

FOCUS ON RESEARCH

THE MOLECULAR ECOLOGY OF VIRULENCE GENES IN THE PNEUMOCOCCUS

Researchers

AJ Smith, T Mitchell, C Dowson, G Edwards, S Clarke

Aim

The aim of this study was to determine the relationship between disease causing pneumococci in Scotland and their relation to disease causing isolates that are present throughout the World. We also studied the genetic diversity of 3 disease causing proteins (pneumolysin, hyaluronidase and neuraminidase) in this organism and their presence in the closely related oral streptococci.

Project Outline/Methodology

This study utilised and refined Multilocus sequence typing (MLST- a technique for determining the relatedness of bacteria) for the population analysis of pneumococci. 250 Scottish pneumococcal isolates were selected from a collection held at the Scottish Meningococcal and Pneumococcal Reference Laboratory (SMPRL) Isolates included a wide range of serotypes (category into which bacteria is placed based on its cellular antigens), type of disease caused, antimicrobial susceptibility and age of patient. The oral streptococci were obtained from a reference collection of isolates from a number of different clinical sources. The presence of disease causing genes in the pneumococci and oral streptococci were detected by polymerase chain reaction (a molecular technique to detect DNA) and representative isolates for the disease causing genes were sequenced.

Key Results

109 Sequence types (STs- the degree of relatedness determined by MLST) were assigned. 40 new STs were detected during the course of this project and added to the MLST database. A number of disease causing isolates that have been detected World wide were present in the Scottish pneumococcal population. The most common disease causing isolate was ST 9. Scottish isolates had lower antimicrobial susceptibilities than a number of the World wide disease causing isolates. A greater degree of diversity in the form of outer bacterial coating was observed. The three disease causing proteins varied in their structure between isolates and this variability appears independent of ST. Pneumolysin was the

most conserved of the three genes. Two percent of oral streptococci had pneumolysin analogues and six percent for hyaluronidase. Neuraminidase was not detected in the oral streptococci.

Conclusions

There appears to be a greater phenotypic (observable characteristics) and genotypic (genetic constitution) diversity in the pneumococcal population, including World wide disease causing isolates than has previously been estimated. Pneumolysin is genetically less variable than hyaluronidase and neuraminidase. Variants of some pneumococcal virulence genes are present in oral streptococci.

What does this study add to the field?

During the course of the study we have developed an automated MLST protocol and detected 40 new STs of pneumococci. A major finding was the presence of relatively high levels of bacterial capsule switching in our study population. This study adds to a knowledge of the epidemiology of World wide disease causing isolates present in the Scottish pneumococcal population and that the introduction of pneumococcal conjugate vaccines should be closely monitored for changes in disease causing isolates that may escape coverage by these vaccines. We have also contributed to an increased understanding of the role of pneumolysin (a key virulence factor) by the discovery of non-haemolytic (loss of ability to lyse red cells) pneumolysin in serotype one pneumococci.

Implications for Practice or Policy

The introduction of conjugate pneumococcal vaccines by SEHD must be closely monitored to observe for changes in pneumococcal ecology and the appearance of disease causing isolates not covered by current vaccine.

Where to next?

Use of the pneumolysin structure/function data to assess feasibility for inclusion as a conjugate protein carrier for future pneumococcal vaccines

Further details from:

Dr AJ Smith, University of Glasgow.
a.smith@dental.gla.ac.uk

