Misidentification of *Bordetella bronchiseptica* as *Bordetella pertussis* using a newly described real-time PCR targeting the pertactin gene

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Recently, a real-time PCR (RT-PCR) assay based on sequence from the gene for pertactin was proposed for identification of *Bordetella pertussis*. Here, it is reported that the *B. pertussis* pertactin gene sequence for the region that encompasses the RT-PCR probe and primers is nearly identical to that of many *Bordetella bronchiseptica* strains of human and avian origin. Additionally, it is demonstrated that such strains are erroneously identified as *B. pertussis* using the RT-PCR assay. These data suggest that the use of the assay without confirmatory testing may result in erroneous identification of a significant proportion of human isolates of *B. bronchiseptica* as *B. pertussis*.

INTRODUCTION

*Bordetella pertussis* is the aetiologic agent of whooping cough, an acute respiratory disease that occurs exclusively in humans. A rapid, sensitive and specific method for the identification of *B. pertussis* is crucial for the effective management of outbreaks and to monitor prevalence. The repetitive element IS481 is frequently targeted for rapid detection of *B. pertussis* by PCR (Riffelmann et al., 2005). While assays based on this approach are highly sensitive, the presence of IS481 in other species of *Bordetella* compromises their specificity (Diavatopoulos et al., 2005; Register & Sanden, 2006; Riffelmann et al., 2005; van der Zee et al., 1997). Recently, a novel real-time PCR (RT-PCR) assay that targets the gene for pertactin, a *Bordetella* adhesin and virulence factor, was proposed as an alternative (Vincart et al., 2007). Although the authors concluded that the assay alleviates problems related to cross-reactivity with *Bordetella* species other than *pertussis*, only single isolates of other species appear to have been evaluated. The goals of the present study were to determine the sequence of the relevant region of the pertactin gene from a large number of *Bordetella bronchiseptica* strains, including several of human origin, for comparison with the sequence of *B. pertussis*, and to evaluate the potential for false-positive results using the pertactin RT-PCR.

METHODS

**Bacterial isolates.** This study includes data derived from 88 isolates of *B. bronchiseptica*, obtained from at least 11 different host species. Initial identification of isolates was based on colony morphology and standard biochemical testing, and was confirmed by subsequent ribotype analysis (Register et al., 1997). Information related to individual isolates is available in Supplementary Table S1. *B. pertussis* Tohama I was used as a positive control in the pertactin RT-PCR. All isolates were grown at 37°C for 36 h (*B. bronchiseptica*) or 72 h (*B. pertussis*) on Bordet–Gengou agar supplemented with 10% sterile, defibrinated sheep’s blood.

**PCR and sequence analysis.** Chromosomal DNA was purified with a commercially available kit (Genta Systems) and quantified with PicoGreen (Molecular Probes). The Primer Design module of Vector NTI Advance (Invitrogen) was used to select PCR primers for amplification of the pertactin gene region of interest (forward, 5'-GATGATGCCGGCCTGTAACA-3'; reverse, 5'-AGGGTGCCGA-TATGCAAGCC-3'). PCR was carried out using 100 ng purified DNA and the reaction components and cycling conditions described previously (Register, 2004). Five microlitres of each reaction was analysed by agarose gel electrophoresis in 3:1 NuSieve (Cambrex BioScience) containing 0.5 μg ethidium bromide ml⁻¹. Amplicons were purified using spin columns (Qiagen), and were sequenced directly by fluorescence-based cycle sequencing with AmpliTaq and BigDye Terminators on an ABI 377 sequencer, at the National Animal Disease Center Genomics Unit. Sequences were analysed using Vector NTI Suite software.

**RT-PCR.** RT-PCR was carried out using purified DNA from the strains indicated according to the method described elsewhere (Vincart et al., 2007). The detection rate of this assay has been determined to be 90, 100 and 100% at 10 log_{10}(copies ml⁻¹) for *B. pertussis* strains ATCC 9797, ATCC 9340 and Bord 201, respectively. Therefore, 10 log_{10}(copies ml⁻¹) was chosen as the detection limit for all strains evaluated in this report.

**Abbreviation:** RT-PCR, real-time PCR.

The GenBank/EMBL/DDBJ accession numbers for the *Bordetella* sequences determined in this paper are EU031919–EU032001.

A table showing *B. bronchiseptica* isolates used for sequence comparisons is available as supplementary data with the online version of this paper.
Fig. 1. Alignment of the B. pertussis gene comprising covering the pertactin RT-PCR primers and probe with those of the three B. bronchiseptica (BB) sequence variants. Dashes represent conserved bases; substitutions are indicated by the appropriate letter. Although not depicted here, the corresponding sequences of the four currently available strains of B. parapertussis are identical to that of B. bronchiseptica variant 1.

RESULTS AND DISCUSSION

The earlier study that evaluated the performance characteristics of the pertactin RT-PCR included a single, unnamed isolate each of B. bronchiseptica and Bordetella parapertussis (Vincart et al., 2007). A search of the GenBank database identified five B. bronchiseptica isolates and four B. parapertussis isolates for which the pertactin gene sequence corresponding to the RT-PCR probe and primers is available. We additionally determined the corresponding sequence from 83 strains of B. bronchiseptica selected from the National Animal Disease Center collection, representing isolates from humans and a variety of other host species. Alignment of the DNA sequences from the 88 B. bronchiseptica isolates revealed three unique variants, none of which is identical to the sequence reported for B. pertussis (Fig. 1). Variant 1 was found with the highest frequency in the B. bronchiseptica strains examined (64.8%) and in all but one host species of origin (Table 1), as well as in the four B. parapertussis strains evaluated (GenBank accession nos BD409974, AX418063, X54547 and BX640426). One or more base mismatches are evident with respect to both the forward and reverse RT-PCR primers as well as the probe sequence proposed for identification of B. pertussis. Variants 2 and 3 were found in 22.7 and 12.5% of isolates, respectively, with the majority detected in strains of human or avian origin. Variants 2 and 3 contain only one or two base mismatches compared to the corresponding B. pertussis sequence.

These data suggest that some strains of B. bronchiseptica (specifically, those with sequence variants 2 or 3) may be misidentified as B. pertussis using the proposed pertactin RT-PCR (Vincart et al., 2007). To address this possibility, the assay was carried out using purified DNA from B. pertussis and from two representatives each of B. bronchiseptica sequence variants 1, 2 and 3. As shown in Table 2, B. bronchiseptica strains St Louis (variant 2), MBORD839 (variant 2), MO211 (variant 3) and F4563 (variant 3) were falsely identified as B. pertussis by the proposed pertactin RT-PCR assay. As expected, B. bronchiseptica strains RB50 and KM22 (both variant 1) were not identified as B. pertussis.

It has been suggested that the pertactin RT-PCR alleviates the problem of cross-reactivity with Bordetella species other than pertussis and may not require a confirmatory test (Vincart et al., 2007). The specificity of the assay is purported to be superior to that of PCRs that target the repetitive insertion sequence IS481. However, these conclusions appear to have been based on the analysis of only a single strain from each of the other Bordetella species tested. Our results indicate that the pertactin RT-PCR is likely to incorrectly identify a large proportion of human B. bronchiseptica isolates as B. pertussis, since 43.5% of the human isolates examined here possess sequence demonstrated to return a false-positive result. In fact, IS481-based assays may provide a specificity superior to that of the pertactin RT-PCR, since the insertion element has so far not been detected in any human B. bronchiseptica isolate (Diavatopoulos et al., 2005; Register & Sanden, 2006; van der Zee et al., 1997).

Other investigators have recently analysed the region of the pertactin gene that encodes the extracellular domain from 50 B. bronchiseptica isolates different from those in the present study (Diavatopoulos et al., 2006). Those sequences overlap the region evaluated here, but do not include the 4 bp at the extreme 5′ end. All but a single sequence, obtained from a seal isolate, match those reported here for variant 1, 2 or 3. The unique sequence in the seal isolate is identical to that of variant 1, except for an additional base

Table 1. Distribution of B. bronchiseptica pertactin RT-PCR sequence variants among host species of origin

<table>
<thead>
<tr>
<th>Sequence variant</th>
<th>Dog</th>
<th>Human</th>
<th>Turkey/avian</th>
<th>Pig</th>
<th>Horse</th>
<th>Guinea pig</th>
<th>Rabbit</th>
<th>Seal</th>
<th>Sea otter</th>
<th>Koala</th>
<th>Leopard</th>
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mismatch relative to \textit{B. pertussis} in the region comprising the RT-PCR probe. Based on our RT-PCR results with variant 1 \textit{B. bronchiseptica} strains, isolates with the novel sequence are not likely to be mistakenly identified as \textit{B. pertussis}, although we have not directly tested this assumption. Due to the absence of sequence data for the bases corresponding to the extreme 5’ end of the forward pertactin RT-PCR primer, it is not possible to conclude with certainty whether additional variants might exist among the remaining 49 \textit{B. bronchiseptica} strains examined elsewhere (Diavatopoulos \textit{et al.}, 2006).

Given the lack of specificity demonstrated by the results reported here, the proposed pertactin RT-PCR cannot be recommended for identification of \textit{B. pertussis} in the absence of additional confirmatory testing. Further efforts are required to identify highly sensitive and specific targets suitable for definitive identification of \textit{B. pertussis} by PCR.

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### References


