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Authors

Dr Chris Rands

christopher.rands@phgfoundation.org

Dr Sobia Raza

sobia.raza@phgfoundation.org

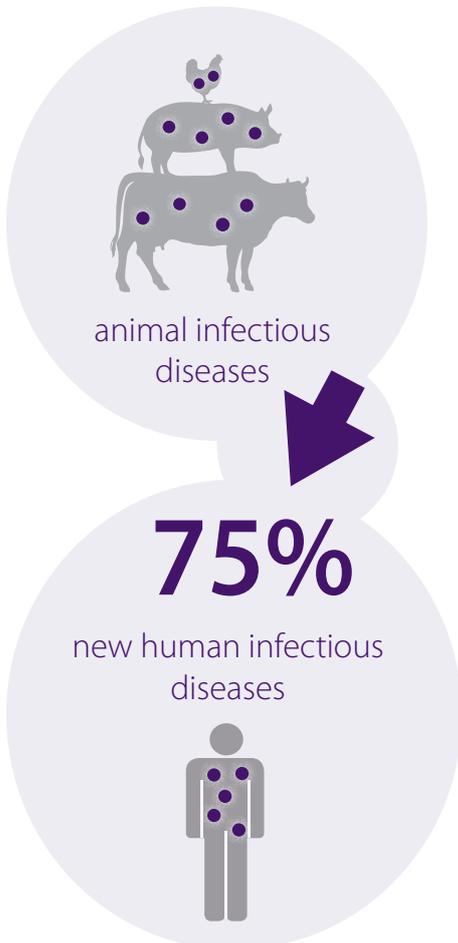
Dr Leila Luheshi

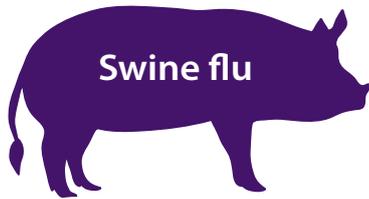
leila.luheshi@phgfoundation.org

One health genomics - why animal diseases matter for human health

In humans, pathogen genomics is beginning to improve diagnosis of infections, tracking of outbreaks and identification of antimicrobial resistance. Could a cross-species ('one health') approach, to include similar efforts with animals, benefit both animal and human populations?

- Animals are the source of around **75%** of newly emerging human infectious diseases
- The use of antibiotics to treat bacterial infections in livestock means that if these infections are transmitted to humans they may already be **resistant** to many of the antibiotics we use to treat them
- Epidemiological analyses to trace the transmission between animal populations and / or between animal and humans are rarely conducted
- Pathogen whole genome sequencing (WGS) has several advantages over conventional methods for diagnosing pathogen infections and characterising outbreaks, namely rapid diagnosis, high sensitivity, and flexible analysis
- Implementing a genomic cross-species surveillance (**one health**) would enable earlier detection of pathogens and their transmission within and between species
- Wider policy issues surrounding the prospective implementation of pathogen genomics in a clinical and public health context are detailed in our report [***Pathogen Genomics Into Practice***](#)





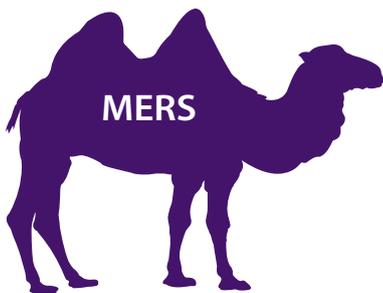
How is surveillance of animal pathogens currently performed in Great Britain?

The Animal and Plant Health Agency (APHA), together with Scotland's Rural College (SRUC), are responsible for performing testing for animal pathogens in Great Britain, through a network of national laboratories. The diagnostic methods currently used include pathology, serology (examining antibodies in the blood) and a relatively small number of specific molecular tests.



Only a handful of known pathogens are monitored by prospective (or routine) surveillance of livestock and the number of animals tested is a small proportion. However the economic burden of such testing may be considerable.

Retrospective surveillance, *i.e.* detection of trends in data from samples submitted following suspicion of disease, or having died from a disease, is most common. Animal to human transmission of infection is determined retrospectively through the combination of surveillance information from animal and human samples. Although less costly to do, the outcomes of retrospective surveillance often come too late to intervene.



Case study 1

Retrospective sequencing and analysis of influenza A (H1N1) samples from the 2009 swine flu outbreak suggested that the virus had been circulating unnoticed in a pathogenic form for years in pigs prior to the human outbreak. If prospective genomic surveillance was in place in pigs then this information could have helped prevent the human outbreak.



Case study 2

While camels were implicated as potential vectors for transmission of the MERS virus to humans prior to genomic analysis, it was only once the virus isolated from camels could be shown to be genetically identical to that found in people who had been in contact with camels that the health authorities, such as the [WHO](#), were able to issue clear advice on staying away from the camels. Asking camel farmers to do this has significant social and economic cost, and so accurate information is important.





How can genomics contribute to the surveillance of animal pathogens?

Pathogen whole genome sequencing (WGS) using next generation sequencing, with downstream bioinformatics analyses, has several advantages over conventional methods for diagnosing animal pathogen infections and characterising outbreaks:

Rapid diagnosis

Genomic analysis could turn around diagnostic results faster than other approaches once a routine service has been setup, potentially taking less than 48 hours from clinical sample to whole genome sequence. However, culturing samples, which is required for current genomic methods that do not employ a **metagenomic** approach, takes considerably longer (sometimes over one month).

High sensitivity

Epidemiological information can be inferred from WGS analyses about the relationship between different individual pathogens, allowing outbreak clusters to be accurately identified. By contrast, traditional microbiological approaches are limited in the sensitivity and specificity with which they can detect transmission events.

Flexible analysis

Once setup, the protocols are fairly generically applicable regardless of the specific type of pathogen being investigated and can incorporate additional analyses such as testing for antibiotic resistance. Under traditional workflows, separate tests need to be conducted to determine drug susceptibility.



Implementing genomic cross-species surveillance - what needs to be considered?

There are several considerations that need to be addressed in order to achieve effective and efficient implementation of genomic cross-species surveillance:

Investment

Animal pathogen genomic surveillance services need to be established. With sequencing infrastructure already at APHA, the main additional costs would be setting up new workflows and recruiting additional bioinformatics expertise. Closer collaboration with Public Health England (PHE), the governmental body responsible for human pathogen surveillance, could help mitigate these costs.

Collaboration and evaluation

Research between medical and veterinary practices, and academic institutes, such as the [cGPS](#), [GMI](#), [COMPARE](#), and other [initiatives](#), should be encouraged to facilitate the development of more standardised analytical methods and better databases for human-animal pathogen surveillance. Systematic health economic analyses is needed to determine when implementing WGS is cost-effective for the public health utility it provides.

Accreditation

Accreditation is required at national and international levels for both laboratories and diagnostic tests. NGS methods for detecting animal pathogens have not yet been approved. Until they are, NGS cannot replace existing accredited methods.

Coordination

APHA and PHE are working on parallel methodological protocols for conducting genomic analyses and guidelines for sharing their data and sensitive metadata. Further strategic coordination and knowledge sharing across government departments is desirable, building on the [HAIRS](#) initiative. Ultimately surveillance should be coordinated at an international level.

Prospective surveillance?

Prospective molecular surveillance, if well coordinated with related human pathogen surveillance, could detect disease outbreaks sooner, acting as an early warning system to reduce the risk of transmission to humans, decreasing the mortality and morbidity costs. Such surveillance could [minimise the economic costs](#) of controlling the outbreaks within the livestock. However, for very rare animal diseases it may not be cost effective. Context specific cost-benefit analysis is required to determine when prospective surveillance is feasible and desirable.