



FOCUS ON RESEARCH

DESIGN OF A NEW METHOD FOR TRACING HOSPITAL OUTBREAKS OF MRSA AND INVESTIGATION INTO THE THEIR EMERGENCE AND NATIONWIDE SPREAD

Researchers

Prof Ross Fitzgerald, Dr Kate Templeton, Dr Giles Edwards, Ms Kirsty Girvan, Dr Anne Holmes

Aim

1. Develop a new method for tracing the transmission of MRSA
2. to investigate the evolution of hospital associated MRSA in Scotland

Project Outline/Methodology

We determined the entire genetic code for representative MRSA isolates from different parts of Scotland and identified genetic differences which could be used to identify different strains. Selected differences were then incorporated into a novel method for discriminating between strains based on DNA sequence variation (genotyping) which could be used for tracing outbreaks in hospitals. In addition, the genetic code of different isolates was used to investigate the emergence and evolution of hospital MRSA in Scotland and the UK.

Key Results

Successful design and validation of a highly useful MRSA genotyping method which performs better than existing methods for investigating the spread of MRSA infections in hospitals.

Analysis of the genetic code of many MRSA samples from Scotland and the UK revealed the basis for the emergence of antibiotic resistance, and the ability of MRSA to survive in hospitals. It was shown that the antibiotic sensitivity of MRSA can be predicted by looking at its genetic code.

The study demonstrated that hospitals in major cities such as Glasgow act as a hub for the spread of MRSA to regional hospitals in the UK.

Scotland has strains of MRSA which are unique to specific geographic regions or hospitals.

Conclusions

The new genotyping method should be more effective for tracing the spread of hospital MRSA outbreaks.

Hospital MRSA strains have evolved by acquiring antibiotic resistance but are less likely to cause disease outside hospitals.

Transmission pathways of MRSA around the UK have been identified. Determining the entire genetic code of bacterial pathogens is an effective way of understanding their transmission, and predicting an effective antibiotic treatment.

What does this study add to the field?

Existing methods for tracing MRSA outbreaks are limited for differentiating closely-related strains and are difficult to compare between laboratories. In this regard, the new genotyping method described here is a significant improvement on existing methods. In addition, the study resulted in the identification of MRSA transmission pathways and factors associated with bacterial survival in hospitals providing new targets for controlling infections.

Implications for Practice or Policy

Determining the genetic code of bacterial pathogens will become a routine approach for treatment of infectious disease and controlling infections. Identification of transmission pathways allows the rational design of methods for blocking transmission. The identification of genetic differences associated with hospital MRSA may indicate new drug targets.

Where to next?

A comprehensive study of the spread of MRSA in Scottish hospitals, in the community and the movement of MRSA between hospital and community is required.

In addition, further development of genome sequencing for routine clinical applications is required.

Further details from:

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