INTRODUCTION

At the time of writing, the genus *Bordetella* includes eight species. Of these, *Bordetella pertussis*, *Bordetella parapertussis* and *Bordetella bronchiseptica* are closely related with relatively little genetic variation (Musser et al., 1986). The causative agent of whooping cough (*pertussis*), *B. pertussis*, is exclusively a human pathogen, whereas *B. parapertussis* and *B. bronchiseptica* may infect both humans and animals. In humans, *B. parapertussis* causes pertussis-like disease that is often milder than pertussis, although severe cases have been reported (Heininger et al., 1994; He et al., 1998). Much less is known about the epidemiology of *B. parapertussis* than about that of *B. pertussis*. When enhanced pertussis surveillance was carried out in Finland in 1994–1997 by using PCR and culture, about one-third of *Bordetella* cases were found to be caused by *B. parapertussis*, suggesting that the incidence of parapertussis is underestimated (He et al., 1998).

*B. pertussis*, *B. parapertussis* and *B. bronchiseptica* share a number of virulence factors. The most important difference between them is that pertussis toxin is produced only by *B. pertussis*; *B. parapertussis* and *B. bronchiseptica* possess, but do not express, the complete toxin operon. Pertactin (*Prn*), an outer-membrane protein that is expressed by *B. pertussis*, *B. parapertussis* and *B. bronchiseptica*, is an important virulence factor and is known to confer protective immunity to *Bordetella* infection in animals and humans (Charles et al., 1989; Kobisch & Novotny, 1990; Leininger et al., 1992). Thus, it is a component of some acellular pertussis vaccines. *Prn* is proposed to function as an adhesin by promoting the attachment of bacteria to certain host cells via the RGD motif (Leininger et al., 1991). *Prn* has two regions that are composed of amino acid repeats (Charles et al., 1991): region 1 includes repeats of GGxxP (Charles et al., 1988), is located near the RGD motif and is polymorphic in *B. pertussis* (Mooi et al., 1998) and *B. bronchiseptica* (Boursaux-Eude & Guiso, 2000; Register, 2001). Region 2 is composed of PQP repeats (Charles et al., 1988) and is polymorphic in *B. bronchiseptica* (Li et al., 1992; Boursaux-Eude & Guiso, 2000; Register, 2001). *Prns* expressed by *B. pertussis*, *B. parapertussis* and *B. bronchiseptica* are highly similar (>90%), with the major differences occurring in the number of repeats in regions 1 and 2 (Charles et al., 1988; Li et al., 1991, 1992). Polymorphism of *B. pertussis* and *B. bronchiseptica* *Prn* has been characterized, but variation of *B. parapertussis* *Prn* has not

The outer-membrane protein pertactin (*Prn*) of *Bordetella pertussis*, *Bordetella parapertussis* and *Bordetella bronchiseptica* is believed to function as an adhesin and is an important immunogen. The emergence of *B. pertussis* and *B. bronchiseptica* *Prn* variants has been reported. The aim of this study was to determine whether similar variation is found in *B. parapertussis* *Prn* and to characterize Finnish clinical *B. parapertussis* isolates that were collected in 1982–2000. Of 76 *B. parapertussis* isolates studied, seven (9%) were found to have silent and non-silent nucleotide changes. In addition, one (1%) had eight PQP repeats instead of nine. Three closely related *B. parapertussis* XbaI PFGE patterns were found. Genetic variation of *B. parapertussis* was found to be very limited, suggesting that *B. parapertussis* is a stable organism that is well-adapted to its own ecological niche.

Abbreviation: *Prn*, pertactin.

The GenBank/EMBL/DDJB accession numbers for the sequences of polymorphic regions 1 and 2 of *Bordetella parapertussis* pertactin are AF503929 and AF503928, respectively.

**PFGE and pertactin gene sequencing suggest limited genetic variability within the Finnish *Bordetella parapertussis* population**

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been observed previously (Boursaux-Eude & Guiso, 2000). The aim of this study was to characterize the Prn proteins expressed by Finnish B. parapertussis isolates by sequencing part of the prn gene and to follow the recent evolution of the B. parapertussis population in Finland by using PFGE.

**METHODS**

**Clinical isolates.** In this study, we sequenced 76 B. parapertussis isolates that were collected from patients resident in Finland during the years 1982–2000 (Table 1). Calcium alginate swabs and Regan–Lowe medium that contained charcoal agar and defibrinated sheep blood, supplemented with cephalcin, were used for primary cultures. After collection, swabs were inoculated onto plates at the local health centre or school. Plates were incubated in a humid atmosphere at 35°C and monitored daily for 7 days. Suspected colonies were Gram-stained and further confirmed by GLC and they were stored at −80°C.

**PCR, sequencing and PFGE.** PCR, sequencing and PFGE were performed according to standardized recommendations for typing of B. pertussis (Mooi et al., 2000). Bacteria were cultivated on Regan–Lowe medium that contained charcoal agar and defibrinated sheep blood at 35°C for 2 days. For PFGE, B. pertussis strains 134 (USA), 287 (France) and B902 (Sweden), French B. parapertussis strain CIP 64.11T and B. parapertussis XbaI ATCC 15311T were used as reference strains. Briefly, a 1000 bp segment of the prn gene (covering regions 1 and 2) was sequenced from the 76 B. parapertussis strains. Forty-seven of the isolates included the strains that possessed a variant form of Prn and at least one invariant strain from each community, were genotyped by PFGE with the restriction enzymes SpeI and XbaI (New England Biolabs), with a CHEF Mapper II apparatus (Bio-Rad). PFGE reference strains and λ ladder PFGE markers (New England Biolabs), used as molecular size standards, were included in each run. Nucleotide sequences were analysed with the Vector NTI Suite 6.0 software (InforMax) and compared by using the Vector NTI AlignX program with the CLUSTAL W algorithm. PFGE patterns were analysed both visually and with the assistance of Bionumerics version 2.5 software (Applied Maths) by using UPGMA with the Dice coefficient and 1% position tolerance settings for cluster analysis.

**Western blotting.** Prn expression was demonstrated by Western blotting using an anti-Prn mAb, BPE3 (Brennan et al., 1988) (data not shown). Bacterial cell lysates (20 × 10^6 bacteria per well) and purified Prn protein (144 ng per well), provided by GlaxoSmithKline, were separated by SDS-PAGE on a 10% resolving gel. Proteins were transferred to a Hybond ECL nitrocellulose membrane (Amersham Pharmacia Biotech), which was blocked with 5% milk powder/0.1% Tween 20/PBS at 4°C overnight. After washing, the membrane was incubated with a 1:1000 dilution of BPE3 antibody (obtained from Michael Brennan, FDA, Bethesda, USA) at 25°C for 1 h. Immunochemical detection was performed with 1:1000-diluted horseradish peroxidase-conjugated rabbit anti-mouse immunoglobulins (DAKO A/S), using an enhanced chemiluminescence system (Amersham), and analysed visually as positive or negative.

**RESULTS AND DISCUSSION**

Of the 76 B. parapertussis isolates studied, seven (9%) were found to have both silent and non-silent nucleotide changes (arbitrarily designated as BPP Prn2). In addition, one (1%) had eight PQP repeats instead of nine (arbitrarily designated as BPP Prn3) (Table 1 and Fig. 1). The silent mutation occurred at nucleotide 1078 (C→T). The non-silent mutations change the codon of glutamine (Q311) to serine (S). S and Q are both polar amino acids with uncharged side chains that are usually found at the surface of water-soluble proteins, where they contribute to both the water solubility and formation of binding sites for charged molecules. Therefore, the predicted Q→S change would probably not affect the conformation or function of Prn. However, to confirm this, the functionality of these Prn variants should be studied. In one of the variant isolates, the predicted amino acid sequence has eight PQP repeats instead of nine in region 2. The effect of variation in the number of PQP repeats on protein function is not known. Variation in region 2 has been observed in only two B. pertussis isolates, but in several isolates of B. bronchiseptica (Boursaux-Eude & Guiso, 2000; Register, 2001). However, variation in region 2 of B. pertussis has only been investigated in a limited number of studies.

The presence of Prn in bacterial cell lysates was analysed by Western blotting using the anti-Prn mAb BPE3. It was confirmed that the variant forms of B. parapertussis Prn are expressed. However, the method was not quantitative; thus, we do not know whether the level of protein expression was the same in all isolates.

Three closely related B. parapertussis XbaI PFGE patterns were found among the 47 isolates studied. The isolates were considered to be closely related, as the PFGE patterns differed considerably from those of B. pertussis. However, B. parapertussis Prn variants were not detected in any of the isolates,

Table 1. B. parapertussis clinical isolates used in this study

<table>
<thead>
<tr>
<th>Community</th>
<th>No. isolates</th>
<th>Year of isolation</th>
<th>No. Prn variants found</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sirkkala school</td>
<td>16</td>
<td>1982–1983</td>
<td>1</td>
</tr>
<tr>
<td>Uittamo</td>
<td>1</td>
<td>1990</td>
<td>0</td>
</tr>
<tr>
<td>Paimio</td>
<td>1</td>
<td>1993</td>
<td>0</td>
</tr>
<tr>
<td>Salo</td>
<td>2</td>
<td>1994</td>
<td>0</td>
</tr>
<tr>
<td>Somero</td>
<td>16</td>
<td>1994</td>
<td>3</td>
</tr>
<tr>
<td>Litonienen</td>
<td>14</td>
<td>1995</td>
<td>0</td>
</tr>
<tr>
<td>Halikko</td>
<td>1</td>
<td>1995</td>
<td>0</td>
</tr>
<tr>
<td>Ulvila</td>
<td>1</td>
<td>1996</td>
<td>1</td>
</tr>
<tr>
<td>City of Turku</td>
<td>1</td>
<td>1996</td>
<td>0</td>
</tr>
<tr>
<td>Masku</td>
<td>5</td>
<td>1996</td>
<td>1</td>
</tr>
<tr>
<td>City of Tampere</td>
<td>1</td>
<td>1996</td>
<td>0</td>
</tr>
<tr>
<td>Salo</td>
<td>2</td>
<td>1999</td>
<td>0</td>
</tr>
<tr>
<td>Raisio</td>
<td>12</td>
<td>2000</td>
<td>1*</td>
</tr>
<tr>
<td>Somero</td>
<td>3</td>
<td>2000</td>
<td>0</td>
</tr>
<tr>
<td>Total</td>
<td>76</td>
<td></td>
<td>7</td>
</tr>
</tbody>
</table>

*This isolate had both the non-silent nucleotide change and eight PQP repeats instead of nine, arbitrarily designated as BPP prn3.
by only one or two bands (there was 96.21 % similarity between the profiles). These changes are consistent with a single genetic event, i.e. a point mutation or an insertion or deletion of DNA (Tenover et al., 1995). The isolates collected in 1982–1995 (n = 30) exhibit an A1 pattern (Fig. 2a). The majority of the isolates collected in 1996 (n = 6) exhibit an A2 pattern, like reference strains ATCC 15311T and CIP 64.11T, and only one isolate exhibited the A1 pattern. The A2 pattern is slightly different from the A1 pattern and is characterized by a fragment of 262 kb instead of the 250 kb fragment (Fig. 2a). In 1999–2000, all isolates (n = 15) exhibited an A2 pattern. The isolate that harbours eight

![Fig. 1. Finnish B. parapertussis pertactin variants. DNA and corresponding amino acid sequences of polymorphic regions are depicted. Dots indicate identical bases; lines indicate deletion of bases. Numbers refer to position of bases in the pertactin gene. Complete sequences can be obtained from GenBank, accession numbers AF503929 (polymorphic region 1) and AF503928 (polymorphic region 2).](image)

![Fig. 2. PFGE profiles of (a) Xba I- and (b) Spe I-digested chromosomal DNA of B. parapertussis isolates. Lanes 1 and 15, molecular size markers; 2 and 8, B. pertussis PFGE reference strains 134 and 287; 14, B. parapertussis PFGE reference strain CIP 64.11T; 3–7, 9, 10, DNA from isolates harbouring PFGE pattern A1 (isolated in 1982–1995); 11 and 12, DNA from isolates harbouring pattern A2 (isolated in 1999 and 2000); 13, DNA from the isolate harbouring pattern B (isolated in 2000).](image)
PQP repeats exhibits a unique PFGE type, arbitrarily designated as pattern B (Fig. 2a). Other isolates from the same outbreak that were submitted to PFGE \( (n = 6) \) exhibit the predominant pattern, A2. \( XbaI \) was found to be more discriminatory than \( SpeI \), as patterns A1 and A2 could not be distinguished when examined with the restriction enzyme \( SpeI \) (Fig. 2b). The isolate that harbours the \( XbaI \) B pattern also produced a unique \( SpeI \) restriction pattern. As we only observed one B-type isolate, which contained eight PQP repeats, it remains to be seen whether the B-type strains will emerge in Finland and whether this PFGE pattern correlates with Prn type. However, there is no correlation between PFGE types A1 and A2 and \( prn \) sequences.

We do not know the importance of differences between groups A1 and A2 on the pathogenicity of \( B. parapertussis \) isolates. However, the same \( XbaI \) PFGE patterns were observed during a vaccine trial in 1992 and 1993 in Italy (Mastrantonio et al., 1998); the PFGE patterns of the isolates did not correlate with duration of coughing or severity of illness. In Italy, both strain types were co-circulating at the time, but the A1 isolates were found to be limited to the northern regions of the country (Mastrantonio et al., 1998). In Finland, it seems that type A2 has recently replaced type A1. However, to confirm this, historical Finnish \( B. parapertussis \) isolates would be needed. Unfortunately, Finnish \( B. parapertussis \) isolates collected before 1982 are not available.

In conclusion, analysis of the \( B. parapertussis \) isolates obtained from various communities in Finland during the past 20 years shows that the \( B. parapertussis \) population is very homogeneous, confirming the results of previous studies (Yuk et al., 1998; Boursaux-Eude & Guiso, 2000). In this study, we showed that \( B. parapertussis \) Prn of seven of 76 isolates (9%) had both non-silent and silent mutations and that one of the seven isolates had eight PQP amino acid repeats instead of nine in the second domain that contains repeated sequences (a domain that is very polymorphic in \( B. bronchiseptica \), but not in \( B. pertussis \)). Several studies indicate that natural selection favours residue charge changes in the surface proteins of pathogens (Hughes, 1999), possibly allowing the pathogen to escape host defences. This might not be the case with \( B. parapertussis \) Prn, where Q311 can be changed to a similar amino acid, S. Our data confirm that repeated regions of \( B. parapertussis \) are very important for protein function, as they are conserved. It has been suggested that \( B. pertussis \) Prn variants have emerged as a result of vaccine-driven evolution, as strains used for whole-cell vaccines harbour a different Prn allele from that of most of the currently circulating \( B. pertussis \) strains (Mooi et al., 1998). The low level of variation in \( B. parapertussis \) Prn could indicate that \( B. parapertussis \) is not under similar selection pressure and has therefore remained stable. However, PFGE analysis clearly shows that the \( B. parapertussis \) population that infects humans is highly clonal and, thus, differences seen in the level of antigenic variation probably reflect differences in the overall stability of these organisms, rather than different selection pressures. Currently, acellular vaccines that contain only a few \( B. pertussis \) antigens are replacing whole-cell vaccines in the industrialized world. Surveillance should be continued to address whether the vaccine change affects the incidence of infection by \( B. parapertussis \).

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