

Whole genome sequencing provides researchers with a better understanding of bovine TB outbreaks

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The use of whole bacterial genome sequencing will allow scientists to inexpensively track how bovine tuberculosis (TB) is transmitted from farm to farm, according to research presented this week at the Society of General Microbiology Autumn Conference.

Bovine TB is primarily a disease of cattle, caused by the bacterium *Mycobacterium bovis*. The disease is hugely expensive, costing the Government over £91 million in England in 2010/11.

Researchers from the University of Glasgow, working in collaboration with the Agri-Food and Biosciences Institute and the Department of Agriculture and Rural Development, Northern Ireland, sequenced the genomes of 147 *M. bovis* samples, collected over a decade of outbreaks in Northern Ireland. By combining the genomic sequences of the bacteria with information about when and where the sample was isolated, in addition to data on the movement of cattle from farm to farm, the researchers were able to build a detailed forensic map of bovine TB spread.

The results showed that, even on a scale of few kilometres, *M. bovis* samples from neighbouring farms were more closely genetically related than geographically distant farms that had had cattle moved between them. This finding confirms that, while long distance spread via cattle movements plays a role, local transmission mechanisms appear to drive

the spread of the disease, although the researchers are unable to determine what these are at the present time.

Hannah Trewby, who is presenting this work says, "The inclusion of whole [genome](#) information in our data will give us unprecedented insight into how bovine TB spreads, and will help us to develop better control methods for the disease."

The role of infected wild badgers in spreading bovine TB remains controversial. This work will help to clarify the role that badgers may have in [spreading the disease](#) and continue to build a sound scientific evidence base on which [control measures](#) can be built.

Professor Rowland Kao, the Principle Investigator of the project, explains, "Our results suggests that the establishment and local persistence of the pathogen in cattle has a distinct spatial signature—we believe that explaining this signature is the key to quantifying the role that badgers play in the persistence of bovine TB in Britain and Ireland. While we do not yet have sufficient data to be definitive, it is clear that whole [genome sequencing](#) of the bacterium will play an important part in solving this puzzle. Given the extensive collection of samples already collected from [cattle](#) and badgers, we are optimistic that this approach will help accumulating the right scientific evidence over the coming years to tackle this important problem."

Provided by Society for General Microbiology

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