Incidence and Pathogenic Effect of Streptococcus pseudopneumoniae

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We evaluated the incidence of Streptococcus pseudopneumoniae in clinical isolates by phenotypic methods and DNA-DNA hybridization. The pathogenic role of this organism was investigated with the mouse peritonitis/sepsis model. Our results show a low incidence (1/120 pneumococcal isolates) and a potential pathogenic effect for S. pseudopneumoniae.

Streptococcus pneumoniae, a major cause of morbidity and mortality worldwide, remains a significant health threat. Correct identification of pneumococci from clinical samples and differentiation from other oral streptococci are essential for appropriate diagnosis and treatment. A novel species of viridans group streptococci resembling S. pneumoniae was recently described as Streptococcus pseudopneumoniae (1); phenotypic identification is based on susceptibility to optochin (OPT) in ambient atmosphere and OPT resistance in a 5% CO2 atmosphere, bile salt insolubility, and the absence of pneumococcal capsule. Genotypic identification is based on DNA-DNA hybridization, whereas sodA sequencing and 16S rRNA gene sequencing are not discriminating. While the new species tested positive for the pneumolysin gene (ply), its pathogenic role was not investigated. In the present study, we assessed the clinical significance of this new species by examining its incidence among pneumococci from clinical samples and investigating its virulence in a mouse peritonitis/sepsis model system.

In total, 120 isolates presumptively identified as S. pneumoniae on the basis of Gram stain, catalase activity, and OPT susceptibility in ambient atmosphere were obtained from consecutive clinical samples of patients admitted to University Hospital, Strasbourg, France, during the period October 2004 to April 2005. Single pneumococcal isolates/patients/infections were analyzed. Eighteen isolates were collected from the lower respiratory tract, 37 were collected from the upper respiratory tract, 24 were collected from blood, 1 was collected from cerebrospinal fluid, 3 were collected from pleural fluid, and 12 were collected from other sterile body sites. Controls (S. pseudopneumoniae CCUG 494557 and S. pneumoniae CCUG 285887) were included in all assays. Additional clinical strains (S. pseudopneumoniae CCUG 48465, CCUG 50866, CCUG 50867, CCUG 50868, CCUG 50869, CCUG 50870, and CCUG 50871) described by Arbique et al. (1) were included in virulence assays.

OPT susceptibility testing was performed by the disk diffusion method with a 6-mm disk (Bio-Rad) on sheep blood agar (Trypticase soy agar [bioMérieux] supplemented with 5% sheep blood); plates were incubated for 18 to 24 h at 35°C in ambient air and in a 5% CO2 atmosphere. Solubility in bile salt (sodium deoxycholate [Merck]) was determined in tubes (4). Capsules were detected by observing a halo around pneumococci with India ink at a ×100 to ×400 magnification. Capsular agglutination tests were performed by the Pastorex test (Bio-Rad) according to the instructions of the manufacturer.

DNA-DNA hybridization was performed as described previously (8). Hybridization between labeled DNA and the fragmented DNA preparation was carried out at 60°C for 16 h in 0.42 M NaCl by the nuclease-trichloroacetic acid method (3). The values of DNA-DNA relatedness given are the means of the results of three independent experiments. Detection of ply in the extracted DNA was performed by PCR with primers specific for a 170-bp region, as described previously (1, 9). The PCR products were analyzed by electrophoresis on 2% agarose gels, with visualization of the ampiclon with ethidium bromide.

Immunocompetent 6-week-old Swiss mice were infected by intraperitoneal injection (0.5 ml) of an exponential-phase culture in brain heart infusion broth (Bio-Rad) (106 CFU per mouse) (2) and observed for a 7-day period. Controls received identical injections of broth. The experiments were performed in triplicate for each isolate and were repeated twice. Dead and sacrificed animals were examined; bacterial cultures of peritoneal fluid and spleen sections were performed on sheep blood agar, and spleen section imprints were Gram stained.

All 120 isolates were OPT susceptible in ambient atmosphere. Six strains (5%) were OPT resistant (zone size, 6 mm) when incubated in CO2. Among the six OPT-resistant isolates, three were capsular agglutination test negative, and two showed no capsule with India ink. All isolates were soluble in bile salt, except one (IBS-370), which was identified as S. pseudopneumoniae (OPT resistant in CO2, insoluble in bile salt, capsular agglutination negative, nonencapsulated).

DNA-DNA hybridization assays performed between strain IBS-370 and the type strains S. pneumoniae CCUG 28588 and S. pseudopneumoniae CCUG 49455 yielded values of 47% and 90%, respectively (Table 1). DNA-DNA similarities of the other five OPT-resistant isolates were low (<50%) for S. pseudopneumoniae and varied for S. pneumoniae, being high (82%) for one S. pneumoniae isolate and low for the other (two unidentified isolates will need further study, and two isolates were identified phenotypically as S. constellatus and S. para-sanguis). Both type strains as well as IBS-370 tested positive for ply (Table 1). Virulence assays resulted in 100% dead mice for S. pneumoniae CCUG 285887 and S. pseudopneumoniae.
Additional S. pseudopneumoniae clinical strains

In conclusion, our results highlight a low incidence and potential pathogenic role of S. pseudopneumoniae. Furthermore, they underscore the complexity of oral streptococci regarding the relationship between their identification and the virulence factors produced. This may lead to laboratories taking account of oral streptococci isolated from specimens of patients suffering from severe lower respiratory tract infections.

**References**


**Table 1. Genotypic and virulence test results**

<table>
<thead>
<tr>
<th>Strain</th>
<th>% DNA-DNA hybridization with:</th>
<th>Virulence in mice</th>
<th>Death/survival status&lt;sup&gt;b&lt;/sup&gt;</th>
<th>Result for spleen samples</th>
<th>Result for peritoneal swabbing</th>
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<tbody>
<tr>
<td></td>
<td>S. pneumoniae CCUG 28588&lt;sup&gt;T&lt;/sup&gt;</td>
<td>S. pseudopneumoniae CCUG 49455&lt;sup&gt;T&lt;/sup&gt;</td>
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<tr>
<td>S. pneumoniae CCUG 28588&lt;sup&gt;T&lt;/sup&gt;</td>
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<td>48</td>
<td>D 24</td>
<td>+</td>
<td>+</td>
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<tr>
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<td>47</td>
<td>90</td>
<td>D 36</td>
<td>+</td>
<td>+</td>
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</table>

<sup>a</sup> All strains had the ply gene.

<sup>b</sup> D 24, death after 24 h; S, survival; D 36, death after 36 h.

<sup>c</sup> CCUG 48465, CCUG 50866, CCUG 50867, CCUG 5086, CCUG 5089, CCUG 50870, and CCUG 50871, described by Arbique et al. (1).