



FOCUS ON RESEARCH

Genomic epidemiology of Legionnaires' disease in Scotland: Towards effective outbreak investigation

Researchers

Prof Ross Fitzgerald, Prof Andrew Smith, Dr. Diane Lindsay, Prof. Nick Loman, Dr. Bryan Wee,

Aim

1. Investigate the relationship between strains of bacteria (*Legionella*) that cause sporadic cases and outbreaks of Legionnaires' disease in Scotland since 1984.
2. Develop novel methods to detect and identify the subtype of *Legionella* in high risk environments, such as cooling towers.
3. Apply an understanding of the above to inform improved measures for tracing future outbreaks of Legionnaires' disease.

Project Outline/Methodology

The complete genetic code for 132 *Legionella* isolates that were responsible for human infections in Scotland since 1984 was determined using an approach called whole genome sequencing. We compared these isolates with the genetic code of 268 environmental samples as well as publicly available data for an additional 500 isolates.

Key Results

All major outbreaks of Legionnaires' disease in Scotland were caused by distinct strains of bacteria.

The increased resolution provided this method revealed clusters of sporadic infections caused by closely related strains that were previously unrecognised. This suggests the presence of persistent sources of infection in hospitals and in the community.

Statistical analysis of the genetic code was also able to identify signals that are more commonly associated with isolates from human infections compared to environmental isolates. Laboratory experiments are being performed to understand the precise role of these signals in the infection process.

Information gained from the complete genetic code was used to develop an innovative, real-time

sequencing-based detection and typing approach that can be deployed to identify reservoirs of *Legionella* during outbreaks.

Conclusions

This study identified genetic features of *Legionella* strains that poses a higher risk of causing human disease. We can use this information to detect these high-risk strains in water systems that are suspected to be contaminated to pinpoint the source of future outbreaks and to limit the severity of an outbreak.

What does this study add to the field?

This study has resulted in the largest and most diverse collection of the genetic code of *Legionella*, the causative agent of Legionnaires' disease that is currently available. This makes it a unique resource to help us understand the differences between bacteria that have a history of causing human disease and those that are more commonly found in the environment. This dataset also provides unparalleled resolution into relationships of *Legionella* strains that have caused infections in Scotland.

Implications for Practice or Policy

The results of this study demonstrates the usefulness of whole genome sequencing and justifies the routine use of whole genome sequencing for the investigation of outbreaks of Legionnaires' disease. This will enable detailed and more accurate relationships to be determined in order to identify the origin of Legionnaires' disease in the environment.

Where to next?

Sequencing efforts targeting regions in Scotland where high-risk reservoirs are suspected in the community can help to prevent future outbreaks.

Further details from:

Prof Ross Fitzgerald
The Roslin Institute, University of Edinburgh,
Edinburgh EH259RG
Email: Ross.Fitzgerald@ed.ac.uk