Household Transmission of *Streptococcus pneumoniae* among Siblings with Acute Otitis Media

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Nasopharyngeal colonization with potential middle ear pathogens is an important first step in the development of AOM. Especially heavy growth of a particular pathogen in nasopharyngeal specimens may correlate well with the organism causing otitis media. *Streptococcus pneumoniae*, *Haemophilus influenzae*, and *Moraxella catarrhalis* are considered normal flora of the nasopharynx in children; however, these microbes are very likely to be causative pathogens of AOM. Moreover, there has been an alarming increase in the antimicrobial resistance of *S. pneumoniae* that may be responsible for treatment failures. The standard method for differentiating strains of *S. pneumoniae* is serotyping based on capsular antigens. However, this approach is limited because of the potential for horizontal transfer of capsular genes. Pulsed-field gel electrophoresis (PFGE) is currently considered the most reliable and practical tool for epidemiological analysis of bacterial infections. The present study was designed to investigate household transmission of *S. pneumoniae* among siblings with AOM utilizing restriction fragment length polymorphism analysis by PFGE.

Twenty-three siblings in 11 families (A through K) with concurrent or closely related episodes of AOM were enrolled in this study (Table 1). Nasopharyngeal isolates were obtained with a transnasal swab (Carry Mate calcium alginate swab; Kimiidera, Wakayama City, Wakayama 641-0012, Japan). Specimens were cultured on sheep blood agar (Nippon Becton Dickinson, Tokyo, Japan) at 37°C with 10% CO₂ through the nose. Specimens were cultured on sheep blood agar (Nippon Becton Dickinson, Tokyo, Japan) at 37°C with 10% CO₂. 

Acute otitis media (AOM) is the most common infectious disease during childhood. Approximately one-third of children experience three or more episodes in the first 3 years of life. Nasopharyngeal colonization with potential middle ear pathogens is an important first step in the development of AOM. Especially heavy growth of a particular pathogen in nasopharyngeal specimens may correlate well with the organism causing otitis media. *Streptococcus pneumoniae*, *Haemophilus influenzae*, and *Moraxella catarrhalis* are considered normal flora of the nasopharynx in children; however, these microbes are very likely to be causative pathogens of AOM. Moreover, there has been an alarming increase in the antimicrobial resistance of *S. pneumoniae* that may be responsible for treatment failures. The standard method for differentiating strains of *S. pneumoniae* is serotyping based on capsular antigens. However, this approach is limited because of the potential for horizontal transfer of capsular genes. Pulsed-field gel electrophoresis (PFGE) is currently considered the most reliable and practical tool for epidemiological analysis of bacterial infections. The present study was designed to investigate household transmission of *S. pneumoniae* among siblings with AOM utilizing restriction fragment length polymorphism analysis by PFGE.

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between the siblings in 12 clusters (92%). One common PFGE pattern (S9, A9) was seen in siblings of three different families (families G, H, and J). Although these three families lived in different districts of the same town and the children attended different day care centers (families H and J), they might have had some contacts or there might be endemic dissemination of the specific pathogen in a small town. Four different serotypes were detected. Serotype 19 was the most prevalent, and serotypes 23 and 19 accounted for the majority of the isolates. Antimicrobial susceptibility tests showed that 10 (37%) strains were penicillin-susceptible S. pneumoniae. Seventeen strains (63%) displayed reduced susceptibility to penicillin (penicillin-intermediately resistant S. pneumoniae). Resistance to two or more antibiotics was observed among 20 strains (74%).

Typing by PFGE, capsular serotype determination, and antibiotic susceptibility testing were equally able to demonstrate homology between pairs of organisms from siblings; however, only PFGE was able to distinguish pairs in the population of 27 organisms since there were 12 PFGE types, four capsular serotypes, and 16 antimicrobial resistance patterns.
Subsequent studies used capsular typing to demonstrate the epidemiology of colonization within individuals over time (3, 5). More recent studies have utilized DNA fingerprinting to study the spread of resistant strains in a day care setting (11). Sluijter et al. (12) compared restriction fragment end labeling, capsular typing, and penicillin binding protein genotyping for effectiveness in the characterization of \textit{S. pneumoniae} colonization in children from birth to 2 years of age. They concluded that restrictions fragment end labeling was superior to capsular typing in distinguishing strains, and they observed horizontal transfer of capsular genes between strains. Chromosomal analysis by PFGE in the present study allowed the identification of one endemic multi-drug-resistant strain (S9, A9) in three unrelated families, which were otherwise indistinguishable by serotyping or antibiogram. In conclusion, the PFGE analysis clearly demonstrated person-to-person transmission of \textit{S. pneumoniae} among siblings with AOM and clinicians should take account of the likelihood of a single pathogen causing AOM among siblings.

**REFERENCES**


