

ETM/421 - Genomic epidemiology of Legionnaires' disease in Scotland: towards effective outbreak investigation

The environmental bacterium *Legionella pneumophila* can cause human infections (legionellosis) including the severe community-acquired pneumonia known as Legionnaires' disease (LD). In recent years, Scotland has had multiple outbreaks of legionellosis that have caused significant morbidity, mortality and public health concern. Our recent investigation into the Edinburgh LD outbreak of 2012 revealed that outbreaks may be caused by multiple genetic subtypes of pathogenic *Legionella* which are persisting in environmental water sources, complicating source attribution. In the current project, we will employ whole genome sequencing to investigate the evolutionary history of legionellosis in Scotland, leading to the identification of all genetic subtypes of clinically-relevant Scottish *Legionella* spp. In addition, we will test the potential for metagenomic analysis to allow culture-independent identification of the diversity of *Legionella* spp in environmental and patient samples. The proposed study should lead to the design of more effective investigations into source attribution in complex outbreaks.