Pathogen adaptation has been proposed to contribute to the resurgence of pertussis. A striking recent example is the emergence of isolates deficient in the vaccine component pertactin (Prn). This study explores the emergence of such Prn-deficient isolates in six European countries. During 2007 to 2009, 0/83 isolates from the Netherlands, 0/18 from the United Kingdom, 0/17 Finland, 0/23 Denmark, 4/99 Sweden and 5/20 from Norway of the isolates collected were Prn-deficient. In the Netherlands and Sweden, respectively 4/146 and 1/8 were observed in a later period (2010–12). The Prn-deficient isolates were genetically diverse and different mutations were found to inactivate the prn gene. These are indications that Prn-deficiency is subject to positive selective pressure. We hypothesise that the switch from whole cell to acellular pertussis vaccines has affected the balance between ‘costs and benefits’ of Prn production by Bordetella pertussis to the extent that isolates that do not produce Prn are able to expand. The absence of Prn-deficient isolates in some countries may point to ways to prevent or delay the spread of Prn-deficient strains. In order to substantiate this hypothesis, trends in the European B. pertussis population should be monitored continuously.

**Introduction**

Introduction of whole cell pertussis vaccines (WCVs) 50 to 60 years ago has greatly reduced the pertussis burden worldwide [1]. However, despite a vaccine coverage between 80% and 96%, pertussis has resurfaced in many countries [2,3]. In particular, in the last few years, high incidences have been observed in the Netherlands, the United Kingdom (UK) and the United States (US) [4-6]. Several causes have been proposed for the resurgence of pertussis, including waning immunity and pathogen adaptation [7].

In the 1990s, less-reactive acellular pertussis vaccines (ACVs) replaced WCVs. ACVs contain between one and five pertussis proteins: (i) pertussis toxin (Ptx); (ii) pertactin (Prn); (iii) serotype 2 fimbriae (Fim2); (iv) serotype 3 fimbriae (Fim3); and (v) filamentous haemagglutinin (FHA). All ACVs contain Ptx. The effectiveness of the different available WCVs was highly variable [8], which complicates evaluation of the protection that ACVs induce compared with that of WCVs. However, recently, several studies have indicated that the immunity induced by ACVs is less long-lasting compared with effective WCVs, resulting in a higher pertussis burden, particularly in children aged 6 to 10 years [9-12].

The effect of waning immunity may have been aggravated by pathogen adaptation [7], which is reflected in large shifts in Bordetella pertussis populations [13-15]. Observed adaptations include antigenic divergence between circulating strains and vaccine strains, and the emergence of strains with a novel promoter for Ptx (ptxP3) [16]. In addition, most recently, strains have emerged that do not express Prn, hereafter named Prn-deficient strains [17-22]. Isolates with the ptxP3 promoter increased in frequency in the 1980s and at present they predominate in many countries, reflecting a global selective sweep [6,13,16,23-26]. The ptxP3 isolates produce higher amounts of Ptx in vitro (1.6-fold increase), when compared with the ptxP1 isolates they replaced [16]. It has been suggested that this may result in a more effective suppression of host immunity [16]. In agreement with this, ptxP3 isolates reach higher bacterial densities than ptxP1 isolates in mice [27]. Prn-deficient isolates emerged around 2000 and have been found in Finland, France, Japan and the US [18-20,22]. In addition, less frequently, isolates were found that
do not produce FHA or Ptx. Hegerle et al. reported one isolate lacking both Prn and FHA, and one isolate lacking Ptx [17,19]. Bouchez et al. have suggested that the emergence of such isolates is related to the introduction of ACVs [17,28]. Prn-deficient isolates have been isolated from pertussis patients and seemed to be as virulent as isolates expressing Prn in infants less than six months of age as well as in a mouse model [17,29]. A better understanding of the epidemiology and virulence of Prn-deficient isolates is crucial for the development of next-generation pertussis vaccines.

In this study, we investigated the emergence and spread of Prn-deficient isolates in Europe. To do so, we combine single nucleotide polymorphism (SNP) typing, antigen expression analysis and DNA sequencing with epidemiological data. The diversity of vaccination programmes in Europe (Table 1) offers a unique opportunity to study the effect, if any, of vaccination policy on the emergence of Prn-deficient strains. Ultimately, we aim to define conditions that could prevent or hamper the emergence of vaccine-adapted strains. This study provides a baseline for future European studies in which the occurrence and spread of Prn-deficient strains will be investigated.

### Methods

#### Analysis of Bordetella pertussis isolates

Six countries provided a total of 665 strains isolated from nasopharyngeal swabs from confirmed pertussis patients for this study: Denmark (n=43), Finland (n=56), Netherlands (n=311), Norway (n=20), Sweden (n=197) and the UK (for the purposes of this article, the UK is considered as one country) (n=38) (Table 2). These countries were selected as they are members of European research programme for improved pertussis strain characterisation and surveillance (EUPERTSTRAIN) network and were able to contribute strains. The strains were isolated during 1996 to 2012. In the countries studied, primary immunisation with ACVs was introduced between 1996 and 2005 (Table 1). Furthermore, in these countries, different ACVs and different vaccine strategies were used and the vaccine coverage varied (Table 1). Strains were grouped into three periods, 1996–2006, 2007–09 and 2010–12 (periods I, II and III, respectively). Bacteria were cultured on Bordet Gengou agar plates supplemented with 15% sheep blood and incubated at 35 °C for 3 to 4 days.

#### PCR and DNA sequencing

DNA isolation was performed using the GenElute Bacterial Genomic DNA Kit (Sigma-Aldrich, Zwijndrecht, Netherlands) according to the manufacturer's instructions.
the Netherlands), following the manufacturer’s instructions for Gram-negative bacteria. For multi-antigen sequence typing (MAST), the pertussis toxin promoter (ptxP), regions 1 and 2 of the pertactin gene (prn), the genes for serotype 2 fimbriae (fim2) and serotype 3 fimbriae (fim3) were sequenced in order to determine polymorphisms [16,30].

To determine the location and size of the mutation causing non-expression of Prn, four sets of primers were selected for PCR amplification of the prn gene (Table 3). Prn PCR products were visualised and sized by capillary electrophoresis on a QIAxcel instrument (Qiagen Benelux), using the QIAxcel high-resolution kit, QX DNA size marker 250–8,000 base pairs (bp) and QX alignment markers 15/8,000 bp. Each type of mutation was verified in at least one isolate by Sanger sequencing using an ABI 3700 DNA sequencer (Perkin-Elmer Applied Biosystems).

### Identification of vaccine antigen-deficient isolates

A microsphere-based Multiplex Immunoassay (Luminex, Austin, TX, US) [31] was developed to measure the expression of Ptx and Prn. Isogenic ptx (BooB5) and prn (B1686) knockout strains were used as negative controls [32,33]. Analyses of these negative controls resulted in values <5 ng/ml. Therefore, isolates with antigen concentrations <5 ng/ml were considered deficient isolates. All deficient isolates were tested at least twice, starting from independent cultures. In addition, Prn deficiency was verified with an immunoblot using the monoclonal antibody Prn Ab 62, E4D7 [34] (Figure 1).

### Single nucleotide polymorphism typing and clustering analysis

SNP typing was used to establish genetic relationships between *B. pertussis* isolates [35,36]. A total of 113 SNPs that are useful for discriminating between isolates were selected after comparing whole genome data of a selection of 74 worldwide isolates (data not shown). In order to study the origin and spread of European Prn-deficient isolates, SNP typing was performed on 261 isolates from all six countries using the Sequenom technology (Sequenom, San Diego, CA, US) [35]. At least 40 randomly selected strains (using the function RAND in Microsoft Excel) per country were typed, if available. A tree was constructed in Bionumerics 6•6 (Applied Maths, Sint-Martens-Latem, Belgium), treating the SNPs as character data and using the neighbor-joining algorithm. The vaccine strains Boo6 (from the Netherlands, 1950, ptxP2), Bo499 (ACV strain 10-536, 1951, ptxP2) and Boo005 (from the Netherlands, 1950, ptxP1) were included as outgroups.
Primers used for the characterisation of mutations leading to non-expression of pertactin in *Bordetella pertussis* isolates in six European countries, 1996–2012

<table>
<thead>
<tr>
<th>PCR</th>
<th>Primer name</th>
<th>Primer sequence (5' to 3')</th>
<th>Positiona</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>prn-SPF1</td>
<td>TCC CTG TTC CAT GGC GGT G</td>
<td>1098036–1098054</td>
<td>[44]</td>
</tr>
<tr>
<td></td>
<td>prn-SPR1</td>
<td>CCT GAT CCT GGA GAC TGG</td>
<td>1100878–1100895</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>prn-BF</td>
<td>AGC TGG GGC GTTCAA GGT</td>
<td>1099289–1099306</td>
<td>[45]</td>
</tr>
<tr>
<td></td>
<td>prn-BR</td>
<td>CGG AT CAG GGC CAA CTC</td>
<td>1100006–1100024</td>
<td>[this work]</td>
</tr>
<tr>
<td>3</td>
<td>prn-D1F</td>
<td>CTA GAT CTC CGC CAT CCG CT</td>
<td>1095755–1095774</td>
<td></td>
</tr>
<tr>
<td></td>
<td>prn-D1R</td>
<td>ACT GGC CCC CAA CAC AGA CA</td>
<td>1098750–1098769</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>prn-D2F</td>
<td>TAC TTT TGC TGC GCC CAT T</td>
<td>1098015–1098033</td>
<td>[this work]</td>
</tr>
<tr>
<td></td>
<td>prn-D2R</td>
<td>TCT GAT GGT GGT TCC GCT G</td>
<td>1098283–1098301</td>
<td></td>
</tr>
</tbody>
</table>

F: forward primer; R: reverse primer.

* Position of the primer, relative to the origin of replication of reference strain Tohama (National Center for Biotechnology Information (NCBI) reference sequence NC_002929).

### Results

#### Frequency of pertactin-deficient isolates in six European countries

Expression of Prn was assessed by a multiplex Immunoassay assay and immunoblotting (Figure 1) for 576 of the 665 strains from the six countries, of which 14 (2.4%) were shown to be Prn deficient (Tables 2 and 4). All 576 strains tested positive for Ptx production. For period I (1996–2006), only strains from the Netherlands (n=82) and Sweden (n=80) were available for this analysis. One Prn-deficient isolate from Finland was obtained in period I: this isolate was not included in the Prn-deficiency frequency analysis because no other Finnish isolates were analysed for Prn expression in that period. For period II (2007–2009), between 17 and 99 strains from each of the six countries were analysed for Prn expression. Prn-deficient strains were observed in Norway (5/20 strains) and Sweden (4/99), but not in Denmark (0/23), Finland (0/17), the Netherlands (0/83) or the UK (0/18). As for period I, for period III (2010–12) only strains from the Netherlands (n=146) and Sweden (n=8) were available for this analysis. In that period, 4/146 Dutch strains and 1/8 Swedish strains were found to be Prn deficient. Thus, Prn-deficient isolates in the frequency analysis were detected in periods II and III. All isolates produced Ptx. The vaccination status of 14 of the 15 patients from whom the Prn-deficient isolates were recovered was unknown (Table 4). Therefore, we cannot relate the infection with a Prn-deficient strain to the degree of immunisation.

#### Mutations causing non-expression of pertactin

Previous studies observed five types of mutations that inactivate the *prn* gene: inversion, deletion of (part of) the gene, insertion of IS481 into *prn*, insertion of a single nucleotide resulting in a frameshift mutation, or a SNP resulting in the introduction of a stop codon [17–22] (Figure 2, Table 5). We used PCR and sequencing of the *prn* gene to determine the cause of non-expression of the Prn-deficient isolates we analysed (Table 4). PCR fragment analysis showed that three Prn-deficient isolates (B3545, B3748, B3865) had an insertion of approximately 1 kilobase pair (kb) proximal to region 2 (Figure 3). We assumed this is the result of an insertion of IS481 into this region and no further sequencing analysis was performed on these isolates. Sequence data of the remaining 12 Prn-deficient isolates showed that in two isolates, the promoter region was inverted as described by Pawloski et al. [22]. Another three isolates (B3582, B3640, B3891) had an IS element inserted proximal to one of the two repeat regions of the *prn* gene, designated region 2 (Figure 2). This mutation has also been found previously in French Prn-deficient isolates [17]. Sequence data of a sixth isolate (B3771), which originated from Finland in period I, contained a deletion of 49 bases in the signal sequence. This isolate was not included in the Prn-deficiency frequency analysis because no other Finnish isolates were analysed for Prn expression in period I. The seventh isolate, B3876 from The Netherlands, contained a SNP at position 223 that introduces a premature stop codon in the *prn2* gene. An eighth isolate (B3658), originating from Norway, also contained a SNP that introduces a premature stop codon in *prn2*, but at position 1,273. Sequencing of the *prn* gene around position 1,273 showed that the other four Norwegian Prn-deficient isolates also harboured this SNP.

#### Phylogenetic relationships of European pertactin-deficient *Bordetella pertussis* isolates

Typing of 261 isolates from the six different European countries using 113 SNPs allowed us to distinguish 20 STs.

Phylogenetic analysis revealed a closely related European *B. pertussis* population (Figure 4). The tree topology showed two distinct clades containing *ptxP1* and *ptxP3* isolates. In addition, a *fim3.1* and a *fim3.2* cluster could be observed within the *ptxP3* clade (Figure 4).

The 12 European Prn-deficient isolates included in the phylogenetic analyses were found in four different STs: ST13, ST14, ST17 and ST19 (Figure 4). These STs were among the predominant types and contained 70% (184/264) of the isolates analysed.
All Prn-deficient isolates analysed in this study were found in the ptxP3 clade but were associated with both fim3.1 and fim3.2 alleles. ST14 contains two types of prn mutations (Table 4). In contrast, the five Prn-deficient isolates that belong to ST13 all harboured the same mutation in prn: a SNP resulting in premature translational termination of prn. All five isolates were from Norway. The prn mutation, in which IS481 was inserted proximal to region 2, was found in three STs that were dispersed across the ptxP3 clade. This mutation was associated with both the fim3.1 and fim3.2 alleles. Thus, identical mutations were observed in different STs, while within a single ST, different mutations were found.

**Discussion**

The diversity in immunisation programmes in Europe offers an opportunity to explore the effect of vaccination strategies on adaptation of *B. pertussis* in populations with a vaccine coverage between 80% and 96%. In this study, the overall mean of Prn-deficient strains from six European countries isolated between 2007 and 2012 was 3.4% (14/414 isolates). Bouchez et al. suggested that the emergence of French Prn-deficient isolates was driven by the switch from WCVs to ACVs [17]. Indeed, Prn-deficient isolates were rarely found before the introduction of ACVs, when WCVs were used [37]. Compared with the mean of Prn-deficient strains found in the six countries studied here (3.4%), higher percentages of Prn-deficient isolates were observed in France (13% in 2011), Japan (32% in 2005–09) and the US (53% in 2012) [18,19,22]. In Japan, ACVs were introduced in 1981 [18], and in the US, the first ACV was marketed in 1991. Thus, these countries have a longer history of ACV immunisation compared with the six countries included in this study, where ACVs vaccines for the primary series were introduced between 1996 and 2005 (Table 1). Interestingly, the early Prn-deficient strains found in this study were mainly from Norway and Sweden, where ACVs for the primary series were introduced in 1996 and 1998, respectively, which is earlier than in the UK (in 2000), Finland and the Netherlands (both in 2005) (Table 1). Notably, in France an ACV booster was introduced in 1998, while the WCV for the primary series was replaced with an ACV in 2004 [29]. The timing of these changes is similar to that in Norway which, as in France, has a relatively high percentage of Prn-deficient strains. In Denmark, an ACV was introduced relatively early in 1997, while Prn-deficient strains were not detected. Unlike the vaccine in the other five countries in this study, which use ACVs containing Prn (Table 1), the Danish ACV contains Ptx only. As the Danish vaccine does not induce Prn antibodies, it is conceivable that Prn-deficient strains will not emerge in Denmark, if Prn-deficiency does not contribute to strain fitness, although overflow of Prn-deficient strains from neighbouring countries is possible.

In 2007–09, five of the 20 Norwegian strains were Prn-deficient. Although the number of isolates tested was

---

**Figure 1**

Immunoblot to confirm absence of pertactin (69 kD) expression in *Bordetella pertussis* isolates in six European countries, 1996–2012

![Immunoblot](image)
### Table 4
Pertactin-deficient *Bordetella pertussis* isolates analysed from four European countries, 2004–12 (n=15)

<table>
<thead>
<tr>
<th>Isolate name</th>
<th>Patient’s age</th>
<th>Patient’s country of residence</th>
<th>Patient’s vaccination status</th>
<th>Year isolate recovered</th>
<th>Sequence type</th>
<th>Mutation</th>
</tr>
</thead>
<tbody>
<tr>
<td>B3771</td>
<td>2 years</td>
<td>Finland</td>
<td>Vaccinated</td>
<td>2004</td>
<td>ST19</td>
<td>#6: prn2 (32_80Δ[49])</td>
</tr>
<tr>
<td>B3645</td>
<td>7 months</td>
<td>Norway</td>
<td>Unknown</td>
<td>2007</td>
<td>ST13</td>
<td>#12: prn2 (1273STOP;C&gt;T)</td>
</tr>
<tr>
<td>B3652</td>
<td>14 years</td>
<td>Norway</td>
<td>Unknown</td>
<td>2008</td>
<td>ST13</td>
<td>#12: prn2 (1273STOP;C&gt;T)</td>
</tr>
<tr>
<td>B3654</td>
<td>14 years</td>
<td>Norway</td>
<td>Unknown</td>
<td>2008</td>
<td>ST13</td>
<td>#12: prn2 (1273STOP;C&gt;T)</td>
</tr>
<tr>
<td>B3655</td>
<td>Unknown</td>
<td>Sweden</td>
<td>Unknown</td>
<td>2008</td>
<td>ST17</td>
<td>prn2 (PCRregion::1kb)</td>
</tr>
<tr>
<td>B3657</td>
<td>2 months</td>
<td>Norway</td>
<td>Unknown</td>
<td>2009</td>
<td>ST13</td>
<td>#12: prn2 (1273STOP;C&gt;T)</td>
</tr>
<tr>
<td>B3658</td>
<td>7 months</td>
<td>Norway</td>
<td>Unknown</td>
<td>2009</td>
<td>ST13</td>
<td>#12: prn2 (1273STOP;C&gt;T)</td>
</tr>
<tr>
<td>B3954</td>
<td>1 month</td>
<td>Sweden</td>
<td>Unknown</td>
<td>2009</td>
<td>ST14</td>
<td>#1: prn2 (PCRregion::1kb)</td>
</tr>
<tr>
<td>B3659</td>
<td>0 months</td>
<td>Sweden</td>
<td>Unknown</td>
<td>2009</td>
<td>ST17</td>
<td>prn2 (PCRregion::1kb)</td>
</tr>
<tr>
<td>B3660</td>
<td>13 years</td>
<td>Netherlands</td>
<td>Unknown</td>
<td>2010</td>
<td>ST14</td>
<td>#4: prn2 (1613*1614::IS481[1049])</td>
</tr>
<tr>
<td>B3865</td>
<td>Unknown</td>
<td>Netherlands</td>
<td>Unknown</td>
<td>2011</td>
<td>ST14</td>
<td>#4: prn2 (PCRregion::1kb)</td>
</tr>
<tr>
<td>B3876</td>
<td>2 years</td>
<td>Netherlands</td>
<td>Unknown</td>
<td>2011</td>
<td>NI</td>
<td>#10: prn2 (223STOP;C&gt;T)</td>
</tr>
<tr>
<td>B3991</td>
<td>Unknown</td>
<td>Sweden</td>
<td>Unknown</td>
<td>2011</td>
<td>NI</td>
<td>#4: prn2 (1613*1614::IS481[1049])</td>
</tr>
<tr>
<td>B3977</td>
<td>69 years</td>
<td>Netherlands</td>
<td>Unknown</td>
<td>2012</td>
<td>NI</td>
<td>#1: prn2 (-20892,-750::22kb)</td>
</tr>
</tbody>
</table>

NI: not included in the SNP analysis; SNP: single nucleotide polymorphism; #: mutation number.

* Sequence type as presented in Figure 2A.

† Mutation causing the non-expression of pertactin. Numbers correspond to those in Table 5 and Figure 2A.

‡ This isolate was not included in the frequency analysis, because it was a single analysed Finnish strain that was isolated before 2007, but was included in SNP analysis and prn mutation analysis.

### Figure 2
Mutations in prn2 causing non-expression of pertactin in *Bordetella pertussis* isolates in six European countries, 1996–2012

A. prn2 is shown with the surrounding genes. The arrowheads indicate the transcription direction. The variable regions 1 (R1) and 2 (R2) of prn are indicated in red. Numbers 1 to 13 refer to mutations (†) in prn2 and correspond to the numbers in Table 5.

B. Detailed representation of mutation †6: a deletion of 49 bases in the signal sequence: prn2 (32_80Δ[49]): • identical bases/amino acids, ‑ deleted bases/amino acids.

C. Detailed representation of mutation †10: a SNP leading to a stop codon: prn2 (223STOP;C>T). Base and amino acid numbering is relative to the prn2 initiation codon.
low, this proportion is relatively high compared with the overall mean of the six countries in this period (3.4%, 14/414). This implies that in Europe, besides France, Norway may also have elevated levels of Prn-deficient isolates. Comparisons of frequencies of Prn-deficient isolates should, however, be made with caution, as differences in the period investigated, vaccination policies and isolate collection are among the factors that can influence the outcome. It seems valid, though, to conclude that the fraction of Prn-deficient strains in several countries of Europe is relatively low, with the exception of France [19] and Norway, as stated above. In order to confirm these findings, further studies are required that include more isolates for each country. The analyses of larger amounts of Prn-deficient strains may also reveal if these strains are found in higher frequencies in particular age groups. Future studies should include more southern European countries.

Mutations that were previously found to inactivate the prn gene [17,19,21] were also observed in the Prn-deficient isolates analysed in this study. We found that the mutations in prn occurred several times independently in different lineages, which is an indication that it has been fixed in the population by positive selection. The European Prn-deficient isolates seem to have originated from distinct lineages, but within the diverse nature of the mutations causing non-expression, we also observed possible signs of clonal expansion of a Prn-deficient strain in Norway. Notably, the specific point mutation that occurred in five Norwegian isolates was also found in seven of 12 Prn-deficient isolates collected in Philadelphia in the US [21]. It was previously suggested that the spread of Prn-deficient isolates in Japan was the result of clonal expansion [18].

The production of bacterial virulence factors, such as pertactin, involves ‘costs and benefits’ for the bacteria. Costs include the energy used to express the virulence factors and activation of the host immune response against these antigens. Benefits comprise attachment to host tissues and manipulation of host defences. We hypothesise that the switch from WCV to ACV has affected the balance between these costs and benefits of Prn production to the extent that strains that do not produce Prn are able to expand. In support of this, our phylogenetic analysis indicates Prn-deficiency is subject to positive selection. We postulate that, because non-expression of one of the

### Table 5

<table>
<thead>
<tr>
<th>Number of the mutation</th>
<th>Name of the mutation</th>
<th>Note</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>n1</td>
<td>prn2 (20892-75&lt;22Kb])</td>
<td>Inversion of about 22 kb in the promoter</td>
<td>[21, this work]</td>
</tr>
<tr>
<td>n2</td>
<td>prn2 (-1846_553&lt;2399)]</td>
<td>Deletion of the first part of prn2 and upstream BP1053</td>
<td>[16]</td>
</tr>
<tr>
<td>n3</td>
<td>prn2 (245&lt;246::IS481[1049])</td>
<td>Insertion of IS481 in prn2, between position 245 and 246</td>
<td>[20]</td>
</tr>
<tr>
<td>n4</td>
<td>prn2 (1613&lt;1614::IS481[1049])</td>
<td>Insertion of IS481 in prn2, between position 1,613 and 1,614</td>
<td>[16, this work]</td>
</tr>
<tr>
<td>n5</td>
<td>prn2 (2735&lt;2736::IS481[1049])</td>
<td>Insertion of IS481 in prn2, between position 2,735 and 2,736</td>
<td>[21]</td>
</tr>
<tr>
<td>n6</td>
<td>prn2 (32_80&lt;49])</td>
<td>Deletion in prn2 signal sequence</td>
<td>[this work]</td>
</tr>
<tr>
<td>n7</td>
<td>prn2 (Aprrn)</td>
<td>Deletion of the entire prn gene</td>
<td>[18]</td>
</tr>
<tr>
<td>n8</td>
<td>prn2 (1043_1067&lt;25])</td>
<td>25 bp deletion in first repeat region</td>
<td>[18]</td>
</tr>
<tr>
<td>n9</td>
<td>prn2 (Δ[89])</td>
<td>89 bp deletion at 5’ of prn</td>
<td>[18]</td>
</tr>
<tr>
<td>n10</td>
<td>prn2 (223STOP:C&gt;T)</td>
<td>SNP C&gt;T, leading to a stop codon</td>
<td>[this work]</td>
</tr>
<tr>
<td>n11</td>
<td>prn2 (760STOP:C&gt;T)</td>
<td>SNP C&gt;T, leading to a stop codon</td>
<td>[21]</td>
</tr>
<tr>
<td>n12</td>
<td>prn2 (1273STOP:C&gt;T)</td>
<td>SNP C&gt;T, leading to a stop codon</td>
<td>[20, this work]</td>
</tr>
<tr>
<td>n13</td>
<td>prn2 (1479STOP)</td>
<td>SNP leading to a stop codon</td>
<td>[18]</td>
</tr>
<tr>
<td>n14</td>
<td>prn1 (1598&lt;1599::IS481[1049])</td>
<td>Insertion of IS481 in prn1, also found in reverse direction</td>
<td>[17]</td>
</tr>
<tr>
<td>n15</td>
<td>prn1 ΔSS</td>
<td>Deletion in prn1 signal sequence</td>
<td>[17,19,21]</td>
</tr>
</tbody>
</table>

bp: base pairs; IS: insertion element; kb: kilobase pairs; SNP: single nucleotide polymorphism; n: mutation number.

a As presented in Figure 2, except for n14 and n15.
b The name is composed as follows: pertactin gene (prn) allele (position from open reading frame of the prn gene/type of mutation/size of the mutation)).

x_y from position x to y
x^y between position x and y
Δ inversion
::IS481 insertion of IS481
Δ deletion
STOP:C>T SNP (C to T) leading to a premature stop codon
**Figure 3**

Characterisation of the prn gene from pertactin-deficient *Bordetella pertussis* isolates by polymerase chain reaction, from six European countries, 1996–2012

A. The prn gene and surrounding genes.

B. The grey bars represent the regions targeted in the PCR that were used to identify insertion and deletion mutations in prn. For the primers, see Table 3.

C. The PCR products of the WT prn allele were compared with PCR products derived from Prn-deficient strains. PCR fragments were sized by capillary electrophoresis. On the basis of the primers used and the size of the PCR fragments, the type of mutation was derived, as shown above the lanes. Designation of PCR fragments as in (B) and mutations as in Table 5. The first lane contains the size marker DNA (in bp). PCR2 distinguishes Δ4 from Δ3 or Δ5, which does not result from PCR1. Mutations 10–13 yielded WT products for the PCRs.

bp: base pairs; kb: kilobase pair; PCR: polymerase chain reaction; WT: wild type.

A. The prn gene and surrounding genes.

B. The grey bars represent the regions targeted in the PCR that were used to identify insertion and deletion mutations in prn. For the primers, see Table 3.

C. The PCR products of the WT prn allele were compared with PCR products derived from Prn-deficient strains. PCR fragments were sized by capillary electrophoresis. On the basis of the primers used and the size of the PCR fragments, the type of mutation was derived, as shown above the lanes. Designation of PCR fragments as in (B) and mutations as in Table 5. The first lane contains the size marker DNA (in bp). PCR2 distinguishes Δ4 from Δ3 or Δ5, which does not result from PCR1. Mutations 10–13 yielded WT products for the PCRs.
Figure 4
Genetic relationship between European *pertactin*-deficient *Bordetella pertussis* isolates

A total of 113 predefined SNPs were used to construct a neighbor-joining tree of 261 European strains collected between 1998 and 2011. The STs are listed next to the branch tips and circle sizes are scaled to the number of isolates in each ST. Colours indicate the country from which the isolates originate. The bold sectors are STs containing Prn-deficient strains and the number in the centre of the segment represents the number of Prn-deficient isolates. The *ptxP* alleles are indicated next to the tree arms (*ptxP2*: orange line; *ptxP1*: green line; *ptxP3*: red line) and the *fim3* types are presented at the tips of the branches. Branch labels give the distance between the STs followed by the bootstrap values as percentages (200 replicates). ST01 and ST02 respectively consist of two and one vaccine strain(s), which are used as an outgroup.

SNP: single nucleotide polymorphism; ST: sequence type.

Denmark
Finland
Netherlands
Norway
Sweden
United Kingdom

ST containing Prn-deficient clinical isolate(s)

Fim3.1
Fim3.2
Fim3.3

Denmark
Finland
Netherlands
Norway
Sweden
United Kingdom

PT: pertactin

ptxP alleles

ptxP1
ptxP2
ptxP3

fim3 types

fim3.1
fim3.2
fim3.3

Branch labels give the distance between the STs followed by the bootstrap values as percentages (200 replicates). ST01 and ST02 respectively consist of two and one vaccine strain(s), which are used as an outgroup.
The emergence of Prn-deficient strains raises questions about its role in pertussis. An analysis of clinical symptoms caused by Prn-positive and Prn-negative isolates in infants did not reveal major differences between the two groups, which suggests that lack of Prn in B. pertussis does not affect virulence in infants substantially [29]. Other important questions that should be addressed in the future are the effect, if any, of Prn-deficiency on the efficacy of pertussis vaccines and whether Prn-deficient strains prevail more in groups with a particular level of immunity. This study establishes a baseline for investigations into the emergence and spread of Prn-deficient strains in Europe.

Acknowledgements

This project was supported by the National Institute of Public Health and the Environment (RIVM), The Netherlands (SOR project S/23046). All the authors are members of the European research programme for improved pertussis strain characterisation and surveillance (EUPERTSTRAIN) network.

Conflict of interest

None declared.

Authors’ contributions

FRM obtained funding and supervised the study. QH and JM organised the EUPERTSTRAIN 2 and 3 collections from the network members. Isolates, epidemiological data and isolate characteristics were provided by all authors. AZ, MvG, KH, HvdH, MB and FRM were responsible for the study concept and practical work. AZ and FRM analysed and interpreted data and wrote the manuscript. All authors were responsible for the critical revision of the manuscript.

References
