Towards Improved Accuracy of *Bordetella pertussis* Nucleic Acid Amplification Tests

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Abstract
In many clinical microbiology laboratories, nucleic acid amplification tests such as PCR have become the routine methods for the diagnosis of pertussis. While PCR has greatly increased the ability of laboratories to detect *Bordetella pertussis* infections, it has also been associated with false-positive results that can, given the tendency of *B. pertussis* to cause outbreaks, result in unnecessary and costly control measures. The species-specificity of *Bordetella* gene targets and their number of copies per genome greatly impact the performance characteristics of nucleic acid amplification tests for *B. pertussis*. It is crucial that laboratorians recognize these characteristics, to limit false-positive test results and prevent pseudo-outbreaks.
The laboratory diagnosis of pertussis has gone through fundamental changes in the last twenty years. Culture and direct fluorescent antibody (DFA) staining of nasopharyngeal secretions have been largely replaced by nucleic acid amplification tests (NAATs) such as PCR. PCR has undergone substantial changes as a clinical diagnostic tool during this time, from conventional PCR with agarose gel or microwell plate detection of amplicons, to real-time amplification and detection. A number of *Bordetella* gene targets have been described and applied to diagnostic PCR tests. These include the single-copy pertussis toxin operon, and multiple-copy insertion sequences. The extent to which these gene targets are shared among *Bordetella* species, and their copy number per genome greatly affect the performance characteristics of NAATs. Herein I provide an update on NAATs for the diagnosis of pertussis, with an emphasis on gene targets and their impact on test accuracy, as well as the “real world” performance of PCR, including its role in pseudo-outbreaks.

**EPIDEMIOLOGY**

Whooping cough, or pertussis, is a highly contagious respiratory disease caused by *Bordetella pertussis*. In spite of widespread childhood vaccination, over 27,000 cases were reported in the U.S. in 2010 ([http://www.cdc.gov/pertussis/outbreaks.html](http://www.cdc.gov/pertussis/outbreaks.html), last accessed 26 February 2012). These reported cases may represent the “tip of an iceberg” that consists of 800,000 to 3.3 million cases in the U.S. every year (3). Worldwide, an estimated 50 million cases and 300,000 deaths occur annually ([http://www.who.int/immunization_monitoring/diseases/pertussis_surveillance/en/index.html](http://www.who.int/immunization_monitoring/diseases/pertussis_surveillance/en/index.html), last accessed 26 February 2012). Epidemics of pertussis often occur in 3 to 5 year cycles,
interspersed with local outbreaks. Humans are the sole reservoir for *B. pertussis*. Adolescent and adults, in whom immunity wanes several years after prior infection or vaccination, transmit the organism to susceptible infants. Pertussis in older children and adults is generally characterized by prolonged cough without the inspiratory whoop or posttussive vomiting typically observed in infants. While the incidence of pertussis in the U.S. is highest among children under one year of age, the incidence among older age groups increased substantially during the past decade (http://www.cdc.gov/pertussis/surv-reporting.html, last accessed 26 February 2012). In response, acellular vaccines are now recommended as a booster for adolescents and adults.

**MICROBIOLOGY AND CLINICAL SIGNIFICANCE**

The genus *Bordetella* is composed of eight species, four of which are responsible for respiratory disease in humans: *B. bronchiseptica, B. holmesii, B. parapertussis, and B. pertussis*. *B. parapertussis* may be responsible for up to 20% of pertussis-like disease, more often in young children (20). Illness is generally milder than that caused by *B. pertussis*, but young patients frequently present with the symptoms of classic pertussis (20). *B. bronchiseptica* is an infrequent cause of respiratory disease in humans, usually occurring in persons with underlying immunodeficiency diseases. Cases often involve exposure to mammals—usually farm animals or pets (38). *B. holmesii* is the most recently identified species associated with pertussis-like illness in humans. Yih et al. were the first to report a pertussis-like illness in patients with *B. holmesii* infections, isolating the organism from less than 1% of nasopharyngeal specimens collected from patients with suspected pertussis between 1994 and 1998 (39). A study using PCR failed to
detect *B. holmesii* DNA in any nasopharyngeal swabs collected from patients (no age information provided) in Finland and the Netherlands with suspected pertussis between 1992 and 2003 (1). However, another studying using PCR detected *B. holmesii* DNA in 20% of samples collected from adolescents and adults in France with suspected pertussis from 2009 to 2011 (21).

In total, the role that these “non-pertussis” *Bordetella* species play in human respiratory disease is not insignificant; they should be considered when designing a nucleic acid amplification-based diagnostic test, whether that test is *B. pertussis*-specific or a multispecies assay. Perhaps more than any other *Bordetella* species, *B. bronchiseptica* has been shown to possess a number of gene targets initially thought to be specific to *B. pertussis*. Some of these gene targets may be present in few isolates of *B. bronchiseptica* – as will be discussed later in this review – necessitating the analysis of a large number of diverse isolates to rule out cross-reactivity with *B. pertussis*-specific PCR assays.

LABORATORY DIAGNOSIS

**Direct fluorescent antibody staining and culture.** Because of their increased sensitivity, NAATs such as PCR have replaced DFA and culture for the detection of *B. pertussis* in many laboratories. DFA staining of nasopharyngeal secretions for *B. pertussis* has both poor sensitivity and specificity; a positive result is no longer part of the U.S. Centers for Disease Control and Prevention (CDC) pertussis case definition (http://www.cdc.gov/vaccines/pubs/surv-manual/chpt10-pertussis.html, last accessed 26 February 2012). Culture remains the gold standard for laboratory diagnosis of pertussis due to a specificity of essentially 100%. The CDC recommends that culture be performed during a suspected outbreak to confirm positive PCR.
results. However, culture is usually much less sensitive than NAATs in part because the organism is highly labile and does not survive well during specimen transport. Rapid specimen transport and the use of a suitable transport medium are critical for optimal culture sensitivity.

Serology. Serology can be a useful diagnostic method, but with important caveats. The presence of IgG antibodies as a result of vaccination or past infection limits the specificity and confounds interpretation of IgG-based tests. Repeated infections over a person’s lifetime can result in a muted IgM response, and poor sensitivity of tests that detect this class of antibody. Detection of IgA antibodies provides a specific diagnosis, but infants often have inconsistent IgA responses (20), limiting the sensitivity of IgA-based tests in this important age group. The most accurate serologic diagnosis of pertussis is retrospective, and requires two serum specimens collected several weeks apart to demonstrate a 4-fold or greater change in the IgG titer. In the United States, serologic tests for \textit{B. pertussis} are usually performed in public health and commercial reference laboratories. At the time that this manuscript was written, there were no U. S. Food and Drug Administration (FDA)-cleared serology-based tests for \textit{B. pertussis}.

Nucleic acid amplification. PCR tests for the detection of \textit{B. pertussis} in clinical specimens were first described in 1989 and targeted the pertussis toxin operon and an insertion element (11). Early PCR assays relied on agarose gels or microwell plates for the detection of amplified DNA. Real-time PCR for the detection of \textit{B. pertussis} was first described in 2001 (15, 28). Almost immediately upon its initial description as a diagnostic tool, PCR was shown to be substantially more sensitive than culture and DFA (7, 10, 18). Not unexpectedly, PCR remains positive longer during the course of disease and after initiation of antibiotic therapy than culture (5, 33). PCR sensitivity decreases substantially with increasing patient age and duration of
symptoms (33). Some individuals exposed to pertussis cases, who never went on to develop symptoms, were positive by PCR (10). These asymptomatic, transient infections are likely due to full or partial immunity.

While PCR is the NAAT most frequently used for the detection of *B. pertussis*, an assay based on loop-mediated isothermal amplification has been reported in the literature (13). At the time that this manuscript was written, there were no FDA-cleared NAATs for *B. pertussis* or other *Bordetella* species. There are several CE-marked real-time PCR kits for the detection of *B. pertussis* and *B. parapertussis*, all targeting insertion sequences; either IS481 alone, or both IS481 and IS1001.

**GENE TARGETS IN BORDETELLA NAATs**

**Insertion sequences (Table 1).** Most PCR tests are based on detection of insertion sequences—transposable DNA elements approximately 1000 base pairs in length that can be inserted into multiple sites on the same chromosome. Insertion sequences are usually present in multiple copies per genome, increasing the sensitivity of PCR tests. The insertion sequence IS481 is perhaps the most well described and validated target for *B. pertussis*. There are more than 50 copies of IS481 per *B. pertussis* genome (28). However, IS481 is also present in *B. holmesii* at eight to ten copies per genome (28), and in rare human isolates of *B. bronchiseptica* (1 of 73 isolates tested) (31). While *B. holmesii* has been associated with pertussis-like disease, it has not been identified as a cause of outbreaks. Therefore, NAATs based on IS481 alone have limited clinical value, particularly when used in outbreak settings. This will be discussed in...
more detail later in this review. IS1001 is found in *B. parapertussis* at approximately 20 copies per genome (35), and has been used in multiplex PCR with IS481 to detect and differentiate *B. pertussis* and *B. parapertussis* (14, 16, 29, 31). IS1001 is also present in isolates of *B. bronchiseptica* [4 of 73 human-derived isolates tested by Tatti et al. (31), and 26 of 38 animal-derived isolates tested by van der Zee et al. (34)] at 1 to 7 copies per genome (34). IS1001 has not been reported in *B. holmesii*. Therefore, multiplex assays based on IS481 and IS1001 will not differentiate *B. pertussis* and *B. holmesii*. An IS1001-like element, hIS1001, is found in *B. holmesii* at 3 to 5 copies per genome (1). Tatti et al. did not detect hIS1001 in any isolates of *B. pertussis*, *B. parapertussis*, or *B. bronchiseptica* (31). Consequently, multiplex PCR assays or testing algorithms that include hIS1001 in addition to IS481 and IS1001 would differentiate *B. pertussis* and *B. holmesii*. IS1002 is found in *B. pertussis* (4 to 8 copies per genome) and *B. parapertussis* (9 copies per genome) (34), but apparently not in *B. holmesii* or *B. bronchiseptica* (the number of isolates tested was not provided) (29). van der Zee et al. found IS1002 in 1 of 38 animal-derived *B. bronchiseptica* isolates tested (34). Therefore, a multiplex PCR containing IS1002, IS481 and IS1001 may allow detection and differentiation of *B. pertussis*, *B. parapertussis* and *B. holmesii*. A PCR that detects IS1002 alone would detect both *B. pertussis* and *B. parapertussis*, without differentiation (may not be important). The sequence identity of *B. pertussis* and *B. parapertussis* IS1002 is 93% (34), which may allow for differentiation of these species by distinct melting peaks. To my knowledge, this has not been reported in the literature. An IS1002 PCR may not cross-react with *B. holmesii* or *B. bronchiseptica*, but analysis of a large number of diverse isolates is necessary to confirm this.

**Single-copy targets (Table 2).** Pertussis toxin, the major virulence factor of *B. pertussis*, is a multi-subunit complex whose genes are organized as an operon. The promoter region of the
pertussis toxin operon is well characterized and an often used target in diagnostic PCR assays (11, 25, 31, 32). The pertussis toxin operon is also present in *B. parapertussis* and *B. bronchiseptica*, but due to mutations in the promoter region is not expressed by these species. The presence of these mutations also allows the differentiation of PCR amplicons produced by *B. pertussis*, *B. parapertussis* and *B. bronchiseptica* by size (22) or melting temperature in real-time PCR (25). Without post-amplification analysis, pertussis toxin-based PCR assays cannot distinguish between *B. pertussis*, *B. parapertussis* and *B. bronchiseptica*. Since the pertussis toxin promoter is not found in *B. holmesii*, primers targeting this have been combined with IS481 to differentiate *B. pertussis* and *B. holmesii* (32). Pertactin is a major virulence factor produced by *B. pertussis*, *B. parapertussis* and *B. bronchiseptica*, associated with adherence to ciliated epithelial cells of the respiratory tract. A real-time PCR assay designed to detect pertactin gene sequences of *B. pertussis* reportedly did not detect *B. parapertussis*, *B. bronchiseptica*, or *B. holmesii* (36). However, the number of isolates tested was not provided. A later study of a large number of human and animal-derived *B. bronchiseptica* isolates demonstrated cross-reactivity (27). Filamentous hemagglutinin is a major virulence factor of *B. pertussis*, mediating adherence to ciliated epithelial cells. It is also produced by *B. parapertussis* and *B. bronchiseptica*. A real-time PCR assay that detects these three *Bordetella* species, followed by post-amplification differentiation of filamentous hemagglutinin amplicons by melting-curve analysis, was recently described (14). A PCR assay targeting the *Bordetella* adenylate cyclase gene was described by Douglas et al. (4). *B. pertussis*, *B. parapertussis* and *B. bronchiseptica* were detected by the assay (*B. holmesii* was not tested). Farrell et al. described a PCR assay based on detection of the outer membrane porin gene, and differentiation of *B. pertussis*, *B. parapertussis* and *B. bronchiseptica* using species-specific probes (6). None of the probes detected *B. holmesii.*
However, few *B. bronchiseptica* and *B. holmesii* isolates were tested. recA is a protein involved in recombinational DNA repair. Depending on the design of PCR primers and probes, real-time PCR assays targeting the recA gene detected *B. pertussis*, *B. parapertussis* and *B. bronchiseptica* but not *B. holmesii* (25), or detected *B. holmesii* only (1, 8). The *B. holmesii*-specific recA primers have been incorporated with IS481 primers in an assay to differentiate *B. pertussis* and *B. holmesii* (8). The flagellin gene was the target of an early PCR assay. PCR primers amplified *B. pertussis*, *B. parapertussis* and *B. bronchiseptica*, but *B. pertussis* produced an amplicon of a different size that was distinguished in agarose gels (12). *B. holmesii* was not evaluated.

BP3385, a gene of unknown function, was the target of a *B. pertussis*-specific real-time PCR assay that did not detect *B. parapertussis*, *B. hinzii*, *B. holmesii*, or *B. bronchiseptica* (9). However, the number of isolates of each species was not provided. A later study with a large number of isolates found that BP3385 is present in some strains of *B. hinzii* and *B. bronchiseptica* (26). A duplex real-time PCR assay targeting the thiolase gene BP283 and undefined gene BP485 was described by Probert et al. (24). The assay did not detect isolates of *B. holmesii*, *B. parapertussis*, or *B. bronchiseptica*. However, only five *B. bronchiseptica* isolates were tested. With the exception of the pertussis toxin gene, PCR assays based on single-copy targets have not been extensively evaluated, and require further analytical and clinical validation.

In addition to the multiplex assays described above, a two-tiered or reflex testing approach can provide adequate species-specificity when using an IS481-based PCR. In this approach, IS481 PCR serves as a highly sensitive screening assay. A specimen positive by IS481 PCR would require further testing using an assay that detects pertussis toxin or another target specific for *B. pertussis* (or conversely, a *B. holmesii*-specific assay to rule it out as the cause of the
positive IS481 PCR result). If unable to verify the positive IS481 result, the laboratory could report either negative or indeterminate for *B. pertussis*. This approach has been used retrospectively by the CDC to investigate pertussis outbreaks (2), but could also be used prospectively in the diagnostic laboratory. A two-tiered testing algorithm would likely miss some true pertussis infections, but the data in the literature suggest that these false-negatives would be relatively few in number (25). In my opinion these few false-negatives from an overall highly sensitive assay would be heavily outweighed by the benefit of fewer false-positives and pseudo-outbreaks.

REAL WORLD PERFORMANCE OF PCR TESTS FOR BORDETELLA: THE GOOD, BAD AND THE UGLY

The widespread use of PCR to diagnose pertussis has provided many benefits, primarily as a result of its high sensitivity relative to other laboratory methods. These benefits include detection and treatment of additional infections (particularly among adolescents and adults) and hence, better control and prevention of outbreaks. The use of PCR has increased our understanding of the effect of patient age and duration of symptoms on the sensitivity of not only PCR, but also culture. It has revealed the significance of pertussis in older persons, and the important role that these age groups play in disease transmission. As a result, vaccine boosters are now available and recommended for adolescents and adults.

Laboratory testing during pertussis outbreaks is often conducted under such stresses as demand for rapid turn-around of test results, higher than normal testing volume (often including
specimens from individuals with low pre-test probability of disease) and the co-circulation of
other respiratory pathogens. Weaknesses of any diagnostic test are more likely to be revealed
during these conditions, and NAATs for *B. pertussis* are no exception. Pseudo-outbreaks of
pertussis due to false-positive PCR results have been reported in the literature and have a variety
of different root causes. They result in the unnecessary expenditure of considerable resources by
healthcare institutions and public health departments. Cross-reactivity of a *B. pertussis* IS481
PCR test with *B. holmesii* in a specimen from an emergency department nurse resulted in the
contact or evaluation of a number of pediatric patients and their caregivers, additional healthcare
workers, and persons who attended a conference with the index patient (37). Weakly positive
results from real-time PCR assays that target IS481 have contributed to pseudo-outbreaks (2, 19).
Many of these weakly positive samples were not verifiable by alternate PCR assays that targeted
different genes. Additionally, the majority of PCR positive cases tested by IgG enzyme-linked
immunosorbent assay were negative for anti-pertussis toxin IgG (2). PCR-positive cases with
weakly positive results by IS481 real-time PCR (crossing threshold values >35) were unlikely to
meet the clinical case definition, and more likely to be false-positive (9, 23). Environmental
contamination in patient clinics, and the resulting contamination of specimens, has contributed to
pseudo-outbreaks (19). Some *B. pertussis* vaccines have been shown to contain genomic DNA,
and aerosolization of vaccine likely results in the contamination of the hands of health care
providers and environmental surfaces (30). Performing specimen collection and vaccination in
the same room was linked to false-positive PCR results (19). Many of the false-positive patient
specimens from the pseudo-outbreak, as well as environmental swabs from the clinics had high
crossing threshold values (>35). Contamination occurring in the laboratory has also contributed
to a pseudo-outbreak (17). The contamination was resolved after the laboratory switched to new
PCR primers that amplified a different gene target. Details of the PCR method were not provided. However, as this contamination event occurred in the late 1990’s, it is likely that a conventional PCR assay was used. Real-time PCR, which does not require the opening of tubes following PCR, greatly reduces the risk of contamination from amplicons.

**SUMMARY**

NAATs such as PCR are the most sensitive laboratory methods routinely available for the detection of *B. pertussis*. With a rapid turn-around time and a capacity for high throughput, PCR testing can have a substantial positive impact on patient care and the management of outbreaks. The predictive value of positive NAAT results is perhaps the greatest limitation of these methods. IS481-based NAATs will detect *B. holmesii*, which for epidemiologic and clinical purposes is considered a false-positive. Environmental contamination in patient clinics has been identified as a source of false-positive test results. The positive predictive value of *B. pertussis* NAATs can be improved by amplifying gene targets that are not shared among species, using multiplex assays or a two-tiered testing algorithm to confirm positives, implementing an indeterminate range for assays that target multiple-copy insertion sequences, segregation of “clean” and “dirty” areas both in patient clinics and the diagnostic laboratory, and testing only symptomatic persons. Additional guidance for healthcare professionals on PCR testing for *B. pertussis* – including specimen collection and interpretation of test results – is available from the CDC (http://www.cdc.gov/pertussis/clinical/diagnostic-testing/diagnosis-pcr-bestpractices.html, last accessed 26 February 2012).
REFERENCES


TABLE 1. *Bordetella* insertion sequences

<table>
<thead>
<tr>
<th>Insertion sequence</th>
<th>B. pertussis</th>
<th>B. parapertussis</th>
<th>B. holmesii</th>
<th>B. bronchiseptica&lt;sup&gt;a&lt;/sup&gt;</th>
<th>References</th>
</tr>
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<tbody>
<tr>
<td>IS481</td>
<td>+ / &gt;50</td>
<td>− / NA</td>
<td>+ / 8-10</td>
<td>(+)&lt;sup&gt;b&lt;/sup&gt; / ND</td>
<td>11, 28, 31</td>
</tr>
<tr>
<td>IS1001</td>
<td>− / NA</td>
<td>+ / ~20</td>
<td>− / NA</td>
<td>(+)&lt;sup&gt;c&lt;/sup&gt; / 1-7</td>
<td>29, 31, 34</td>
</tr>
<tr>
<td>hIS1001</td>
<td>− / NA</td>
<td>− / NA</td>
<td>+ / 3-5</td>
<td>− / NA</td>
<td>1, 31</td>
</tr>
<tr>
<td>IS1002</td>
<td>+/4-8</td>
<td>+ / 9</td>
<td>− / NA</td>
<td>−&lt;sup&gt;d&lt;/sup&gt; / 1</td>
<td>29, 34</td>
</tr>
</tbody>
</table>

Symbols and abbreviations: +, present in all isolates; (+), present in some isolates; −, absent in all isolates; NA, not applicable; ND, not determined.

<sup>a</sup> Human-derived *B. bronchiseptica* isolates only.

<sup>b</sup> 1 of 73 human-derived isolates was positive (ref #31).

<sup>c</sup> 4 of 73 human-derived isolates were positive (ref #31).

<sup>d</sup> Found in rare animal-derived isolates (ref #34).
<table>
<thead>
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<th>Target</th>
<th>References</th>
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<tbody>
<tr>
<td><em>B. pertussis</em>-specific</td>
<td></td>
</tr>
<tr>
<td>BP283 (thiolase)</td>
<td>24</td>
</tr>
<tr>
<td>BP485</td>
<td>24</td>
</tr>
<tr>
<td>Shared among <em>Bordetella</em> species</td>
<td></td>
</tr>
<tr>
<td>Adenylate cyclase</td>
<td>4</td>
</tr>
<tr>
<td>BP3385</td>
<td>9, 26</td>
</tr>
<tr>
<td>Filamentous hemagglutinin&lt;sup&gt;b&lt;/sup&gt;</td>
<td>14</td>
</tr>
<tr>
<td>Flagellin&lt;sup&gt;b&lt;/sup&gt;</td>
<td>12</td>
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<tr>
<td>Pertactin</td>
<td>27, 36</td>
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<tr>
<td>Pertussis toxin&lt;sup&gt;b&lt;/sup&gt;</td>
<td>11, 22, 31, 32</td>
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<tr>
<td>Porin&lt;sup&gt;b&lt;/sup&gt;</td>
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<tr>
<td>recA&lt;sup&gt;b&lt;/sup&gt;</td>
<td>1, 8, 25</td>
</tr>
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</table>

<sup>a</sup>With the exception of pertussis toxin, PCR assays targeting these genes have not been well validated.

<sup>b</sup>Species-specific primers, or PCR assays using post-amplification differentiation of species have been described.