O157 both between animals and from the environment within a typical beef suckler herd. More specifically, the model aims to simulate the transmission of VTEC within the herd through the summer grazing period and during winter housing. To achieve this, the model is developed to consider the single field environment in which the spatial dispersion of VTEC O157 is accounted for and to consider the specific spatial aspects of the animals in the group pens in winter housing accommodation. Several control measures are investigated including more frequent cleaning out of the housing, and reduction in herd size.

The poster will include a brief background to VTEC O157 in cattle, an outline of the model framework including a description of the mathematical approach and the results. Further, the

effect of the investigated control measures on the transmission of VTEC O157 within the herd will be provided. Finally, some overall conclusions will be drawn and presented.

Poster number 3

Bayesian approaches to the assessment of uncertainty in Microbial Risk Assessment

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Quantitative Risk Assessment is becoming an important tool for managing microbial environmental and food chain risks. Within the food production context, Microbial Risk Assessment (MRA) utilises a body of statistical, probabilistic and mathematical approaches to construct a mechanistic model of the food production chain of interest. As important as constructing a model which is plausible structurally, is the issue of reflecting input parameter uncertainty. Fundamental to the validity of MRA models is the correct identification, quantification and incorporation of the relative uncertainties at the different levels of the food production chain.

The Bayesian statistical approach provides a rigorous means by which parameter uncertainty can be modelled. It has the advantage that, as well as being applicable to the description of uncertainty in parameters which can be derived simply, it has the flexibility to respond to more complex, non-standard problems; in such cases the technique can be used to derive meaningful estimates of uncertainty, and to quantify the relative plausibility of different parameter values. Within the context of a farm-to-fork assessment of the risk posed by VTEC O157 in milk sold as pasteurized, I will describe a number of studies which have been carried out in specific areas where the parameters of interest are not estimable using standard statistical approaches. As examples, I will describe a Bayesian approach to estimating bacterial concentration in a substance, given microbial count data together with a confirmatory test result. I will also describe a Bayesian approach to estimating the animal-level prevalence of a particular organism using samples taken from faecal pats on the ground.

Poster number 4

Using a visual simulation model of *Campylobacter* in poultry from retail to consumer to show country to country differences

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Campylobacter is one of the leading causes of food borne illness in countries throughout Europe. Broiler meat may be the source of many cases of campylobacteriosis making *Campylobacter* in chicken an issue for all European countries. There are however, major differences in the prevalence of *Campylobacter* in the retail products, broiler production and chicken meat processing methods and in the level of imported chicken in the different countries. Microbiological risk assessments addressing this pathogen-commodity combination will prove useful for decision makers such as Codex committees, food industries, food control authorities, regulators and other stake holders. However, the general *Campylobacter* models need to be adapted to answer the specific risk management questions in the different countries. We have developed a retail product to consumer simulation model in Extend software. The model aims to increase transparency in the risk assessment process, and allows a visual understanding of the entire process being modelled while also clearly showing the input values used in the model. We have compared the data from Germany (provided by BfR -The Federal Institute for Risk Assessment, Berlin), the Netherlands (CARMA project data) and Norway. These countries have very different levels of *Campylobacter* in broilers and chicken meat, as well as import, production and consumption differences. The differences in the effects on human health from various risk management strategies available to countries with very different *Campylobacter* levels and poultry production differences are illustrated.

Poster number 5

Risk assessment of BSE in changing the cut-off age of BSE testing

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The Food Safety Commission's expert committee on prions, on the request of the Ministry of Health and the Ministry of Agriculture, Forestry and Fisheries, evaluated both qualitatively and quantitatively, the risk of slaughter cattle being infected with BSE and of bovine meat being contaminated with the BSE agent, when replacing the current scheme of testing all cattle for BSE by testing of cattle over 20 months of age. The risk of bovine meat being contaminated with the BSE agent was found to be 'negligible' or 'very low' regardless of the cut-off age for BSE testing. A quantitative assessment resulted in a similar estimation. From these results, the committee concluded that the proposed change of cut-off age for BSE testing would result in only a very small increased risk to consumers, even under a worst-case assumption.

Poster number 6

Providing answers to the Query? Improving understanding of an infection affecting rural populations in SW England and Northern Ireland

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Q (Query) fever is a disease caused by the organism *Coxiella burnetii* most commonly found in sheep, cattle and goats in the UK, and transmitted to humans by inhalation of infected aerosols. The disease occurs most frequently in humans exposed to farm animals or in areas where animal products are handled.

The South West Region consistently reports the highest number of cases in England and Wales, and an epidemiological review, showed that the region reported one third of all cases. Northern Ireland reports higher rates of Q Fever per 100,000 population, with between 21 and 75 cases per year since 1990.

Although outbreaks have been reported world wide, the causes have often not been clearly identified and there have been no case control studies to determine risk factors among sporadic cases. We collaborated with laboratories in the South West and Northern Ireland to identify cases of acute Q Fever for a case control study to determine risk factors for this disease.

There were 50 eligible cases identified during the study period, of which 38 (76%) returned completed questionnaires. This was a lower number than anticipated possibly due to the impact of foot and mouth disease the previous year. Of these cases, the average age was 46 years old and the majority (74%) were male. Ninety (50%) of the 180 controls responded. Preliminary analysis has not indicated statistically significant findings so far, but this may be due to the unusually low number of cases. Further results and conclusions will be presented.

*Members of the Q Fever Study Group are: David Dance, David Carrington, John Hartley, Simon Hill, Graham Lloyd, Conall McCaughey, Marina Morgan, Isabel Oliver, Hilary Orr, Mike Smith, Robert Smith, Brian Smyth and James Stuart

Poster number 7

Twenty years of *Mycobacterium bovis* infection in humans and cattle in Scotland

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Human cases of confirmed *M. bovis* (n=155) and cattle herd breakdowns (n=168) in Scotland in the period 1985-2004 were analysed and compared by geographical distribution. The number of both confirmed cattle herd breakdowns and single human isolates of *M. bovis* over the 20 year period averaged around eight per year, as compared to an average of around 290 human cases of *M. tuberculosis* over the same period. However, there was a marked rise in the number of cattle breakdowns from 2002, but to date there has been no corresponding increase in human cases of *M. bovis*. The recent increase in cattle herd breakdowns is almost certainly due to (a) re stocking with cattle from high incidence (of bovine tuberculosis) areas, such as the South West of England and South Wales following the foot and mouth epidemic of 2001; (b) catch up following the suspension of cattle testing in 2001 and (c) a reflection of the worsening disease incidence in England and Wales.

The geographical distributions by NHS Health Board areas of confirmed cattle breakdowns and human isolates over the twenty year study period were compared. The highest numbers of cattle breakdowns were in Dumfries and Galloway and Grampian. Although Dumfries and Galloway was most affected by foot and mouth in Scotland, both areas are traditionally high importers of cattle from areas such as the South West of England and Ireland. Lothian and Greater Glasgow NHS Board areas have the highest numbers of human isolates over the study period. Both are high density population areas and contain the two major cities in Scotland, Edinburgh and Glasgow. It is likely that almost all of these human cases contracted their infection several years (probably decades) before their diagnosis and location at diagnosis may not necessarily reflect location at the time of exposure. The age distribution of human cases is heavily skewed to the over 60s suggesting exposure prior to the success of the cattle tuberculosis eradication scheme and the introduction of compulsory heat treatment of cows' milk in Scotland in 1983.

Scotland is now in the elimination phase of all tuberculosis infections in the indigenous human population, and while there is now no significant correlation over time ($r=-0.372$, $p=0.116$) or by geographical distribution ($r=-0.007$, $p=0.979$) of cattle and human disease, the recent upsurge of infection in cattle suggests that enhanced surveillance in humans is a necessary tool to monitor the situation.

Poster number 9

Surveillance of zoonoses in Scotland

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Health Protection Scotland (HPS) – formerly the Scottish Centre for Infection and Environmental Health (SCIEH) - is the national surveillance centre for infectious disease in Scotland and uniquely captures data from both human and animal sources via medical, reference and some veterinary laboratories. These data were analysed and compared by geographical distribution for the period 1993-2004.

There were 26,859 isolates of animal pathogens reported and 108,850 (17%) of 631,850 human pathogens reported over the twelve year period 1993 -2004, which were considered to be potential zoonoses. The potentially food and water borne pathogens, *Campylobacter*, *Salmonella*, *Cryptosporidium*, *Giardia* spp. and *E.coli* O157 were the most important in Scotland in terms of human infection with zoonoses, with these five organisms representing 95% (102,998) of all human zoonotic pathogens recorded over the twelve year period. The most common laboratory reports of zoonoses from animals over the same period were *Salmonella*, *Cryptosporidium*, *Chlamydia*, *Campylobacter* spp and *Mycobacterium avium* *paratuberculosis*

For all zoonoses in people, NHS Board areas Borders, Dumfries and Galloway, Forth Valley, Grampian, Lanarkshire and Lothian had a higher than expected standardised incidence rate (SIR) of infection, while Ayrshire and Arran, Fife, Greater Glasgow, Shetland, Tayside and Western Isles had a lower than expected SIR. Organisms and diseases considered to be new and emerging were *Rhodococcus equi*, *Cyclospora cayetanensis*, *Leishmania* spp, *Pneumocystis carinii* (*jiroveci*) and BSE/vCJD.

Within limitations, particularly that of data capture, this study demonstrates the importance of zoonotic disease in developed countries such as Scotland and the need for continued and robust surveillance. Surveillance is necessary not only to monitor trends of existing disease but also to be able to recognize new and emerging disease so that appropriate action can be taken by all those involved in the control of zoonotic disease, such as health professionals, politicians and those responsible for the allocation of scarce health resources.

Poster number 10

Assessment of the stability of *Brucella* VNTR loci in outbreak situations and in experimental infection.

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Variable Number Tandem Repeat (VNTR) based typing offers great promise as a tool to differentiate *Brucella* isolates and enhance the ability to use molecular approaches for epidemiological studies. One requirement that needs to be formally investigated is the stability of markers within an outbreak and within animals. We have now applied a VNTR typing scheme to some 400 *Brucella* isolates using the original eight 'Hoofprints' octamers and an additional seven novel loci of varying sizes. The genetic diversity of loci was found to differ markedly and it is clear that different loci may be required to assess diversity within different populations. Included in these studies were multiple isolates obtained from outbreak situations following importation of *Brucella* into the UK, as well as isolates obtained following experimental infection of pigs with *B. suis*. We have used these isolates to assess the stability of the various VNTR loci within such defined situations and report on our findings here.

Poster number 11

Sero-epidemiology of brucellosis in the UK, 2002-2004

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Introduction The clinical microbiology laboratory at University Hospital Aintree provides a national brucella serology service for England, Wales and Northern Ireland. Approximately 2,500 tests are performed annually. The results of positive serological tests between 2002-2004 are presented.

Methods The micro-agglutination test (MAG) has been used by the laboratory as a screening test for a number of years. It is simple to perform, well standardised and measures both IgG and IgM antibody. A MAG titre of $\geq 1:160$ is normally considered diagnostic for brucella infection at some time. Additional antibody tests are performed on positive samples.

Results 44 cases of brucellosis were diagnosed serologically between 2002-2004. Age range was 2 to 72 years (mean 41.2 years). Of these cases, 79% were male and 73% were reported from Northern Ireland.

Conclusion The sero-epidemiology of human brucellosis in the UK appears to be strongly linked to brucella infected dairy herds in Northern Ireland and consequent occupational exposure.

Poster number 12

Seroepidemiology of Q fever in Northern Ireland

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Q fever is a common zoonotic disease caused by the organism *Coxiella burnetii*. Compared to the rest of the British Isles, Northern Ireland (NI) reports particularly high rates of Q fever in humans, with between 10 and 75 cases per year since 1990 in a population of 1.6 million. The source of human infection in the British Isles is believed generally to be sheep and cattle, and transmission to humans is believed to be by inhalation of infected aerosols. The disease occurs frequently in humans exposed to farm animals or in areas where animal products are handled.

We studied Q fever seroepidemiology using a variety of serological methods in humans and animals in NI in the following populations: General human population 3328 sera using existing serum collections from cardiovascular studies (PRIME, Change of Heart, CINDI) and over 200 sera from farmers. Animal sera included 4963 bovine sera, as well as sera from sheep, pigs, goats, rats and mice.

Preliminary analysis indicates that the seroprevalence in the general human population is 8% (PRIME 7.8%, COH 15.1% CINDI 6.3%) differences between the surveys such as age and urban/rural recruitment bias probably explain the differences. Seroprevalence in farmers is 50.8% and in veterinary practitioners is 33%. Overall bovine seroprevalence is 6% (with 0 - 50% within herd prevalence) and the ovine seroprevalence is 13.7% (with 0-83% within herd prevalence)

The results underline the ubiquity of infection with this zoonotic agent in human and animal populations in Northern Ireland.

Further results and conclusions will be presented.

Poster number 14

FOOD BORNE ZOOSES

Epidemiology of *Mycobacterium bovis* infections in England, Wales and Northern Ireland between 1993 and 2003

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Mycobacterium bovis is a zoonotic bacterium with a wide host range, infecting cattle especially, but also wildlife in England, Wales and Northern Ireland. Human infections are, at present, rare in these countries, but the recent resurgence of *M. bovis* infections in cattle since the 1980s has increased concern about a risk to human health. Between 1993 and 2003, 315 human *M. bovis* infections were identified. Of these cases, 83% were born before 1960 and are likely to represent infections acquired in the distant past. The most frequently reported exposures in this group were consumption of unpasteurised dairy products and exposure to cattle either by occupation or by living or staying on a farm. Only 14 of the cases were born in the UK after 1960, by which time pasteurisation of milk and animal health measures were in place to safeguard human health. There were 332 and 1749 new confirmed herd incidents in 1993 and 2003, respectively. At present, the number of new incidents is estimated to be increasing at a rate of 18% annually. Testing for bovine tuberculosis and culling of reactor cattle is a statutory requirement of the European Union; the costs for testing and culling the cattle were £74 million in 2003/2004 in the UK. It is reassuring that despite the increase in infections in cattle over the last two decades there has been no increase in human disease. Due to the long latency of the disease, however, it is important to continue to monitor human cases, to reinforce the importance of pasteurisation of milk, to enforce the enhanced

surveillance of unpasteurised milk by additional routine testing and to ensure adequate protection for those at occupational risk.

Poster number 8

Food-borne zoonotic pathogens: a multidisciplinary study of transmission, pathogen evolution and control

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Successive reports have identified a developing “knowledge gap” in research in Britain – making both the farming community and the nation as a whole more and more vulnerable to the effects of major outbreaks of animal disease. The Veterinary Training Research Initiative (VTRI) aims to fill this knowledge gap, and the Faculty of Veterinary Science at the University of Liverpool, with the University of Lancaster, HPA and VLA, has been awarded £4.2M for a package of interdisciplinary research and training focussed on the epidemiology of food-borne zoonotic infections <http://pcwww.liv.ac.uk/vets/research/vtri/vtri.htm>.

This comprises four interlinked research programmes

- Origins, transmission pathways and emergence of human campylobacter infections
- The role of wildlife in the epidemiology of campylobacteriosis, salmonellosis and VTEC infections
- Between animal and between farm transmission: the role of behaviour, signalling and host genetics
- Verocytotoxin-encoding bacteriophages – ecology and role in disease

and a package of training opportunities including an Intercalated MSc for veterinary students in Veterinary Infection and Disease Control, PhD and MPhil training, undergraduate vacation scholarships, and short courses and CPD.

Poster number 22

Response of *Campylobacter* spp. to cold

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Despite the importance of *Campylobacter* spp. as human pathogens, little is known about their ability to cope with hostile conditions within the transmission chain from animal to man. *Campylobacter* spp. are perceived to be sensitive to the extra-intestinal environment yet they appear to maintain their infectious potential. In this study, gene-expression in NCTC 11168 at chill and host like temperatures was investigated and various strains were examined for their chill tolerance.

Duplicate biological replicates of NCTC 11168 were exposed to 6°C for 10 min and 24 h and gene expression was determined using RNA microarray technology, which identified 127 significantly up- and 104 significantly down-regulated genes at 6°C compared to 37°C. The greatest differences were identified in synthesis and modification of macromolecules, cell envelope, transport and binding proteins and conserved hypothetical genes. This indicates that there are considerable changes in transcriptional levels at lower temperatures.

NCTC 11168 and campylobacter strains isolated from broiler flock caeca at slaughter, from the raw chicken carcasses post in-out wash and at post-chill were exposed to 6°C over 50 d in triplicate. The strains represented two different MLST types, and all of the strains belonging to one MLST type survived chilling better than the strains belonging to the other MLST type.

This could suggest that different genotypes of campylobacter vary in their ability to survive low temperatures. We are currently investigating whether expression of chill related genes differ in different MLST types.

Poster number 23

***Campylobacter* and the environment: a geographical pattern in the timing of the peak week in the UK.**

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Even though *Campylobacter* has become the single biggest identified cause of bacterial infectious intestinal disease in the UK, the epidemiology and ecology of this infection remains far from clear. A number of risk factors for sporadic *Campylobacter* infection have been identified but none to date can explain the remarkable and consistent seasonal pattern. Consistent differences in the peak week between northern European countries suggest there could be some, as yet, unexplained environmental risk factors in operation.

Using British data at health authority level over a 13 year period, we explore variation of seasonality by geographical location concentrating on the timing of the peak (peak week) and on the estimated start of the exponential growth leading to the peak (start week).

In searching for environmental factors that might explain the seasonality of human *Campylobacter* infection, we have identified a geographical pattern in the timing of the peak in the UK with a gradient across the country in an unexpected direction. We have shown, for the first time, within-country variation in the seasonality of *Campylobacter* infection and we generate further hypotheses as to the sources of infection. We did not find a significant within-country variation in the UK in the start week. It appears, therefore, that spatial variation affects the time from the start to the peak, and hence the rate of increase of incidence. Our findings may provide further clues to the precise aetiology of this disease.

Poster number 24

The epidemic rise and fall of human campylobacteriosis in Scotland

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Campylobacter is the largest cause of bacterial gastrointestinal infection in the developed world. It was first isolated from stools of patients with acute enterocolitis in the 1970s. In Scotland the reported incidence is approximately 10 cases/10,000.

There was a 78% rise in human *Campylobacter* infections in Scotland between 1990-2000. This epidemic rise occurred in the adult population, predominantly in the highly populated central belt of Scotland whilst *Campylobacter* infections in children fell marginally during the same period. The cause for the rise is unclear due to the limitations of surveillance data in human populations and lack of surveillance in key animal reservoir populations. A 31% fall in human *Campylobacter* infections took place during the period 2000-2003. The gradient of this epidemic fall was greater than that of the rise and was consistent across all regions of Scotland except for the Borders. This fall occurred across all age groups but was most pronounced in the 0-9 and 20-29 year age groups, the groups having greatest incidence at the onset of the fall.

These data suggest that acquired immunity in the human population may have played a role in the reduction but it is also plausible that it could be due to a reduction within the animal

reservoir of *Campylobacter*. However, a comprehensive explanation of the fall in human campylobacteriosis and more importantly the ability to predict future disease trends is only likely to be achieved when prevalence and loading in animal reservoirs and foods, human seroprevalence and human exposure studies have been conducted.

Poster number 25

Three-year surveillance programme in Wales and Northern Ireland examining the prevalence of *Campylobacter* and *Salmonella* in retail raw chicken

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A 38-month study of *Campylobacter* and *Salmonella* contamination rates in retail raw whole chicken was carried out in Wales and Northern Ireland between 2001 and 2004. In total, 2508 samples were taken and overall rates 71% for *Campylobacter* and 5.7% for *Salmonella* were found. Results indicated that the annual rates for *Campylobacter* were unchanged over the three years of the study, ranging from 70-73%, and that the *Salmonella* rates declined between 2001 and 2004, falling from 8.4 to 3.9%. There were some significant differences noted between fresh and frozen samples, samples taken from retailers and local butchers, and between samples taken in Wales and Northern Ireland. There was also some seasonality in *Campylobacter* rates in fresh samples, with distinct peaks occurring every year. When compared to human infection rates, there was some limited similarity in the shape of the curves and the timings of monthly peaks in Wales, but not in Northern Ireland.

Poster number 26

***Salmonella* Enteritidis phage type 36 outbreak in Austria, 2004**

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In June 2004, an egg trader (packing station) was epidemiologically suspected of distributing the vehicles for a *Salmonella* Typhimurium phage type (PT) U291 outbreak, which - at that time - affected more than 100 people all over Austria and 8 German tourists and which began in September 2003. All 68 egg producing farms that delivered their eggs to the suspected packing station were screened for salmonella, but *S. Typhimurium* PT U291 could not be found in any of those. One holding was identified as being heavily contaminated with *S. Enteritidis* PT 36, a rare phage type in Austria. This phage type was isolated from diverse specimen sampled in that holding, 6 of 7 drag swabs, 1 of 4 samples of pooled egg yolks, and viscera of 7 of 11 killed hens.

In 2004, a total of 36 culture confirmed human PT 36 infections (19 manifest cases, 12 asymptomatic carriers and 5 carriers with unknown clinical status) were documented in 4 of the 9 Austrian provinces. It was possible to demonstrate that table eggs from this single farm were the probable source of infection for 30 of 31 culture confirmed human infections. Only in the case of one patient, who regularly purchased his eggs at a local market place, no connection to the farm could be proven due to non-traceability of the market's egg source. The PT 36 outbreak ceased after culling the contaminated flock.

This episode underlines the considerable potential of adequate epidemiological and microbiological investigations of food borne outbreaks to improve the prevention and control of communicable diseases. The source of the *S. Typhimurium* PT U291 outbreak - which initially prompted this investigation - is still not identified, accounting for more than 300 human cases as of April 2005.

Poster number 27

Characterisation of *Listeria monocytogenes* isolated from *alheiras*

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In Portugal, epidemiological information regarding listeriosis is scarce. This might be due to the fact that there is no obligatory notification of this food borne zoonosis in Portugal. However, *Listeria monocytogenes* has been isolated from different food products throughout various *ad hoc* studies in our country.

The microbiological characterisation of the Portuguese traditional fermented meat product *alheira* showed that *L. monocytogenes* was the most prevalent microbiological hazard. Therefore a characterisation of a random selection of *L. monocytogenes* isolates (116) from *alheiras* was accomplished based on their susceptibility to arsenic, cadmium and tetracycline, as well as serogroup identification by a multiplex PCR assay.

All five serogroups which may be identified by this technique were observed. The most prevalent groups were 1/2b-3b, 1/2a-3a and 4b-4d-4e respectively. Unique arsenic, cadmium and tetracycline susceptibility/serogroup patterns were found in *alheiras* produced in the same plant. However, most of the distinguished groups were detected in isolates from more than one producer.

Further characterisation of these isolates will be accomplished by antibiotic susceptibility and molecular typing by RAPD in order to ascertain the origin of this food borne pathogen.

Alheiras are stored at refrigeration temperatures and can be consumed after being cooked, grilled, roasted, microwaved or even fried. Due to the ability of this bacterium to survive in adverse environmental conditions as well as the high case fatality ratio of listeriosis, it will be imperative to evaluate if temperatures reached during cooking are able to inactivate this food borne pathogen efficiently.

This work was supported by FCT/FEDER project POCTI/AGG/39587/2001 and M.T.S. Felício was financially supported by PRODEP III (Programa de Desenvolvimento Educativo para Portugal, Medida 5, Acção 5.3).

Poster number 28

Food borne pathogens monitoring in animal populations: the experience of the Veneto Region of Italy

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The control of food borne diseases must be based on a “farm to fork” approach, in which primary production represents a critical point for contamination spreading, and is therefore a key point for any control activity. At the European level, such a strategy is clearly identified by the new zoonoses legislation (Directive 2003/99/CE and Regulation (CE) 2160/2003), which provides for the monitoring and the control of food borne zoonoses at primary production. Regulation 2160/2003 points out the necessity, for some zoonoses, to establish specific control measures, which should be based on targets for prevalence reduction. In order to apply the legislation, Member States will have to define sampling programmes, pursuing two different aims:

- to estimate infection prevalence in different animal species and categories;
- to follow trends over time, in order to evaluate target achievement after the application of control measures.

From 2002 to 2004 baseline studies have been performed in the Veneto Region of Italy to define the prevalence of *Salmonella*, *Campylobacter*, antimicrobial resistance indicators in the most important animal species farmed and slaughtered in this area (cattle, pigs, chickens, turkeys, laying hens, rabbits), with the aim of evaluating methods for zoonoses legislation implementation, studying and defining a sampling system running “*in continuum*” and

detecting specific risk situations. The monitoring scheme applied allowed us to assess precisely the prevalence for different pathogens and animal species, and was adjusted after the first year of application in order to detect defined variations in prevalence with a reduced number of samples.

Poster number 29

Domestic and travel-related foodborne gastrointestinal illness in a population health survey

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Routine surveillance data underestimate incidence of gastrointestinal (GI) illness and provide little information on illness related to travel.

We analysed data from the 1998 Welsh Health Survey to estimate population incidence, and to examine risk factors for domestic and travel-related GI illness and factors associated with consulting a doctor. The survey comprised a self-completed postal questionnaire that was sent to 50,023 adults in Wales (a 2% population sample). It included the question 'Have you had stomach upset with diarrhoea in the past 3 months, which you think was due to something you ate?' and whether this occurred at home or abroad.

The response rate was 61.4% and there were 28,423 responses to the GI illness question available for analysis. Reported frequency of food borne GI illness in the three months before interview was 20.0% (95% confidence interval (CI) 19.5 to 20.4%; equivalent to 0.8 episodes per person-year), including 18.3% (95% CI 17.9 to 18.8%) domestic and 1.6% (95% CI 1.5 to 1.8%) travel-related. In the final model, sex, age group, marital status, self-reported health, long term illness, smoking and alcohol consumption were predictors of domestically-acquired illness, and employment status, self-reported health, smoking and alcohol consumption of travel-related illness. People with travel-related illness (11.9%; 95% CI 9.3 to 15.2%) were less likely to consult than those with domestic illness (16.5%; 95% CI 15.5 to 17.5%).

Foodborne GI illness is common but risk factors for illness and consultation differ for domestic and travel-related illness.

Poster number 30

General practitioner sentinel surveillance for traveller's diarrhoea

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Over 60 million visits abroad are now made from the United Kingdom each year. Traveller's diarrhoea (TD) is the most common health problem among international travellers. Much of the burden falls on general practitioners although very little is known about general practice consultations for TD.

A sentinel surveillance scheme of 30 volunteer general practices distributed throughout Wales (combined practice population 215,642; 7.5% of the population) routinely provides weekly reports of consultations for eight infectious diseases to the Communicable Disease Surveillance Centre. TD, defined as 'diarrhoea (three or more loose stools in 24 hours) starting whilst abroad or within seven days of return', was introduced as a new reportable infection in July 2002.

Between 1 Jul 2002 and 31 Oct 2004, there were 85 reports of TD, with peaks during the summer months. The mean annual rate was 16.9 consultations (95% confidence interval 13.5 to 20.9) per 100,000 population, with slightly higher rates in men. There was considerable

variation in rates between age groups with the highest rate (34 (95% CI 21 to 53) per 100,000) occurring in the 15-24 year age group and affecting both sexes equally. Most travellers had returned from Europe, predominantly Spain and the Canary Islands. However, about 1 in 5 travellers had visited intermediate or developing countries, including North Africa and India.

This study shows the feasibility of incorporating TD in a sentinel general practice scheme, and the possibility of collecting data that may help characterise population groups or travel destinations associated with higher risk.

Poster number 31

GLOBALISATION AND ZONOSSES

West Nile virus in Canada: Continuing to Ride the Learning Curve

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Background: The purpose of surveillance is to identify West Nile (WN) virus in birds, mosquitoes, or horses as early as possible so that steps can be taken to reduce the risk of exposure of humans to WN virus.

Methods: The 2004 mosquito season was the fifth season for which the Public Health Agency of Canada has been involved in national coordination, surveillance, and testing for WN virus. Surveillance activities for 2004, as in previous years, focussed on birds, mosquitoes, horses and humans. In 2004, a wide array of diagnostic protocols were utilized for front-line and confirmatory testing in the various species. Results were tabulated, mapped, and shared broadly with surveillance partners and public health personnel.

Results: During 2004, WN virus activity was reported in five Canadian provinces. This was based on positive test results from humans, dead birds, mosquitoes, and/or horses. Twenty-six (26) human cases were reported to the Public Health Agency of Canada: Quebec (3); Ontario (14); Manitoba (3); Saskatchewan (5); and Alberta (1). During 2003, 1494 human cases of illness due to WN virus were reported in nine provinces/territories, including ten deaths.

Conclusions: West Nile virus is here to stay in Canada. Public health will continue to focus their efforts on surveillance, education, prevention and response to this emerging disease. There was a considerable decrease in the level of WN virus activity between 2003 and 2004 in Canada. Several possible factors may have contributed to this observed decrease, and discussions are ongoing.

Poster number 15

Potential for hantavirus transmission in Great Britain

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Hantavirus is an important worldwide zoonosis, the incidence of which appears to be increasing. In north-west Europe, the serotypes associated with human infection are Puumala virus (PUUV), occurring in *Clethrionomys glareolus* (bank vole), and Dobrava virus (DOBV), occurring in *Apodemus flavicollis* (yellow-necked mouse). Both of these rodent species are present in Great Britain; however, there is currently insufficient evidence to confirm transmission of the disease to humans. This may be due to limited surveillance or

ecological/social scenarios that prevent or limit virus transmission to humans. This work investigates the current ecological scenario for PUUV transmission in north-west Europe and assesses the potential for hantavirus transmission in Great Britain.

An analytical review of human and rodent hantavirus outbreaks in north-west Europe, together with knowledge of the distribution and population dynamics of British mammal fauna in response to (a)biotic factors, has enabled an assessment of the potential for PUUV transmission to humans.

Climatic factors, such as temperature, rainfall and sunshine hours, are crucial to the occurrence of beech masting (large increases in beech nut production). Basing threshold criteria upon intensity of specified climatic factors, a quantification of the relationship between each factor enables the prediction of 'mast years' and, in turn, subsequent fluctuations in bank vole population and changing risk of potential hantavirus transmission.

The reasons for the apparent absence of Puumala hantavirus in Great Britain may be manifold. This paper discusses the likely contributory or confounding ecological risk factors that would promote or prevent transmission, and identifies key areas for hantavirus surveillance.

Poster number 19

Possible eco-epidemiology of mosquito-borne arbovirus transmission in Great Britain: an entomological perspective

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There is currently considered to be no transmission of mosquito-borne arboviruses to humans in Great Britain, despite a number of mosquito-borne arboviruses being endemic in other parts of Europe, where they are known to cause human disease. In light of the recent emergence of West Nile virus in the USA and Usutu virus in Austria, an understanding of the potential for arbovirus transmission in Great Britain. and the likely effects of climate change are an important consideration for studies into new and emerging vector-borne infectious diseases.

In Great Britain, Buckley *et al.* (2003) provided evidence that suggested the presence of West Nile, Sindbis and Usutu virus neutralising antibodies in British resident birds. In addition, earlier work by Chastel *et al.* (1985) provided serological evidence of Tahyna virus in small mammals in Devon. Great Britain has about 30 endemic mosquito species, several with seasonal abundance and other eco-behavioural characteristics predisposing them to serve as potential arbovirus vectors from birds and mammals to humans.

This poster reviews briefly the potential for transmission of these arboviruses and studies the possible eco-epidemiology of such mosquito-borne arbovirus transmission in Great Britain.. Information on mosquito and animal host distributions and seasonality has been incorporated with ecological habitat preferences to assist with understanding the likely spatio-temporal dynamics of arbovirus transmission in Great Britain to help direct any subsequent surveillance programmes.

Poster number 20

A Cluster of Melioidosis in A School in Sarawak, Malaysia, 2003

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Background: In September 2003, Sarawak Health Department received notification of three students from a school with melioidosis (caused by *Burkholderia pseudomallei*). The three

students were among a group of 57 students who participated in an outdoor telematch in the school field. Investigations were initiated to characterise the outbreak.

Methods: Retrospective cohort study was conducted for those who participated in the telematch. A comparative cross-sectional study was conducted among a group of 51 students (randomly selected) who did not participate in the telematch. Blood samples were taken for melioidosis serology (IgM/IgG) from both groups. Soil samples from school field were taken and analysed for *Burkholderia pseudomallei*.

Results: This is the first time that a cluster of melioidosis has been detected in Sarawak. Ten students (attack rate of 17.5%{all positive serology, 3 confirmed by culture}) had multiple abscesses over their body with onset of two weeks after the telematch. Twenty-one (58.8%)(telematch group) were found to be serology positive compared to nine (25.7%) of the non-telematch group. Attributable Risk Percent (serology positive) for the telematch group was 56.3% (baseline serology positive non-telematch = 43.7%). Twenty (21.1%) out of the 95 soil sampling points were positive for *Burkholderia pseudomallei*.

Conclusions: Detection of *Burkholderia pseudomallei* in soil samples taken from the school field indicate a high possibility that the source of infection was from the school field. Baseline serology positive of 43.7% was attributed to exposure of the students to *Burkholderia pseudomallei* not related to the telematch. Teachers, students and parents were given health education on prevention of melioidosis.

Poster number 32

The Human Animal Infections and Risk Surveillance group

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The Human Animal Infections and Risk Surveillance (HAIRS) group acts as a forum to identify and discuss infections with potential for interspecies transfer (particularly zoonotic infections). The meetings are chaired by the HPA Department of Emerging infections and attended by members from Defra (New, Endemic and Zoonotic Disease Division), VLA (Emerging Disease Programme and Food and Environmental Safety Programme), National Public Health Service for Wales, the Department of Health, Food Standards Agency and the Chair of the National Expert Panel on New and Emerging Infections.

The remit of the group includes:

1 Hazard Identification

Identify and review UK or international incidents of potential zoonotic implication including:

- ▶ Acute cluster or outbreaks
- ▶ Increasing trends of known infections/ syndromes
- ▶ New infections or undiagnosed syndromes
- ▶ Novel presentations of known conditions

2 Risk assessment

If potentially zoonotic incident or trend, HAIRS can recommend:

- ▶ Negligible potential risk to public health
- ▶ As above but will be monitored
- ▶ More information needed to assess the incident
- ▶ Formal risk assessment

3 Risk management

Reduce risk by:

- ▶ Identifying
- ▶ Selecting
- ▶ Advising or
- ▶ Implementing measures that would reduce risk to public health

4 Risk communication

- ▶ Monthly summary of notable events of Public Health significance

- ▶ Informing within participating Agencies
- ▶ Informing other relevant Agencies
- ▶ Inform UK Zoonoses Group
- ▶ Write up and communicate any qualitative risk assessments

Examples of the infections considered by the group and the process of risk assessment will be shown on the poster

*Members of the HAIRS group are:

Health Protection Agency, Centre for Infections: Dilys Morgan (Chair) David Brown, Kirsty Hewitt, Katri Jalava, Mandy Walsh; Centre for Emergency Preparedness and Response: Jolyon Medlock; Defra: Harry Bailie, Paul Gayford, Ruth Lysons, Giles Paiba; VLA: Graham David, Geoff Pritchard; FSA: Judith Hilton; NPHS Wales: Robert Smith; Department of Health: Maggie Tomlinson; NEPNEI: Chris Bartlett

Poster number 33

Surveillance for West Nile Virus in the Netherlands, 2002–2004

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Introduction and objectives: In October 2002, after the West Nile Virus (WNV) epidemic in the United States and reports on a changing epidemiology for flaviviruses in Europe, the National Institute for Public Health and the Environment (RIVM) launched a surveillance for WNV by monitoring patients with unexplained meningoencephalitis and conducting additional laboratory testing for WNV.

Methods: Because neurological illness of possible viral etiology other than acute flaccid paralysis is not notified in the Netherlands, RIVM 1) examined medical registration data of 104 Dutch hospitals covering 16.3 million persons to identify all discharge diagnoses for unexplained meningo-encephalitis; 2) examined data from 11 laboratories covering 2.5 million persons to study trends in submissions of cerebrospinal fluid (CSF) for virologic testing for common neurotropic viruses (e.g., herpes and enteroviruses); and 3) actively collected CSF samples from six virology laboratories for further exclusion of WNV infection.

Results: Hospital surveillance indicated that approximately 500 patients per year had meningitis or encephalitis (unspecified viral or unexplained) diagnosed. In 2002, 87% of CSF submissions tested negative for common viruses; none of these samples was tested for WNV. Samples that were subsequently collected by RIVM for further WNV testing (150 in 2002, 294 in 2003, 337 in 2004) tested negative for antibodies to WNV. At this level of testing, the probability to detect WNV meningo-encephalitis would have been 0.99 had there actually been five WNV-caused meningo-encephalitis patients among the 500 hospital patients but only 0.59 had there been one WNV-caused patient.

Conclusion: No endemic WNV transmission has been detected in the Netherlands since 2002. On the basis of available data, no substantial endemic transmission of WNV occurred. However, a limited outbreak of WNV meningo-encephalitis might not be detected. Ruling out WNV as an etiologic agent in all CSF samples when no common pathogen is detected would improve surveillance.

Poster number 34

Neuropathological studies of Japanese encephalitis virus in humans and the mouse model

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Zoonotic flaviviruses (*Flaviviridae*, *Flavivirus*) have grown in importance worldwide, with the increasing spread of Japanese encephalitis virus (JEV) across Asia, and West Nile virus (WNV) in America and Europe. The viruses are transmitted naturally among birds by mosquitoes, especially *Culex* species. For JEV, waterbirds, primarily egrets and herons (*Ciconiiformes*, *Ardeidae*) are important hosts, and pigs, which may have abortions, amplify the virus. Humans become infected following the bite of an infected mosquito. After a brief viraemia, the virus enters the central nervous system (CNS), but the means by which it crosses the blood brain barrier is not certain. We therefore conducted a neurohistopathological study of four fatal human JE cases and made comparisons with the mouse model.

In human material there were perivascular inflammation, punched out lesions (foci of malacia) and microglial nodules that are characteristic of JE. In addition, we saw damaged astrocytic foot processes and indirect evidence of endothelial cell damage (reduced Ulex staining and expansion of the rough endoplasmic reticulum) which may have contributed to impairment of the blood brain barrier. Oedema and demyelination were seen in the malacic foci and an increase in MHC Class II expression was noted in gitter cells, microglial cells and pericytes. A similar inflammatory infiltrate was observed in murine CNS tissue. In addition, axonal damage was detected in areas of inflammation by beta-amyloid precursor protein staining and, although small areas of malacia were observed, the characteristic punched out foci were not identified. Our preliminary study shows similar pathology in human disease and the mouse model and is consistent with JEV crossing the blood brain barrier by replicating in endothelial cells; damage to glial foot processes may also be important.

Poster number 43

Phylogenetic analysis of Japanese encephalitis virus from swine in the Philippines.

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Since it emerged in Japan in the 1870s, Japanese encephalitis virus (JEV) has spread across Asia and has become numerically the most important cause of epidemic encephalitis worldwide, with an estimated 50,000 cases and 15,000 deaths annually. This zoonotic flavivirus is thought to have originated from an ancestral virus in the Indonesia-Malaysia region and evolved there into four or five different genotypes, which then spread across Asia. The Philippines is geographically close to this region, but there is little information about JEV isolates circulating in this country. We therefore examined previously uncharacterised isolates of JEV from the Philippines to determine their genotype.

We determined the nucleotide sequence of the NS5 gene for six JEV strains isolated from pig serum in Luzon, Philippines between 1984-1986. The sequences were compared with representative data from other JEV strains, published in Genbank, and phylogenetic analysis was performed to determine the genotypes. The six strains had high sequence homology (99-100% at the nucleotide level), and all belonged to genotype III. This genotype has been found previously in the Philippines, and is the most widely spread JEV genotype. Why genotype III appears to spread most easily is not known.

Poster number 44

NEW AND EMERGING ZONOSSES

Response to re-emergence of brucellosis as a significant occupational zoonosis in Northern Ireland

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Background: An outbreak of bovine brucellosis in Northern Ireland which commenced in 1996 and peaked in 2002 when 1390 reactor cattle were destroyed is still ongoing. In the human outbreak there have been 101 cases between 1998 and 2004 with a peak in 2002 when 29 cases were reported. The establishment of a Brucellosis Advisory Group by the Health and Safety Executive for Northern Ireland sought to prevent this occupational zoonosis and to provide guidance to general practitioners on best practice in patient management.

Aims: To explore the best methods of providing guidance to primary care doctors on best practice in the diagnosis, investigation and management of brucellosis as part of an overall strategy to prevent and treat human disease.

Methods: A multi professional team was established to consider the content and format of the guidance.

Outcome: The team developed a Pathway of Care for general practitioners and an accompanying patient information leaflet. The Pathway describes the clinical features of brucellosis and the epidemiology of human and bovine infections and guides general practitioners through the stages of diagnosis, management and referral.

Conclusion: A multi disciplinary approach is necessary when a rare zoonosis re-emerges. In the period before eradication of the disease in animal hosts, systems which seek to prevent disease and enable its early recognition can be developed using an inclusive multidisciplinary approach.

Poster number 13

Analysis of the potential for survival and seasonal activity of *Stegomyia albopicta* in the United Kingdom using Geographic Information Systems

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The ability to lay non-desiccating eggs in tyres, coupled with the international trade in used-tyres, has enabled the Asian tiger mosquito, *Stegomyia albopicta* (formerly *Aedes albopictus*), to travel globally and become established in North, Central and South America, the Caribbean, Australasia, Africa and Europe. Concerns have been raised over its potential role in the transmission of arboviruses and *Dirofilaria* nematodes. Photoperiodically-induced egg diapause enables establishment of *St. albopicta* following its importation into northerly latitudes. A number of abiotic factors subsequently determine its seasonal activity, raising questions over its ability to establish and act as a disease vector in the United Kingdom (U.K.).

The U.K. imports >5 million used-tyre casings annually, and this seems the most likely route by which *St. albopicta* would be imported. The anthropophilic and container-breeding nature of *St. albopicta* could cause an urban human biting nuisance with the potential for involvement in human and veterinary disease transmission cycles. This paper addresses the likelihood for importation of *St. albopicta* into the U.K., and assesses, using a GIS-based model, the ability for *St. albopicta* to establish, and its likely seasonal activity. It also reviews the possible role of *St. albopicta* as a potential disease vector in the U.K..

The model predicts that abiotic risk factors would permit establishment of *St. albopicta* throughout large parts of lowland U.K., with at least 4-5 months of adult activity (May-September), being more prolonged in the urban centres around London and the southern coastal ports. Pre-emptive surveillance of possible imported *St. albopicta*, through a targeted approach, could prevent the establishment of this exotic mosquito and mitigate any subsequent human and animal health implications for the UK, either now or in the future.

Poster number 21

Antimicrobial resistance monitoring in animals in Switzerland

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According to directive 2003/99/EG, all EU member states and trade partners such as Switzerland will be required to implement monitoring programmes for antimicrobial resistance in bacteria of animal origin. Switzerland is currently developing such a national programme based on international recommendations and results of our own research projects.

Concerning resistance monitoring, the following design questions are addressed:

- Which animal species and production classes should be monitored?
- Which combinations of bacteria and antimicrobial substances should be considered?
- At which point(s) in the production chain should samples be collected?
- How many samples need to be collected at which level (herd, animal) to achieve a pre-defined precision of the result?

The Swiss monitoring programme will include information on healthy animals from beef and dairy cattle, pork, chicken and turkey production. Risk ranking and risk profiling are used to prioritise combinations of bacteria and antimicrobial substances. Efficacy and cost-effectiveness of samples collected from live animals, at slaughter, and meat at retail were compared. The programme will closely interlink with the monitoring of antimicrobial resistance in bacteria of human origin. In Switzerland, we also have a legal basis to systematically collect data on the usage of antimicrobial substances in animals. Relevant data can be obtained from importers, marketing authorization holders, medicated feed producers, veterinarians and farmers.

In this presentation, further details of the design issues of our resistance monitoring programme will be discussed.

Poster number 35

High-level fluoroquinolone resistant *Salmonella* Typhimurium in Japan

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Fluoroquinolones are antimicrobials that are commonly used for treatment of gastro-intestinal infections. Until recently, there have been a limited number of reports of high level fluoroquinolone resistant salmonellae, although the reports on salmonellae with decreased susceptibility to fluoroquinolones are increasing. Since 2000, we have identified more than ten cases infected with high-level fluoroquinolone resistant *Salmonella* enterica serovar Typhimurium (*Salmonella* Typhimurium). Their MICs to ciprofloxacin were 24 ug/ml or more. All but one had a total of three point mutations in quinolone-resistance determination regions (QRDRs) in GyrA and ParC; two in GyrA (S83F, TCC to TTC; and D87N, GAC to AAC) and one in ParC (S80R, AGC to CGC). One showed higher MIC to ciprofloxacin (>32 ug/ml), and had a total of four point mutations in QRDRs in GyrA, ParC and ParE; two in GyrA (S83F, TCC to TTC; and D87G, GAC to GGC), one in ParC (S80R, AGC to CGC) and one in ParE (S458P, TCG to CCG). Almost all of them showed indistinguishable or similar PFGE profiles. We also identified several high-level fluoroquinolone resistant *Salmonella* Typhimurium strains from animals, including cattle and pets. They had the same point mutations, and also showed similar PFGE profiles, as those observed in human isolates. These results suggest

that relatively clonal *Salmonella* Typhimurium strains with high-level fluoroquinolone resistance are prevailing in Japan.

Poster number 36

New and emerging Methicillin-Resistant *Staphylococcus aureus* (MRSA) in the horse.

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A preliminary survey was carried out in 2004 to investigate whether horses are carriers of methicillin-resistant *Staphylococcus aureus* (MRSA) in the UK. Sixty-seven horses were sampled at a large equine hospital and 41 other horses (privately owned and riding school horses) were also sampled.

Eight horses at the equine hospital were found to be nasal carriers of MRSA, with a further three horses with clinical infections due to MRSA. Staff at the hospital were also screened for MRSA, but none was found to be positive. Horses sampled outside the hospital were negative for MRSA. Methicillin-resistant coagulase-negative staphylococci (MR-CNS) were isolated from horses at the equine hospital, as well as outside the hospital.

MRSA isolates were confirmed by PCR for the *mecA* and *femA* genes and were found to contain the SCC_{mec} type IV gene cassette. The MR-CNS isolates had a different SCC_{mec} cassette from the MRSA, ruling them out as a likely source for the *mecA* gene. Restriction-fragment length polymorphism-pulsed-field gel electrophoresis (RFLP-PFGE) demonstrated five different MRSA strains from these horses, of which none was related to the two most common human UK MRSA strains, EMRSA-15 and EMRSA-16, or to the Canadian strain, CMRSA-5, which has been associated with human and equine infection in Canada.

The results from this study suggest unique or rare MRSA strains are present in the UK horse population. MRSA was not isolated from horses sampled outside the hospital. However, this may be a reflection of the small number sampled and/or that horses presented to the veterinary hospital may be subject to selective pressure due to treatment with antimicrobials.

Poster number 37

Antibiotic resistance in wildlife

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Antibiotic resistance is an important problem in farm animal and human medicine. The increasing prevalence of resistance is assumed to be largely due to selection through the use of antibiotics. There is considerable ignorance, however, concerning the sources of resistant strains and the genetic elements that encode resistance, and the dynamics and persistence of resistance under different antibiotic-use regimens. Here, we describe an investigation of the role of wildlife as sources of antibiotic resistance for domestic animals and man, and the likely sources and mechanisms of persistence of antibiotic resistance in wildlife in the absence of obvious exposure to antibiotics.

We have found that antibiotic resistance is common in the normal bacterial flora of wildlife, and that the prevalence varies between individual animals, host species, environment and time of year – but that there is no clear association with contact with livestock or the intensity of farming, both of which might be taken as proxies for exposure to exogenous antibiotics.

The antibiotic resistance genes in wild mammal isolates were most often the same as those most commonly found in domestic animals and human beings. This, with the identification of some resistance strains with identical PFGE profiles, suggests that transfer between wildlife and domestic livestock is possible. However, the ecology of resistance appears to be very dynamic, with evidence for some resistant strains of *Escherichia coli* having wide mammalian host ranges, but with resistance genes also moving regularly between host strains of *E. coli*.

Poster number 38

Rabies in NW England: Experience, Extent and Education

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Experience

Recently in Lancashire a sick bat was found by a member of the public. The bat died and was much later found to be infected with European Bat Lyssavirus type 2 (EBLV-2), which is closely related to classical rabies virus and is transmissible to humans via infected saliva, a bite or scratch. The bat handlers and the member of the public were given a course of rabies vaccine; none became ill. This is the second incident in the NW Region.

Extent

The Lancashire incident is the fourth time a UK bat has tested positive for EBLV-2 since 1996. EBLV-2 has not been found in the common Pipistrelle bats [*Pipistrellus pipistrellus* and *Pipistrellus pygmaeus*]. It is estimated that about 2% of the less common Daubenton's bats [*Myotis daubentonii*], which live near rivers or canals, roosting in the stonework of bridges, have specific neutralising antibodies to EBLV-2.

Education

The local health community was informed of both incidents and advice on prevention and management of exposed individuals given.

Following the earlier incident a scenario on rabies was developed for the NW Zoonoses Group [<http://www.northwest-zoonoses.info/>]. The increased awareness of rabies in the Group led to the lessons being incorporated in a national Standard Operating Procedures on Rabies, jointly developed by the Health Protection Agency and DEFRA.

The scenario has also been used locally and nationally in training. Further education to improve the awareness of at-risk groups such as fishermen and walkers on canal and river banks is planned. It is expected that such developments will also be able to be shared with other regions in the country.

Poster number 39

The ecology of some rodent-borne zoonoses

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We have been carrying out empirical (and theoretical) studies of pathogen dynamics in natural populations of wild rodents. As well as revealing the effects of host dynamics on infection, this research has demonstrated subtle but important effects of endemic pathogens on host demographic parameters, and enabled us to question hitherto untested, widely-made assumptions about the transmission dynamics of pathogens in natural populations. Furthermore, we have been able to quantify the transmission dynamics directly from data from natural populations, both within and between species.

The zoonotic pathogens studied include: cowpox virus, LCMV, *Anaplasma phagocytophilum* (granulocytic ehrlichiosis), and tuberculosis (*M. microti*). The techniques and concepts developed have recently also been applied to longitudinal studies of *Yersinia pestis* in wild rodents in Central Asia. Current studies, through a multicentre EU-funded study, also include hantaviruses, and the effects of environment on population and disease dynamics.

Understanding the ecology of infections in their natural hosts is essential if rational, effective and efficient control programmes are to be established, and conflicts with the need to conserve our natural biodiversity are to be avoided.

Poster number 40

Wild Rabbits as Potential Carriers of *Escherichia coli* VTEC

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Infections caused by verocytotoxigenic *Escherichia coli* (VTEC) 0157 have received much attention within the environmental and public health context. In 2001, a total of 1049 confirmed cases of VTEC 0157 were reported in the UK. In many instances, the routes of infection, such as poor butchering practices, direct animal contact, or human-to human transmission via the faecal-oral route, are quickly identified. However, the mode of infection may occasionally be less obvious.

In 2001, wild rabbits were newly implicated as a possible vector for the transmission of VTEC to humans. HSE became involved with an incident that prompted a wider study of the potential for rabbits to pass VTEC on to humans via exposure to contaminated rabbit droppings. Cattle faecal samples were taken from sixteen herds that lived in close proximity to wild rabbits. Analysis by culture and polymerase chain reaction (PCR) showed seven herds to be positive for *E. coli* 0157. Faeces were collected from individual rabbits at six farms at times of low (late winter) and high (summer) rabbit density. None of the 32 samples collected on two farms in late winter was positive for *E. coli* 0157, but eight out of 97 (8.25%) rabbit samples collected in summer were positive on four out of six farms. PCR analysis for VTEC *E. coli*, including non-0157, showed 20 (20.6%) of 97 samples to be positive. Our investigations indicate wild rabbits may carry VTEC including *E. coli* 0157 and suitable precautions are recommended to prevent human infection.

Poster number 41

Understanding the impact of biotic and abiotic factors on the distribution of *Ixodes ricinus* in Great Britain

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Emerging and re-emerging tickborne zoonotic diseases from resident wildlife and livestock, such as Lyme borreliosis, ehrlichiosis and babesiosis, have heightened concerns over diseases already endemic in our wild population, in addition to the potential introduction of exotic pathogens, resulting from international animal movements, increasing animal populations, climate change and natural importation and migration.

Ixodes ricinus is the most abundant and widely distributed tick in the British Isles and is vector for a number of bacterial, viral and protozoal pathogens of both medical and veterinary importance. We present an update to the historical distribution of this species, using data from historical records, published scientific literature and unpublished field studies. This has been supplemented with contemporary data gathered through a newly established 'tick watch' scheme.

Throughout its range, the distribution of *I. ricinus* is governed by specific environmental conditions that impact upon its survival and development, in particular microclimate and host abundance and distribution. Through field studies on Gower Peninsula, Wales, a better understanding of the impact of abiotic and biotic factors on the distribution and activity of *I. ricinus* have been developed.

These data have been used in conjunction with historical distribution data of *I. ricinus* to produce a predictive habitat suitability map, which identifies areas which may be more suitable for the establishment of *I. ricinus* and hence identifies areas of potential tickborne disease transmission.

Poster number 42