HM Government

Zoonoses Report
UK 2015

June 2017

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Contents

Preface

This annual report on zoonoses in the United Kingdom (UK) includes reported cases of zoonotic infection in humans and animals during 2015. The data have been compiled from statutory notifiable or reportable disease reports, national scanning surveillance systems, national laboratory reporting, control programmes, research programmes and from data submitted to the European Community via the Trends and Sources Report under the Zoonoses Directive 2003/99, by agencies contributing to the Report.

This report is a collaborative publication produced by:

- Public Health England (PHE): lead organisation for this year's report
- Department for Environment, Food and Rural Affairs (Defra)
- Food Standards Agency (FSA)
- Department of Health (DH)
- Animal and Plant Health Agency (APHA)
- Health Protection Scotland (HPS)
- Scottish Government (SG)
- Scotland's Rural College (SRUC)
- Food Standards Scotland (FSS)
- Agri Food and Biosciences Institute (AFBI)
- Public Health Agency (PHA), Northern Ireland
- Department of Agriculture, Environment and Rural Affairs (DAERA, Northern Ireland)
- Public Health Wales (PHW)
- Welsh Government (WG)

Occasional corrections and amendments to the data, many of which are derived from dynamic databases, may occur following publication and will result in minor changes to subsequent annual reports.

We would very much appreciate comments and suggestions for items in future reports. Please send these to Zoonoses@phe.gov.uk.

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For safe food and healthy eating

Executive summary

This year's UK Zoonoses Report continues to include feature articles which highlight human and animal incidents and issues of public health significance which occurred during 2015, as well as a summary of reported cases of zoonotic infection in humans and animals. As usual, the report highlights significant trends in a number of zoonoses, and whilst these will continue to be monitored, they also emphasise the need for continued surveillance and collaboration between veterinary and human health practitioners. Interpreting trends in veterinary data in particular needs to be done with care, as the number of submissions to the various Government laboratories involved in supplying data for this report may vary from year to year for a number of reasons. These may include weather conditions, concerns about disease or financial factors, and are likely to affect the various livestock sectors and types of submissions in different ways.

Anthrax

During 2015, the first cases of anthrax in animals in the UK since 2006 occurred at a farm in Wiltshire. Human cases of anthrax are very rare and the risk to human health was considered to be very low, but all potential contacts were offered public health advice. A risk assessment considered animal and human health, and potential sources of the infection. Since anthrax had been confirmed on the farm previously (most recently in 1996), the local environment was considered to be the most likely source. Some specific restrictions on farm management have been implemented to reduce the likelihood of further cases.

Hantavirus

Hantavirus infections associated with pet rats have been highlighted in previous years, but in 2015 a cluster of locally acquired hantavirus infections occurred in south Wales. Three acute cases were epidemiologically linked by the transfer, breeding and husbandry of fancy and/or breeder/feeder rats. In addition, of 14 individuals identified through contact tracing, eight were seropositive for hantavirus and several reported a previously undiagnosed viral illness compatible with hantavirus infection.

Bovine TB

Bovine TB (bTB) continues to be one of the most serious animal health problems for the cattle industry in the UK. A total of 6,534 new bTB incidents were recorded in the UK during 2015, an increase from 6,115 new bTB incidents reported in 2014. The majority of incidents were reported in England (3,960), whereas Wales recorded the lowest number of new bTB incidents since 2008 (836). A total of 47,251 cattle in the UK were slaughtered as tuberculin skin or interferon-gamma (blood) test reactors in 2015, an increase of 12.9% from 2014 (n=41,869). In 2015, there were 42 human *M. bovis* cases diagnosed in the UK, a slight increase from 39 in 2014.

Gastrointestinal infections

Gastrointestinal infections in humans showed some interesting trends in 2015. Laboratory reports of *Campylobacter* in the UK (63,292) showed a decrease of 10% when compared with 2014, and the reporting rate decreased from 109.2 per 100,000 population in 2014 to 97.2 per 100,000 in 2015. This decrease was particularly noted in England where the rate of reported *Campylobacter* infections has decreased to the lowest since 2008. Northern Ireland continues to report rates lower than the rest of the UK. The FSA surveys to assess *Campylobacter* contamination of fresh chickens at retail, found that for the period Oct-Dec 2015, 59% of skin samples were positive for *Campylobacter* and 11% of chickens on sale had high levels of *Campylobacter* (over 1,000 cfu/g). These figures show statistically significant reductions in comparison to 74% and 19% respectively over the same period in 2014.

The number of cryptosporidiosis cases reported in the UK was greatly increased in 2015, with 6,149 cases. This is a 33.7% increase on 2014. This increase was observed across the UK and represented an excess of *C. hominis* cases between July and September, of whom a greater proportion than expected had travelled to Spain. There was also an excess of cases of *C. parvum* that began in November 2015. Investigations suggested that consumption of salad or sandwich items in a specific coffee chain, sometimes situated within supermarkets, was a likely route of exposure.

The number of reported human salmonella infections in 2015 in the UK (n=9,485) increased by 17% compared to 2014 (n=8,078), reversing a trend of a year-to-year decrease since 2006.

Laboratory reports of Shiga toxin producing Escherichia coli (STEC, also known as VTEC) fell to 867 compared to 1,186 in 2014. This is the first time the number of reports has fallen below 1,000 per annum since 2005. Although still greatly underdiagnosed, non-O157 STEC reports increased to 372 from 306, a modest increase compared to the tripling of numbers between 2013 and 2014.

Swine influenza

The number of diagnoses of swine influenza in pigs remained high in 2015, possibly because testing continued to be offered free of charge in some circumstances. All diagnoses in 2015 were in pigs from farms in England. The predominant strain of swine influenza circulating in the pig population in 2015 was again the pandemic strain which emerged in 2009 (termed A(H1N1)pdm09), whilst H1N2 was also reported. Co-circulation of multiple strains raises questions as to the long term dynamics of virus strain dominance or coexistence, particularly the potential for further genetic reassortment.

Introduction

Zoonoses are defined by the World Health Organisation as “diseases and infections which are transmitted naturally between vertebrate animals and man”. Transmission may occur by a number of routes, from indirect contact through food or drink to direct contact through occupational exposure on farms, from pets or through leisure pursuits. Data on zoonotic diseases in human and animal populations are sourced from laboratory-confirmed infections, enhanced surveillance schemes for specific zoonoses and notification of infectious diseases.

Notification and reporting of zoonotic diseases

Some (but not all) zoonotic infections are statutorily notifiable or reportable under veterinary and/or human health legislation. A list of these can be seen in Appendices 1 and 2. Relevant animal legislation includes: the Animal Health Act 1981 and its subsequent amendments; the Zoonoses Order 1989; the Specified Animal Pathogens (Amendment) (England) Order 2008; the European Communities Act 1972 and the Transmissible Spongiform Encephalopathies (England) Regulations 2010. The Devolved Governments have equivalent legislation.

Relevant human legislation includes the Public Health (Control of Disease) Act 1984, the Public Health (Infectious Diseases) Regulations 1988, the Public Health etc. (Scotland) Act 2008 and the Public Health Act (Northern Ireland) 1967. The Public Health (Control of Disease) Act 1984 was amended in 2010 to include a revised list of notifiable diseases, and for the first time a list of notifiable organisms in England and Wales. Similar lists for Scotland and Northern Ireland are included in the legislation cited above. In addition to the public health legislation, employers and the self-employed are required to report work-related incidents and diseases (including specified infections) to the Health and Safety Executive (HSE) under the Reporting of Injuries, Diseases, and Dangerous Occurrences Regulations (RIDDOR), 1995 (www.hse.gov.uk/riddor/).

The significance of notification differs in human and veterinary contexts. For human cases, registered medical practitioners in England and Wales have a statutory duty to notify the proper officer of the Local Authority (usually the Consultant in Communicable Disease Control (CCDC) of Public Health England (PHE) in England or Public Health Wales (PHW) immediately on suspected clinical diagnosis of a notifiable disease. Similar processes exist in Scotland and Northern Ireland though the list of notifiable diseases varies slightly by country. A summary is provided in Appendix 1. For more detail of the specified notifiable diseases and causative organisms see:

England: www.legislation.gov.uk/uksi/2010/659/contents/made
Northern Ireland: www.legislation.gov.uk/apni/1967/36/contents
Scotland: www.legislation.gov.uk/asp/2008/5/contents
Wales: www.legislation.gov.uk/wsi/2010/1546/contents/made

In animals, there is an obligation on any person having in their possession, or under their charge, an animal affected or suspected of having a notifiable disease (as listed in Appendix 2) to immediately notify the local Animal and Plant Health Agency (APHA) Field Office in England, Wales and Scotland (http://www.defra.gov.uk/ahvla-en/) or the local Divisional Veterinary Office in Northern Ireland. Procedures for notification and control of specified diseases are outlined in the legislation detailed above.

Surveillance and recording of zoonotic diseases

Humans

In addition to statutory notification of specified infectious diseases (as above), voluntary laboratory reporting (Appendix 3) and outbreak surveillance are conducted in each of the constituent countries of the United Kingdom (UK). Due to under-diagnosis and under-reporting, the cases recorded in national surveillance databases tend to be biased towards more clinically severe cases or outbreak related cases.

The national surveillance centres receive and collate reports of outbreaks of foodborne gastrointestinal disease from laboratories, local health protection teams and Local Authority environmental health (Public Protection) departments. The minimum dataset on each outbreak is then collected through a standardised questionnaire. Each year a summary report of the results of the investigations are reported as required under article 8 of the European Union Zoonoses Directive 2003/99/EC[1]. Surveillance provides information on specific risk factors associated with different pathogens and their trends. Enhanced surveillance schemes, either nationally or locally, provide information on specific aspects of a zoonosis.

Data from the zoonoses surveillance schemes are reported on national surveillance centre websites and for England and Wales quarterly in the Health Protection Report available at https://www.gov.uk/government/publications/common-animal-associated-infections-quarterly-reports-2015

[1] OJ L 325, 12.12.2003, p. 31. Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and Zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/11/EEC

Health Protection Scotland (HPS) and Northern Ireland's Public Health Agency (PHA) provide surveillance data on their websites:
www.hps.scot.nhs.uk/giz/index.aspx
www.publichealth.hscni.net/directorate-public-health/health-protection/surveillance-data.

Animals

In GB, livestock are monitored for the appearance of notifiable or novel diseases or changing trends in endemic diseases, including actual and potential zoonoses. This is done by the APHA, Scotland's Rural College (SRUC), Food Standards Agency (FSA) Operations and Food Standards Scotland (FSS) Operations. A similar function is performed by the Agri-Food and Biosciences Institute (AFBI) and the Department of Agriculture, Environment and Rural Affairs (DAERA) in Northern Ireland. In addition, information may be available from universities, veterinary research organisations and other private veterinary laboratories.

The APHA undertakes scanning surveillance for new and re-emerging animal diseases on behalf of the Department for Environment, Food and Rural Affairs (Defra) and the Welsh Government (WG). The SRUC performs a similar role for the Scottish Government (SG). Surveillance is achieved primarily through the collection, collation and analysis of disease data arising from material submitted for diagnostic purposes. Diagnostic samples are submitted to APHA Regional Laboratories and post mortem examination sites and to SRUC Disease Surveillance Centres. The results are entered onto the Veterinary Investigation Diagnostic Analysis (VIDA) database and collated into reports covering GB which are published monthly, quarterly and annually. The results are available at:
https://www.gov.uk/government/uploads/system/uploads/attachment_data/file/524585/pub-zoo0415.pdf. SRUC reports can be found at:
http://www.sruc.ac.uk/downloads/120613/monthly_reports. In Northern Ireland the AFBI publish quarterly Disease Surveillance Reports:
https://www.afbini.gov.uk/publications/animal-disease-surveillance-reports-2015.

Appendix 4 records results for zoonotic diseases identified via testing undertaken by Government veterinary laboratories. However many veterinary samples are submitted to private laboratories for diagnosis and so may not be included in the data in this report.

Risk assessment and control of animal associated threats to public health

The UK Zoonoses, Animal Diseases and Infections (UKZADI) is an executive group that enables effective join-up at a strategic level across UK Government and devolved administrations' public health interests and co-ordinates cross-departmental and intergovernmental action, contributing to effective and efficient protection of the public, and to minimising the risk of disease outbreaks and the impact of any outbreaks that do occur. The multi-agency, cross-disciplinary Human Animal Infections and Risk Surveillance (HAIRS) group acts as a forum to identify and assess infections with potential for interspecies transfer (particularly zoonoses) both nationally and internationally (if there is the potential to impact the UK). The HAIRS group also undertakes epidemic intelligence activities for potential threats outside the UK. In addition the Veterinary Risk Group (VRG) was established in response to the Anderson Review (Lessons Learned from the Foot and Mouth Disease outbreak in 2007) which recommended that government should establish a standardised and systematic process for identifying, assessing, characterising, prioritising and escalating unexpected animal-related threats. The VRG is a cross-directorate and cross-administration UK-level body which reports to the four UK Chief Veterinary Officers.

Control policies have been introduced to reduce the prevalence of pathogens in the food chain and other areas. These include the implementation of legislation relating to the production of drinking water and food. The FSA, PHE and devolved equivalents and Local Government Regulation operate national microbiological food sampling programmes and carry out studies focusing on particular foods, food processes and the production environment. This work enables potential food safety issues to be identified, as well as establishing current levels of microbial contamination. Local authorities also carry out food sampling activities.

Under the auspices of the FSA, the Epidemiology of Foodborne Infections Group and the Advisory Committee on the Microbiological Safety of Food (ACMSF) bring together UK surveillance data on humans, animals and food to consider foodborne risks.

Further information on the human aspects of infection is available from the PHE webpages: https://www.gov.uk/government/collections/zoonotic-diseases-zoonoses-guidance-data-and-analysis

Information on the animal aspects of infection is available:

https://www.gov.uk/government/collections/notifiable-diseases-in-animals
https://www.gov.uk/government/publications/salmonella-in-livestock-production-in-great-britain-2015
https://www.gov.uk/government/publications/non-statutory-zoonoses-disease-surveillance-reports-2015

Feature Article 1: Northern Ireland's *Brucella*-free status

Author: Paddy McGuckian (Department of Agriculture, Environment and Rural Affairs)

Northern Ireland gained Officially Brucellosis Free (OBF) status for *Brucella abortus* in 2015. It was also officially free of *B. melitensis*, *B. ovis* and *B. suis* which have never been recorded in the UK.

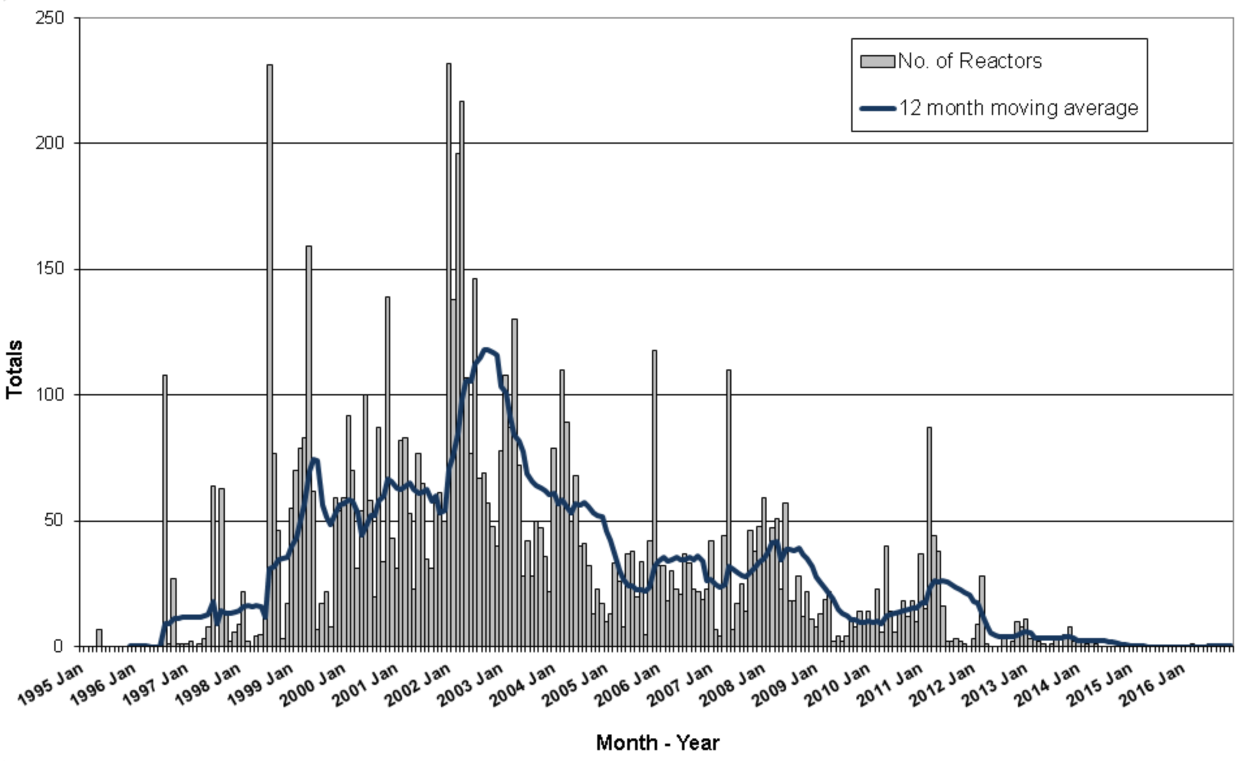
Screening for brucellosis comprises serological testing of eligible cattle, sampling at slaughter of cattle, and monthly testing of bulk milk tank samples from dairy herds. The testing commenced in 2001 and all dairy herds were included in the screening programme within the following year. The requirement for pre-movement testing was introduced in December 2004 and continued until its abolition in September 2015.

In Northern Ireland, DAERA carries out a programme of blood testing of all herds containing breeding stock and milk testing of all dairy herds. Routine brucellosis blood sampling was carried out on beef cattle herds on an annual basis until June 2015, when testing frequency was changed to a biennial basis. Dairy herds were routinely blood sampled biennially until November 2015, when the frequency of testing was decreased to once every five years. Monthly bulk milk enzyme-linked immunosorbent assay (ELISA) testing continues.

During the period 1990 to 1996, outbreaks of brucellosis were sporadic, with significant clustering restricted to the southern part of the province. During 1997, three primary outbreaks resulted in secondary and tertiary spread to more than 60 farms. There was a fall in brucellosis incidence in Northern Ireland from its peak (annual herd incidence of 1.43%) at the start of 2002 to a low point in October 2005 (0.34%). Subsequently there was a rise in herd incidence, however a marked decrease occurred from the end of 2008 to the end of December 2012 (Figure 1).

In 2015, 20,806 herds were checked and 584,988 animals were tested individually. No herds or animals were detected as positive. The annual herd incidence was 0.00% in December 2014 and the annual animal incidence was 0.000% in the same month compared to an annual herd incidence of 0.04% and an annual animal incidence of 0.001% for the same period in 2014. There have been no confirmed breakdowns since February 2012.

Figure 1. Brucellosis reactors in Northern Irish cattle herds (beef and dairy), January 1995-July 2014



Feature Article 2: Anthrax in cattle

Author: Brendan Walsh (Department for Environment, Food and Rural Affairs)

In October 2015, the first cases of anthrax in animals in the UK since 2006 occurred at a farm in Wiltshire. The sudden death of a single 6 year old suckler cow aroused suspicion of anthrax. Anthrax is a notifiable disease, and as such, the farm's private veterinary surgeon reported this suspicion to the APHA. APHA investigations could not rule out anthrax, and samples were taken for laboratory testing and submitted to PHE (Porton Down). The premises were placed under formal restrictions, a local footpath was closed as a precaution and the Local Authority (LA) was instructed to incinerate the carcase and arrange safe disposal of the ash.

[Image from Freeimages.com]

Within two days of the initial report, a Chief Veterinary Officer case conference was held to discuss the polymerase chain reaction (PCR) results which confirmed anthrax in the cow.

Three days later, a second dead bovine animal was found at the same premises as the first confirmed case. Samples were again taken, and results were strongly positive on PCR and microscopy of blood smear. Culture results were also positive. The incineration of this carcase was also carried out by the LA.

PHE advised that human cases of anthrax were very rare and the risk to human health was considered to be very low, however all potential contacts were offered public health advice. PHE informed their stakeholders and sent a draft risk assessment to the Vice Chair of the Local Resilience Forum. The Environment Agency, in liaison with Wessex Water, confirmed there were no current public water supply abstractions operating in the area. Neighbouring farms and local veterinary practices were advised of the situation and asked to remain vigilant for signs of disease.

Anthrax had been confirmed on the farm previously in 1996 and thorough epidemiological investigations took place to better understand the 2015 cases. These focused on the pasture where the cows were grazing prior to the deaths, and a former tannery site approximately 1.5 km upstream along a brook that ran through the premises. Following a site visit by the Environment Agency and the LA to a fenced off area close to the former tannery where excavation works had been reported, the

Scientific and Technical Advisory Cell concluded that this site was unlikely to be the source of the spores.

The identification of anthrax in UK animals had potential trade implications. APHA International Trade identified affected export health certificates. European Union (EU) trade (at a national level) was not impacted by the identification of anthrax. There were limited implications for exports to countries outside the EU, with the biggest impact being on hides and skins exports to China. One export certificate was permanently placed on hold. Other certificates were evaluated for use subject to restrictions including products not coming from within 50 km of the infected premises.

APHA worked with the FSA to identify the premises of origin for animals going into abattoirs to ensure traceability of relevant material to hide and skin yards.

No further animal cases occurred and there were no related cutaneous symptoms in the identified contacts. After 20 days with no new cases, restrictions on the farm were lifted. The following conditions remain in place on the affected areas of the farm for the next three years:

- mandatory vaccination of ruminants grazing the affected land
- forage produced on affected land may only be fed to vaccinated animals
- prohibition on use of affected land for arable purposes.

Feature Article 3: Hantavirus in pet ‘fancy’ and commercial rats bred for reptile food

Authors: Rob Smith (Public Health Wales)

Since 2012, a small number of confirmed symptomatic cases of Seoul hantavirus (SEOV) infection have been reported in patients with no travel history. Most of these UK-acquired cases have been in individuals exposed to: infected domestic (“fancy”) or other pet rats; rats bred to produce feeding material for reptiles (“feeder rats”); and wild rats. The presence of SEOV in UK pet and breeder rat populations has been reported, with evidence of hantavirus infection found in 26 of 79 (33%) pet rat owners tested [1].

In 2015, a cluster of locally acquired hantavirus infections occurred in south Wales. Three acute cases were epidemiologically linked by the transfer, breeding and husbandry of fancy and/or breeder/feeder rats.

The first case was a 26 year old male who became unwell in July 2015, was hospitalised twice and diagnosed with acute hantavirus infection. Follow-up determined that he had several hundred rats which he bred as feed for his reptiles and to sell, along with a small number of fancy rats, mostly via the internet. He was unaware of the potential risk of hantavirus and did not wear any protective equipment whilst cleaning the cages. A multiagency incident management team was convened by PHW, which included local authorities, APHA and PHE.

The infected individual agreed to euthanasia of his rats, and a sample of 30 rats was sent to APHA Weybridge for testing. Of these, 20 were Real Time PCR positive for hantavirus, and SEOV ribonucleic acid (RNA) was detected in the rat kidneys. Whilst this individual was ill, his father who had also looked after the rats became unwell in September 2015. He too was diagnosed with acute hantavirus infection. About the same time, a third case was identified who had both household contact with pet rats and occupational contact at a commercial breeder where his job was to clean and feed thousands of rats destined for the commercial reptile food market. The biosecurity was extremely poor with limited provision of personal protective equipment which was not routinely used.

A selection of rats from each of the premises implicated in the cluster was tested with an overall PCR positivity rate of 53% (48/91). All of the positive rats were older animals, and the majority were female. Partial gene sequence analysis indicated the SEOV strain to have a high degree of similarity to those detected in previous UK pet rat cases. Work is being conducted by PHE and APHA to compare human and rat-derived sequences. Additional testing of a further 14 individuals identified through contact tracing initiated by PHW revealed a further eight seropositive individuals. Some reported with previously undiagnosed viral illness compatible with hantavirus infection. Questionnaires administered to household contacts suggested high levels of close contact between rats and humans.

This incident has highlighted a number of issues for further consideration:

- reptile owners may breed rats as reptile feed
- the level of rat contact/exposure within households may be underestimated – there were indications of high risk exposures and free-ranging of the rats in all areas of the home for some cases
- the number of commercial rat farms in the UK is unknown but these establishments may not be uncommon
- there may be additional implications for the pet shop trade which may sell rats, both live and frozen, for reptile feed
- whilst the risk of hantavirus from frozen baby rats is likely to be low as vertical transmission is considered unlikely for SEOV, it is known that within households they may be thawed with resultant contamination of the kitchen environment with various zoonoses
- the HAIRS risk assessment on hantaviruses was updated [2].

References

1 PHE. Hantavirus infection in people with contact with wild and pet rats in England – preliminary results of a sero-surveillance study https://www.gov.uk/government/uploads/system/uploads/attachment_data/file/385205/Public_Health_England_Hantavirus_Sero-surveillance_study_Report_of_preliminary_results_final_version_180914.pdf

2 HAIRS. Qualitative assessment of the risk that Hantaviruses present to the UK population. https://www.gov.uk/government/uploads/system/uploads/attachment_data/file/496674/Hanta_RA_2016_PHE_format_FINAL_290116.pdf

Feature Article 4: Whole Genome Sequencing and *Salmonella* surveillance

Authors: Lukeki Kaindama, Tim Dallman and Lesley Larkin (Public Health England)

Whole Genome Sequencing (WGS) is increasingly being used in disease surveillance due to its unprecedented sensitivity and accuracy in identifying linked cases of infection. PHE now routinely performs WGS for several gastrointestinal pathogens, including *Salmonella* spp., *Shigella* spp., *Listeria monocytogenes* and pathogenic strains of *Escherichia coli*.

A key aim in the application of WGS for public health is to detect clusters of cases that are microbiologically linked. This is achieved by identifying Single Nucleotide Polymorphisms ('SNPs') across the genome, which allows the generation of a 'SNP address' for each isolate sequenced. This represents a particular genetic profile down to the single nucleotide resolution. Genetically related human cases of *Salmonella* can then be easily identified. If available, isolates from food or animal samples can also be assessed for potential links using the SNP address. Identified clusters can be analysed phylogenetically to study the variation between isolates and elucidate their ancestral relationships. Classical descriptive epidemiology is used to define the characteristics of the identified clusters and to inform hypothesis generation and subsequent analytical epidemiological studies.

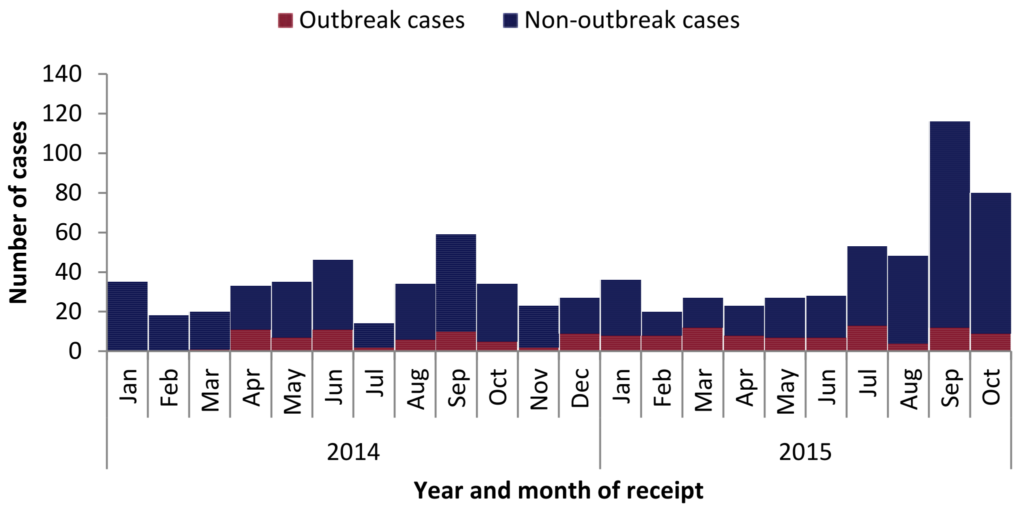
WGS is useful not only for detecting related cases, but also for excluding unrelated cases, providing robust case definitions to refine outbreak investigations. Assurance that cases are truly genetically related means that when exposure information is assessed, the strength of any associations is amplified. This makes hypothesis generation and the identification of a common exposure or vehicle of infection easier, giving greater confidence in the result so that appropriate control action can be taken. Recent examples of this were a *S.* Enteritidis phage type 14b (PT14b) outbreak in 2014 linked to imported eggs [1] and a *S.* Enteritidis outbreak in 2015 linked to snake ownership [2].

The investigation into the *Salmonella* Enteritidis PT14b outbreak was the first time WGS was used 'near real time' to investigate a multi-country outbreak of *Salmonella* and to inform public health control measures [1]. There were several outbreaks of *S.* Enteritidis PT14b identified, linked to a hospital and restaurants in England. At the same time, France was investigating a *Salmonella* outbreak associated with a German egg producer and there was also an outbreak of *Salmonella* in Austria. Both countries reported a matching Multiple Locus Variable-number Tandem Repeat Analysis (MLVA) profile to the one seen in the UK.

Overall, 322 human *S.* Enteritidis PT14b isolates from France, Austria, Germany, Luxembourg, the UK, environmental isolates from the UK hospital and restaurants, and egg and farm samplers from Germany were shown to be very closely genetically related with a minimum SNP distance between strains of 0 and a maximum difference of 23. The ability to establish this clear link between human disease cases, contaminated eggs and the farm premises resulted in robust public health protection action being taken under the requirements of EU *Salmonella* control legislation. The unique identifier provided by the SNP address also means that the process for detecting cases and monitoring the effectiveness of the interventions is greatly simplified.

Between January and December 2015, a cluster of 101 cases of *S.* Enteritidis PT8 with a specific genetic profile was reported, with cases geographically dispersed across all countries of the UK [2]. Upon interview, 30% of cases reported exposure to pet reptiles, and a case control study confirmed that exposure to snakes was the only variable independently associated with infection (Odds Ratio=810, 95% confidence interval (85-7715), p<0.001). Reptile feeder mice sourced from retail outlets in the UK tested positive for the outbreak strain. Detection of this outbreak would not have been possible without the use of WGS to delineate the outbreak strain from background numbers of S. Enteritidis PT8 as this is a common serovar in the UK (Figure 2). Retrospective analysis and sequencing of *S.* Enteritidis PT8 isolates provided evidence that transmission of this strain had been occurring undetected by normal surveillance procedures since at least 2011.

Figure 2. Distribution of *S.* Enteritidis PT8 cases by month of sample receipt, England, January 2014 – October 2015[2]



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[2] Routine phagetyping ceased in November 2015

The effective implementation of WGS for routine surveillance of gastrointestinal pathogens is not without difficulties. A large amount of data is generated for analysis, and requires a high-level of expertise to interpret it in combination with the epidemiological evidence. Since April 2014, 334 clusters of five or more genetically related isolates, clustering at the 5-SNP level, of *Salmonella* spp. have been detected and assessed. The majority of reported clusters are small, but all need to be assessed in order to effectively prioritise clusters that warrant further investigation. A further significant complication is that knowledge of the potential genetic variation within and between genetically related clusters of *Salmonella* spp that can be expected over time and under certain conditions defined by host, pathogen and environment interactions is still limited. However, despite these complications, the high resolution WGS typing of isolates at a national level for routine surveillance is clearly facilitating the improved detection of smaller or geographically widespread clusters, detection of outbreaks of genetically monomorphic clones of *S.* Enteritidis, and is helping to refine case definitions and focus outbreak investigations. Whole genome SNP typing is likely to continue to change the nature of and the approach to surveillance and outbreak investigations for many years to come.

References

1 Inns T, Lane C, Peters T, Dallman T, Chatt C, McFarland N, *et al.* on behalf of the Outbreak Control Team. A multi-country Salmonella Enteritidis phage type 14b outbreak associated with eggs from a German producer: ‘near real-time’ application of whole genome sequencing and food chain investigations, United Kingdom, May to September 2014. *Euro Surveill.* 2015;20(16):pii=21098. Article DOI: http://dx.doi.org/10.2807/1560-7917.ES2015.20.16.21098

2 Carrion, I. Uncovering the scale of a reptile associated salmonellosis outbreak in the United Kingdom (UK) 2015: a recent history. (2015) http://ecdc.europa.eu/en/ESCAIDE/programme/abstract-book/Documents/escaide-2015-abstract-book.pdf

Zoonoses A-Z

Anthrax (*Bacillus anthracis*)

Anthrax is caused by the bacterium *Bacillus anthracis*. Under certain environmental conditions *B. anthracis* can convert into a spore which may survive in the environment for many decades in an inert state. In this form the organism shows great resistance to the effects of heat, drying, ultra-violet light and many disinfectants.

Anthrax can occur in all mammalian species, and has also been reported in some birds. The clinical presentation in animals varies between species with three forms of anthrax recognised: peracute/ apoplectic, acute and chronic. Sporadic anthrax cases still rarely occur in cattle in the UK, presumably from exposure to anthrax spores present in soil and originating from cases that occurred decades earlier.

Anthrax infection in humans mainly causes one of three types of disease that affect either the lungs (inhalation/ pulmonary), the digestive tract (intestinal) or the skin (cutaneous). In 95% of naturally-acquired human cases, the infection is cutaneous. Recent human cases of anthrax in the UK have been associated with drums made from imported animal hides, or with contaminated heroin.

Infection in humans

There were no human cases of anthrax reported in the UK in 2015.

Infection in animals

There was one anthrax incident detected in animals in the UK in October 2015, when anthrax was confirmed in two cows at a farm in Wiltshire (see Feature Article 2).

Previously, the last outbreak of anthrax in animals in the UK occurred in 2006 when six cattle died on a farm in Wales (two confirmed and four suspected cases). The cause was thought to be river flooding and damage in a field that had been contaminated with anthrax during an outbreak three decades previously.

Avian and animal influenza

Influenza is a respiratory infection caused by viruses of the Orthomyxoviridae family. Animal-adapted influenza viruses do not readily infect people. However, spontaneous mutation or re-assortment of influenza virus genes between human and animal strains can occur. Some of these strains have the potential to be readily transmitted between people and can lead to pandemic spread in humans.

Avian influenza (AI), also referred to as ‘Fowl Plague’ or ‘Bird Flu’, is a disease of birds caused by type A influenza viruses. It is one of the most important poultry diseases as it is highly infectious, can produce significant mortality and can affect many species of birds. Avian influenza viruses are classified according to the severity of disease (pathogenicity) they cause in kept birds as either highly pathogenic or of low pathogenicity. Highly pathogenic avian influenza (HPAI) viruses can cause severe disease in poultry, with a high death rate (up to 100% in affected flocks). HPAI disease can develop so rapidly that birds may die without showing any previous signs of disease. Low pathogenicity avian influenza (LPAI) viruses result in milder, less significant disease, but can mutate into highly pathogenic strains. All HPAI and LPAI strains of H5 or H7 subtypes are notifiable in birds. There are other influenza A viruses that affect other species of animals. None of these infections are notifiable and different virus strains can cause varying degrees of disease in their specific animal host. Most generally cause mild disease in comparison to the severity associated with HPAI virus infection in poultry.

The highly publicised H5N1 HPAI virus strains have been responsible for considerable poultry losses across Asia and other parts of the world. In addition, other H5 and H7 strains have been observed in wild birds and poultry worldwide including H5N8 HPAI and H5N6 HPAI. As a result the UK has maintained a high vigilance for avian influenza with established surveillance systems, in response to the potential for sporadic incursions of influenza A (H5) viruses.

Infection in humans

Human cases of avian influenza in the UK are very rare. There were no human cases reported in 2015.

In 2006, there was one confirmed case of H7N3 in a farm worker. In 2007, there were four cases of AI in owners who kept birds, associated with a H7N2 poultry outbreak. All viruses were of low pathogenicity for poultry. There have been no deaths reported as a result of AI viruses in the UK.

Infection in animals

In 2015, avian influenza was detected on two occasions in England: LPAI (H7N7) in broiler breeder chickens, and HPAI (H7N7) in layer chickens.[3]

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[3] https://www.gov.uk/government/publications/reports-relating-to-recent-cases-of-avian-influenza-bird-flu

Avian influenza surveillance

Active surveillance of UK poultry for viruses of H5 and H7 subtypes has been undertaken annually since 2003. During 2015, none of the 327 holdings sampled in the UK had birds with antibodies to AI viruses of subtypes H5 or H7 (0/359 holdings sampled in 2014).

The UK undertakes EU-mandated AI wild bird surveillance activities on dead wild birds. Wild bird surveillance activities include patrols of designated reserves and wetlands around the UK and the investigation of wild bird 'mass mortalities' (defined as five or more wild birds of any species in any location in the UK). In Northern Ireland individual dead gulls, waders, ducks, geese and swans are investigated, in addition to mass mortality events. In 2015, a total of 479 wild birds were sampled in the UK. All of the birds sampled were found dead by the public or warden patrols of wetlands and reserves. H5N1 HPAI (notifiable in wild birds since 2003) was not detected.

Infection via the food chain

In 2015, the FSA carried out an updated assessment of the risk to consumers from AI viruses via the food chain.[4] The assessment concluded that for thoroughly cooked and hygienically handled and stored food, the risk of infection with AI viruses via handling and consumption is considered to be very low.

Non-avian influenza

The most significant non-avian influenza virus associated with animals in recent years has been swine influenza pandemic H1N1 virus which emerged in 2009 (termed A(H1N1)pdm09). There were 28 cases of swine influenza reported in the UK in 2015, compared with 32 in 2014. Twenty-five of 171 submissions (14.6%) in 2015 were in pigs from farms in England. This relatively high proportion may be because testing continued to be offered free of charge in some circumstances.

The predominant strain of swine influenza virus circulating in the pig population in 2015 was A(H1N1)pdm09. Endemic H1N2 was also reported and, since 2010, some 2010 H1N2-pdmH1N1 reassortants. Co-circulation of multiple strains raised questions as to the long term dynamics of virus strain dominance or coexistence, particularly the potential for further genetic reassortment. Swine influenza diversity across the globe is being driven by reassortment between the endemics and the pdmH1N1 strain.

[4] ACMSF. Assessment of the risk of avian influenza viruses via the food chain. https://acmsf.food.gov.uk/sites/default/files/acm_1192_avian%20influenza.pdf

Bovine tuberculosis (*Mycobacterium bovis*)

The *Mycobacterium tuberculosis* complex includes *M. tuberculosis, M. bovis* and *M. microti.* Bovine tuberculosis (bTB) is caused by *M. bovis*, a zoonotic organism that can give rise to tuberculosis in humans that is virtually indistinguishable from the disease caused by *M. tuberculosis,* the major cause of human tuberculosis (TB).

Bovine TB is one of the most serious animal health problems for the cattle industry in the UK. Over the last ten years the disease has cost the Government more than £500 million and could cost another £1 billion in the next ten years unless the current trends are reversed[5]. *M. bovis* infection has also been reported in many mammalian species, including other livestock, wildlife and domestic animals. In the UK, cattle and badgers are considered the main maintenance hosts, with other mammals regarded as spill-over or dead-end hosts.

A compulsory area eradication campaign for bTB began in GB in 1950 and in Northern Ireland in 1959. This was underpinned by routine screening of herds using the comparative tuberculin skin test, slaughter of all test reactors and cattle movement restrictions in infected herds. This programme gradually reduced the incidence of infection in cattle herds to a very low level by the early 1980s. However, since then, the incidence and geographical distribution of bTB in cattle herds (‘breakdowns’[6]) increased in England and Wales. This increasing trend accelerated immediately after the foot and mouth disease outbreak in 2001, during which the routine bTB testing and slaughter programme was suspended for almost ten months. However, since 2012 it appears to have stabilised in England and, in the case of Wales, reversed.

M. bovis is currently endemic in cattle and badgers in most of Northern Ireland and large tracts of south west England and south and mid-Wales. Herd incidence and prevalence of bTB are also very low in most counties of the North and East of England (Low Risk Area), where pre- and post-movement testing of cattle entering this region from the rest of England and Wales are in force. Scotland was declared an officially bTB free region of the UK by the European Commission in 2009 (Decision 2009/761/EC) and, as such, it also implements strict controls regarding the movement of cattle from the rest of the UK.

Human infection with *M. bovis* most often occurs through inhalation of aerosols containing the organism, but can also occur by eating or drinking unpasteurised milk and dairy products. The consumption of such products from infected cattle was an

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[5] Defra. The Strategy for achieving Officially Bovine Tuberculosis Free status for England. April 2014. https://www.gov.uk/government/uploads/system/uploads/attachment_data/file/300447/pb14088-bovine-tb-strategy-140328.pdf
[6] Incidents of bovine TB are also known as ‘breakdowns’, i.e. herds in which at least one animal was identified as a reactor to the tuberculin skin test or where one or more *M. bovis* culture-positive tuberculous lesions were detected by post-mortem meat inspection during commercial slaughter of a non-reactor animal.

important cause of childhood tuberculosis in the UK until pasteurisation became widespread in the mid-20th century.

Infection in humans

Over the last five years, *M. bovis* has accounted for 0.8% (193/23,646) of culture confirmed *M. tuberculosis complex* human cases notified in the UK. In 2015, there were 42 UK cases, a slight increase from 39 in 2014. The majority (n= 32) of *M. bovis* cases were reported from England, with a smaller number in Northern Ireland (n=5), Wales (n=3) and Scotland (n=2).

In 2015, approximately half of all *M. bovis* cases were male (n=22). Case numbers peaked in the 45 to 64 year age group (n=15) and only two cases were notified in children under 15 years old. Place of birth was known in nearly all cases, with the majority born in the UK (n=30/38). The majority of non-UK born cases were 15 to 44 years old (5/8), whilst 80.0% (24/30) of the UK-born cases were 45 years or older.

Infection in animals

In 2015, the GB registered cattle population comprised 76,124 herds and 9.59 million cattle. A total of 4,846 new bTB incidents were recorded (3,960 in England, 836 in Wales, 40 in Scotland, and a 'balancing amount'[7] of 10 further GB cases), a 2.7% increase on the 4,718 new bTB incidents recorded in 2014. Post-mortem evidence of bTB (characteristic lesions in test reactors and/or culture of *M. bovis*) was detected in 67% of the new GB incidents (1,118 confirmed slaughterhouse cases out of 1,665 slaughterhouse cases reported to APHA). A total of 36,255 cattle in GB were slaughtered as tuberculin skin test or interferon-gamma (blood) test reactors in 2015, an increase of 9.8% from 2014 (n=33,031). Nevertheless, the majority of individual cattle herds in the UK do have official bTB free (OTF) status at any given time (93% of all herds in GB at the end of 2015). The overall aim of the government's current bTB strategy for England is to secure OTF status for the whole of the country by 2039[8]. As an interim goal, the UK government intends to apply to the European Commission in 2018 for the Low Risk Area of the North and East of England to be recognised as an OTF region.

In 2015 Wales recorded the lowest number of new bTB incidents since 2008, with only 836 cases. Officially bTB free status was withdrawn from 475 Welsh herds during 2015 compared with 525 in 2014. The number of animals slaughtered in Wales as bTB test

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[7] A 'balancing amount' refers to any cases that are known to have occurred in GB, but which cannot be allocated to a specific nation.

[8] www.gov.uk/government/publications/a-strategy-for-achieving-officially-bovinetuberculosis-free-status-for-england

reactors[9] during 2015 was 7,553 compared with 5,851 in 2014. The number of suspect bTB cases from Welsh herds identified in the slaughterhouse in 2015 was 148 (of which 92 were bacteriologically confirmed as *M. bovis* infections), compared with 150 (96 confirmed) in 2014. In December 2015 there were 721 herds under movement restriction in Wales due to a bTB incident or overdue bTB test, compared with 854 in December 2014.

In Scotland, there were 40 new bTB herd incidents in 2015, down from 47 in 2014. There were 10 incidents where OTF herd status was withdrawn. Animals with either visible tuberculous lesions at slaughter or positive *M. bovis* culture were only detected in five of the 40 new herd incidents (12.5%) in 2015. The majority of these Scottish bTB incidents were associated with inward movements of cattle from high risk areas elsewhere in the UK and Ireland.

In 2015, the Northern Irish registered cattle population comprised 24,539 herds and 1.66 million cattle. During 2015, 1,688 new bTB reactor herds and 10,996 reactor animals were identified, and at the end of the year 2,993 herds were under movement restriction due to either a bTB incident or overdue bTB test, compared with 2,782 in December 2014.

One hundred and forty five incidents of M. bovis infection in non-bovine domestic animals (mainly sheep, goats, pigs, camelids, dogs, cats and farmed deer) and wild deer in GB were confirmed by culture during 2015. In Northern Ireland in 2015, samples from 6 non-bovine domestic animals were submitted with one pig confirmed *M. bovis* positive.

Further information

Epidemiology of *M. bovis* in humans in England, Wales and Northern Ireland (2002 – 2014):
https://wwwnc.cdc.gov/eid/article/23/3/pdfs/16-1408.pdf

Bovine TB infection status in cattle in GB in 2015:
http://veterinaryrecord.bmj.com/content/180/7/170

Cross Government guidance:
https://www.gov.uk/government/publications/bovine-tuberculosis-tb-public-health-management

The latest and historical statistics about TB in cattle in GB:
https://www.gov.uk/government/collections/bovine-tb

[9] TB reactors to the tuberculin skin test or the interferon-gamma blood test.

The GB data provided above on TB incidents in cattle were derived from the TB in cattle in Great Britain National Statistics, issued by Defra on 17 February 2017[10].

The bovine TB statistics are updated monthly and are available on the above link. All bovine TB data in this Defra TB database are provisional and subject to change as more data become available.

Brucellosis (*Brucella* spp.)

The cattle population of GB has been officially brucellosis free (OBF) since 1985. The history of bovine brucellosis in Northern Ireland is described in Feature Article 1. Northern Ireland was declared OBF on 6 October 2015[11].

Infections with *Brucella ovis*, *B. melitensis*, *B. suis* and *B. microti* have never been detected in the animal population in the UK. The marine species *B. ceti* and *B. pinipedalis* are occasionally isolated from marine mammals washed up on the coast around the UK.

Cases of *B. abortus* in humans have occasionally been acquired in Northern Ireland, and peaked in 2002 along with the peak of infection in cattle. These infections can be as a result of occupational exposure through the handling of infected afterbirths and products of conception (e.g. in farmers, veterinarians or abattoir workers). Otherwise, human cases of brucellosis are generally acquired outside the UK (usually *B. melitensis*) through the consumption of unpasteurised milk and dairy products.

Infection in humans

In 2015, 12 cases of brucellosis in humans were identified in the UK (Table 1), all of which were acquired abroad. This compares with 11 cases in 2014.

[10] https://www.gov.uk/government/uploads/system/uploads/attachment_data/file/577177/bovinetb-country-14dec16.ods
[11] Commission Implementing Decision ((EU) 2015/1784

Table 1 Reports of *Brucella* infection in humans in the UK, 2015

	England & Wales	Scotland	Northern Ireland	United Kingdom
B. abortus	1	0	0	1
B. melitensis	9	0	0	9
Brucella spp. unknown	1	0	1	2
Total	11	0	1	12

Infection in animals

The OBF status and trading rules underpin international trade and it is important to detect an incursion as quickly as possible. A programme of surveillance is therefore carried out in GB to ensure the OBF status is not compromised. Cattle surveillance includes targeted post-import testing of breeding cattle, risk-based investigations of cattle abortions and premature calvings, and testing of bulk milk samples from all dairy herds. An annual survey to demonstrate the absence of *B. melitensis* in sheep and goats, as required by EU Council Directive 91/68/EEC, is conducted in the UK. Evidence of absence of *B. melitensis* is also supported through the testing of submissions of abortion samples from sheep and goats.

No cases of brucellosis were detected in terrestrial animals in GB during 2015. Tests were carried out on: 37,847 bulk milk samples; 6,270 cattle abortions and premature calvings; 118 post importation tests of breeding cattle; and 6,294 tests of imported cows at their first calving following importation. The annual sheep and goat survey which tested 11,277 sheep from 801 flocks and 492 goats from 120 herds in GB and 4,155 sheep from 255 flocks and 141 goats from 28 herds in Northern Ireland, also found no evidence of *B. melitensis*.

In Northern Ireland in 2015, 584,988 eligible animals in 16,051 cattle herds were tested for *B. abortus*. No herds were positive (compared to eight herds (0.04%) in 2014, none of which were confirmed by bacteriological culture).

There were ten diagnoses of *Brucella* sp. in marine mammals in 2015. Nine were identified following positive culture results in Scotland and one from Wales. In 2014 there were five diagnoses, three from Scotland and two from England.

Campylobacteriosis (*Campylobacter* spp.)

The *Campylobacter* species of greatest public health importance are *Campylobacter jejuni* and *C. coli* (thermophilic campylobacters) which can be found in a wide range of livestock, poultry, and wildlife species. They do not generally cause disease in animals, apart from occasional abortion in sheep and enteritis in young mammals. *C. fetus fetus* is a common cause of abortion in sheep and may occasionally cause serious systemic disease in humans. Other *Campylobacter* species, such as *C. sputorum*, *C. hyointestinalis* and *C. lari* are present in mammals and birds in the UK, but are not generally considered of public health importance.

Campylobacter was first confirmed to cause human illness in 1972, and by 1986 it became recognised as the most commonly reported gastrointestinal pathogen in the UK. Transmission to humans is through the faecal-oral route, usually by the consumption of contaminated foods or water. *C. jejuni* accounts for approximately 90% of *Campylobacter* infections in humans. However, most laboratories do not routinely speciate strains isolated from human clinical specimens, so changes in relative incidence may not be detected.

Infection in humans

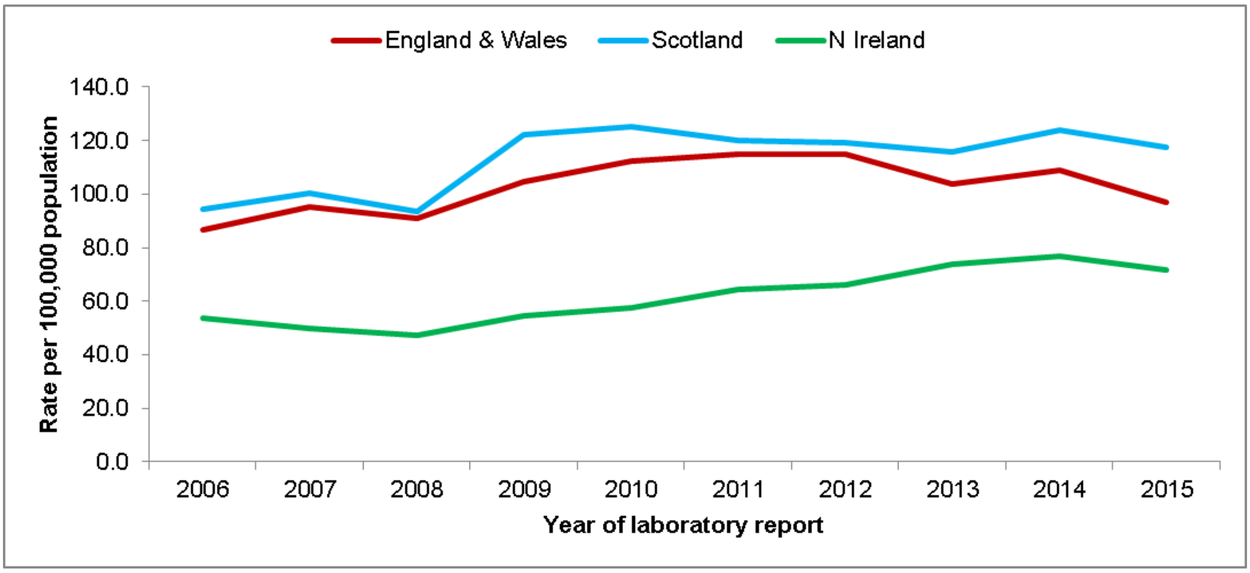
In 2015, there were 63,292 laboratory reports of *Campylobacter* in the UK, a decrease of 10.3% compared with 2014 (n=70,540). The reporting rate in the UK decreased from 109.2 per 100,000 population in 2014 to 97.2 per 100,000 in 2015. This decrease was particularly noted in England where the rate of reported *Campylobacter* infections has decreased to the lowest rate since 2008. Northern Ireland continues to report rates lower than the rest of the UK. The reasons for this are currently not known (Table 2 and Figure 3).

Table 2 Number of *Campylobacter* reports in humans 2013-2015

Year	England & Wales	Scotland	Northern Ireland	United Kingdom
2013	59,040	6,163	1,355	66,558
2014	62,494	6,632	1,414	70,540
2015*	55,697	6,275	1,320	63,292

*These figures are provisional

Figure 3. Rate of reported *Campylobacter* infections by region per 100,000 population, 2006-2015



The Second Study of Infectious Intestinal Disease in the Community established that the ratio of unreported human *Campylobacter* disease to reports to national surveillance is 9.3 to 1[12] (95% CI 6-14.4). This suggests that, in 2015, there were approximately 600,000 (with 95% CI, 383,574 – 920,578) *Campylobacter* cases in the UK. Since this is a population estimate, the confidence intervals need to be taken into consideration, but nevertheless, this is the most accurate measure we have of the unavoidable under-reporting to laboratory surveillance systems. This is required to give more accurate estimates of the true number of cases in the community.

In 2015, there were 11 foodborne outbreaks of campylobacteriosis reported in the UK, similar to the 12 outbreaks recorded in 2014. Seven outbreaks were associated with the consumption of poultry meat products, of which five were chicken liver parfait or pate and two were chicken meat dishes. One outbreak was associated with red meat (calves liver); another with mixed meats; one with pasta/noodle salad; and for one the implicated food vehicle was unknown. A summary of foodborne outbreaks by zoonotic pathogens, broken down by food vehicle category, is given in appendix 5.

Infection in animals

There were 265 confirmed cases of campylobacter identified in animals in the UK in 2015 (England and Wales: 182, Scotland: 64, Northern Ireland: 19). This compares with 185 cases in 2014, an increase of 43.2%.

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[12] Tam CC, *et al.* Longitudinal study of infectious intestinal disease in the UK (IID2 study): incidence in the community and presenting to general practice. *Gut,* 2012; 61(1):69-77.

Campylobacter isolates may not always be considered clinically significant in a disease investigation. Therefore, discrepancies may exist between the figures reported below (which relate solely to testing of individual bacterial isolates) and those provided above and in Appendix 4 (which relate to clinical diagnoses of campylobacteriosis in animals). The majority of livestock derived samples are from ruminant abortion investigations. There was a significant decrease in the incidence of campylobacter-associated abortion in sheep in GB in 2015 compared to 2014, despite comparable submission levels. Incidences of campylobacter fetopathy recorded by APHA appear to follow a cyclical pattern, with significant rises in infection rates observed every three years. This is thought to be due to immunity waxing and waning in the national flock.

Of the 186 ovine isolates from GB, 149 (80.1%) were confirmed as *C. fetus fetus (*a similar proportion to that seen in 2014), and 37 (19.9%) as a mixture of enteric strains (*C. jejuni*, *C. coli* and *C. sputorum* of those that have been typed). Of the 57 bovine isolates from GB, 16 (28.1%) were identified as *C. fetus venerealis intermedius* (31% in 2014) and seven (12.3%) were *C. fetus fetus* (12% in 2014). Thirty four (59.6%) were a mixture of enteric (thermophilic) strains: 24 *C. sputorum* (70.6%) and six *C. jejuni* (17.6%). The remaining four were unspecified. All isolates from pet animals in Table 3 were from testing undertaken by SRUC*.*

In Northern Ireland, there were 14 ovine isolates and 5 porcine isolates.

In addition to the data in Table 3, which relates to investigation of clinical disease, there was a survey of broilers at slaughter in 2015 as part of a structured official monitoring programme based on Decision 2007/516/EC. In the survey, 501 neck skin samples were tested, with 55 positive for *C. coli* and 299 positive for *C. jejuni*, and of 501 caecal contents samples were tested, 81 were positive for *C. coli* and 269 were positive for *C. jejuni.*

Infection in food

Campylobacter spp. are present in a significant proportion of animals and poultry entering slaughterhouses, resulting in potential for widespread contamination of meat (especially poultry meat) during the slaughter process and at retail. It was estimated that handling, preparation and consumption of broiler meat may account for 20% to 30% of human cases of campylobacteriosis, while 50% to 80% may be attributed to the chicken reservoir as a whole13. As a result, the FSA sees the reduction of Campylobacter in poultry as a key priority.

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[13] EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on Quantification of the risk posed by broiler meat to human campylobacteriosis in the EU. EFSA Journal 2010; 8(1):1437. [89 pp.]. doi:10.2903/j.efsa.2010.1437.Available online: www.efsa.europa.eu

Table 3: Number of *Campylobacter* spp. isolates identified by Government laboratories in animal derived samples in the UK in 2015

	Total units tested positive for Campylobacter	C. coli	C. jejuni	C. sputorum	C. upsaliensis	Campylobacter spp, unspecified	C. fetus subsp fetus	C. fetus subsp venerealis*	C. lari
Cattle	57		6	24		4	7	16	
Pigs	5		2			3			
Sheep	200	8	21	8		11	151		1
Goats	1						1		
Chickens**	2	1	1						
Cats***	27		4		21	2			
Dogs***	158	2	44		106	5			1
Macaques***	7					7			
Total**	457	11	78	32	127	32	159	16	2

* Also includes *C. fetus* subsp *venerealis* biovar *intermedius* (Cfvi) isolates, although not all laboratories test isolates to this level.
** There was a single diagnosis of *C. jejuni* and one of *C. coli* identified by APHA that were isolated from birds examined for diagnostic reasons. Both positive birds were submitted from farms in England.
*** SRUC routinely receives and tests diagnostic samples from companion animals in Scotland (and elsewhere in the UK) and this data has been included in the above table for interest, but is not included in appendix 4.

Each year, the FSA conducts surveys to assess campylobacter contamination of fresh chickens at retail[14]. For the period Oct-Dec 2015, 58.9% of skin samples were positive for *Campylobacter* and 10.7% of chickens had high levels of *Campylobacter* (over 1,000 cfu/g). These figures are both statistically significant reductions in comparison to 74.3% and 18.9% respectively over the same period the previous year (Oct-Dec 2014). In addition, 5.7% of packaging samples were positive for *Campylobacter* (compared with

[14] https://www.food.gov.uk/science/microbiology/campylobacterevidenceprogramme/retail-survey

7.3% Oct-Dec 2014) and 0.1% of packaging samples had a level *Campylobacter* above 1,000 cfu/swab.

To measure progress on the effectiveness of this work, a joint government and industry target to 'reduce Campylobacter in UK produced chickens by 2015' had been set, to reduce the most contaminated carcases (>1,000 cfu/g) in UK poultry houses from 27% to 10% by 2015[15]. The target was not achieved, but due to the measurable progress being made by the industry, it was agreed to roll the target over to the end of 2016. The FSA is leading a campaign (Acting on *Campylobacter* Together – ACT) to bring together the whole food chain to tackle *Campylobacter,* from farm to fork. Further details can be found at: www.food.gov.uk/actnow

Chlamydiosis[16] and psittacosis

Ovine chlamydiosis (*Chlamydia abortus*)

Infection of pregnant ewes with *Chlamydia abortus* may result in enzootic abortion of ewes (EAE). *C. abortus* may also cause abortion in goats and cattle.

Human infections appear to be rare but can cause serious disease in pregnant women, resulting in stillbirth or abortion. The main route of transmission to humans is through the inhalation of aerosols and contaminated dusts.

Infection in humans

The number of human cases of *C. abortus* occurring annually is uncertain as routine serological testing does not distinguish between *C. abortus* and other *Chlamydia* species. Diagnosis of *C. abortus* is dependent primarily on clinical suspicion in a person with positive serology for *Chlamydia* infection and relevant exposure to sheep/ lambing. There were no human cases reported in 2015 in the UK.

Infection in animals

In 2015, there were 336 incidents of abortion in animals due to *C. abortus* infection in the UK: 332 in sheep (Table 4) and four in cattle.

15 http://www.food.gov.uk/science/microbiology/campylobacterevidenceprogramme/
16 The nomenclature has reverted from chlamydophila back to chlamydia

Table 4 Laboratory confirmed reports of *C. abortus* in sheep and goats in the UK, 2015

		GB	NI	UK
Sheep and goat abortions submissions*		829	246	1075
C. abortus confirmed as cause of abortion	in goat abortion material	0	0	0
	in sheep abortion material	292	40	332

* To APHA and SRUC in GB, and AFBI in NI, where a diagnosis is reached

Psittacosis (*Chlamydia psittaci*)

Psittacosis (also known as ornithosis or chlamydiosis) is an infection caused by *Chlamydia psittaci*. It has been described in over 130 species of birds but is most common in psittacines (parrots and parakeets). Bird species of the economically important poultry industries, for example turkeys, geese and ducks, are also natural hosts.

Transmission of *C. psittaci* from birds to humans most often occurs via infectious aerosols, although it is not always possible to attribute individual cases to a particular source.

Infection in humans

In 2015, there were 24 laboratory reports of *C. psittaci* infections in the UK (compared with 32 cases reported in 2014): 22 cases in England and Wales and two in Scotland. No cases were diagnosed in Northern Ireland.

A lack of specific serological testing means that reported cases could have been caused by *Chlamydia* species other than *C. psittaci*.

Infection in animals

No cases of avian chlamydiosis (presumed *C. psittaci*) were diagnosed by government laboratories following testing of samples from UK birds during 2015 (compared to one case in 2014).

Further information

Chlamydiosis (Enzootic Abortion in Ewes) and risks in lambing season:
https://www.gov.uk/guidance/chlamydophila-abortus

Cryptosporidiosis (*Cryptosporidium* spp.)

Cryptosporidiosis is a disease caused by protozoan parasites of the genus *Cryptosporidium*. *C. hominis* is normally only isolated from humans, whilst *C*. *parvum* is found in both animals and humans. Together, these *Cryptosporidium* species are responsible for up to 96% of diagnosed cases in the UK and have different risk exposures and seasonal and geographical distributions[17].

Young calves (particularly those aged between 10-20 days) are considered to be the major animal reservoir for *C*. *parvum*, but infection can also be acquired from other species, particularly lambs and goat kids. *C. parvum* is considered to be endemic on the majority of cattle holdings in the UK, and is also common in sheep flocks and deer. Clinical disease (diarrhoea) is seen in young animals, but may not always be apparent. Human infection is acquired through the consumption of contaminated food or water, contact with infected animals, exposure to faeces (human or animal) in the environment or through person-to-person spread. Confirmed reports of cryptosporidiosis in humans in the UK follow a bimodal seasonal pattern, with higher incidence occurring in spring and early autumn. The spring peak consists predominantly of *C. parvum* cases, which are most likely acquired from animal sources. In contrast, the larger, early autumn peak has a greater rise in *C. hominis* cases, many of which are associated with travel outside the UK.

Infection in humans

The number of cryptosporidiosis cases reported in the UK in 2015 was 6,149. This is a 33.7% increase on 2014 (n=4,598). This increase was observed across the UK (Table 5) and largely comprised two separate, widespread events. The first involved an excess of *C. hominis* cases between July and September, of whom a greater proportion than expected had travelled to Spain. Enhanced surveillance and questionnaires did not identify any specific exposures.

The second involved an excess of cases of *C. parvum* that began in November 2015. Cases were more common in females, and were mainly aged 15-44 years. Investigations suggested that consumption of salad or sandwich items from a specific coffee chain, sometimes situated within supermarkets, was a likely exposure. The vehicle could have been a food item sold in coffee shops, including those operating inside supermarkets. Alternatively, a contaminated salad item might have been supplied to both coffee shops and supermarkets, explaining the geographical spread of this outbreak.

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[17] Chalmers RM, *et al.* Epidemiology of anthroponotic and zoonotic human cryptosporidiosis in England and Wales, 2004 to 2006. *Epidemiol Infect,* 2011; 139(5): 700-712.

Table 5 Number of Cryptosporidium reports in humans 2013-2015

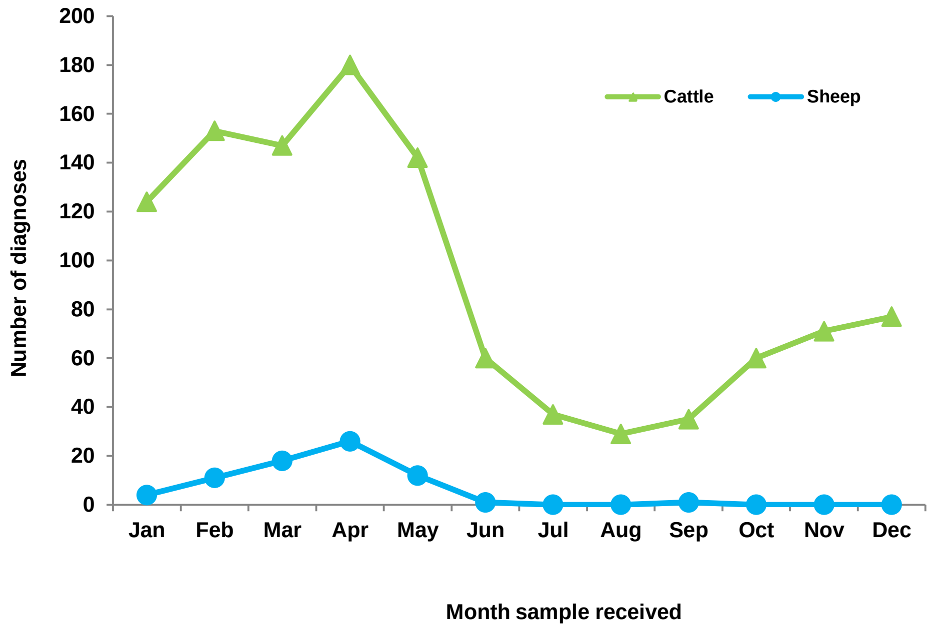
Year	England & Wales	Scotland	Northern Ireland	United Kingdom
2013	3,520	430	161	4,111
2014	4,023	432	143	4,598
2015	5,222	723	204	6,149

The Second Study of Infectious Intestinal Disease in the Community indicated that the ratio of human cryptosporidiosis disease in the community to reports to national surveillance is approximately 8.2 to 1[11] (95% CI 2.1 – 31.7). This suggests that in 2015 there were approximately 51,000 (with 95% CI 12,913 – 194,923) cases of cryptosporidiosis in the UK. Since this is a population estimate, the confidence intervals need to be taken into consideration, but nevertheless, this is the most accurate measure we have of the unavoidable under-reporting to laboratory surveillance systems. This is required to give more accurate estimates of the true number of cases in the community. In 2015, there were 15 outbreaks of *Cryptosporidium* infection. One outbreak was foodborne and 14 were non-foodborne (seven were associated with swimming pools and seven with petting/ open farms).

Infection in animals

Clinical cryptosporidiosis is relatively common in animals in the UK. In 2015, there were 1,191 (762 in GB and 429 in Northern Ireland) diagnoses of infection with cryptosporidia recorded by UK Government veterinary laboratories. Of these, 1,108 (697 in GB and 411 in Northern Ireland) were diagnosed in cattle; 73 (55 in GB and 18 in Northern Ireland) were diagnosed in sheep (Figure 4); and ten GB diagnoses were made in other species, mostly in goats.

Figure 4. Recorded diagnoses of cryptosporidiosis in cattle and sheep in UK, 2015



During 2015 APHA were involved in the investigation of three of the seven petting/ open farm-associated human outbreaks of *Cryptosporidium*:

- a protracted outbreak of *C. parvum* infection (two different subtypes), affecting six people who visited an open farm in South East England. The farm was in full compliance with the guidelines outlined in the Industry Code of Practice, however low numbers of *Cryptosporidium* oocysts were detected in faecal samples from lambs and goat kids. Veterinary advice was given on how environmental contamination could be reduced further.
- an outbreak of three cases of *C. parvum* infection in visitors to an open farm in North Wales. Low levels of Cryptosporidium oocysts were identified in lambs on the farm. Concerns relating to manure management and environmental hygiene were also raised, and advice was given in accordance with existing guidelines.
- twenty-nine confirmed or possible cases of *C. parvum* in visitors to an open farm in the Midlands. *Cryptosporidium* oocysts were identified in samples from lambs and further testing of these isolates confirmed the same subtype as the human cases (*C. parvum* IIaA17G1R1). There were concerns with the presence of diarrhoeic animals in animal contact pens, poor environmental hygiene and also inadequate separation of picnic areas and animal contact areas. Advice was given in accordance with existing guidelines.

Further information

An industry Code of Practice (CoP) on preventing or controlling ill health from animal contact at visitor attractions is available:
http://www.face-online.org.uk/CodeofPractice

Echinococcosis

Alveolar echinococcosis (*Echinococcus multilocularis*)

Echinococcus multilocularis is a tapeworm that causes alveolar hydatid disease. Its life-cycle normally involves foxes and raccoon dogs as definitive hosts and small rodents, particularly voles, as intermediate hosts. Dogs, cats and wolves may also act as definitive hosts to a lesser extent.

E. multilocularis has a wide geographical distribution across the Northern hemisphere throughout Europe, North America and Asia, although it is not known to be present in indigenous animals in the UK (rarely cases have been identified in imported animals). Dogs entering the UK are required to receive treatment for *E. multilocularis*. There is evidence that the distribution of *E. multilocularis* is spreading in northern Europe[18,19,20]. Given the large number of urban foxes in the UK[21], trends within Europe are of interest and are being closely monitored.

The European Commission adopted Regulation (EU) No 1152/2011 on 14 July 2011, as preventive health measures for the control of *E. multilocularis* infection in dogs[22]. It lays out the requirements for implementing a pathogen-specific surveillance programme regarding sampling, detection techniques and reporting which allows the UK, Ireland, Finland and Malta to maintain disease free status. Under this regulation, a programme is in place to carry out surveillance in foxes sufficient to detect not more than 1% prevalence with a confidence of 95% (at least 300 foxes sampled). As with previous surveys, the 2015 surveillance of the UK fox population (691 foxes tested) did not identify any *E. multilocularis.*

Cystic hydatidosis (*Echinococcus granulosus*)

Echinococcus granulosus is a tapeworm that inhabits the small intestine of canines and causes cystic hydatidosis, a less invasive disease than alveolar hydatid disease. The *E.*

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[18] Takumi K, *et al.* Evidence for an increasing presence of *Echinococcus multilocularis* in foxes in The Netherlands. *Intl J Parasitol,* 2008; 38(5):571-578.
[19] Berke O, *et al.* Emergence of *Echinococcus multilocularis* among red foxes in northern Germany 1991-2005. *Vet Parasitol,* 2008; 155(3-4):319-322.
[20] Vervaeke M, *et al.* Spatial spreading of *Echinococcus multilocularis* in red foxes across nation borders in Western Europe. *Prev Vet Med,* 2006; 76(3-4):137-150.
[21] Irwin, A. There are five times more urban foxes in England than we thought. New Scientist, 4 January 2017. https://www.newscientist.com/article/2116583-there-are-five-times-more-urban-foxes-in-england-than-we-thought/
[22] OJ L 296, 15.11.2011, p.6. http://eur-lex.europa.eu/JOIndex.do?year=2011&serie=L&textfield2=296&Submit=Search&_submit=Search&ihmlang=en

granulosus complex consists of 10 *E. granulosus* genotypes,[23] two of which are present in the UK in indigenous animals: a sheep adapted strain involving a dog to sheep life-cycle, and a horse adapted strain involving a dog to horse life-cycle.

The main cycle of infection in GB is between farm dogs (the definitive host in the UK) and sheep (the main intermediate host). Sheep acquire hydatidosis by grazing on pastures contaminated with dog faeces or by ingesting other contaminated feed. Cattle can also be infected with the sheep strain, but resultant cysts are usually sterile. Dogs are infected by ingesting animal viscera containing viable cysts.

Humans can act as an accidental intermediate host through direct contact with infected dogs or their faeces. The current incidence of human hydatid disease in the UK is considered to be very low. Over 95% of new cases identified in the UK are diagnosed in non-UK nationals and have a history of prior residence in, or travel to, countries where cystic echinococcosis is endemic.

Developing cysts may grow for 20 or more years before becoming large enough to cause a range of symptoms depending on the affected organ and the location of the cyst. This long incubation period means that new autochthonous cases may occur occasionally in people who have been exposed in the UK many years previously but who have remained asymptomatic for a substantial part of their lives.

Infection in humans

During 2015, 16 confirmed cases of hydatid disease in humans were reported in the UK (the same number as in 2014). Thirteen of the cases were from England and Wales (all imported infections) and three were from Scotland (travel histories unknown).

Infection in animals

In GB, *E. granulosus* is present in the sheep and cattle population. Hydatid disease in animals is not notifiable in the UK and the identification of the parasite in animal tissues is not reportable, however visual inspection for cysts is undertaken at abattoirs. Detection of the cyst at meat inspection requires the condemnation of all or part of the carcase and/ or the offal. As no definitive diagnoses of *E. granulosus* are made at abattoir, the FSA no longer report findings of suspected hydatid disease at post mortem. However carcase rejection figures for both sheep and cattle are routinely monitored.
In Northern Ireland, there were 3 cases of hydatid disease in sheep reported at abattoir in 2015,[24] and no cases were reported in 2014.

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[23] Boubaker G, *et al*. (2013) A Multiplex PCR for the Simultaneous Detection and Genotyping of the *Echinococcus granulosus* Complex. *PLoS Negl Trop Dis,* 2013; 7(1): e2017. doi:10.1371/journal.pntd.0002017
[24] Abattoir cases are not included in Appendix 4

Dog owners are advised to consult their private veterinary surgeon for specific guidance for their own animals (pets and farm dogs). Worming dogs regularly with an appropriate treatment remains highly effective and a key personal health protection measure.

Further information

Detailed information on hydatid disease control is available on the Welsh Government website:
http://gov.wales/topics/environmentcountryside/ahw/disease/hydatiddisease/?lang=en

Hantavirus

There are many different hantaviruses, some of which have a defined geographical distribution. They are rodent-borne and each is specific to a different host. They are not usually associated with overt disease in rodents (although domesticated animals can develop clinical signs with some hantaviruses), and once infected, the rodent may shed infectious virus for prolonged periods. The first human case of Seoul hantavirus infection in the UK was confirmed in 2012 (unspeciated hantavirus infections had been diagnosed previously).

Transmission of hantaviruses to humans occurs through the inhalation of infected animal excreta and saliva. Although some hantaviruses are associated with asymptomatic infections or mild disease, most can cause serious infections in humans ('haemorrhagic fever with renal syndrome' and 'hantavirus pulmonary syndrome'). Case fatality rates vary greatly with disease syndrome and specific viruses, ranging from 0.1% to in excess of 50%.

Infection in humans

In 2015, there were four confirmed cases of Seoul hantavirus infection in the UK. One case occurred in England with exposure from a pet rat. The other three occurred in a small cluster in Wales (Feature Article 3). This compares with four cases reported in 2014.

A retrospective data cleaning exercise has resulted in some changes to the historical data. New case numbers are given in Table 6 (Northern Ireland reported no cases between 2006 and 2015).

Table 6 Laboratory confirmed reports of hantavirus in UK residents, by travel-history

Year		2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
England & Wales	Indigenous		1					2	3	1	4
	Travel-associated					1				2	
Scotland	Indigenous									1	
	Travel-associated										
United Kingdom	Total		1			1		2	3	4	4

Infection in animals

Seoul hantavirus causes asymptomatic infection in rats, and there are no routine surveillance systems in place in the UK.

Hepatitis E

Hepatitis E virus (HEV) is an enteric virus which is found worldwide. It is endemic throughout Europe, including the UK. There are four main genotypes: genotype 1 is usually found in Asia and Africa, type 2 in Mexico, type 3 in North America and Europe, and type 4 in China. Types 1 and 2 are only found in humans while types 3 and 4 can infect humans and other animal species, particularly pigs and deer (although they do not appear to cause illness in these animals).

In humans HEV infection is usually a mild, self-limiting illness, however in rare cases fulminant disease (acute liver failure) may develop and can prove fatal. Clinical symptoms are variable and appear to be associated with the viral genotype. For example, genotype 1 is known to cause high mortality in pregnant women, while genotype 3 infections can progress to chronic hepatitis in immuno-compromised individuals, mainly among solid organ transplant recipients. Mortality in the general population is usually 1-3%.

In developed countries, including the UK, HEV genotype 3 is the indigenous genotype and is transmitted mainly through ingestion of undercooked products from infected animals. Most cases are sporadic, however occasional outbreaks have followed consumption of undercooked pork or deer meat, or uncooked shellfish. Other routes of transmission include transfusion of infected blood products.

Infection in humans

Hepatitis E cases have significantly increased in recent years, with 1,154 cases reported in the UK in 2015. There is a degree of under-reporting as many infections are asymptomatic and only confirmed cases are reported. Seroprevalence rates in the general population are high at around 13%[25] with data from modelling work and extrapolation of HEV-infected donors indicating up to 100,000 infections per year in England[26].

The majority of hepatitis E cases in the UK are indigenous. In 2015, 82.6% of cases (n=791) in England and Wales were assessed as being non-travel associated, compared with an average of 57.3% between 2006 and 2014 (Table 7). A large proportion of cases (45.7%, n=438) were in males over 50 years of age. There was no geographical clustering.

Table 7 Laboratory confirmed reports of Hepatitis E in UK residents, 2006-2015

Year	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
England & Wales	289	162	176	175	276	464	604	731	924	958
E&W: non travel associated cases*	175	63	72	79	145	252	430	512	762	791
Scotland	3	4	4	3	13	15	78	95	193	186
Northern Ireland**	0	0	0	0	0	1	0	1	9	10
United Kingdom	292	166	180	178	289	480	682	827	1,126	1,154

*Please note some numbers have been updated following a data cleaning exercise

**Northern Ireland does not routinely test for Hepatitis E

Molecular characterisation data of HEV genotype 3 viruses linked to indigenous infections in England shows that they divide into two phylogenetically distinct groups; group 1 and group 2. Since 2011 genotype 3 group 2 viruses have predominated[27]. Similar trends of increased HEV case numbers linked to genotype 3 group 2 (also known as 3c) have been reported from a number of other European countries[28].

The increase in indigenous cases and the observed viral shift or emergence of indigenous viruses not commonly circulating prior to 2010, suggests that there has been

[25] Ijaz S, *et al*. Indigenous hepatitis E virus infection in England: more common than it seems. *J Clin Virol,* 2009; 44: 272-76
26 Hewitt PE, et al. Hepatitis E virus in blood components: a prevalence and transmission study in southeast England. Lancet 2014; 384: 1766-73
[27] Ijaz S, *et al*. Indigenous hepatitis E in England and Wales from 2003 to 2012: evidence of an emerging novel phylotype of viruses. *JID,* 2014; 209:1212-18
[28] Adlhoch C, *et al*. Hepatitis E virus: assessment of the epidemiological situation in humans in Europe, 2014/5. *J Clin Virol,* 2016; 82:9-16

a change in the magnitude of risk of acquiring HEV in the UK. However, the question remains as to how the risks have been altered, with changes in animal husbandry, farming practices, food processing and meat importation potentially being key factors.

A joint PHE and NHSBT (National Health Service Blood and Transplant) study provided novel data on the impact of HEV on blood safety[29], and suggested that the HEV genotype 3 is widespread in blood donors. Selective screening to reduce exposure to HEV in immune-suppressed patients was introduced in 2016.

Infection in Animals

Hepatitis E does not cause disease in pigs and in the UK there are no routine surveillance systems in place.

A pig abattoir survey was undertaken in early 2013 (as part of a multi-agency project with PHE, Defra, the Veterinary Medicines Directorate (VMD), FSA, APHA and the British Pig Executive (BPEX) [30]) to better understand the possible role of infection in pigs on human disease incidence. It showed a sero-prevalence of 92.8% for HEV in 629 pigs at UK abattoirs[31]. Where samples could be analysed, pigs generally had the genotype 3 group 1 virus suggesting that the likely source of human infections with genotype 3 group 2 in the UK is not UK pigs.

Leptospirosis (*Leptospira interrogans* serovars)

Leptospirosis is caused by the spirochaete bacterium *Leptospira interrogans*, of which only some strains are pathogenic. *L.* Icterohaemorrhagiae is the main serovar causing human disease.

Leptospires are globally widespread amongst wild and domesticated mammals. The serovars encountered most frequently in farm livestock in the UK are *L.* Hardjo (cattle), *L*. Bratislava (pigs) and *L*. Icterohaemorrhagiae (which affects a wide range of wild and domestic species). Leptospirosis may present in a number of clinical syndromes in animals, commonly abortion or milk drop, but also as systemic infection. The disease is a major cause of economic loss to intensive cattle and pig industries in developed countries. Clinical disease can be controlled by vaccination in cattle and dogs, and is

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[29] Hewitt PE, *et al.* Hepatitis E virus in blood components: a prevalence and transmission study in southeast England. *Lancet,* 2014;384(9956):1766-73.
[30] Name changed to AHDB Pork in 2015
31 Grierson S et al. Prevalence of Hepatitis E Virus Infection in Pigs at the Time of Slaughter, United Kingdom, 2013. Emerg Infect Dis, 2015; 21(8): 1396-1401

frequently undertaken in the UK. Clinical disease in animals in GB is less common than in the past, although it remains a significant problem in Northern Ireland.

Humans mainly acquire infection by direct contact with the urine of chronically infected animals. Infection may occur when spirochaetes in contaminated water or soil come in contact with cuts or abrasions, with mucous membranes or with conjunctiva. Spirochaetes may also cross the nasal mucosa and pass through the lungs (from inhalation of aerosolised body fluids). Most reported cases occur in men, probably due to greater occupational and recreational exposures.

Infection in humans

During 2015, 68 cases of leptospirosis were reported in the UK (Table 8), 63 in England and Wales. The following serovars were determined: *L.* Copenhageni (n=6), *L.* Icterohaemorragiae (n=3), *L.* Australis (n=2), *L.* Canicola (n=2), *L.* Mini (n=2), *L.* Poi (n=2), *L.* Saxkoebing (n=2), *L.* Bataviae (n=1), *L*. Hardjo (n=1). It was not possible to determine the infecting serovars for the remaining cases.

In April 2015, there was a change in the PHE reference laboratory service in England and Wales. The reference laboratory moved from Hereford to a joint service split between PHE Colindale and PHE Porton Down.

Table 8 Laboratory confirmed reports of leptospirosis in UK residents, 2013-2015

Year	England & Wales	Scotland	Northern Ireland	United Kingdom
2013	47	1	2	50
2014	76	2	0	78
2015	63	3	2	68

Twenty-nine of the 63 cases in England and Wales were likely to have been acquired through travel, with the largest number of cases (n=16) returning from South East Asia (including Indonesia, Malaysia and Thailand).

Twenty of the 63 cases were likely to have been acquired through exposures in the UK, two of which were fatal. An occupational exposure was reported for six of these cases (two sewage workers; two farmers; a park worker; and an abattoir worker). A further nine cases were likely to have acquired their infections through non-occupational rodent exposure: four through recreational or non-occupational contact with water; and one through exposure to sewage.

Of the remaining 14 cases, limited information was available on potential exposures to leptospirosis. One case was reported only to have no recent travel history abroad and, for 13 cases, no travel history or exposure information was provided.

Infection in animals

Countries within the UK use different methods for diagnosing leptospirosis, and the diagnostic criteria required for disease confirmation has also changed in recent years. It is therefore difficult to make comparisons between countries and time periods.

There were 34 incidents of leptospirosis diagnosed in the UK in 2015, of which five were in Great Britain. Four of the incidents occurred in cattle (two in Scotland involving abortions, one presenting as milk drop in a dairy unit in Wales, and one outbreak of abortion in a dairy farm in England), and one diagnosis was made in a pig in England.

Bulk milk testing of dairy herds in 2015 to monitor *L.* Hardjo status in England and Wales continued to show evidence of potentially active infection and/ or extensive vaccination in 50-60% of dairy herds from the population submitting samples, a figure which has remained stable for the previous four years. [32] [33]

The remaining 29 incidents in 2015 occurred in Northern Ireland. There has been a decreasing number of positive incidents in Northern Ireland from 20% of randomly selected aborted foetuses/stillborn calves in the mid-1990s to around 3-4% in recent years. While there have been temporary increases along the way, the decreasing trend is most likely as a result of vaccine pressure, and in particular the use of modern monovalent *L.* Hardjo vaccines.

During 2015 the APHA tested 5,345 serum samples from a range of species for diagnostic, monitoring and export purposes (mainly dogs). A summary of the positive samples is given in Table 9. These data only indicate serological evidence of exposure and/ or vaccination, and not clinical disease.

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[32] https://www.gov.uk/government/uploads/system/uploads/attachment_data/file/524585/pub-zoo0415.pdf

[33] The significance of these observations is heavily influenced by persistence of antibody, vaccination status and selection bias. However, it is unlikely that many fully vaccinated herds submitted samples for testing so these results are expected to be fairly representative of unvaccinated herds in England and Wales.

Table 9 Detection of antibody (possibly vaccination associated) to pathogenic leptospires in serum samples submitted to APHA for testing using the microscopic agglutination test (MAT), 2015*

	Dogs	Cattle	Pigs	Horses
Total samples	938	2,521	428	23
Positive *L.* Canicola	85**	0	0	0
Positive *L.* Icterohaemorrhagiae	84**	1	0	8
Positive *L.* Hardjo	5	428**	0	1
Positive *L.* Bratislava	40	1	103	1
Positive *L.* Copenhageni	23	1	0	0
Positive *L.* Pomona	2	0	1	0
Positive *L.* Grippotyphosa	11**	0	0	0
Positive *L.* Australis	2**	1	0	1
Positive *L.* Hebdomanis	0	2	0	1
Positive *L.* Javanica	0	3	0	0
Positive *L.* Mini	0	1	0	1
Positive *L.* Prajitno	0	0	0	1

* Results only reflect the serological tests requested for each submission, and therefore significant titres to other *Leptospira* serovars may have been missed.

** Serovars for which a vaccine is available in this species.

Listeriosis (*Listeria monocytogenes*)

Listeria monocytogenes is widely distributed in the environment, including in soil, decaying vegetation and fodder such as silage in which the bacteria can multiply. In animals, listeriosis is mainly a disease of farmed ruminants, with cattle and sheep considered the most important species. Infection occurs due to direct ingestion of soil or through soil-contaminated feed, notably spoilt silage.

In humans, listeriosis most commonly occurs in pregnant women, neonates and people over the age of 60 years with underlying medical conditions. Consumption of foods contaminated with *L. monocytogenes* is the main route of transmission to humans. Zoonotic infection acquired directly from animals is also possible, although cases reporting animal contact are rare.

Infection in humans

There were 189 cases of listeriosis reported in the UK in 2015, compared to 188 in 2014. The number of cases in the UK has remained relatively stable since 2010. Twenty-eight of the cases in 2015 were pregnancy-associated (Table 10). There were no outbreaks of listeriosis reported in the UK in 2015.

Table 10 Laboratory reports of listeriosis in humans in the UK, 2013-2015

		2013	2014	2015
England and Wales	Pregnancy-associated cases	16	22	26
	Others	144	147	144
	Total England and Wales cases	160	169	170
Scotland	Pregnancy-associated cases	1	1	1
	Others	15	14	12
	Total Scotland cases	16	15	13
Northern Ireland	Pregnancy-associated cases	0	0	1
	Others	2	4	5
	Total Northern Ireland cases	2	4	6
United Kingdom	Total	178	188	189

Infection in animals

The majority of listeriosis cases in UK animals typically occur between January and April when many animals, especially cattle, are housed. This peak in cases is considered to be linked to the feeding of soil-contaminated silage.

During 2015, 157 diagnoses of listeriosis in animals were made in the UK (Table 11), a 23.8% decrease from 206 cases in 2014. This reflects a decrease in diagnoses in both GB and Northern Ireland.

Table 11 Confirmed *Listeria* cases (all species) in animals in the UK, 2013-2015

Animal	2013	2014	2015
Birds (at farm)	3	1	0
Cattle	63	69	43
Sheep and goats	133	134	113
Other	2	2	1
Total	201	206	157

Lyme Borreliosis (*Borrelia burgdorferi*)

Lyme borreliosis (or 'Lyme disease') is caused by the bacterium *Borrelia burgdorferi* and is transmitted to humans and animals through the bite of an infected *Ixodes* tick. It is the most common tick-borne infection in humans in the temperate northern hemisphere. The majority of UK cases are indigenously acquired, usually through recreational activities including country or hill walking, running, orienteering or gardening.

Well known regional foci of Lyme borreliosis in England and Wales include the New Forest, Salisbury Plain, Exmoor, the South Downs, Thetford Forest and parts of Wiltshire and Berkshire. Similar foci are known on the west coast and Highlands and Islands of Scotland.

Infection in humans

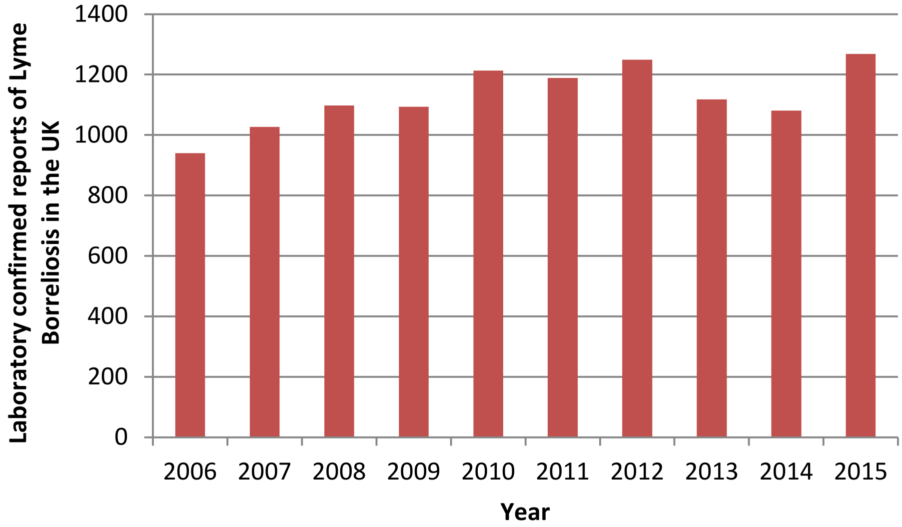
There were 1,262 serologically confirmed cases of *B. burgdorferi* infection in humans in the UK in 2015: 1,060 in England and Wales (of which 747 were acute infections), 200 in Scotland, and two in Northern Ireland. This is an increase of 16.7% from 2014 (n=1,081) (Table 12, Figure 5).

As a result of improvements made to the surveillance system following an extensive validation exercise, the data for 2013 and 2014 has changed from previously cited figures. The changes have been made to ensure harmonised data going forward. In addition, from 2013, cases in England and Wales have been separated into acute and longstanding infections.

Table 12 Reference laboratory reports of Lyme disease in humans in the UK, 2013-2015

		2013	2014	2015
England and Wales	Acute	656	449	747
	Longstanding or equivocal*	280	407	313
	Total	936	856	1,060
Scotland		176	224	200
Northern Ireland		6	1	2
United Kingdom		1,118	1,081	1,262

Figure 5. Number of laboratory confirmed human cases of Lyme borreliosis in the UK, 2006-2015



Of the 1,060 cases in England and Wales, 8.8% (n=93) reported recent travel (compared with 11.1% in 2014). The seasonal pattern in 2015 was similar to previous years, with infections reported throughout the year and peaking in the third quarter. This is consistent with the major tick feeding period which occurs in the late spring and early summer months.

Case reports were received from all regions of England and Wales in 2015, with the South of England contributing around 55%.

Pasteurellosis (*Pasteurella* spp.)

Pasteurellosis is a bacterial disease with a worldwide distribution. Within the *Pasteurella* genus, *P. multocida* is the most commonly reported organism, and is well known as both a common commensal and pathogen in a variety of animal species.

The most common mode of zoonotic transmission to humans is via dog or cat bites and scratches. These frequently lead to cutaneous infections, which may be severe. Systemic disease can also occur.

Infection in humans

There were 855 laboratory confirmed reports of human pasteurellosis in the UK in 2015 (Table 13), a 10.2% increase from the 776 cases reported in 2014. Infection with *P. multocida* accounted for 65.6% of reports (n=561).

Table 13 Laboratory confirmed reports of pasteurellosis in humans in the UK, 2015

Serovar	England and Wales	Scotland	Northern Ireland	United Kingdom
P. canis	28	56	0	84
P. multocida	443	116	2	561
P. pneumotropica	14	14	0	28
P. other named	58	5	0	63
Pasteurella spp	98	21	0	119
Total	641	212	2	855

Infection in animals

There were 384 cases of *P. multocida* diagnosed by government laboratories in animals in the UK in 2015[34] (Table 14).

Table 14 Laboratory confirmed reports of *P. multocida* in animals in the UK, 2014-2015

Year	2014			2015		
	GB	NI	UK	GB	NI	UK
Cattle	96	78	174	116	91	207
Sheep	123	3	126	107	4	111
Pigs	50	18	68	17	28	45
Birds	7	10	17	10	6	16
Miscellaneous / wildlife	2	2	4	3	2	5
Goats	1	0	1	0	0	0
Total	279	111	390	253	131	384

In addition, SRUC isolated *P. multocida* from 5 cats and 17 dogs in 2015. These were not submitted to APHA's VIDA database, and are therefore not included in the routine pasteurellosis data.

Q Fever (*Coxiella burnetii*)

Q fever is caused by the bacterium *Coxiella burnetii*. This can survive for long periods in the environment and is generally transmitted in aerosols or by fomites, including dust

[34] Current diagnostic criteria only consider *P. multocida.*

particles. *C. burnetii* infection occurs mainly in domesticated ruminants (cattle, sheep and goats), where it can cause abortion. Most cases of livestock abortion due to Q fever are sporadic, although outbreaks can occur.

Transmission to humans mostly occurs through exposure to aerosols containing *C. burnetii*. These may arise via bacterial shedding in products of abortion or normal parturition, or result from contaminated dust particles or bedding. Most human infections are asymptomatic, but cases may present as acute or chronic disease, and relapses may occur. Since 1999, the Health Protection Agency/ PHE data show that on average, 16% of annually diagnosed cases are chronic infections.

Infection in humans

In 2015, 21 cases of Q fever were reported in the UK, a large reduction from the 61 cases reported in 2014 (Table 15). This followed an increase in cases in 2011-2012, and numbers have now fallen back to expected levels. The reasons for the increase remain unclear.

Table 15 Laboratory confirmed reports of Q fever in humans in the UK, 2013-2015

Year	England & Wales*	Scotland	Northern Ireland	United Kingdom
2013	45	2	0	47
2014	56	5	0	61
2015	19	2	0	21

* Acute and chronic cases

Infection in animals

There were eight incidents (three cattle, one sheep and four goats) of Q fever abortion in England and Wales confirmed in 2015. Two of the cattle incidents involved dairy herds in England where single or multiple abortions had been reported. The third cattle incident was identified in a suckler herd in Wales. In sheep, Q fever infection was confirmed as the cause of abortion in one ewe on a smallholding of 17 pedigree sheep in England.

The four goat incidents all occurred in England. In the first incident, Q fever was confirmed as the cause of abortion in five dairy goats which had recently been dried off in a milking herd of 800. The second and third incidents[35] involved the same newly established goat herd which had sourced animals from multiple farms, and which experienced abortions and maternal deaths affecting 10 out of 80 young goats which

[35] These were counted differently in the Trends and Sources report.

had arrived on the farm a few days earlier. The final incident of Q fever in goats involved a large milking herd, where eight out of a group of 200 lactating does aborted.

There were no confirmed diagnoses of Q fever in Scotland from abortion specimens submitted to SRUC and no reported cases of Q fever in Northern Ireland in 2015.

Further information

Information on Q fever infection risks during the lambing season are available at:
https://www.gov.uk/government/news/pregnant-women-advised-to-avoid-animals-that-are-giving-birth--2

Q fever information for farmers is available at:
https://www.gov.uk/government/publications/q-fever-good-practice-for-farmers

Rabies (Rhabdoviridae)

Rabies is an acute viral infection of the central nervous system, caused by a lyssavirus in the family *Rhabdoviridae*. It affects all mammals, including humans, cats, dogs, wildlife and farm animals. In animals, three forms are classically described: prodromal, excitement (furious) and paralytic (dumb). The disease is absent from land mammals in the UK. The last case of rabies in an animal outside of quarantine in GB was a dog in Newmarket in 1970[36]. In Northern Ireland the last case was reported in 1923. The last case of rabies in quarantine in the UK was reported in 2008 in England.

The virus is present in the saliva of affected animals, and the most frequent method of transmission to humans is by bites, scratches or licks to broken skin or mucous membranes. In humans, post exposure treatment with vaccine, and if indicated rabies immunoglobulin, is very effective in preventing disease. Once symptoms develop in untreated individuals, death is almost inevitable with very few documented survivors[37].

Infection in humans

The last case of human terrestrial rabies acquired in the UK was in 1902; however occasional travel-related cases do occur. Between 2000 and 2014, there were five cases of imported human rabies, the last in 2012.

There were no human cases of rabies in the UK in 2015.

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[36] Pethece CK, Hopes R. A case of rabies at Newmarket. *Vet Rec,* 1970;86(10):299.b www.ncbi.nlm.nih.gov/pubmed/5461596
[37] Jackson AC. Why does the prognosis remain so poor in human rabies? *Expert Rev. Anti Infect Ther,* 2010; 8(6): 623-625

Infection in animals

In 2015, two cats, six dogs, a rabbit and 27 zoo bats were submitted to the APHA for laboratory testing. None of the samples were positive for rabies virus.

The UK Pet Travel Scheme was launched in 2000 to allow people to bring in or travel with their pets (dogs, cats and ferrets), while ensuring the UK remains free from rabies and certain other exotic diseases. On 1st January 2012 the UK harmonised its pet movement controls with the rest of the EU, but retained *Echinococcus multilocularis* tapeworm treatment controls (for dogs only). Under the EU scheme, the risk of rabies entering the UK remains very low, and these controls make it easier to travel with pets. During 2015, 165,154 dogs, 14,501 cats, and 90 ferrets entered GB under the EU pet travel scheme[38], compared to 155,510, 15,081 and 69 respectively in 2014.

Further information

Further information on pet movement rules are at: https://www.gov.uk/take-pet-abroad

Bat rabies (European Bat Lyssavirus)

European Bat Lyssaviruses (EBLVs) 1 and 2 are commonly referred to as ‘bat rabies’. EBLVs have been known to infect other animals and humans, presumably through a bite or scratch from an infected bat. EBLV-2 was first recognised in UK bats in 1996.[39]

Since 1977, there have been 4 human cases of EBLV in Europe, including two cases of EBLV-2. In all cases the person had not received rabies vaccination either before or after the incident.

Infection in humans

One case of EBLV-2 occurred in 2002 in Scotland, when a bat handler was diagnosed following multiple bites from Daubenton’s bats (*Myotis daubentonii*)[40]. There have been no human cases of bat rabies in the UK since.

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[38] This data was extracted from the APHA’s Pets Database and represents information supplied by third parties (pet transport carriers).
[39] Harris SL *et al.* Passive surveillance (1987 to 2004) of United Kingdom bats for European bat lyssaviruses. *Vet Rec* 2006; 159(14):439-46.
[40] Crowcroft N. Rabies-like infection in Scotland. *Euro Surveill*. 2002;6(50):pii=1984.

Infection in animals

Both active and passive surveillance is undertaken by APHA. A seroprevalence study conducted in England between 2003 and 2006 found EBLV-2 antibodies in 2.2% of Daubenton's bats, and EBLV-1 antibodies in <1% of Serotine bats[41].

Since 1996, eleven bats have tested positive (virus isolation) through APHA's passive lyssavirus surveillance scheme, and one bat in Scotland tested positive (EBLV-2 RNA detected) through active surveillance (Table 16). In 2015, 430 dead bats from the UK were submitted to the passive surveillance scheme, and one tested positive for EBLV-2.

Table 16: Detection of EBLV-2 in Daubenton's bats in the UK (1996 to 2015)[42]

Date	No. isolations	County	Sex and age
1996	1	Sussex	Female, Adult
2002	1	Lancashire	Female, Juvenile
2003	1*	Lancashire	Male, Adult
2004	1	Surrey	Female, Juvenile
2006	1	Oxfordshire	Female, Juvenile
2007	1	Shropshire	Female, Adult
2008	3**	Surrey Shropshire Perthshire	Female, Adult Male, Juvenile Male, Adult
2009	1	West Lothian	Female, Juvenile
2014	1	Shropshire	Male (no data on age)
2015	1	Powys	Male, Juvenile

* Carcase frozen and submitted for testing October 2004

** One incident of EBLV-2 RNA detected in an oral swab taken as part of surveillance for lyssaviruses in Scotland

Further information

General information including guidance on post exposure prophylaxis is available from PHE:
https://www.gov.uk/government/collections/rabies-risk-assessment-post-exposure-treatment-management

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[41] Harris SL, *et al.* Targeted surveillance for European bat lyssaviruses in English bats (2003-06). *J Wildlife Disease* 2009; 45(4):1030-41.
[42] Johnson N. Two EBLV-2 infected Daubenton's bats detected in the north of England. *Vet Rec* 2016; 179:311-312 (Errata)

Information on bats is available online from the Bat Conservation Trust at:
www.bats.org.uk
Results of the Scottish Natural Heritage bat lyssavirus monitoring programme:
www.snh.org.uk/press/detail.asp?id=2104

Salmonellosis (*Salmonella* species)

There are more than 2,600 *Salmonella* serovars, but salmonellosis in humans and animals is largely caused by a small number of the over 1,500 identified serovars of *S. enterica* subspecies *enterica.* In animals, clinical cases of salmonellosis are most common in cattle. Subclinical carriage is most common in poultry, reptiles and pigs. However, reports of clinical disease in weaned pigs have increased in recent years as a result of the emergence of monophasic *S.* Typhimurium in the pig sector.

Most human salmonellosis is acquired via the foodborne route. *Salmonella* Typhi and *S*. Paratyphi A are adapted to humans and are thus not considered to be zoonotic. Illness in humans associated with other *Salmonella* serovars is known as non-typhoidal salmonellosis. Two of these serovars, *S.* Enteritidis and *S.* Typhimurium, account for over half of all human salmonellosis cases.

Infection in humans

In 2015, 9,485 cases of laboratory confirmed salmonellosis were reported in the UK (Table 17). For every laboratory confirmed report of disease made to national surveillance schemes, there are estimated to be 4.7 cases in the community[11] (95% CI 1.2 – 18.2). This suggests the total number of cases in the UK in 2015 was approximately 45,000 (with 95% CI 11,382 – 172,627). Since this is a population estimate, the confidence intervals need to be taken into consideration, but nevertheless, this is the most accurate measure we have of the unavoidable under-reporting to laboratory surveillance systems.

The number of reported infections in 2015 in the UK increased by 17.4% compared to 2014 (n=8,078) (Figure 6). Reporting of *Salmonella* spp shows a consistent seasonal pattern with a distinct peak of infection observed in the third quarter of the year. Due to a change in laboratory reporting, the data for 2015 now includes untyped *Salmonella* isolates in England and Wales tested at regional microbiology laboratories but not submitted to the *Salmonella* Reference Service for confirmation and serotyping. Previous years did not include these isolates. However, the reference service has reported an overall increase in *Salmonella* isolates in 2015 compared to previous years.

Salmonella Enteritidis remained the most commonly reported serovar in 2015, accounting for 33.2% of cases for which a serovar result was available (Table 18, and Figure 7). Overall, in 2014 and 2015 there was an increase in reports in all UK countries, a reversal of the general trend of decreasing reports seen in the last decade. *Salmonella* Typhimurium (including monophasic strains) was the second most commonly reported serovar and increased by 23.8% from 2014. This increase is mostly attributable to the increase in the number of cases reported in England.

Whole genome sequencing (WGS) has been used routinely by PHE for identifying and characterising *Salmonella* isolates from April 2014. Since November 2015, following extensive evaluation and validation, this approach has now fully replaced phage typing for strain characterisation. As a result, information on phage types of *S*. Typhimurium and *S*. Enteritidis is not reported for 2015 (see Feature Article 4).

Table 17 Laboratory confirmed reports of non-typhoidal *Salmonella* infection in humans in the UK, 2013-2015*

Year	England & Wales	Scotland	Northern Ireland	United Kingdom
2013	7,493	813	155	8,461
2014	7,250	717	111	8,078
2015	8,558	803	124	9,485

* From the end of 2014 PHE moved to a new laboratory reporting system. Direct comparisons between the data derived from the previous system (LabBase2) and the new system (SGSS) should take this into consideration.

There was one large *S.* Enteritidis PT8 outbreak identified in 2015 linked to reptile ownership, specifically the handling and feeding of ‘feeder mice’ to pet snakes. This was the second largest *Salmonella* outbreak in recent years associated with non-foodborne transmission of salmonellosis.

Eleven foodborne outbreaks of *Salmonella* were reported in the UK in 2015, compared with ten in 2014. Eight were caused by *S*. Enteritidis, one by *S.* Typhimurium and two by other *Salmonella* serovars. The most common food type associated with *Salmonella* outbreaks in 2015 was poultry products (eggs and chicken meat). A summary of foodborne outbreaks by zoonotic pathogen, broken down by food vehicle category, is given in Appendix 5.

Figure 6. Rate of reported non-typhoidal *Salmonella* infections by region per 100,000 population, 2006-2015

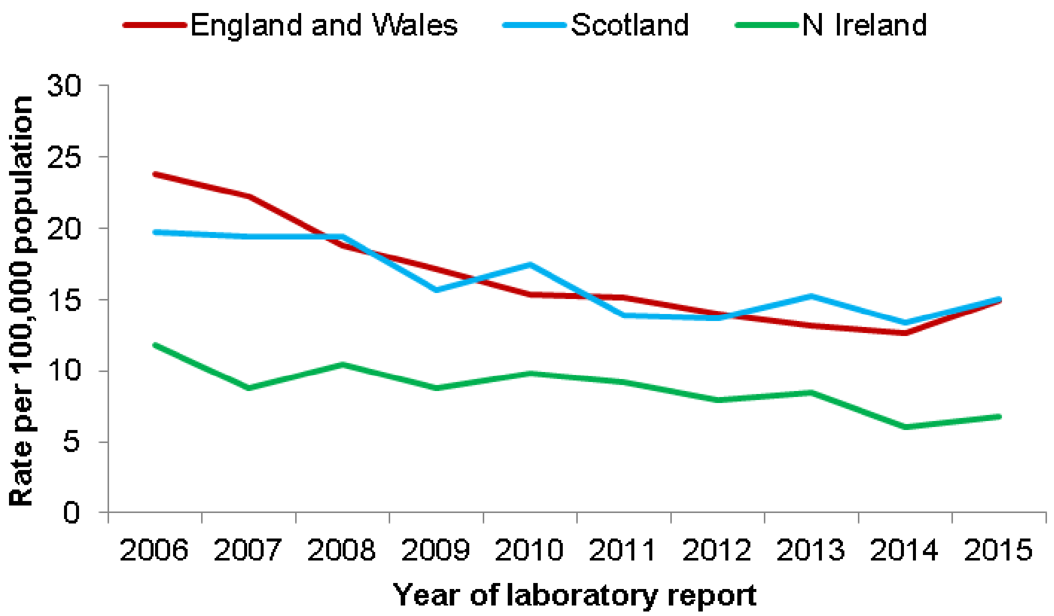

Figure 7. Laboratory reports of non-typhoidal human *Salmonella* cases in the UK for which a serovar result is confirmed, 1996-2015

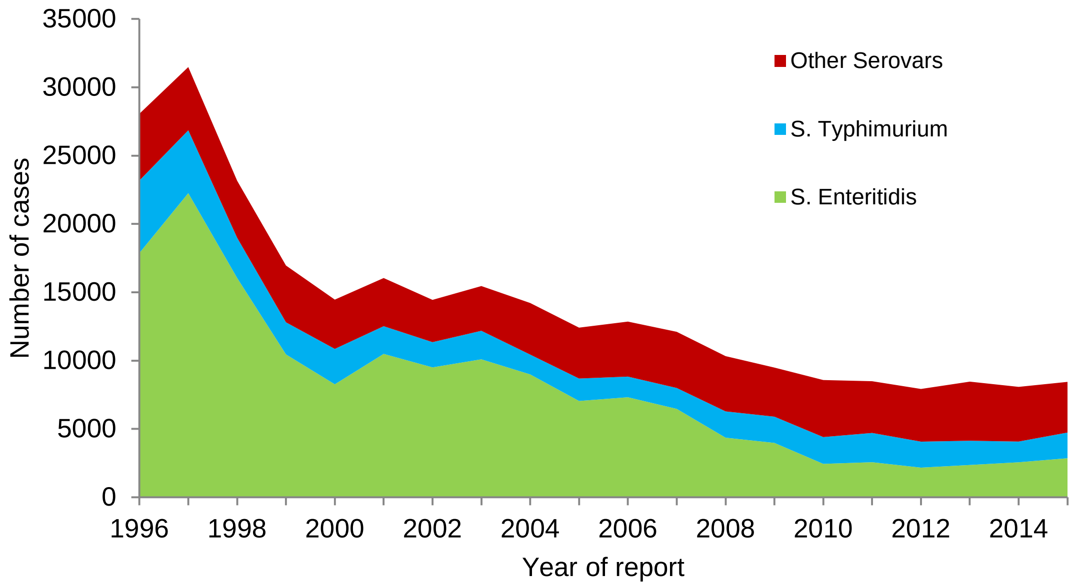

Table 18 The ten most common non-typhoidal *Salmonella* serovars in humans isolated in 2015 in each country of the UK

England		Wales		Scotland		Northern Ireland	
Serovar	n	Serovar	n	Serovar	n	Serovar	n
Enteritidis	2,362	Enteritidis	132	Enteritidis	315	Enteritidis	48
Typhimurium	1,620	Typhimurium	82	Typhimurium	133	Typhimurium	43
Newport	219	Infantis	15	Group B	41	Infantis	3
Virchow	185	Newport	12	Stanley	20	Stanley	3
Stanley	158	Java	10	Infantis	19	Agona	2
Infantis	153	Kentucky	8	Agona	16	Heidelberg	2
Kentucky	132	Virchow	7	Arizonae	16	Muenchen	2
Agona	131	Agona	5	Group C1	15	Nachshonim	2
Oranienburg	101	Saint Paul	5	Newport	14	Saint Paul	2
Braenderup	100	Stanley	5	Virchow	13	*	

*All other serovars have no more than one case

Infection in animals

The majority of *Salmonella* isolations in farm livestock in the UK are detected as a result of testing diagnostic samples from clinically diseased cattle, or as a result of statutory surveillance under legislative programmes to control salmonella in flocks of domestic fowl and turkeys. The poultry *Salmonella* National Control Programmes (NCPs) are required under EU regulation[43]. All NCPs focus on reducing the prevalence of the most important serovars of *Salmonella* that can affect human health and, as such, specific reduction targets are set for *S.* Enteritidis and *S.* Typhimurium (including monophasic strains). In the NCP for breeding chicken flocks, *S.* Hadar, *S.* Infantis and *S.* Virchow are also included in the reduction target. *Salmonella* NCPs have been implemented in the breeding chicken, laying chicken, broiler chicken and turkey breeding and fattening industry sectors.

For poultry populations (chickens and turkeys) subject to *Salmonella* NCPs, results are reported as the number of positive flocks detected under the programmes. Trends in the number of *Salmonella* reports in animal species not subject to an NCP also need to be treated with caution in view of the inherent biases associated with the data, e.g. the level of diagnostic and surveillance testing carried out.

[43] Regulation (EC) No. 2160/2003

There were 3,055 isolations of *Salmonella* in the UK in 2015, compared with 2,691 in 2014. Of isolations in 2015, 2,783 were reported by GB. This comprised 2,565 isolations from species covered by statutory reporting requirements[44] (929 from chickens, 619 from turkeys, 381 from cattle, 310 from ducks, 145 from pigs, 66 from sheep, 47 from horses, 34 from pheasants, 23 from pigeons, six from partridges, four from quail and one from guinea fowl) plus 218 isolations from non-statutory species (e.g. cats, dogs and reptiles).

There were 272 isolations of *Salmonella* in 2015 from animals and poultry as covered by statutory reporting requirements in Northern Ireland[45]. These were 175 isolations from chickens, 2 from turkeys, 70 from cattle, 13 from pigs, and 12 from sheep. No isolations from other species were reported.

Farmed livestock (excluding species in the NCPs) and horses

There were 381 *Salmonella* isolations from cattle in GB during 2015, an 18.1% decrease compared with 2014 (n=465) (Figure 8). There were also fewer isolations from sheep (66 compared to 70), and pigs (145 compared to 163).

In Northern Ireland, there were 70 *Salmonella* isolates from cattle, 12 from sheep and 13 from pigs in 2015. This compares to the 2014 figures of 96 isolates from cattle, 12 from pigs and 9 from sheep.

Cattle

There were 451 isolations in cattle in the UK during 2015 (compared with 559 in 2014). *S.* Dublin, which seldom causes disease in humans, accounts for the majority: 299 in 2015 compared with 395 in 2014. There were also 19 isolations of *S.* Typhimurium, three isolations of *S.* Enteritidis and 11 monophasic *S.* Typhimurium strains from cattle during 2015 plus a number of other serovars and a few untypable strains.

In Great Britain, there were 238 isolations of *S.* Dublin (compared with 309 in 2014), 17 of *S.* Typhimurium, two of *S.* Enteritidis and 10 monophasic *S.* Typhimurium strains. In Northern Ireland, there were 61 reported isolations of *S.* Dublin (compared with 86 in 2014), two of *S.* Typhimurium, and one each of *S.* Enteritidis and monophasic *S.* Typhimurium.

Sheep and goats

There were 78 isolations from sheep during 2015 (compared with 80 during 2014): 66 from Great Britain (compared with 71 in 2014), and 12 from Northern Ireland (compared with 9 in 2014). There were no isolations in goats.

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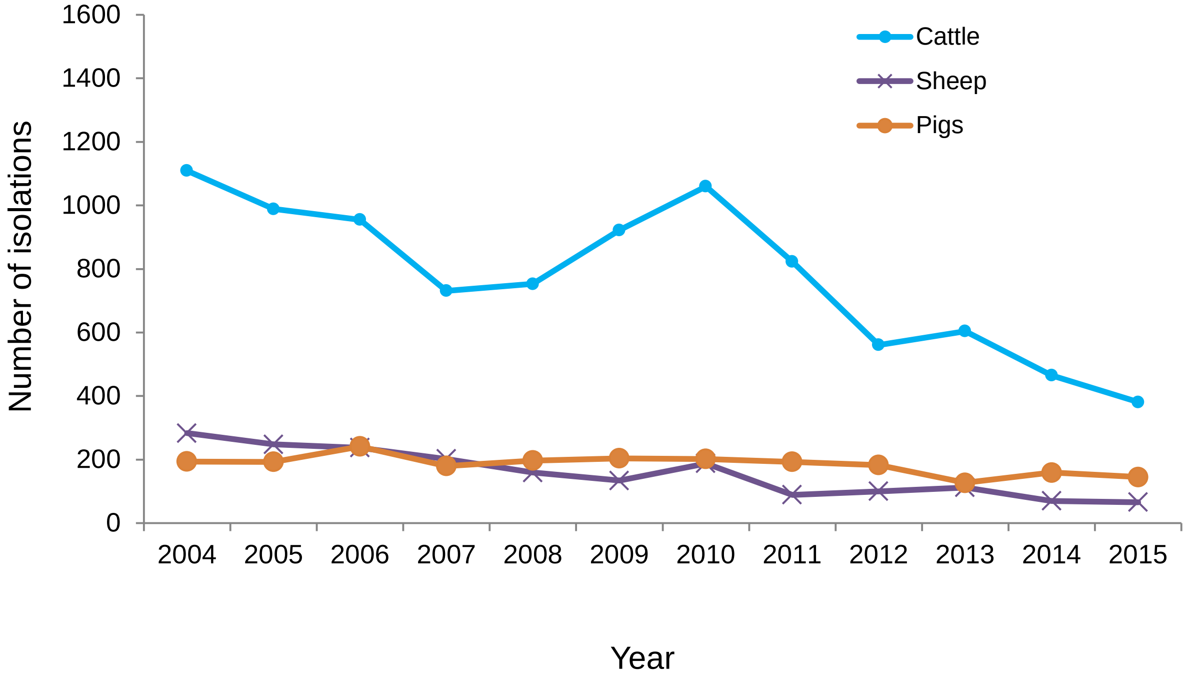
[44] Zoonoses Order 1989
[45] Zoonoses Order (Northern Ireland) 1991

Figure 8. Number of laboratory-confirmed isolations of *Salmonella* in animals in GB, 2005-2015



Pigs

There were 158 isolations from UK pigs during 2015 (compared with 169 in 2014). *Salmonella* Typhimurium accounted for 48 isolations. For the monophasic *Salmonella* Typhimurium strains, there were 39 reported isolations of *S.* 4,5,12:i:- and 53 isolations of *S.* 4,12:i:-. These results indicate the continued maintenance of monophasic *S.* Typhimurium strains in pigs in the UK. The remaining 18 isolates were of other serovars.

In Great Britain in 2015, there were 145 isolations from pigs (compared with 159 in 2014). Of these, 42 were *S.* Typhimurium, 39 were monophasic Typhimurium *S.* 4,5,12:i:-, and 49 were monophasic Typhimurium *S.* 4,12:i:. There were 15 isolates of other serovars reported during the year.

In Northern Ireland, there were 13 isolations in 2015 (compared with 10 in 2014): six *S.* Typhimurium; four Monophasic *S.* Typhimurium *S.* 4,12:i:-; and three of other serovars.

Horses

Forty seven isolations of *Salmonella* were received from horses during 2015, all in Great Britain. This is a decrease from the 62 isolates reported in 2014 (58 from Great Britain and four from Northern Ireland).

Ducks and geese

There were 310 isolations in ducks during 2015, all from Great Britain (compared with 321 in 2014). There were no such reports from Northern Ireland (and no reports in 2014).

There have been very few isolations of *Salmonella* from geese in recent years, with none in 2015 or 2014 and one isolation in 2013.

Results from the UK Salmonella NCPs in chickens and turkeys

The NCPs have been operating for varying lengths of time. The breeding chicken NCP is the longest-established (2015 was its ninth year) whereas the turkey NCP is the most recent addition at six years. Each year, the UK NCP results have been significantly below EU reduction targets.

- in 2015, one adult breeding chicken flock was positive for *S.* Enteritidis, in Northern Ireland. This gives an overall prevalence of 0.06% UK breeding chicken flocks testing positive for the regulated *Salmonella* serovars.
- out of the total 4,093 laying hen flocks included during the year, one adult flock was positive for monophasic *S.* 4,12:i:- , giving an overall prevalence of 0.02%.
- the prevalence of the target serovars in broiler flocks was 0.15% in 2015. Sixty broiler flocks were detected as positive for *S*. Enteritidis, three flocks for *S*. Typhimurium, and one flock for monophasic *S.* 4,12:i:- out of a total of approximately 44,082 flocks tested. The large number of *S*. Enteritidis cases seen in flocks in 2015 was primarily related to an outbreak involving a hatchery in GB. How the hatchery became contaminated remains unclear. This outbreak was unusual in that it included six hatchery workers and a farmer who contracted infection through occupational exposure. Unusually, the *S*. Enteritidis serovar that caused this outbreak caused some illness in the birds, and a number of flocks were culled.
- no regulated serovars were isolated from breeding turkey flocks (0% prevalence), whilst the prevalence in fattening turkey flocks was 0.34% (9/2,618 flocks). *S.* Enteritidis was detected in one fattening flock (identical to the serovar that caused the hatchery associated outbreak seen in broiler chickens) and eight fattening flocks tested positive for monophasic *S.* Typhimurium (*S*. 4,5,12:i:-).

Animal feed surveillance for Salmonella

Feedstuff contaminated with *Salmonella* may be a source of infection for animals. Due to the large quantity of feed that is consumed, such contamination is considered to be a significant risk. In order to reduce this risk, salmonellae are monitored and controlled, according to guidelines described in Codes of Practice[46], at a number of points in the feed production process. The isolation rate of *Salmonella* from animal feedstuffs and feedstuff ingredients in GB has remained stable since 2014. The percentage of total positive tests in 2015 was 0.7%, the same as in 2014 (298 positive tests compared with

46 England: https://www.food.gov.uk/sites/default/files/multimedia/pdfs/enforcement/feed-law-code-england.pdf ; NI: https://www.food.gov.uk/sites/default/files/feed_law_enforcement_guidance_ni_0.pdf ; Wales: https://www.food.gov.uk/sites/default/files/wales-feed-law-code.pdf ; Scotland: http://www.foodstandards.gov.scot/sites/default/files/Feed%20Law%20Code%20of%20Practice%20Scotland%20-%202016.pdf

277 in 2014). In Northern Ireland, 146 isolations of *Salmonella* were made under the animal feed surveillance programme during 2015.

Further information

A description of *Salmonella* data collection and reporting in animals in Great Britain is included in the Salmonella in Livestock Report:

https://www.gov.uk/government/publications/salmonella-in-livestock-production-in-great-britain-2015

Shiga toxin producing *Escherichia coli* (STEC)

NB: Nomenclature has changed from VTEC to STEC

Escherichia coli (*E. coli*) are a normal component of the bacterial fauna in the gastrointestinal tracts of humans and other animals. Although many strains are considered to be harmless, there are a number of subgroups associated with human disease. These include shiga toxin producing strains of *E. coli* (STEC) which cause gastrointestinal disease in humans with potentially severe complications, such as haemolytic uraemic syndrome (HUS). HUS is a severe multi-system disorder characterised by acute kidney failure, although other complications, including those of the central nervous system can occur. Children are at most risk of developing HUS following STEC infection.

Ruminants, particularly cattle and sheep, are the main reservoirs for STEC in the UK although the bacterium can also be found in a wide range of other animals, including birds, goats and deer. STEC does not cause disease in these animals but can be excreted in their faeces and can survive in the environment for months. Direct or indirect contact with animals, their faeces or environment, person to person spread, and consumption of food or water contaminated with STEC are the primary modes of transmission.

From 1st May 2012, PHE used Multilocus variable number tandem repeat analysis (MLVA), a molecular technique, to routinely type all isolates of STEC serogroup O157[47]. In June 2015, this was superseded by routine WGS for all STEC serotypes commonly identified or associated with outbreaks in England and Wales. It is sufficiently discriminatory to identify cases that are likely to have had a common exposure or be epidemiologically linked (see Feature Article 4).

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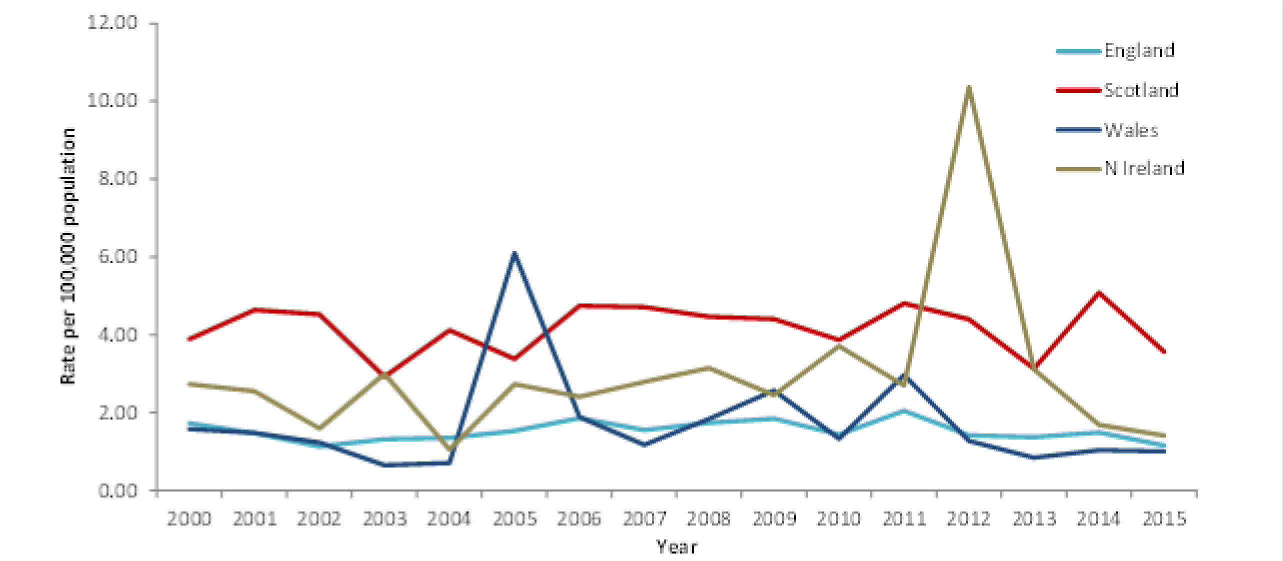
[47] Byrne L *et al*. Evaluating the Use of Multilocus Variable Number Tandem Repeat Analysis of Shiga Toxin-Producing *Escherichia coli* O157 as a routine public health tool in England. *PLoS One,* 2014; 9(1): e85901

Infection in humans

STEC are distinguished by serogroup and there are 174 known serogroups based on O (somatic) antigen polysaccharides, of which O157 is currently the most commonly diagnosed in the UK. The predominance of STEC O157 in national datasets should be interpreted with caution as most hospital laboratories use testing algorithms which are specific to the detection of STEC O157. For cases of severe disease consistent with STEC infection, where O157 is not isolated at the frontline hospital laboratory, it is recommended that faecal specimens are referred to the Gastrointestinal Bacteria Reference Unit for re-testing for the presence of both O157 and non-O157 STEC (PHE STEC Operational Guidelines)[48].

In 2015, there were 867 laboratory confirmed human cases of STEC O157 reported in the UK (665 in England and Wales, 170 in Scotland, and 32 in Northern Ireland)[49]. There are clear variations in the geographical distribution of laboratory confirmed cases within the UK. With the exception of years with large outbreaks (2005 and 2012), Scotland has consistently recorded the highest rates of infection per 100,000 head of population (Figure 7). The unusually high rate for Northern Ireland in 2012 was due to 145 cases associated with a single outbreak.

Figure 7 Annual rates of laboratory confirmed reports of human STEC O157 infections in the UK, 2006–2015



The burden of disease due to non-O157 STEC is underestimated, but since December 2012 a number of frontline laboratories have introduced a PCR to directly detect shiga

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[48] https://www.gov.uk/government/uploads/system/uploads/attachment_data/file/323416/VTEC_operational_manual.pdf

[49] The figures presented in this report are culture positive cases only. Other reports use the ECDC definition which includes serology-only positive cases that either had HUS or were epidemiologically -linked to a culture positive case. Those figures will therefore be slightly higher.

toxin genes. This should improve the detection of serogroups other than O157, but the proportion of laboratories implementing the new method is still relatively low (~ 10%). In 2015 there were 372 laboratory confirmed cases of non-O157 STEC identified in the UK (210 cases in England, 1 in Wales, 78 in Scotland and 83 in Northern Ireland), a notable increase in reports compared to previous years.

Eleven outbreaks of STEC in the UK were detected and investigated affecting a total of 130 cases in 2015. Ten of the outbreaks involved STEC O157 and one involved STEC serogroup O26. These included:

- one petting farm outbreak
- one nursery school outbreak, where the source of infection was unknown
- six foodborne outbreaks linked to consumption of burgers; venison; coconut; mixed salad leaves; cross-contamination of raw and cooked foods at a butcher's shop; and associated with a local restaurant where the source was not determined
- one waterborne outbreak due to contamination of a private water supply at a holiday cottage after a period of high rainfall
- one localised outbreak of STEC O157 in England, and a dispersed outbreak in England and Scotland (serogroup O26) were detected, but no common source of infection was determined through investigations in either outbreak

An outbreak of STEC O55:H7 in the South of England originally detected and investigated during 2014 recurred in 2015. STEC O55:H7 is a rare strain causing very severe illness, and cases were detected for the first time in England in 2014. Cases were highly clustered both geographically and phylogenetically (within 5 SNPs). The strain was unusually severe with 43% of cases developing HUS, compared to a 5% progression rate typically seen in STEC O157 cases, although this varies with age, gender, STEC toxins and other factors[50]. Although no common exposures could be identified, extensive investigations were carried out including food trace-back, animal contact and animal movement studies. Investigations to identify the source are still on-going.

Infection in animals

STEC O157 infection is widespread in cattle and sheep in the UK. However, because it does not cause disease in the animal population and shedding of the organism is intermittent, prevalence figures are of limited help in assessing the degree of risk to humans. It is therefore assumed that all ruminants are potentially infected with STEC O157.

[50] Launders N *et al*. Disease severity of Shiga toxin-producing E. coli O157 and factors influencing the development of typical haemolytic uraemic syndrome: a retrospective cohort study, 2009-2012. *BMJ Open*, 2016; 6(1):e009933

Information regarding STEC outbreak investigations is given in the APHA non-statutory zoonoses reports at: https://www.gov.uk/government/publications/non-statutory-zoonoses-disease-surveillance-reports-2015

Further Information

Advice leaflets on minimising the risk of infection with STEC can be found at:

- http://adlib.everysite.co.uk/resources/000/264/533/sci_vtec_leaflet.pdf
- http://www.face-online.org.uk/resources/preventing-or-controlling-ill-health-from-animal-contact-at-visitor-attractions-industry-code-of-practice
- www.scotland.gov.uk/Publications/2005/03/20839/54388
- http://www.wales.nhs.uk/sitesplus/888/page/43884
- http://www.food.gov.uk/science/research/foodborneillness/ecoliresearch/fs421009/

Toxoplasmosis (*Toxoplasma gondii*)

Toxoplasmosis is caused by the protozoan parasite *Toxoplasma gondii*. Cats are the definitive host for the organism, although many warm-blooded animal species can be infected as intermediate hosts. The resistant oocysts excreted by cats can remain viable in the environment for many months.

Humans are infected with *T. gondii* by three main routes:

- ingesting sporulated oocysts from water, food or soil or other materials contaminated with the faeces of infected cats
- ingesting undercooked or raw meat (mainly pork or lamb) that contains tissue cysts
- transmission from a newly infected mother to the foetus

There are also less common routes of transmission, such as receiving organ transplants or blood products from donors with toxoplasmosis, and ingesting the parasite following direct contact with products of conception during lambing.

Infection in humans

A total of 371 laboratory confirmed cases of toxoplasmosis were reported in the UK during 2015 (Table 19), compared with 370 in 2014. In England and Wales, 342 cases of toxoplasmosis were reported: 324 cases had acute infection (94.7%); two had reactivated infection (0.6%); and the remaining 16 types of infection were undetermined (4.7%).

Table 19 UK confirmed human cases of toxoplasmosis, 2013-2015

Year	England & Wales	Scotland	Northern Ireland	United Kingdom
2013	311	14	0	325
2014	344	26	0	370
2015	342	29	0	371

Infection in animals

In 2015, there were 298 toxoplasmosis incidents diagnosed in the UK (248 in GB) compared with 275 in 2014. Of the cases in GB, 241 were diagnosed in sheep, five in goats, and one each in a camelid and an oryx. This was an increase in comparison with the number of GB diagnoses in 2014 (n=212), despite 2015 submissions of ovine abortion material to GB government laboratories decreasing to levels comparable with those pre-Schmallenberg virus (which was considered to have been a driver of increased submissions). In Northern Ireland, there was a decrease in the number of *T. gondii* incidents diagnosed during 2015 (n=50) compared to 2014 (n=63).

Table 20 presents the serological testing results for toxoplasmosis in animals in the UK in 2015. This testing does not distinguish between antibody as a result of vaccination and that produced by natural infection; therefore the vaccination status of the animal must be considered. However, as most of these samples will have been taken from animals with a recent history of abortion it is likely that the majority of positives were associated with natural infection.

Table 20 Serological testing for toxoplasmosis in animals in the UK, 2015

Sera testing	GB	NI	UK
No. separate sheep submissions (total number of samples)	136 (795)	207(598)	343 (1,393)
No. positives *T. gondii* : sheep	373	375	748
No. separate goat submissions (total number of samples)	16 (134)	3 (8)	19 (142)
No. positives *T. gondii* : goats	81	5	86
No. separate pig submissions (total number of samples)	4 (102)	11 (71)	15 (173)
No. positives *T. gondii* : pigs	0	31	31

In addition to the data in the table, Northern Ireland diagnosed *T. gondii* in 31 of 41 submissions from cattle during 2015. Three sera from three alpaca submissions from GB were also tested, one of which was positive.

Trichinellosis (*Trichinella* spp.)

Trichinellosis is caused by a parasitic nematode worm (*Trichinella* spp.) known as 'the muscle worm', which can infect many species of mammals and some birds. There are nine species of *Trichinella*, of which *T*. *spiralis* is the most common in Europe[51]. It is a foodborne disease that is spread primarily by the consumption of raw or undercooked meat products from horses and pigs containing trichinae, the infective, immature (larval) stage of the worm.

In humans, European outbreaks of trichinellosis are regularly reported and are mainly linked to the consumption of raw or undercooked meat from wild boar, back yard pigs or horses. In contrast, there have been no human cases acquired from meat produced in the UK for over 30 years.

Infection in humans

There were no human cases in 2015 in the UK.

Eleven cases of trichinellosis were diagnosed in the UK between 2000 and 2014, including an outbreak of eight cases in England and Wales in 2000 associated with the consumption of imported meat products. The remaining three cases were travel related: one in England and Wales in 2001, one in Scotland in 2010 in a person who had eaten partially cooked meat in France, and the other in Scotland in 2014 which had been acquired in the Czech Republic.

Infection in animals

Pigs and horses are routinely monitored at abattoir for the presence of *Trichinella*. In 2015, FSA received test results for 6,112,998 farmed pigs (tests are undertaken by food business operators). In addition, 3,595 horses, 1,120 farmed wild boar and 14 feral wild boar in the UK were tested. All samples examined were negative.

A UK monitoring programme for *Trichinella* in wildlife began in November 1999 and ended in March 2015. This programme initially tested only foxes for *Trichinella* but, from 2006, other susceptible wildlife were also considered. *T. spiralis* was found in a fox in

[51] Pozio E. World distribution of Trichinella spp. Infections in animals and humans. *Vet Parasitol,* 2007; 149(1-2) p3-21

Northern Ireland in both 2007 and 2009, and a fox in England was positive for *T. pseudospiralis* in 2013. In 2015, 39 foxes, 114 badgers, 232 rats, 7 gulls and 139 corvids all tested negative for *Trichinella*.

Variant Creutzfeldt-Jakob disease (vCJD) in humans and Bovine Spongiform Encephalopathy (BSE) in animals

Infection in humans

Creutzfeldt-Jakob disease (CJD) is a rare and fatal transmissible spongiform encephalopathy (TSE) of humans. Sporadic CJD is the most common form and was initially described in 1921. In 1996, a new variant, vCJD, was recognised and was strongly linked to bovine spongiform encephalopathy (BSE), which was first recognised in cattle in 1986.

The last death from definite or probable vCJD in the UK occurred in 2013, making a total of 177 deaths recorded since 1995. The number of deaths per year peaked at 28 in 2000. There have been no cases of vCJD in people born after the 1980s in the UK.

Further information

The National Creutzfeldt-Jakob Disease Research & Surveillance Unit:
www.cjd.ed.ac.uk/

Report on the incidence of variant Creutzfeldt-Jakob disease diagnoses and deaths in the UK, January 1994 – December 2011:
http://www.cjd.ed.ac.uk/sites/default/files/cjdq72.pdf

Infection in animals

BSE is a TSE disease of domestic cattle. BSE caused a major epizootic in cattle and smaller epizootics in exotic ruminants and domestic and exotic felines. The UK BSE epidemic peaked in 1992 with over 37,000 cases in cattle and has since declined steadily. The annual incidence of BSE cases in the EU has declined since targeted surveillance started in 2001. There have also been a small number of cases in North America, the Middle East, and Asia. Worldwide there have been two naturally occurring cases of BSE in goats: one in France and one in the UK.

The transmissible agent in TSEs is widely suspected to be an abnormal form of a host-encoded protein called the ‘prion protein’, although some research[52,53] suggests that in some TSEs, infectivity may be associated with low levels of detectable abnormal prions, or that abnormal prion protein may not always be infectious.

In 2015, 2 cases of BSE were diagnosed in cattle in the UK, 1 from Wales and 1 from England.

Yersiniosis (*Yersinia* spp.)

Yersiniosis in the UK is caused by *Yersinia enterocolitica* and *Y. pseudotuberculosis.* Plague is caused by *Y. pestis* but this specific pathogen does not occur in the UK.

Y. enterocolitica has been isolated from many domestic and wild mammals, birds and some cold-blooded animals. More than 50 serotypes have been identified, not all of which cause disease in animals and man. *Y. pseudotuberculosis* has been isolated from various species of wild and domestic mammals, birds and reptiles. Yersiniosis in humans is mostly caused by *Y. enterocolitica,* and humans usually acquire infection through food contaminated with the faeces of infected animals.

Infection in humans

In 2015 there were 44 cases of human yersiniosis reported in the UK (Table 21), compared with 65 in 2014.

Table 21 Confirmed human cases of yersiniosis in the UK, 2015

	England & Wales	Scotland	Northern Ireland	United Kingdom
Y. enterocolitica	33	5	0	38
Y. pseudotuberculosis	3	0	0	3
Yersinia spp	3	0	0	3
Total	39	5	0	44

[52] Barron RM, *et al.* High titres of TSE infectivity associated with extremely low levels of PrPSc in vivo. *J Biol Chem*, 2007; 282:35878-35886
[53] Piccardo P, *et al.* Accumulation of abnormal prion protein that is not infectious. *PNAS*, 2007; 104: 4712-4717

Infection in animals

During 2015, 143 cases (126 in Northern Ireland and 17 in GB) of yersiniosis were diagnosed in animals in the UK, a decrease from 2014 case numbers (147 in Northern Ireland and 22 in GB). The 2015 cases were diagnosed in cattle (n=92), sheep (n=39), wildlife and miscellaneous (n=10), and there was a single case diagnosed in both a goat and a bird.

Further information

Reports on *Yersinia* in animals in GB are produced by the APHA in the Non-Statutory Zoonoses Reports, which can be found at:
https://www.gov.uk/government/publications/non-statutory-zoonoses-disease-surveillance-reports-2015

Appendix 1: Notifiable zoonotic diseases in humans

Disease	Notifiable in humans under public health legislation in			Reportable under RIDDOR* to HSE
	England & Wales	Scotland	Northern Ireland	
Anthrax	✓	✓	✓	✓
Acute infectious hepatitis/Hepatitis unspecified: viral (e.g. Hepatitis E)	✓		✓	✓
Botulism	✓	✓		
Brucellosis	✓	✓		✓
Chlamydiosis (avian)				✓
Chlamydiosis (ovine)				✓
Diphtheria	✓	✓	✓	
Clinical syndrome due to STEC *E. coli* (including O157) infection		✓		
Gastro-enteritis (under 2 years of age only)			✓	
Haemolytic uraemic syndrome	✓	✓		
Food poisoning	✓		✓	
Infectious bloody diarrhoea	✓			
Leptospirosis			✓	✓
Lyme disease				✓
Plague	✓	✓	✓	
Q fever				✓
Rabies	✓	✓	✓	✓
Clinical syndrome due to *Streptococcus suis*				✓
Tetanus	✓	✓	✓	✓
Tuberculosis (including bovine TB)	✓	✓	✓	✓
Tularaemia		✓		
Viral haemorrhagic fevers	✓	✓	✓	
West Nile Virus		✓		
Yellow fever	✓	✓	✓	

* RIDDOR: Reporting of Injuries, Diseases and Dangerous Occurrences Regulations (not including Part II: Diseases additionally reportable in respect of offshore work places)

The table above lists notifiable zoonotic diseases only; further organisms are notifiable when isolated in laboratories. The lists of notifiable organisms can be found here:

England: www.legislation.gov.uk/uksi/2010/659/contents/made
Northern Ireland: www.legislation.gov.uk/apni/1967/36/contents
Scotland: www.legislation.gov.uk/asp/2008/5/contents
Wales: www.legislation.gov.uk/wsi/2010/1546/contents/made

Appendix 2: Notifiable and reportable diseases in animals which are potential zoonoses in the UK

Notifiable diseases are those where there is a statutory requirement to report a suspicion of a clinical case of disease.

Reportable diseases (in animals) include those where there is a statutory requirement to report laboratory confirmed isolation of organisms of the genera *Salmonella* and *Brucella,* and of *Echinococcus multilocularis,* under the Zoonoses Order 1989 (as amended). In addition further diseases are included in the schedule of the Specified Animal Pathogens Order 2008. The report is to be made by the laboratory which isolated the organism from an animal derived sample.

Disease	Main species	Last Occurred in UK54	Notifiable to APHA in GB, Veterinary Service in NI	Reportable (S= only reportable under SAPO)
Anthrax (*Bacillus anthracis*)	Cattle/other mammals	2015	✓	S
Avian Influenza (HPAI and influenza A virus of H5 or H7 subtype that is not classified as highly pathogenic). LPAI viruses may also be zoonotic even if not notifiable.	Poultry/ waterfowl	2015	✓	S
Bovine Spongiform Encephalopathy	Cattle	Present	✓	
Brucellosis (*Brucella abortus*)	Cattle[55]	2004 GB/ 2012 NI[56]	✓	✓
Brucellosis (*Brucella melitensis*)	Sheep and goats	Never	✓	✓
Brucella suis	Pigs	Never	✓	✓
Echinococcus granulosus	Sheep and dogs	Present		S
Echinococcus multilocularis	Dogs	Not in indigenous animals	✓	✓
Equine Viral Encephalomyelitis	Horses	Never	✓	S

[54] Figures taken are correct as at 31st December 2015.
[55] In the Zoonoses Order 1989 Brucella reporting relates to (a) “animal” meaning cattle (bull, cow, steer, heifer, calf), horse, deer, sheep, goat, pig or rabbit; and (b) “bird” meaning a domestic fowl, turkey, goose, duck, guinea-fowl, pheasant, partridge, quail or pigeon.
[56] NI granted OBF status in 2015, last case identified in 2012; outbreak in Scotland in 2003 and Cornwall, England in 2004.

Glanders & Farcy (*Burkholderia mallei*)	Horses	1928	✓	S
Newcastle disease and paramyxovirus infection	Poultry and pigeons	2006	✓	S
Psittacosis (Ornithosis)	Poultry	Present	Ornithosis (incls. psittacosis) notifiable in Northern Ireland in poultry [57]	
Rabies (Terrestrial)	Dogs and other mammals	1970[58]	✓	S
Rabies (EBLV)	Bats	2015[59]	✓	S
Rift Valley Fever	Cattle, sheep and goats	Never	✓	S
Salmonella	All species	Present	Salmonella, when carried in animals or poultry, which the Department considers to be a risk to human health, is notifiable in Northern Ireland	✓
Trichinella	Pigs, horses and other mammals	Present in wildlife[60]		S
Tuberculosis (*Mycobacterium bovis*)	Domestic cattle, buffalo, bison and deer	Present[61]	✓[62]	✓
Vesicular stomatitis virus (VSV)	Cattle/ other mammals	Never	✓	S
West Nile Virus	Horses	Never	✓	S

[57] The Psittacosis or Ornithosis Order 1953 (S.I. 1953 No. 38) gives discretionary powers to serve notices to impose movement restrictions and require cleansing and disinfection of affected premises so APHA may be involved in the control of Psittacosis, even though it is not a notifiable disease in animals or birds.
[58] A quarantine case was confirmed in 2008, however this does not affect the national disease status.
[59] European bat Lyssavirus type 2 was isolated from a Daubenton's bat in 2015.
[60] *Trichinella* is known to be present in wildlife in Northern Ireland. This follows the identification in Northern Ireland of a single fox positive for *Trichinella spiralis* in 2007 and again in 2009 during wildlife surveillance. A positive fox was found in England in 2013 (*Trichinella pseudospiralis*). An extensive investigation of wildlife and the epidemiology of the *Trichinella* species by the FSA identified no further cases showing this to be an isolated case. SAPO only refers to *T. spiralis.*
[61] Scotland has been officially free since October 2009, although sporadic incidents continue to be identified in cattle herds.
[62] In addition to any bovines and deer with suspect clinical signs of tuberculosis, under the Tuberculosis (England) Order 2007, the Tuberculosis (Wales) Order 2011, and the Tuberculosis (Scotland) Order 2007 (as amended), there is a statutory requirement in GB to notify to the APHA of the presence of suspect TB legions in the carcases of any bovine animals or other farmed or companion (pet) mammals. Furthermore, identification of *Mycobacterium bovis* in samples taken from any mammal (other than man) must also be reported to APHA Weybridge unless the organism was present in the sample as a result of an agreed research procedure. Notifying the suspicion of TB in a living domestic animal in the course of clinical examination, surgery, by radiography or in biopsy material is not mandatory (except for cattle or deer), but submission of clinical samples from such cases to APHA is encouraged.

Appendix 3: Laboratory-confirmed cases of zoonotic disease in humans, 2006-2015 [63]

United Kingdom

	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015*
Anthrax	1	0	1	13	39	0	5	2	0	0
Avian Influenza	1	4	0	0	0	0	0	0	0	0
Mycobacterium bovis	29	24	23	29	36	39	39	30	39	42
Brucellosis	16	15	15	18	12	25	14	14	11	12
Campylobacteriosis	52,550	57,908	55,617	65,077	70,229	72,112	72,588	66,558	70,540	63,292
Cryptosporidiosis	4,728	3,668	4,937	5,647	4,604	3,573	6,655	4,111	4,598	6,149
Hantavirus**	0	1	0	0	1	0	2	3	4	4
Hepatitis E**	292	166	180	178	289	480	682	827	1,126	1,154
Hydatid disease	14	10	18	9	7	15	6	13	16	16
Leptospirosis	50	81	76	56	42	52	78	50	78	68
Listeriosis	208	254	207	234	179	165	185	178	188	189
Lyme disease	940	1,027	1,098	1,093	1,213	1,189	1,249	1,118	1,081	1,262
Pasteurellosis	490	457	497	559	586	668	666	717	776	855
Psittacosis	30	39	63	60	58	41	37	30	32	24
Q fever	200	72	67	31	55	114	124	47	61	21
Rabies 'classical'	0	0	1	0	0	0	1	0	0	0
Rabies EBLV	0	0	0	0	0	0	0	0	0	0
Salmonellosis (non-typhoidal)	14,084	13,279	11,517	10,486	9,692	9,395	8,792	8,461	8,078	9,485
STEC O157	1,286	1,120	1,247	1,315	1,052	1,484	1,260	1,015	1,186	867
Non-O157 STEC	20	25	36	45	44	37	59	100	306	372
Streptococcus suis	4	2	7	2	4	1	3	3	3	4
Taeniasis	89	101	100	72	114	94	70	80	71	85
Toxocariasis	2	1	2	4	12	4	7	3	5	6
Toxoplasmosis	123	146	457	494	414	364	328	325	370	371
Trichinellosis	0	0	0	0	1	0	0	0	1	0
vCJD[64]‡	5	5	2	3	3	5	0	1	0	0
Yersiniosis	62	78	62	62	54	55	55	60	65	44

* Provisional data
** Data has been updated following a data cleaning exercise
‡ Data source: NCJDRSU

[63] Not a definitive list of the zoonotic pathogens reported each year, but covers zoonotic diseases reported annually in the UK Zoonoses Report.
[64] Deaths

England & Wales

	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015*
Anthrax	0	0	1	0	5	0	4	1	0	0
Avian Influenza	1[65]	4[66]	0	0	0	0	0	0	0	0
Mycobacterium bovis	20	22	17	21	31	30	33	24	35	35
Brucellosis	11	8	5	13	11	17	9	12	10	11
Campylobacteriosis‡	46,748	51,831	49,891	57,685	62,588	64,572	65,044	59,040	62,494	55,697
Cryptosporidiosis	3,982	3,073	4,162	4,831	3,901	2,990	5,765	3,520	4,023	5,222
Hantavirus	0	1	0	0	1	0	2	3	3	4
Hepatitis E	289	162	176	175	276	464	604	731	924	958
Hydatid disease	14	10	18	9	6	12	6	10	14	13
Leptospirosis	44	74	62	52	39	44	72	47	76	63
Listeriosis	185	226	181	213	160	148	167	160	169	170
Lyme disease**	768	797	813	863	905	959	1,040	936	856	1,060
Pasteurellosis	430	392	438	455	466	538	535	581	602	641
Psittacosis	30	38	62	58	53	40	27	25	25	22
Q fever[67]	43	64	55	27	52	106	112	45	56	19
Rabies 'classical'	0	0	0	0	0	0	1[68]	0	0	0
Rabies EBLV	0	0	0	0	0	0	0	0	0	0
Salmonellosis (non-typhoidal)	12,849	12,094	10,321	9,482	8,573	8,492	7,919	7,493	7,250	8,558
STEC O157	1,001	828	950	1,034	773	1,182	837	787	883	665
Non-O157 STEC	2	6	11	15	9	12	22	47	169	211
Streptococcus suis	3	1	7	1	3	0	3	1	3	4
Taeniasis	88	99	95	70	108	90	65	74	65	70
Toxocariasis	1	1	2	1	8	0	5	3	5	3
Toxoplasmosis	90	104	405***	422	345	341	311	311	344	342
Trichinellosis	0	0	0	0	0	0	0	0	0	0
Yersiniosis (non-pestis)	33	55	39	47	47	51	44	52	58	39

* Provisional data
** Data has been updated following a validation exercise
*** Enhanced surveillance system introduced
‡ Data for previous years revised through use of an improved database query method and data validation

[65] H7N3
[66] H7N2
[67] Acute and chronic infections
[68] A UK National who visited India

Northern Ireland

	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015*
Anthrax	0	0	0	0	0	0	0	0	0	0
Avian Influenza	0	0	0	0	0	0	0	0	0	0
Mycobacterium bovis	3	1	2	1	1	2	0	4	2	5
Brucellosis	4	5	10	4	0	2	2	0	0	1
Campylobacteriosis	937	885	848	977	1,040	1,175	1,211	1,355	1,414	1,320
Cryptosporidiosis	134	85	119	118	119	140	177	161	143	204
Hantavirus	0	0	0	0	0	0	0	0	0	0
Hepatitis E	0	0	0	0	0	1	0	1	9	10
Hydatid disease	0	0	0	0	0	0	0	0	0	0
Leptospirosis	3	1	1	0	0	3	2	2	0	2
Listeriosis	6	5	11	4	2	3	7	2	4	6
Lyme disease	1	0	0	2	0	1	2	6	1	2
Pasteurellosis	9	3	2	7	0	1	2	3	1	2
Psittacosis	0	0	0	0	0	0	0	0	0	0
Q fever	13	5	11	2	0	1	1	0	0	0
Rabies 'classical'	0	0	1[69]	0	0	0	0	0	0	0
Rabies EBLV	0	0	0	0	0	0	0	0	0	0
Salmonellosis (non-typhoidal)	206	155	185	158	178	166	145	155	111	124
STEC O157	42	49	56	44	67	49	189[70]	61	40	32
Non-O157 STEC	0	0	0	0	0	0	2	1	62[71]	83
Streptococcus suis	0	0	0	0	0	0	0	0	0	0
Taeniasis	0	0	0	0	0	0	1	0	0	0
Toxocariasis	0	0	0	0	0	0	0	0	0	0
Toxoplasmosis	0	2	4	3	2	0	0	0	0	0
Trichinellosis	0	0	0	0	0	0	0	0	0	0
Yersiniosis	3	1	0	0	0	0	0	1	3	0

* Provisional data

[69] UK national who visited South Africa
[70] 142 of these cases were associated with one outbreak
[71] Includes PCR/culture results and all specimen types

Scotland

	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015*
Anthrax	1	0	0	13	34	0	1	1	0	0
Avian Influenza	0	0	0	0	0	0	0	0	0	0
Mycobacterium bovis	6	1	4	7	4	7	6	2	2	2
Brucellosis	1	2	0	1	1	6	3	2	1	0
Campylobacteriosis	4,865	5,192	4,878	6,415	6,601	6,365	6,333	6,163	6,632	6,275
Cryptosporidiosis	612	510	656	698	584	443	713	430	432	723
Hantavirus	0	0	0	0	0	0	0	0	1	0
Hepatitis E	3	4	4	3	13	15	78	95	193	186
Hydatid disease	0	0	0	0	1	3	0	3	2	3
Leptospirosis	3	6	13	4	3	5	4	1	2	3
Listeriosis	17	23	15	17	17	14	11	16	15	13
Lyme disease	171	230	285	228	308	229	207[72]	176	224	200
Pasteurellosis	51	62	57	97	120	129	129	133	173	212
Psittacosis	0	1	1	2	5	1	10	5	7	2
Q fever	144[73]	3	1	2	3	7	11	2	5	2
Rabies 'classical'	0	0	0	0	0	0	0	0	0	0
Rabies EBLV	0	0	0	0	0	0	0	0	0	0
Salmonellosis (non-typhoidal)	1,029	1,030	1,011	846	941	737	728	813	717	803
STEC O157	243	243	241	237	212	253	234	167	263	170
Non-O157 STEC	18	19	25	30	35	25	35	52	75	78
Streptococcus suis	1	1	0	1	1	1	0	2	0	0
Taeniasis	1	2	5	2	6	4	4	6	6	15
Toxocariasis	1	0	0	3	4	4	2	0	0	3
Toxoplasmosis	33	40	48	69	67	23[74]	17	14	26	29
Trichinellosis	0	0	0	0	1	0	0	0	1	0
Yersiniosis (non-pestis)	26	22	23	15	7	4	11	7	4	5

* Provisional data

[72] From 2012, reporting changed to acute cases only
[73] 142 of these cases were associated with one outbreak
[74] From 2011, reporting changed to acute cases only

Appendix 4: Government laboratory-confirmed cases or incidents of zoonotic infection in animals, 2006-2015[A]

United Kingdom [A]

	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
Anthrax	1	0	0	0	0	0	0	0	0	1
Avian Influenza (HPAI)[A]	0	1	2	0	0	0	0	0	1	1
New TB incidents in cattle herds [A]	5,044	5,454	6,286	5,893	5,881	6,300	6,810	6,292	6,115	6,534
M. bovis isolates in non-bovine animals (excludes badgers)	89	77	123	156	142	142	99	138	134	146
Mycobacterium species in non-bovine animals (excluding *M. bovis*)	186	146	107	149	144	140	16	26	16	7
Brucella abortus [A]	118	151	177	71	74	21	23	26	8	0
Brucella melitensis [A]	0	0	0	0	0	0	0	0	0	0
Brucella spp [A] (in marine mammals)	8	11	10	7	7	9	13	6	5	10
BSE	114	67	37	12	11	7	3	3	1	2
Campylobacter [A]	211	251	186	164	280	178	144	259	185	265
Chlamydiosis (*Chlamydia abortus*) fetopathy [A]	508	553	372	406	397	447	539	331	446	336
Cryptosporidiosis [A]	1,348 #	1,043 #	1,311†	1,436	1,768	1,381	1,896	1,874	1,374	1,191
Hydatid [A]	0	0	0	0	0	0	0	1	0	0
Leptospirosis [A]	157	197	238	89	113	50	85	69	59	34
Listeriosis [A]	148	152	216	196	237	165	219	201	206	157
Orf [A]	39	48	44	38	41	36	49	56	31	43
Pasteurella multocida [A]	N/A	336†	394	540	510	464	379	531	390	384
Psittacosis (*C. psittaci*) [A]	1	2	1	3	8	0	2	2	1	0
Q fever [A]	5	4	5	3	5	8	6	3	4	8
Rabies 'classical'	0	0	1	0	0	0	0	0	0	0
Rabies EBLV	1	1	2	1	0	0	0	0	1	1
Salmonella (all types) [A]	3,119	2,352	2,311	2,672	3,513	2,961	3,344	3,321	2,691	3,055
Streptococcus suis [A]	90	100	132	115	139	124	96	146	157	158
Swine Influenza [A]	13	10	16	18	40	37	38	33	32	28
Toxoplasmosis [A]	380	424	257	232	267	189	348	444	275	298
Trichinellosis	0	1	0	1	0	0	0	1	0	0
Yersiniosis [A]	28†	24†	32†	37	23	44	50	82	169	143

[A] The key to the UK and individual nation's data in appendix 4 appears as the final table at the end of this appendix.

† GB data.

Data only includes isolations from cattle and sheep in GB.

England [A]

	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
Anthrax	0	0	0	0	0	0	0	0	0	1
Avian Influenza (HPAI) [A]	0	1	2	0	0	0	0	0	1	1
New TB incidents in cattle herds [A]	2,719	3,196	3,766	3,363	3,632	3,802	3,919	3,890	3,804	3,960
M. bovis isolates in non-bovine animals (excludes badgers) †	78†	68†	119†	144†	134†	133†	98†	132	132†	141
Mycobacterium species in non-bovine animals (excluding *M. bovis*)	138†	104†	77†	122†	130†	140†	14	21	8	7
Brucella abortus [A]	0	0	0	0	0	0	0	0	0	0
Brucella melitensis [A]	0	0	0	0	0	0	0	0	0	0
Brucella spp [A] (in marine mammals)	0	0	6	4	0	1	7	0	2	0
BSE	78	39	25	9	11	5	2	1	1	1
Campylobacter [A]	117	125	94	93	148	93	73	129	105	182*
Chlamydiosis (*Chlamydia abortus*) fetopathy [A]	258	263	201	219	215	226	260	166	220	296†
Cryptosporidiosis [A]	N/A	N/A	1,311†	1,346†	1,674†	1,095†	650	681	549	762†
Hydatid [A]	0	0	0	0	0	0	0	0	0	0
Leptospirosis [A]	26	45	16	5	8	3	15	1	1	2
Listeriosis [A]	118†	132†	191†	177†	215†	146†	85	180†	151†	121†
Orf [A]	25	29	26	26	29	20	30	35	18	43†
Pasteurella multocida [A]	N/A	336†	281†	319†	368†	316†	116	319†	279†	253†
Psittacosis (*C. psittaci*) [A]	0	1	0	1	4	0	1	1	1	0
Q fever [A]	4	4	3	3	5	3	5	3	4	7
Rabies 'classical'	0	0	1	0	0	0	0	0	0	0
Rabies EBLV	1	1	2	0	0	0	0	0	1	0
Salmonella (all types) [A]	2,658*	1,948*	1,729*	2,198*	3,044*	2,392*	2,739*	2,685*	2,263†	2,783†
Streptococcus suis [A]	67	67	96	83	94	94	66	100†	90†	110†
Swine Influenza [A]	12	9	16	13	31	34	36	33	27	25
Toxoplasmosis [A]	170	166	93	115	101	84	146	132	212†	248†
Trichinellosis	0	0	0	0	0	0	0	1	0	0
Yersiniosis [A]	28†	24†	32†	33†	15†	22†	8	7	22†	17†

[A] The key to the UK and individual nation's data in appendix 4 appears as the final table at the end of this appendix.
† GB data.
* England and Wales data.

Northern Ireland [A]

	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
Anthrax	0	0	0	0	0	0	0	0	0	0
Avian Influenza (HPAI) [A]	0	0	0	0	0	0	0	0	0	0
New TB breakdowns in cattle herds per year and the % Herd incidence	1,513 6.23	1,264 5.35	1,274 5.58	1,293 5.61	1,160 5.12	1,386 6.00	1,695 7.32	1479 6.44	1,397 6.03	1,688 6.88
M. bovis isolates in non-bovine animals (excludes badgers)	11	9	4	12	8	9	1	0	2	1
Mycobacterium species in non-bovine animals (excluding *M. bovis*)	48	42	30	27	14	0	0	0	0	0
Brucella abortus- number of reactor herds per year and confirmed infected herds	118 60	151 53	177 34	71 13	74 25	21 4	23 1	26 0	8 0	0 0
Brucella melitensis [A]	0	0	0	0	0	0	0	0	0	0
Brucella spp [A] (in marine mammals)	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	0	N/A
BSE	10	14	4	3	0	2	1	0	0	0
Campylobacter [A]	47	36	35	15	46	25	35	35	13	19
Chlamydiosis (*Chlamydia abortus*) fetopathy [A]	61	40	36	39	55	61	68	51	56	40
Cryptosporidiosis [A]	N/A	N/A	N/A	90	94 Φ	286 Φ	736 Φ	668 Φ	404 ΦC	429
Hydatid [A]	N/A	0	0	0	0	0	0	0	0	0
Leptospirosis [A]	113	106	199	84	105	46	70	65	56	29
Listeriosis [A]	30	20	25	19	22	19	45	21	55	36
Orf [A]	2	3	1	1	1	1	0	3	2	0
Pasteurella multocida [A]	N/A	N/A	113	221	142	148	140	212	111	131
Psittacosis (*C. psittaci*) [A]	0	0	0	0	0	0	0	0	0	0
Q fever [A]	0	0	0	0	0	0	0	0	0	0
Rabies 'classical'	0	0	0	0	0	0	0	0	0	0
Rabies EBLV	0	0	0	0	0	0	0	0	0	0
Salmonella (all types) [A]	184	223	382	252	345	354	426	503	428	272
Streptococcus suis [A]	5	17	10	14	21	12	19	46	67	48
Swine Influenza [A]	0	0	0	5	4	0	0	0	5	3
Toxoplasmosis [A]	53	54	64	44	51	45	100	229	63	50
Trichinellosis	0	1	0	1	0	0	0	0	0	0
Yersiniosis [A]	N/A	N/A	N/A	4	8	22	34	72	147*	126

[A] The key to the UK and individual nation's data in appendix 4 appears as the final table at the end of this appendix.
Φ Data only includes isolations from cattle and sheep.
ΦC Data only includes isolations from cattle.
*Marked increase is a consequence of 2014 being the first full year of using selective media at AFBI, making Yersinia detection much easier.

Scotland [A]

	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
Anthrax	0	0	0	0	0	0	0	0	0	0
Avian Influenza (HPAI) [A]	0	0	0	0	0	0	0	0	0	0
New TB incidents in cattle herds [A]	44	58	47	49	45	43	54	28	47	40
M. bovis isolates in non-bovine animals (excludes badgers) †	78†	68†	119†	144†	134†	133†	98†	0	132†	0
Mycobacterium species in non-bovine animals (excluding *M. bovis*)	138†	104†	77†	122†	130†	140†	2	5	4	0
Brucella abortus [A]	0	0	0	0	0	0	0	0	0	0
Brucella melitensis [A]	0	0	0	0	0	0	0	0	0	0
Brucella spp [A] (in marine mammals)	8	11	4	3	7	8	6	6	3	9
BSE	12	7	1	0	0	0	0	0	0	0
Campylobacter [A]	28	44	35	39	47	34	25	55	36	64
Chlamydiosis (*Chlamydia abortus*) fetopathy [A]	97	140	65	66	52	79	103	53	76	296†
Cryptosporidiosis [A]	N/A	N/A	1311†	1346†	1674†	1095†	309	319	212	762†
Hydatid [A]	0	0	0	0	0	0	0	0	0	0
Leptospirosis [A]	16	41	22	0	0	0	0	3	2	2
Listeriosis [A]	118†	132†	191†	177†	215†	146†	59	180†	151†	121†
Orf [A]	10	8	10	6	8	7	8	13	7	43†
Pasteurella multocida [A]	N/A	336†	281†	319†	368†	316†	99	319†	279†	253†
Psittacosis (*C. psittaci*) [A]	1	1	1	1	4	0	1	1	0	0
Q fever [A]	0	0	0	0	0	0	0	0	0	0
Rabies 'classical'	0	0	0	0	0	0	0	0	0	0
Rabies EBLV	0	0	0	1	0	0	0	0	0	0
Salmonella (all types) [A]	277	181	200	222	124	215	179	133	2,263 †	2,783 †
Streptococcus suis [A]	14	14	26	17	22	18	8	100†	90†	110†
Swine Influenza [A]	1	1	0	0	5	3	2	0	0	0
Toxoplasmosis [A]	94	142	68	52	91	31	66	46	212†	248†
Trichinellosis	0	0	0	0	0	0	0	0	0	0
Yersiniosis [A]	28†	24†	32†	33†	15†	22†	8	1	22†	17†

[A] The key to the UK and individual nation's data in appendix 4 appears as the final table at the end of this appendix.
† GB data.

Wales [A]

	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
Anthrax	1	0	0	0	0	0	0	0	0	0
Avian Influenza (HPAI) [A]	0	0	0	0	0	0	0	0	0	0
New TB incidents in cattle herds [A]	767	935	1,198	1,186	1,039	1,046	1,109	877	858	836
M. bovis isolates in non-bovine animals (excludes badgers) †	78†	68†	119†	144†	134†	133†	98†	6	132†	4
Mycobacterium species in non-bovine animals (excluding *M. bovis*)	138†	104†	77†	122†	130†	140†	0	0	4	0
Brucella abortus [A]	0	0	0	0	0	0	0	0	0	0
Brucella melitensis [A]	0	0	0	0	0	0	0	0	0	0
Brucella spp [A] (in marine mammals)	0	0	0	0	0	0	0	0	0	1
BSE	14	7	7	0	0	0	0	2	0	1
Campylobacter [A]	19	46	22	17	39	26	11	40	31	182*
Chlamydiosis (*Chlamydia abortus*) fetopathy**	92	110	70	82	75	81	108	61	94	296†
Cryptosporidiosis [A]	N/A	N/A	1311†	1346†	1674†	1095†	201	206	209	762†
Hydatid [A]	0	0	0	0	0	0	0	1	0	0
Leptospirosis [A]	2	5	1	0	0	1	0	0	0	1
Listeriosis [A]	118†	132†	191†	177†	215†	146†	30	180†	151†	121†
Orf [A]	2	8	7	5	3	8	11	5	4	43†
Pasteurella multocida [A]	N/A	336†	281†	319†	368†	316†	24	319†	279†	253†
Psittacosis (*C. psittaci*) [A]	0	0	0	1	0	0	0	0	0	0
Q fever [A]	1	0	2	0	0	5	1	0	0	1
Rabies 'classical'	0	0	0	0	0	0	0	0	0	0
Rabies EBLV	0	0	0	0	0	0	0	0	0	1
Salmonella (all types) [A]	2,658*	1,948*	1,729*	2,198*	3,044*	2,392*	2,739*	2,685*	2,263 †	2,783 †
Streptococcus suis [A]	4	2	0	1	2	0	3	100†	90†	110†
Swine Influenza [A]	0	0	0	0	0	0	0	0	0	0
Toxoplasmosis [A]	63	62	32	21	24	29	36	37	212†	248†
Trichinellosis	0	0	0	0	0	0	0	0	0	0
Yersiniosis [A]	28†	24†	32†	33†	15†	22†	0	2	22†	17†

[A] The key to the UK and individual nation's data in appendix 4 appears as the final table at the end of this appendix.
† GB data.
* England and Wales data.

Key to all other tables in appendix 4

The tables in appendix 4 are not intended to provide a definitive list of all zoonotic pathogens, but include those for which data are available (notifiable/reportable and those recorded by the APHA's Veterinary Diagnostic Analysis (VIDA) system (GB data) and /or AFBI systems). The VIDA data provides figures only for new incidents with relevant VIDA codes (although numbers of incidents in this report may differ marginally from those published in the 2015 FZ2100 annual report due to updated database recording). The FSA supplied the Trichinellosis data. The species for which diagnoses may be recorded and other notes relevant in interpreting the other tables in appendix 4 are provided below.

<table>
<tr><th colspan="2">Diagnosis</th><th>Cattle</th><th>Sheep</th><th>Goats</th><th>Pigs</th><th>Birds [1]</th><th>Misc.</th><th>Wildlife [2]</th></tr>
<tr><td colspan="2">Anthrax (incidents)</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td colspan="2">Avian influenza (only highly pathogenic strains). Tables show number of HPAI incidents p.a.</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td colspan="2">New TB incidents in cattle herds
New TB incidents in cattle herds represent herds which were previously OTF but either had cattle that reacted to a tuberculin test or had a tuberculous animal disclosed by routine meat inspection at slaughter, during the period shown. (Figures for Wales include incidents where OTF status has been withdrawn for epidemiological reasons only). Data for GB countries for new TB incidents in cattle herds included in the relevant tables in appendix 4 is not directly comparable across the individual tables. Since 2008 the GB figures are based on data derived from APHA's Sam system. Sam is an APHA IT system that holds information on all customers, and helps manage specific work areas such as TB. Prior to 2008 a different data system was in use and the data produced is not exactly comparable with the statistics produced from Sam. In addition the overall UK totals are not the sum of the number of new incidents in each national table as a balancing amount is included in the overall GB total for cases where the exact region is unknown, and is therefore only reflected in this UK figure. This balancing amount in 2015 was ten, nine in 2014, 18 in 2013, 33 in 2012, 23 in 2011, five in 2010, two in 2009, one in 2008, one in 2007 and one in 2006.</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td colspan="2">M. bovis isolates in non-bovine animals
(excludes badgers)</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td colspan="2">Mycobacterium in non-bovine animals
(excluding M. bovis)</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Brucella abortus</td><td rowspan="3">Confirmed cases are statutorily reportable under Zoonoses Order 1989.</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Brucella melitensis</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Brucella spp.
(in marine mammals)</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
</table>

Diagnosis	Cattle	Sheep	Goats	Pigs	Birds [1]	Misc.	Wildlife [2]
BSE							
Campylobacter Confirmed cases obtained through scanning surveillance. Data for GB countries included in the relevant tables in appendix 4 has been derived from the incidents recorded on APHA's Veterinary Diagnostic Analysis (VIDA) system. This uses strict criteria and so not all isolated pathogens are included in the relevant tables (pet animal diagnoses are not included). In NI data from Campylobacter diagnoses in pigs are also included.							
Chlamydiosis (*Chlamydia abortus*) fetopathy Confirmed cases obtained through scanning surveillance (VIDA database in GB. NI data is only for diagnoses from sheep and goats).							
Cryptosporidiosis Confirmed cases obtained through scanning surveillance (VIDA database in GB).							
Hydatid Confirmed cases obtained through scanning surveillance (from VIDA database in GB). Therefore tables in appendix 4 state laboratory, not abattoir, diagnoses.							
Leptospirosis Confirmed incidents obtained through scanning surveillance (VIDA database in GB).							
Listeriosis Confirmed cases obtained through scanning surveillance (VIDA database in GB).							
Pasteurella multocida Confirmed cases obtained through scanning surveillance (VIDA database in GB).							
Psittacosis (*C. psittaci*) Confirmed incidents obtained through scanning surveillance (VIDA database in GB).							
Q Fever (*Coxiella burnetii*) Confirmed incidents obtained through scanning surveillance (VIDA database in GB).							
Rabies 'classical'							
Rabies EBLV							

Diagnosis	Cattle	Sheep	Goats	Pigs	Birds [1]	Misc.	Wildlife [2]
***Salmonella* (all types)** Confirmed cases statutorily reportable under Zoonoses Order 1989. Data for GB countries included in this table relates only to *Salmonella* isolations from the statutory species (cattle, sheep, goats, pigs, horses, deer, rabbits, chickens, turkeys, ducks, geese, partridges, pheasants, guinea fowl, quail and pigeons). In NI the Zoonoses Order 1991 lists any mammal except man; any 4 footed beast which is not a mammal; snakes; birds of every species as species for which salmonella isolations must be reported. Therefore isolations from all these species are included in the NI data.							
Streptococcus suis Confirmed cases obtained through scanning surveillance (VIDA database in GB).							
Swine influenza Confirmed cases obtained through scanning surveillance (VIDA database in GB).							
Toxoplasmosis Confirmed incidents obtained through scanning surveillance (VIDA database in GB).							
Trichinellosis Data from FSA surveillance.							
Yersiniosis Confirmed cases obtained through scanning surveillance (VIDA database in GB).							

Shaded boxes indicate a diagnosis is not available for that species.

[1] Includes both domestic and wild birds, specific species included = domestic fowl (chickens), turkeys, ducks, geese, guinea fowl, pheasants, partridges, pigeons and quail. For AI any avian species to be included.

[2] Mammals only (includes rabbits and deer).

Misc. = miscellaneous exotic farmed or other species (includes horses and farmed deer).

Appendix 5: Food vehicles associated with foodborne gastrointestinal outbreaks in 2015 in the UK, in relation to *Campylobacter, Listeria monocytogenes, Salmonella*, and STEC O157

Food vehicle category	Campylobacter	Listeria monocytogenes	Salmonella	STEC O157**
Poultry meat	7	0	3	0
Red meat	1	0	1	1
Game	0	0	0	1
Cross contaminated raw and cooked meats	0	0	0	1
Crustacean & shellfish	0	0	0	0
Vegetables, Salads & fruits	0	0	0	2
Eggs & egg dishes	0	0	3	0
Milk & diary product	0	0	0	0
Composite/Mixed foods	2	0	1	0
Unknown	1	0	3	1
Total*	11	0	11	6

* The total may differ from the total number of foodborne outbreaks reported as more than one food vehicle may be identified in a single outbreak.

**Outbreak data derived from both eFOSS and the National Enhanced Surveillance System for STEC (NESSS) in England.

Appendix 6: Animal population

Number of livestock in the UK in 2015

	England*	Wales**	Scotland***	N. Ireland†	UK
Cattle	5,384,753	1,118,979	1,805,986	1,608,851	9,918,569
Sheep	15,141,563	9,503,977	6,701,376	1,989,674	33,336,590
Pigs	3,826,342	25,295	317,748	569,738	4,739,123
Poultry	125,433,109	7,844,922	13,055,168	21,245,736	167,578,935
Goats	82,033	10,116	4,751	3,800	100,700
Farmed Deer	20,138	994	7,236	2,319	30,687
Horses	184,916	50, 462	36, 408	11,000	282,786

Data sourced via the Radar Veterinary Surveillance database (Defra)

* obtained from the June 2015 England Agricultural Census

** obtained from the June 2015 Wales Agricultural Census

*** obtained from the June 2015 Scottish Agricultural Census

† Northern Ireland data provided by Department of Agriculture and Rural Development Northern Ireland, 2015 from Agriculture Survey for 2015 and APHIS records.

Note that figures in the above table are a snapshot of the population at a specific time during the year, as shown in the table footnotes. For further information on data quality including accuracy and comparability contact: vetsurveillance@defra.gov.uk

Number of pets owned in the UK in 2015[75]

PFMA (Pet Food Manufacturers' Association) research shows that in 2015 46% of UK households owned at least one pet. This would be approximately 12million households with pets, out of approximately 26million UK households in total. The pet population stands at around 58 million.

Historically, a sample of over 2,000 people were interviewed each year, but in the last two years a sample of over 4,000 people have been interviewed. In order to further reduce statistical uncertainty, survey results are averaged over 2 years, giving an effective sample of over 8,000 people. In 2015 PFMA teamed up with Cats Protection and Dogs Trust which enabled a larger sample size in 2015.

The table below shows the estimated population of UK pets, as well as a breakdown of the most popular pets, in 2014-2015.

Species	Approximate number of pets (millions)
Dogs	8.5
Cats	7.4
Rabbits	1.0
Birds (indoor)	0.5
Guinea Pigs	0.7
Hamsters	0.4
Outdoor fish	17.1
Indoor fish	19.9
Domestic fowl	0.7
Lizards	0.3

[75] Source: Pet Food Manufacturers' Association: www.pfma.org.uk

Appendix 7: Further reading

General further reading

Advisory Committee on the Microbiological Safety of Food: Report on microbial antibiotic resistance in relation to food safety. The Stationery Office, ISBN 0 11 322283 1.
http://acmsf.food.gov.uk/acmsfreps/acmsfreports

Defra Publications - Zoonoses Reports UK
https://www.gov.uk/government/collections/zoonoses-reports

Food Standards Agency: A report on the study of Infectious Intestinal Disease in England, The Stationery Office, ISBN 0 11 322308 0
www.food.gov.uk/science/research/foodborneillness/microfunders/intestinal

Food Standard Agency – Measuring foodborne Illnesses levels
http://www.food.gov.uk/science/microbiology/fds/58736

Public Health England - Zoonoses web pages
https://www.gov.uk/government/collections/zoonotic-diseases-zoonoses-guidance-data-and-analysis

Health Protection Scotland – Outbreaks in Scotland in 2015
http://www.hps.scot.nhs.uk/outbreaks/

HSE zoonoses guidance:
http://www.hse.gov.uk/agriculture/topics/zoonoses.htm

Joint Agency Guidelines for the Investigation of Zoonotic Disease (England and Wales)
https://www.gov.uk/government/publications/zoonotic-diseases-investigation-guidelines

Guidelines for the investigation of zoonotic disease in Scotland
http://www.documents.hps.scot.nhs.uk/about-hps/hpn/zoonoses-guidelines.pdf

APHA - Non-Statutory Zoonoses Reports
https://www.gov.uk/government/publications/non-statutory-zoonoses-disease-surveillance-reports-2015

Oxford Textbook of Zoonoses: Biology, Clinical Practice and Public Health Control, 2nd Ed. (Palmer, Soulsby, Torgerson and Brown) OUP ISBN 9780198570028

Disease specific further information:

Useful links can also be found at the end of each A-Z section.

Appendix 8: List of Abbreviations/ Acronyms

ACMSF	Advisory Committee on Microbiological Safety of Food
AFBI	Agri-Food and Biosciences Institute
AI	Avian Influenza
APHA	Animal and Plant Health Agency
BPEX	British Pig Executive
BSE	Bovine Spongiform Encephalopathy
bTB	Bovine Tuberculosis
CCDC	Consultant in Communicable Disease Control
CJD	Creutzfeldt-Jakob Disease
DAERA	Department of Agriculture, Environment and Rural Affairs (Northern Ireland)
Defra	Department for Environment, Food and Rural Affairs
DH	Department of Health
EAE	Enzootic Abortion of Ewes
EBLV	European Bat Lyssavirus
EU	European Union
FSA	Food Standards Agency
FSS	Food Standards Scotland
GB	Great Britain (England, Wales, Scotland)
HAIRS	Human Animal Infections and Risk Surveillance Group
HEV	Hepatitis E Virus
HPAI	Highly Pathogenic Avian Influenza
HPS	Health Protection Scotland
HSE	Health and Safety Executive
LA	Local Authority
LPAI	Low Pathogenicity Avian Influenza
NCP	National Control Programme
NHSBT	National Health Service Blood and Transport

OBF	Officially Brucellosis Free
OTF	Officially tuberculosis free
PCR	Polymerase Chain Reaction
PHA	Public Health Agency (Northern Ireland)
PHE	Public Health England
PHW	Public Health Wales
RIDDOR	Reporting of Injuries, Diseases and Dangerous Occurrences Regulations (HSE)
SEOV	Seoul hantavirus
SG	Scottish Government
SNP	Single Nucleotide Polymorphisms
SRUC	Scotland’s Rural Colleges
STEC	Shiga toxin producing *Escherichia coli* (previously termed ‘VTEC’: Verocytotogenic-producing *Escherichia coli*)
TB	Tuberculosis
TSE	Transmissible Spongiform Encephalopathy
UK	United Kingdom (England, Wales, Scotland, Northern Ireland)
UKZADI	United Kingdom Zoonoses, Animal Diseases and Infections Group
vCJD	Variant Creutzfeldt-Jakob disease
VIDA	Veterinary Investigation Diagnosis Analysis Database
VMD	Veterinary Medicines Directorate
VRG	Veterinary Risk Group
VTEC	Verocytotoxigenic *Escherichia coli* (now replaced by ‘STEC’: Shiga toxin producing *Escherichia coli*)
WG	Welsh Government
WGS	Whole Genome Sequencing

Appendix 9: Acknowledgements

This report was produced by a group under the Chairmanship of Dilys Morgan, PHE. The group contained representatives of, or received assistance from, the following organisations:

Agri Food and Biosciences Institute
Veterinary Sciences Division, Stoney Road, Stormont, Belfast, BT4 3SD
www.afbini.gov.uk

Animal and Plant Health Agency (APHA)
New Haw, Addlestone, Surrey, KT15 3NB
https://www.gov.uk/government/organisations/animal-and-plant-health-agency

Brucella reference unit (BRU)
Royal Liverpool and Broadgreen University Hospital, Prescott Street, Liverpool, L9 8XP
https://www.gov.uk/government/collections/brucella-reference-unit-bru

***Cryptosporidium* Reference Unit** (PHE Collaborating Laboratory)
Public Health Wales, Microbiology Swansea, Singleton Hospital, Swansea, SA2 8QA
www.wales.nhs.uk/sites3/page.cfm?orgId=457&pid=25284

Department of Agriculture, Environment and Rural Affairs (Northern Ireland) (DAERA)
Dundonald House, Upper Newtownards Road, Belfast, BT4 3SB
www.daera-ni.gov.uk

Department for Environment, Food and Rural Affairs (Defra)
Area 5A, Nobel House, 17 Smith Square, London, SW1P 3JR
https://www.gov.uk/government/organisations/department-for-environment-food-rural-affairs

Department of Health
Richmond House 79 Whitehall, London, SW1A 2NS
www.dh.gov.uk

Department of Health, Social Services & Public Safety (Northern Ireland)
Castle Buildings, Stormont, Belfast, BT4 3SJ
www.dhsspsni.gov.uk

Food Standards Agency (FSA)
Aviation House, 125 Kingsway, London, WC2B 6NH

www.food.gov.uk

Health Protection Scotland (HPS)
Meridian Court, 5 Cadogan Street, Glasgow, G2 6QE
www.hps.scot.nhs.uk

Hospital for Tropical Diseases
2nd Floor Mortimer Market Centre, Mortimer Market, London, WC1E 6JB
http://www.thehtd.org/

***Leptospira* Reference Unit** (PHE Collaborating Laboratory)
Department of Microbiology and Immunology, County Hospital, Hereford, HR1 2ER
https://www.gov.uk/government/collections/leptospira-reference-unit-lru

National Lyme Disease Testing Service (Scotland)
Microbiology department, Raigmore Hospital, Inverness, IV2 3UJ
http://www.hps.scot.nhs.uk/reflab/STRL.aspx

Public Health Agency (Northern Ireland)
18 Ormeau Avenue, Belfast, BT2 8HS
www.publichealth.hscni.net/

Public Health England (PHE)
PHE Colindale, 61 Colindale Avenue, London, NW9 5EQ
www.phe.gov.uk

Public Health Wales
Communicable Disease Surveillance Centre, Health Protection Division, The Temple of Peace and Health, Cathays Park, Cardiff, CF10 3NW
http://www.wales.nhs.uk/sitesplus/888/page/43899/

Rare and Imported Pathogens Laboratory, Porton
Public Health England Porton Down, Salisbury, Wiltshire, SP4 0JG
https://www.gov.uk/government/collections/rare-and-imported-pathogens-laboratory-ripl

Scotland's Rural College
West Mains Road, Edinburgh, EH9 3JG
http://www.sruc.ac.uk/

Scottish *E. coli* O157/VTEC Reference Laboratory (SERL)
Department of Laboratory Medicine, Royal Infirmary of Edinburgh, Edinburgh, EH16 4SA
http://www.hps.scot.nhs.uk/reflab/SERL.aspx

Scottish Government, Rural Directorate
Saughton House, Broom House Drive, Edinburgh, EH11 3XD
www.scotland.gov.uk

Scottish Parasite Diagnostic and Reference Laboratory
House-on-the-Hill, Stobhill Hospital, 133 Balornock Road, Glasgow, G21 3UW
http://www.nhsggc.org.uk/about-us/professional-support-sites/microbiology/scottish-microbiology-reference-laboratories/scottish-parasite-diagnostic-reference-laboratory/

Scottish *Salmonella* Reference Laboratory
North Glasgow University Hospitals NHS Trust, 133 Balornock Road, Glasgow, G21 3UW
http://www.nhsggc.org.uk/about-us/professional-support-sites/microbiology/scottish-microbiology-reference-laboratories/scottish-salmonella-shigella-c-difficile-reference-laboratory/

Scottish Toxoplasma Reference Laboratory
Microbiology department, Raigmore Hospital, Inverness, IV2 3UJ
http://www.hps.scot.nhs.uk/reflab/STRL.aspx

***Toxoplasma* Reference Unit** (PHE Collaborating Laboratory)
Public Health Wales, Microbiology Swansea, Singleton Hospital, Swansea, SA2 8QA
www.wales.nhs.uk/sites3/page.cfm?orgId=457&pid=25359

Welsh Government (WG)
Cathays Park, Cardiff, CF10 3NQ
www.wales.gov.uk