Bringing genomics into bovine tuberculosis control in Ireland

In association with

Dr Joseph Crispell and Professor Stephen Gordon from University College Dublin, talk about a recently funded project that aims to use bacterial genomics to help control bovine tuberculosis across Ireland

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bTB ERADICATION BY 2030

Control of bovine tuberculosis (bTB) cost more than €84 million in 2017, according to 2018 data from the Department of Agriculture, Food and the Marine (DAFM). Control is essential to reduce the burden of infected animals, to protect animal welfare and public health, and to ensure market access. With the numbers of cattle infected with the bTB causative agent, *Mycobacterium bovis*, gradually falling across the country, the DAFM has called for eradication of bTB by 2030 (More, 2019). To eradicate bTB in Ireland, we will need to use the most up-to-date tools. As *M. bovis* infection levels continue to drop, we'll need to be able to accurately track infection transmission and identify the source of each new herd outbreak.

MOLECULAR TYPING METHODS

Over the last three decades, molecular typing methods that rely on identifying unique DNA patterns in *M. bovis* have been crucial for tracking infection (Allen et al, 2013). Current methods, variable number tandem repeat typing (VNTR) and spacer-oligotyping (spoligotyping), use specific regions of the bacteria's genome to characterise patterns of repeated sets of nucleotides (Roring et al, 1998; Roring et al, 2004). Such molecular methods have led to important insights, such as revealing the role badger populations play as sources of infection (Furphy et al, 2012).

GENOMICS AS THE NEXT MOLECULAR TYPING TOOL

The latest advance in molecular typing is to move beyond specific sequences, and instead examine the entire genome of the pathogen. This approach is termed whole genome sequencing. Instead of being limited to specific regions of the bacterial genome, whole genome sequencing looks at the 4.3 million nucleotides that make up the *M. bovis* genome to identify differences between strains. As such, whole genome sequencing offers a greater degree of resolution to differentiate isolates of *M. bovis* when compared to VNTR or spoligotyping. Whole genome sequencing will provide exquisite detail for tracking

M. bovis transmission. To establish and implement whole genome sequencing for *M. bovis* in Ireland, we have recently started a new project funded by the DAFM and the Department of Agriculture, Environment and Rural Affairs (DAERA) in Northern Ireland: Bovine TuBerculosis GENomics in IrEland (or BTBGENIE).

BTBGENIE will be bringing together a team of key researchers from institutes across the island of Ireland including: the DAFM Central Veterinary Research Laboratory, Queen's University Belfast, the Agri-Food and Biosciences Institute in Northern Ireland, and UCD. This will build upon our previous research, where we have used genomics to reveal that deer may be playing an important role in cattle infection in Co. Wicklow (Crispell et al, 2020). In BTBGENIE, we aim to develop the necessary tools to use genomics in routine bTB surveillance across all of Ireland and, hence, help support the ultimate goal of bTB eradication across the island of Ireland.

References available on request.