

in association with the Health Protection Agency

Antimicrobial resistance in human and veterinary medicine – one medicine, one problem?

Tuesday 2 October 2012, Royal College of Physicians, London NW1 4LE

Speaker Biographies



Name: Professor S Peter Borriello

Role: Chief Executive, Veterinary Medicines Directorate

Affiliation: FRCPath

Biography

Professor Borriello has held senior executive positions in human and in animal health following a successful research career. National laboratory reference work for both human and animal pathogens, and national surveillance for human pathogen resistance have been within his areas of responsibility in the past, and veterinary antibiotics and resistance surveillance are part of his current responsibilities. He is a Fellow of University College London, a holder of a number of university chairs in human and veterinary disciplines, chair of a number of national and international committees, and the newly appointed Editor-in-chief of the *Journal of Medical Microbiology*.



Name: Professor Peter Davey

Role: Lead for Clinical Quality Improvement

Affiliation: Division of Population Health Sciences, Medical Research
Institute, University of Dundee

Biography

Professor Davey trained in Infectious Diseases in Birmingham and completed an MD at the University of London before being appointed to a Senior Lectureship in Clinical Pharmacology and Infectious Diseases at the University of Dundee in 1986.

He has over thirty years of experience in research on the outcomes of antimicrobial chemotherapy and the relationships between prescribing and resistance (<http://medicine.dundee.ac.uk/staff-member/professor-peter-g-davey-0>). Professor Davey is the lead author for the Cochrane Systematic Review of Interventions to Improve Antibiotic Prescribing Practice for Hospital Inpatients. He is Education Secretary of the British Society for Antimicrobial Chemotherapy and was President from 2006-9.

Title of talk

The history of restrictions and their effectiveness in human usage

Abstract

- Collateral damage to the normal bacterial flora of the human body leading to infection with antibiotic resistant bacteria and with *Clostridium difficile* is an inevitable consequence of any antibiotic use.
- The first aim of antibiotic stewardship must be to ensure the rapid identification and effective treatment of patients with bacterial infection who will benefit from antibiotic treatment. The second aim is to minimise collateral damage by reducing unnecessary antibiotic use.
- In Europe progress has been achieved with reduction in unnecessary antibiotic use and in the prevalence of resistance in gram positive bacteria, especially methicillin resistant *S aureus* and penicillin resistant *Streptococcus pneumoniae*. However, resistance is increasing alarmingly in gram negative bacteria.
- *Clostridium difficile* infection is a powerful stimulus to prudent antibiotic prescribing because in comparison with antimicrobial resistance it is a more immediate threat to the health of antibiotic users.
- Public and professional education about antibiotic resistance should focus on effective actions to reduce resistance through prudent use of antibiotics and good infection control practice.
- Significant progress has been made with persuading prescribers to use older, narrow spectrum antibiotics with lower risk of collateral damage. The focus now needs to shift towards reducing exposure to antibiotics by reducing both the number of people who take antibiotics and the duration of treatment.
- Antimicrobial Management Teams are effective provided that team members have dedicated time for antibiotic stewardship in their job plans. There is still insufficient integration of antibiotic stewardship with infection control at the operational level.
- In Scotland we have addressed these issues by embedding antibiotic stewardship within a national plan for improvement in the quality and safety of healthcare and applying the model for improvement that is being used in the Scottish Patient Safety Programme.



Name: Professor Susan Dawson

Role: Head of School of Veterinary Science

Affiliation: University of Liverpool

Biography

Susan Dawson is a veterinary surgeon working at the University of Liverpool and is currently head of the vet school. Her research interests focus on infectious diseases in particular zoonotic infections and antibacterial resistance. She was a member of the Veterinary Products Committee for 10 years until the end of 2011 and was a veterinary representative on ARHAI (antibiotic resistance and healthcare associated infections).

Title of talk

Antibacterial resistance in companion animals and potential risk to human health

Abstract

Companion animals have high levels of contact with humans and over half of households in the UK have a pet, with estimates of up to 7 million dogs and 1 million horses in the UK. Veterinary care of companion animals is on an individual basis and increasingly complex treatments and procedures are available in particular for dogs, cats and horses. Antibacterial treatment prescribing by vets is common with evidence from one study showing that a quarter of small animal consultations involve antibacterial prescribing. In the same study penicillins (including potentiated variants, such as co-amoxycylav) were the most commonly prescribed antimicrobial in dogs and potentiated sulphonamides in horses. Fluoroquinolones and 3rd/4th generation cephalosporins were prescribed to a relatively small proportion of dogs and horses (up to 5.6%).

Cross-sectional studies of dogs and horses show the overall antibacterial resistance in faecal *E.coli* in dogs and horses is relatively high. In both dogs and horses, *E. coli* were most commonly resistant to ampicillin, tetracycline and trimethoprim, with a much lower prevalence of resistance amongst *E. coli* to co-amoxycylav and the fluoroquinolones. The prevalence of ESBL-producing *E.coli* in dogs in the community (0.5%) and in the vet visiting population (4.1%) is low. Hospitalised horses were found to have a higher prevalence of ESBL producing *E.coli* (53.4%).

Low carriage rates of MRSA have been found in healthy dogs and horses although epidemics can occur in sick animal populations.

Due to the high degree of contact between companion animals and humans then there is a risk of transfer of antibacterial resistance between the two species.



Name: Professor Ross Fitzgerald

Role: Professor of Molecular Bacteriology

Affiliation: The Roslin Institute, University of Edinburgh

Biography

Ross Fitzgerald is Professor of Molecular Bacteriology at The Roslin Institute, and Edinburgh Infectious Diseases, University of Edinburgh. He joined the University in 2004 and established the Laboratory for Bacterial Evolution and Pathogenesis which investigates the biology of clinically important species of staphylococci. In particular, his group is currently using next generation sequencing as a platform for tracing *S. aureus* evolution including host-switching events, and investigating the molecular basis of *S. aureus* pathogenesis. A major goal is the translation of fundamental discoveries into novel approaches to controlling infectious disease.

Title of talk

Staphylococcus aureus host-switching events and the evolution of antibiotic resistance

Abstract

Staphylococcus aureus is a major human and animal pathogen responsible for considerable morbidity, mortality and economic loss. In particular, strains of *S. aureus* which are antibiotic-resistant have emerged in both human and animal hosts. Here I will present recent studies of *S. aureus* host jumps between humans and animals which have led to the emergence of new pathogenic clones. The implications of these findings for veterinary and public health will be discussed.



Name: Mr Nigel Gibbens

Role: Chief Veterinary Officer UK

Affiliation: Defra

Biography

Nigel Gibbens is the UK's Chief Veterinary Officer. He was appointed in May 2008 following previous experience in the State Veterinary Service and in policy roles on international trade, TSE research, surveillance and controls, animal welfare and international relations co-ordination for Defra's Food and Farming Group.

Prior to joining the UK government services in 1990, Nigel worked in private practice in his early career and in Government veterinary services in Belize and Yemen.



Name: Professor Stephen Gillespie

Role: Sir James Black Professor of Medicine

Affiliation: University of St Andrews. RCPATH RECP(Edin)

Biography

Professor Gillespie graduated in Medicine in 1908 from the Queen's University Belfast. After clinical training at the Royal Victoria Hospital he was appointed Mercers' Lecturer in Clinical Tropical Medicine (London School of Hygiene and Tropical Medicine) and subsequently Senior Lecturer at the Royal Free Hospital School of Medicine. In 2010 he was appointed as the first holder of the Sir James Black Chair of Medicine at the University of St Andrews. Professor Gillespie's research focuses on the

evolutionary biology of antibiotic resistance and developing new treatments for tuberculosis.
Honorary Consultant Microbiologist at the Victoria Hospital Kirkcaldy.

Title of talk

Antimicrobial resistance: biology and evolution

Abstract

It is now widely recognised that resistance to antibiotics represents a major threat to human health. If we are to generate effective plans to combat it an understanding of the biology of resistance will be required. This talk can provide only a broad overview of the evolutionary biology of resistance because each interaction between a bacterium and an antibiotic reflects a separate biological system.

There are four broad stages whereby resistance is fixed in the bacterial population and distributed globally. The first stage is resistance acquisition that can occur via gene acquisition or gene modification. The dynamic balance between the benefit of resistance and the physiological defines the outcome of this process as it does the adaptation to the new gene or modified gene. We are now starting to understand the molecular mechanism of adaptation with examples of compensatory mutations in related genes.

Resistance determinants can also be transmitted between organisms of the same and of different species as the gene pool of many bacteria is global. Laid on top of this transmission network is the spread of resistant organisms in the human population. Through this mechanism we have seen, for example an inexorable rise in multiple drug resistant tuberculosis and the rate spread of metalloβ-lactamses in a very short time.

Evolution is a slow process but the selective pressure of antibiotics provides a “turbo boost” accelerating the acquisition adaptation and transmission of resistant determinants. It is only by unravelling and understanding the complexity of these biological relationships that we will be able to deliver the public and animal health policies to address the issue.



Name: Professor Peter Hawkey

Roles: Professor of Clinical and Public Health Bacteriology, Lead Public Health Microbiologist for West Midlands. Consultant Medical Microbiologist

Affiliations: University of Birmingham, Health Protection Agency West Midlands Public Health Laboratory, Birmingham NHS

Biography

Peter Hawkey is a practising Clinical Microbiologist and Regional Microbiologist for the West Midlands HPA as well as holding the Chair in Clinical and Public Health Bacteriology at the University of Birmingham. His research has centred on developing and taking findings in molecular microbiology of bacteria (Coliforms, *S. aureus* and *C. difficile*) and applying them to understanding the epidemiology and diagnosis of infections in patient.

He was one of the first researchers to work on ESBLs and identified and characterised the world's second most common ESBL, CTX-M14 in China. Longstanding collaborations in China and India have resulted in studies on the global spread of antibiotic resistance. He is a member of ARHAI and the Defra Antimicrobial Coordination Group.

Title of talk

Antibiotic resistance in animal and man – how big a problem?

Abstract

The broad concept that the greater usage of an antimicrobial results in greater resistance is true but is a generalisation. Often in individual 'drug bug' combinations resistance may be rare or in contrast emerge quickly and become dominant. There are three specific interrelated hazards influencing the rate of emergence, namely antibiotic use, the bacterium and the antibiotic resistance gene(s). Resistance to some antimicrobials can represent a threat in some cases purely to humans (e.g. colistin resistance in *Acinetobacter baumannii*) or animals (e.g. tetracycline resistance in *Arcanobacterium pyogenes* in bovine mastitis). The recognition and control of resistance in those settings will have a very different approach to the more worrying spread of resistance genes amongst bacteria that either cause infections in humans (e.g. Zoonoses) or where commensal bacteria are shared between humans and animals (e.g. *E. coli* or *Staphylococcus aureus*).

A further factor is mobility in the environment of antibiotic resistant bacteria. Are they found in large numbers in material which is easily dispersed into the environment (e.g. faeces) or are they confined to a very localised area of infection or incapable of either survival or significant replication outside a mammalian host (e.g. *Legionella pneumophila*)? The degree of contact amongst human and animal populations is also an important factor in promoting or slowing the spread of antibiotic resistant bacteria. The most obvious example of this being the ease with which antibiotic resistance spreads in countries with poor quality drinking water and/or sewage disposal. The control of the use of antimicrobials in both human use and animals is generally good in Europe and North America but often poor in parts of Asia, Africa and South America. The increasing interconnections in the world both in terms of movement of people (carrying resistant bacteria in their gut or on skin) and food/food animals means that this problem needs to be considered on a worldwide basis rather than an individual town or country.



Name: Professor David Heymann

Role: Chairman, Health Protection Agency

Affiliation: Fellow of the Academy of Medical Sciences

Biography

David Heymann is Chairman of the Health Protection Agency, UK; Head of the Centre on Global Health Security, Chatham House and Professor of Infectious Disease Epidemiology, London School of Hygiene and Tropical Medicine.

He was the World Health Organization's Assistant Director-General for Health Security and Environment. He also represented the Director-General for polio eradication and was Executive Director of the WHO Communicable Diseases Cluster until 2003. Previously, he was Director for the WHO Programme on Emerging and other Communicable Diseases from 1995 to 1998. David Heymann is a Member of the Institute of Medicine of the United States National Academies and the Academy of Medical Sciences (United Kingdom).



Name: Professor Marc Lipsitch

Role: Professor of Epidemiology

Affiliation: Center for Communicable Disease Dynamics,
Department of Epidemiology, Harvard School of Public Health

Biography

Marc Lipsitch is Professor of Epidemiology and Director of the Center for Communicable Disease Dynamics at Harvard School of Public Health. His research studies the impact of human immunity

and antimicrobial use on pathogen populations and the resulting effects on human health. His research group uses a variety of approaches including in vitro and in vivo experiments, epidemiology, population genomics and mathematical modelling. Areas of particular interest include antigenic diversity in *Streptococcus pneumoniae*, antimicrobial resistance in a range of organisms, and seasonal and pandemic influenza.

Title of talk

How do we quantify the effect of animal antibiotic use on human health?

Abstract

Attempts to assess and quantify the impact of animal antimicrobial use on human health must consider at least three different domains: 1) direct ingestion of resistant human pathogens in food, leading to rapid disease onset; 2) transmission of resistant, human commensals/opportunistic pathogens from treated animals to farm workers or via food to healthy humans, who later experience an opportunistic infection; 3) human acquisition of resistant commensals/opportunistic pathogens that then transmit to other humans and/or transmit their resistance elements to other human commensals, before these cause disease, possibly in another host.

Our ability to quantify human health harms declines from domain 1, to 2, to 3, because of the distance in time, and possibly place and person, separating the exposure and the health outcome. In the first domain, multiple studies (summarized by SA McEwen, PubmedID 22849281) have estimated the morbidity and mortality effects of resistant infections (mainly *Salmonella* and *Campylobacter* spp.) that can be attributed to veterinary antimicrobial use; these cluster around estimates of 0.1-40 excess deaths per year in the US (where nearly all quantitative studies have been done) order 10^3 excess hospitalizations and 10^5 excess days of illness, with the largest estimates by far coming from fluoroquinolone use (prior to the US FDA ban on enrofloxacin in poultry). Despite significant uncertainty these estimates give reasonable orders of magnitude of the harm.

For domain 2, there has been genetic documentation of likely transfer of resistant commensals from animals to humans, but only a few studies have documented (and none appear to have quantified) the resulting disease burden.

Domain 3 is even harder to quantify, but important theoretical work by DL Smith and coworkers suggests that the most important risk of transfer of commensals and resistance elements may be in precisely those infections where human-to-human transmission of resistant organisms has not yet become common.

The goal of restrictions on animal use in this domain ought to be the reduction of opportunities for bacterial “research and development” of novel resistance mechanisms and/or novel resistant strains that may become future health problems in humans. While this is the most difficult potential outcome of animal antibiotic use to quantify, it is the one that has the greatest potential to harm human health.



Name: Dr Bharat Patel

Role: Consultant Medical Microbiologist

Affiliations: Health Protection Agency, Royal College of Pathologists

Biography

Dr Patel is a consultant medical microbiologist for the Health Protection Agency and an honorary consultant medical microbiologist for Barts Healthcare. He is a member of the HPA Healthcare associated infections and antimicrobial resistance Programme Board. He helped prepare the HPA/ARHAI Advice on Carbapenemase Producers: Recognition, infection control and treatment. He has advised NHS Trusts and infection prevention control teams on the management of outbreaks of antimicrobial resistance pathogens.

Abstract

Antimicrobial resistance is a major concern to those who manage infections in sick humans and animals. Emerging resistance to pathogens limits the ability of the clinician to manage serious infections and reduces the choice of antimicrobials available for treatment. This limits the potential scope of a good recovery and outcome in animals and humans. Judicious use and stewardship limits the development and spread of antimicrobial resistant pathogens until the appropriate strategies and resourcing is put in place for the development of newer agents.



Name: Professor Laura Piddock

Role: Professor of Microbiology

Affiliation: University of Birmingham

Biography

Professor Piddock's research investigates the mechanisms of action and resistance of antibiotics in bacteria isolated from people and animals. She is an elected Fellow of the American Academy of Microbiology and of the Institute of Biology. She was President of British Society for Antimicrobial Chemotherapy (2004-12), and is Vice-President until 2014. She was a member of MRC Infections and Immunity Board from 2004-10, and a Member of FSA ACMSF from 2004-2006. She has been an invited Expert Advisor to the WHO. Professor Piddock is the first BSAC Chair in Public Engagement, and is the Director of Antibiotic Action.

Title of talk

The worldwide dissemination of a single plasmid encoding an ESBL in bacteria isolated from people and animals.

Abstract

The treatment of infections caused by antibiotic resistant bacteria is one of the great challenges faced by clinicians in the 21st century. Antibiotic resistance genes are often transferred between bacteria by mobile genetic vectors called plasmids. In 2011, we reported the first complete sequence of a *bla*_{CTX-M-14} carrying IncK plasmid, pCT which carried a single antibiotic resistance gene, *bla*_{CTX-M-14}. PCR assays identifying novel features of pCT were used to screen CTX-M-14 producing clinical and veterinary *Escherichia coli* isolates from Europe, Asia and Australia for pCT-like plasmids. We showed that pCT-like plasmids carrying *bla*_{CTX-M-14} have successfully disseminated world-wide. This work provided a paradigm for using a complete DNA sequence as a platform to develop rapid, simple epidemiological tools to identify and trace the spread of large plasmids in clinically relevant pathogens.

It is commonly believed that removal of antibiotic pressure will reduce numbers of antibiotic resistant bacteria due to the perception that carriage of resistance incurs a fitness cost to the bacterium. Therefore, we investigated the ability of pCT to persist and disseminate in the absence of antibiotic pressure. Carriage of pCT was found to impose no detectable fitness cost to various bacterial hosts. An absence of antibiotic pressure and inactivation of the antibiotic resistance gene also had no effect on plasmid persistence, conjugation frequency or bacterial host biology indicating that plasmids such as pCT have evolved to impose little impact on host strains. Therefore, the persistence of antibiotic resistance genes and their vectors is to be expected in the absence of antibiotic selective pressure regardless of antibiotic stewardship. Other means to reduce plasmid stability are needed to prevent the persistence of these vectors and the antibiotic resistance genes they carry.



Name: Professor Stuart W J Reid

Role: Principal

Affiliation: Royal Veterinary College

Biography

Stuart Reid is Principal of the Royal Veterinary College, previously the Dean of the Faculty of Veterinary Medicine in Glasgow. Graduating from the University of Glasgow as a veterinarian in 1987, his research expertise is in quantitative epidemiology applied to human and animal health issues, at all levels of resolution.

With a focus on pathogens of zoonotic and public health significance, his efforts are directed towards understanding the distribution and dynamics of disease determinants at the population level, ensuring engagement with key stakeholders and science-based impact on disease control policy at national and international level. He has over 130 publications and over £15M in competitive grants to his name.

Title of talk

The ecology of antimicrobial resistance; diversity and dogma

Abstract

Antimicrobial resistance (AMR) of bacterial infections represents a serious threat to the health of both humans and animals. Whilst the use of any antimicrobial agent can select for resistance, the relative contributions from use in different populations to the overall resistance burden remain poorly understood.

Here, passive surveillance data on *Salmonella* Typhimurium DT104 isolated between 1990 and 2004 in Scotland were used to investigate the patterns and diversity of resistance, taking an ecological perspective. During the epidemic period, there were 5,200 isolates of DT104 from humans and animals forwarded to the Scottish Salmonella Shigella and Clostridium difficile Reference Laboratory. Phenotypic antimicrobial susceptibility data were used to examine the resistance phenotypes of these isolates and whole genome sequencing performed to investigate the resistance determinants in a subset of 148 isolates of DT104.

Ecological diversity metrics, which included all weightings of numbers of unique profiles and of abundance, demonstrated that the diversity of phenotypic resistance profiles was greater in the human isolates than in the animal isolates, a finding supported by the sequencing data. These results are consistent with the conclusions that (a) there may be more varied selection pressure for resistance in humans than animals in Scotland and (b) the local animals are unlikely to be the principle source of the resistance diversity observed in humans. Other sources of resistance that may be contributing to the diversity of resistance observed in the human bacterial population, such as imported food or the environment, were not measured in this study.

Whilst these conclusions relate to *S. Typhimurium* DT104 in Scotland, the focus on diversity, rather than prevalence, provides a different perspective on the issue of antimicrobial resistance and its emergence, and one that challenges some existing tenets.



Name: Professor Peter Silley

Role: Independent Consultant

Affiliations: MB Consult Limited and the University of Bradford

Biography

Peter Silley is a Microbiologist with a career in academia and pharma, working in human and veterinary medicine. MB Consult formed in 1999 to handle increasing demand for consultancy work. Professor of Applied Microbiology at the University of Bradford. He is a Member of CLSI Veterinary Antimicrobial Susceptibility Testing Sub-Committee and serves as a Member of the Scientific Advisory Board of the US *Healthy People, Healthy Animals Healthy Planet* program.

He works in Europe, North and South America and Japan and is conversant with the regulatory guidelines in these countries as relevant to microbial issues; direct experience of working with all major classes of antimicrobials.

For further information please see: www.mbconsult.com

Title of talk

AMR – the same for humans and other animals?

Abstract

If we are to have a meaningful discussion as we address the challenges of antimicrobial resistance then it is crucial we all speak the same language and understand the different issues facing human and veterinary medicine. Those involved with animals face a dual focus, that of resistance in target animal pathogens and also in foodborne pathogens and commensal organisms.

Fortunately, antimicrobial resistance in target animal pathogens is not a significant clinical problem; the major public health challenge is targeted at foodborne pathogens and commensals. In human medicine the focus is on pathogens. At the outset this seems straightforward, however within Europe, antimicrobial resistance for foodborne pathogens and commensal organisms is measured by the epidemiological cut-off value rather than a clinical breakpoint; this of course contrasts with antimicrobial resistance in human medicine which is determined by the clinical breakpoint.

The consequence of this terminology is that “resistance” rates in foodborne pathogens and commensals cannot be directly related to clinical resistance in human medicine. We are talking a different language and this inevitably leads to misunderstanding if we are trying to integrate respective data sets into a one health paradigm. The complexities of antimicrobial resistance cannot be addressed in generic terms; the issues vary, for example, according to antibiotic class and animal species, and between countries, even within Europe.

There is a clear need to harmonise methodology and analysis such that data can be used as one of the necessary inputs into risk analysis. If surveillance were truly harmonised then there is the potential for data to be appropriately used within risk analysis providing the opportunity to implement appropriate risk management steps as a response to the public health issues arising from changes in antibiotic resistance in food-borne pathogens and commensal organisms.



Name: Mr Christopher Teale

Roles: Veterinary surgeon and veterinary microbiologist

Affiliation: Animal Health and Veterinary Laboratories Agency

Biography

Chris Teale qualified as a veterinary surgeon from the University of Cambridge. He spent two and a half years in general mixed veterinary practice in Somerset and then Leicestershire before joining the

Veterinary Investigation Service of the Ministry of Agriculture, Fisheries and Food (now the Animal Health and Veterinary Laboratories Agency) as diagnostic veterinary pathologist investigating field cases of disease in farmed livestock. He subsequently specialised in veterinary microbiology and is currently head of antimicrobial resistance at AHVLA.

Title of talk

Flow of AMR phenotypes and genotypes – food-producing animals

Abstract

Resistance genes and resistant bacteria can be transferred between animals, humans and the environment. Selected examples will be presented to illustrate the transfer of resistant bacteria or bacterial resistance genes from animals to man via the food chain. However, there is also evidence for transfer of resistance genes in the opposite direction from man to animals via the environment/ sewage contamination. The conditions in which animals are kept can allow faecal-oral recycling to occur and thus organisms that are introduced at a low rate to the animal population can be amplified and returned to man via the food chain or other means (direct contact, environmental contamination). Examples of the spread of resistance genes from man to animals include:

1. Detection of rifampicin and fusidic acid resistance genes in animal wastes in Germany, although these compounds had not been used in animals.
2. Demonstration of aminoglycoside acetyltransferase AAC(3)II, conferring gentamicin resistance, in calves in France in 1986. This gene had emerged and been widely disseminated in French hospitals in the 1970s.



Name: Professor The Lord Trees

Roles: Emeritus Professor of Veterinary Parasitology, RCVS Past President

Affiliations: University of Liverpool, Royal College of Veterinary Surgeons

Biography

Professor the Lord Trees was made a life peer as Baron Trees of The Ross in Perth and Kinross, and was introduced in the House of Lords on 12 July 2012.

He is only the second veterinary surgeon, after Lord Soulsby of Swaffham Prior, to become a Peer.

Lord Trees is an Edinburgh graduate, qualifying from the Royal (Dick) School of Veterinary Studies in 1969. After graduation, he undertook a mixture of research posts at home and overseas, plus over a year in general practice, before completing his PhD in 1976, also at Edinburgh.

He was then appointed to Elanco Animal Health, first as Veterinary Adviser and then as its Head of Animal Science for the Middle East, Turkey and Africa.

In the early 1980s, Lord Trees moved into academia, starting as a lecturer in veterinary parasitology in Liverpool University's Faculty of Veterinary Science, based in the Liverpool School of Tropical Medicine. He was awarded a personal chair in veterinary parasitology and became Head of the Parasite and Vector Biology Division in 1994. He held the post of Dean of Faculty from 2001 until 2008.

Lord Trees has conducted research and published extensively on animal and human parasitic diseases, both endemic in Britain and in hot climates and has a particular interest in the "one world, one health, one medicine" agenda.

He is a former President of the Association of Veterinary Teachers and Research Workers, Vice-President of the European College of Veterinary Parasitology and Chairman of the Heads of Veterinary Schools.

He has been an RCVS Council member since 2000, and was President of the RCVS for 2009-2010.

From 2011, Lord Trees has been a member of the Executive Committee of the World Association for the Advancement of Veterinary Parasitology and is currently Chairman of the Moredun Research Institute.



Name: Professor David Walker

Role: Director of Public Health NHS Midlands and East

Affiliation: Department of Health

Biography

Professor Walker is the Regional Director of Public Health for the East Midlands and for the Midlands and East Cluster of SHAs. He has been a director in the NHS in a number of public health leadership roles for the last 12 years. Prior to this he was a Consultant in Communicable Disease Control in the North of England.

Professor Walker holds a number of academic appointments and has published widely in the field of communicable disease surveillance methodology. He is a former visiting scientist at the Centers for Disease Control in Atlanta, USA.



Name: Professor Elizabeth Wellington

Role: Professor of Environmental Microbiology

Affiliation: School of Life Sciences, University of Warwick

Biography

Professor Liz Wellington is involved in the study of bacteria in the environment. Research work focuses on understanding the ecological roles for specific bacterial activities including antibiotic production, resistance and exoenzyme production in soil and analysing the impact of lateral gene transfer on adaptation.

She reported coevolution of antibiotic resistance and production, in soil demonstrating that important environmental reservoirs of drug resistance exist, continue to evolve and will be augmented by inputs from anthropogenic sources such as sewage sludge, manure, wastewater treatment effluent and storm discharges. Due to co-selection, pollutants such as QACs act to increase prevalence of resistance genes.

Title of talk

The environment as a reservoir of antibiotic resistance: prevalence, selection and transfer

Abstract

E.M.H.Wellington, W.H.Gaze, G.C.A.Amos and P.M.Hawkey.

Antibiosis is an ancient phenomenon in soil and plays an important part in microbial interactions and antagonisms. It is now apparent that a wide diversity of resistance genes can be found in soil bacteria and a significant proportion of this diversity is due to the co-evolution of antibiotic producers with susceptible competing bacteria.

The soil 'resistome' is therefore constantly evolving due to natural selective processes combined with the impacts of anthropogenic inputs. It is the effects of the latter that cause concern as pollutants, waste products and faeces frequently contaminate land and could drive clinically important resistance in pathogens at an increased rate.

The predominance of antibiotic resistant bacteria in clinical environments is now also well documented and mechanisms of dissemination relate to transfer of mobile genetic elements and also the spread of resistant clones. Clinically important bacteria are frequently not indigenous to environments such as soil and water and it might be anticipated that they survive poorly and this would reduce the risk for dissemination of drug resistance to these environments.

Recent research has revealed that a number of factors are responsible for this not being the case. Resistance is disseminated in nature to indigenous bacteria and also pollution with chemicals such as antibiotics and quaternary ammonium compounds (QACs) reinforces selection for mobile elements such as integrons carrying QAC resistance genes often linked to antibiotic resistance gene cassettes.

Culture dependent and independent methods have highlighted class 1 and class 2 integron prevalence in bacteria from agricultural and QAC contaminated soils. Bacterial species found to carry integrons included clinically important pathogens, some of which displayed a multi antibiotic resistant phenotype. Further studies proved 3GC resistant bacteria were found in rivers downstream of sewage works and that CTX-M-15 mobilisation may occur in the environment as the majority of the genetic contexts found were novel.