Characterization of the 10 Most Common Serotypes Causing Invasive Pneumococcal Disease in Canada, 2011-2014

A.R. GOLDEN1, H.J. ADAM2, J. KLASSEN1, M. GILMOUR1, M. BAXTER1, J. MARTIN1, K.A. NICHOL3, W. DEMCZUK1, J. EMBREE1, J.A. KARLOWSKY1,3, D.J. HOBAN1, G.G. HANZEL1, and the CANADIAN ANTIMICROBIAL RESISTANCE ALLIANCE (CARA)

1University of Manitoba, 2Diagnostic Services Manitoba and 3National Microbiology Laboratory, Winnipeg, Canada

ABSTRACT

Although there are over 90 currently identified pneumococcal serotypes, it is widely acknowledged that a small number account for the vast majority of invasive pneumococcal disease (IPD). Serotypes have different invasive capacities, based on their ability to elicit an immune response. The objectives of this study were to identify the contribution and antimicrobial susceptibility patterns of the ten most common serotypes (STs) in IPD in Canada over the years 2011-2014. Ten isolates of each of the ten most common serotypes per year (40 of each serotype, 400 total isolates) were characterized for genetic relatedness by pulsed-field gel electrophoresis (PFGE), and MLST sequence types (STs) were compared to the Pneumococcal Molecular Epidemiology Network (PMEN) database. Ten isolates of each serotype per year were subjected to antimicrobial susceptibility testing by CLSI broth microdilution method. STs were also compared to the MLST types in the PMEN database to establish genetic relationships. The goal of this study was to characterize the antimicrobial resistance and molecular characteristics of the ten most common serotypes causing IPD in Canada in the years 2011-2014.

Background: A significant proportion of invasive pneumococcal disease (IPD) in Canada is caused by a small number of serotypes. The focus of this study was to identify the ten most common serotypes causing IPD in Canada in 2011, and to determine their prevalence to 2014. The objectives of this study were to identify the contribution and antimicrobial susceptibility patterns of the ten most common serotypes (STs) in IPD in Canada over the years 2011-2014. Ten isolates of each of the ten most common serotypes per year (40 of each serotype, 400 total isolates) were characterized for genetic relatedness by pulsed-field gel electrophoresis (PFGE), and MLST sequence types (STs) were compared to the Pneumococcal Molecular Epidemiology Network (PMEN) database. Ten isolates of each serotype per year were subjected to antimicrobial susceptibility testing by CLSI broth microdilution method. STs were also compared to the MLST types in the PMEN database to establish genetic relationships. The goal of this study was to characterize the antimicrobial resistance and molecular characteristics of the ten most common serotypes causing IPD in Canada in the years 2011-2014.

Materials and Methods: Invasive S. pneumoniae isolates from sterile sites were forwarded from Canadian Public Health Laboratories to the Public Health Agency of Canada – National Microbiology Laboratory. Serotyping was performed using specific antisera (Statens Serum Institute, Copenhagen, Denmark) through a collaboration between the Canadian Antimicrobial Resistance Alliance (CARA) and the Public Health Agency of Canada – National Microbiology Laboratory. These S. pneumoniae isolates were forwarded to CARA for further testing. A total of 5,012 isolates were sent to CARA from January 2011 to December 2014, inclusive. Antimicrobial Susceptibility Testing: Antimicrobial susceptibility testing was performed using custom-designed, in-house prepared broth microdilution plates and incubated with Electronic Autobac 2 (Roch, USA). Minimum inhibitory concentrations (MICs) were interpreted using CLSI guidelines. Quality control was performed using ATCC 49619. Minimum inhibitory concentrations (MICs) were interpreted using CLSI guidelines (and multi-drug resistance if defined as resistance to 3 or more antimicrobial classes (penicillin resistant MIC ≥ 12 μg/mL)). Isolates resistant to 3 or more antimicrobial classes were defined as extended-spectrum β-lactamase (ESBL). Characterization of Top 10 Serotypes: Ten isolates of each of the ten most common serotypes per year of 40 isolates for each serotype, 400 total isolates) were characterized for genetic relatedness by pulsed-field gel electrophoresis (PFGE) and multi-locus sequence typing (MLST). PFGE was performed as previously described. MLST was performed using methods and primers previously described. Only particular clones of S. pneumoniae serotypes collected in Canada in 2011-2014. Serotype clones are identified in the pie chart (Figure 2).

Conclusions: The top ten pneumococcal serotypes isolated from Canadian Public Health Laboratories in 2011 were 7F, 19A, 11A, 15A, 15B and 4F. Of these five serotypes, 11A and 19A were the most common serotypes causing IPD in Canada indicating the success of these clones. Serotypes 14A, 9N and 22F demonstrated increased invasive capacities in this study. Resulting from the increased emergence of less common serotypes through conjugate vaccination, overall S. pneumoniae IPD incidence is decreasing. The prevalence of MDR was demonstrated by isolates of serotype 15A related to Sweden-15, 19A related to Taiwan-19A, and 4F related to Taiwan-4F. P. h. pilus was identified in all serotype 7F isolates (ST191) and roughly half of serotype 19A (ST153) isolates. Serotype 15A isolates related to the AID-15A clone demonstrated the presence of P. h. pilus. Only serotype 19A isolates demonstrating MDR and relate to Taiwan-19A demonstrated the presence of P. h. pilus. AID-15A}: 351-3.

Acknowledgments: The authors would like to thank the participating Canadian Public Health Laboratory Network (CPHLN) sites: Saskatchewan (SK), Quebec Public Health Laboratory (Quebec, QC), Ontario (Ontario), British Columbia (BC), and Manitoba (Manitoba). The authors also wish to acknowledge and thank the Canadian Antimicrobial Resistance Alliance (CARA) for providing funding support for the project. The study was supported by the Canadian Antimicrobial Resistance Alliance (CARA) and the Public Health Agency of Canada – National Microbiology Laboratory, Winnipeg, Manitoba, Canada.

References: The authors would like to thank the participating Canadian Public Health Laboratory Network (CPHLN) sites: Saskatchewan (SK), Quebec Public Health Laboratory (Quebec, QC), Ontario (Ontario), British Columbia (BC), and Manitoba (Manitoba). The authors also wish to acknowledge and thank the Canadian Antimicrobial Resistance Alliance (CARA) for providing funding support for the project. The study was supported by the Canadian Antimicrobial Resistance Alliance (CARA) and the Public Health Agency of Canada – National Microbiology Laboratory, Winnipeg, Manitoba, Canada.

Table 1. Antimicrobial susceptibilities and percent MDR determined by the top ten common S. pneumoniae serotypes collected in Canada in 2011-2014.

Table 2: MDR and ST53 types identified by the top ten common S. pneumoniae serotypes.

Table 3. Comparison of the diversity of antimicrobial resistance in S. pneumoniae selected in Canada, 2011-2014.