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# *Bordetella bronchiseptica* in Canine Respiratory Disease: A Review

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**ABSTRACT**

*Bordetella bronchiseptica* is a major bacterial pathogen responsible for canine infectious respiratory disease complex (CIRDC), which affects the upper respiratory tract of dogs and contributes to significant morbidity in canine populations worldwide. The disease spreads primarily through aerosol and direct contact between infected and susceptible dogs, especially in environments with high animal density such as kennels, shelters, and dog daycare facilities. Puppies and immunocompromised dogs are particularly vulnerable due to their immature immune systems, while co-infections with respiratory viruses can exacerbate clinical signs and increase disease severity. Infected animals may shed the bacterium for extended periods, allowing continuous transmission even among clinically healthy carriers. Although human infection is rare, *B. bronchiseptica* poses a potential zoonotic risk, particularly for immunocompromised individuals, underscoring the importance of One Health approach that integrates animal, human, and environmental health. Preventive measures including intranasal vaccination, proper ventilation, strict hygiene, and public education are essential to reduce bacterial spread and disease incidence. Comprehensive control efforts combining vaccination programs, environmental management, and ongoing surveillance are critical to mitigate both animal health impacts and zoonotic transmission risks.

## Introduction

Canine Infectious Respiratory Disease (CIRD), also known as kennel cough or infectious tracheobronchitis, is one of the most common contagious diseases affecting dogs worldwide. CIRD refers to an upper respiratory tract infection caused by one or more pathogens (Schulz *et al*., 2014). Several viral and bacterial agents contribute to the development of CIRD, acting sequentially or synergistically to produce characteristic clinical signs. Dogs of all ages may become infected with respiratory pathogens, however, previous studies have demonstrated that puppies are the most susceptible and frequently affected group (Yondo *et al*., 2023). Canine parainfluenza virus (CPIV), canine adenovirus type 2 (CAdV-2), and *Bordetella bronchiseptica* remains the most commonly detected pathogens in dogs with CIRD (Dong *et al*., 2022).

*B. bronchiseptica* is a primary pathogen associated with CIRD, known for its ability to cause respiratory disease independently as well as its significant role in mixed infections with various viral and bacterial pathogens (Jang *et al*., 2025). Clinically, CIRD is characterized by common respiratory signs such as coughing, nasal discharge, fever, and lethargy. The disease may persist for several weeks and, in some cases, progress to severe bronchopneumonia (De Luca *et al*., 2024). *B. bronchiseptica* is a zoonotic, Gram-negative coccobacillus that is an obligate aerobe and is frequently isolated from the upper respiratory tracts of domestic animals (such as dogs, cats, rabbits, horses, pigs, rats, hamsters, and guinea pigs) as well as wild animals (including voles, seals, rodents, and captive koalas) (Ner *et al*., 2003). The bacterium colonizes ciliated epithelial cells and induces inflammation within the respiratory tract of dogs and various other species, including humans (Ellis, 2015).

*B. bronchiseptica* can colonize both the upper and lower respiratory tracts. A study in Germany reported a prevalence of 78.7% in dogs with Canine Infectious Respiratory Disease Complex (CIRDC) compared to 45.6% in healthy dogs (Lappin *et al*., 2015). Contemporary isolates have shown multidrug resistance and the presence of virulence-associated genes, complicating disease control and treatment efforts (Shang *et al*., 2024). Therefore, comprehensive understanding of the epidemiology, pathogenesis, and prevention strategies of *B. bronchiseptica* is crucial for effective canine health management (Chamorro *et al*., 2023).

Infection with *B. bronchiseptica* not only can cause mild respiratory symptoms such as coughing, sneezing, and nasal discharge but may also progress to pneumonia or systemic complications such as meningoencephalomyelitis in severe cases (Otto *et al*., 2022). Molecular diagnostic methods, including PCR and qPCR, have become more widely used due to their higher sensitivity in detecting *B. bronchiseptica* compared to traditional culture techniques, which may sometimes fail (Jang *et al*., 2025). In terms of prevention, mucosal vaccines (intranasal or oral) have been shown to reduce the duration of coughing and bacterial shedding, although their efficacy varies depending on the administration route and formulation (Ellis *et al*., 2015; Collins *et al*., 2022).

## Etiology

*Bordetella bronchiseptica* is a Gram-negative, rod-shaped bacterium that belongs to the *Bordetella* genus. It is one of the primary causes of respiratory diseases in dogs and cats and can also infect humans, particularly individuals with weakened immune systems. *B. bronchiseptica* has an interesting evolutionary history, as its ancestors are believed to have originated from a free-living environmental lineage before adapting to become a pathogen in warm-blooded animals. Its ability to survive in the environment, such as in hot springs, demonstrates that *B. bronchiseptica* can persist under nutrient-limited conditions and possesses motile flagella that facilitate transmission through environmental reservoirs (Badhai and Das, 2023). Etiologically, *Bordetella bronchiseptica* possesses various virulence factors that play crucial roles in infection processes, including filamentous hemagglutinin (*fha*B), pertactin (*prn*), adenylate cyclase toxin (*cya*A), dermonecrotic toxin (*dnt*), and the type III secretion system (T3SS). These factors enable the bacterium to adhere to the respiratory epithelium, evade the host immune system, and cause tissue damage (Shang *et al*., 2024).

This bacterium is recognized as one of the main pathogens responsible for Canine Infectious Respiratory Disease Complex (CIRDC), commonly known as kennel cough (Al-Kafawi *et al*., 2023). The pathogen can survive outside the host for a certain period, facilitating transmission


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among dogs in high-density environments such as kennels, shelters, or pet shops. Moreover, *B. bronchiseptica* can persist for extended periods in the respiratory mucosa and act as either a primary or secondary pathogen, particularly in dogs with weakened immune systems or those exposed to environmental stress (Wilson *et al*., 2020). *B. bronchiseptica* can also exploit the life cycle of environmental amoebae such as *Dictyostelium discoideum* as an amplifying transmission vector. In the Bvg− phase, the bacterium can survive and replicate within amoebae, evade predation, and spread geographically through the amoebal life cycle. This highlights the significance of environmental reservoirs in the epidemiology of *B. bronchiseptica* (Taylor-Mulneix *et al*., 2017). Furthermore, interactions with *Acanthamoeba castellanii* show that the Bvg− phase is more advantageous for survival outside mammalian hosts, reinforcing the role of environmental adaptation in the bacterium's life cycle (Nugraha, 2022).

Biofilm formation is one of the key survival strategies of *B. bronchiseptica*, particularly for resisting environmental stress and the host immune response. Biofilm development is regulated by the signaling molecule c-di-GMP, where albumin and calcium from respiratory secretions can inhibit biofilm formation by increasing ACT secretion and c-di-GMP degradation (Mugni *et al*., 2025). Additionally, the diguanylate cyclase BdcB promotes biofilm formation while suppressing motility and modulating the host immune response through the regulation of type III secretion system expression (Belhart *et al*., 2023). At the molecular level, the effector protein BteA, secreted via the type III secretion system, can induce host cell death by disrupting calcium homeostasis and mitochondrial function, leading to cellular necrosis. Differences in BteA activity and regulation between *B. bronchiseptica* and B. pertussis also contribute to variations in disease severity (Zmuda *et al*., 2024).

In dogs, *B. bronchiseptica* infection often occurs concurrently with other pathogens, such as *Mycoplasma* and canine respiratory coronavirus, with a co-infection prevalence of up to 47%. This underscores the need for the development of combined vaccines and comprehensive prevention strategies to control contagious respiratory diseases in dogs (Jang *et al*., 2025). From an informative standpoint, understanding the mechanisms of pathogenesis, virulence regulation, and environmental adaptation of *B. bronchiseptica* is essential for developing effective prevention, control, and therapeutic strategies for both animals and humans (Mattoo *et al*., 2001).

## Bacterial morphology

*Bordetella bronchiseptica* is a small, Gram-negative coccobacillus measuring approximately 0.2–0.5 × 0.5–2 µm, typically observed as single cells or pairs under Gram staining (Richter, 1967). Under electron microscopy, *B. bronchiseptica* exhibits distinct surface structures, including a lipopolysaccharide-rich outer membrane and fine filamentous pili associated with adhesion to the respiratory epithelium (Gueirard *et al*., 2005). The bacterium is an obligate aerobe and is generally motile under certain conditions due to flagellar expression, with motility closely linked to phase-variable genetic regulation (Akerley *et al*., 1993). The outer cell surface contains several outer membrane proteins (OMPs) with molecular patterns that vary among isolates, playing roles in host interaction and antigenicity (Friedman *et al*., 2006). The lipopolysaccharide (LPS) component of *B. bronchiseptica* demonstrates structural variation influencing endotoxicity and host immune recognition, as described in analyses of the core LPS and lipid A structures (Vinogradov *et al*., 2000).

Large adhesins such as filamentous hemagglutinin (*Fha*), fimbriae, and pertactin are prominent surface structures that mediate the initial attachment of the bacteria to the cilia of respiratory epithelial cells, as clearly observed in ultrastructural studies of in vivo colonization (Inatsuka *et al*., 2005). In addition to protein adhesins, the production of surface polysaccharides (e.g., Bps in certain *Bordetella* species) and biofilm components facilitates adherence to mucosal surfaces and protection against mucociliary clearance (Conover *et al*., 2010). Biofilm formation by *B. bronchiseptica* has been microscopically demonstrated and is associated with specific surface phenotypes and the expression of certain outer membrane proteins (OMPs), forming compact extracellular matrix communities that protect bacterial cells (Nicholson *et al*., 2012). Signal transduction regulators such as the bvgAS system and cyclic-di-GMP modulate virulence expression and surface motility/morphological phenotypes, which are evident in the phenotypic shift between bvg+ and bvg− phases (Akerley *et al*., 1992).

*B. bronchiseptica* colonies grown on solid media such as Bordet-Gengou or blood agar typically appear as small, shiny, and grayish to cream-colored colonies; some isolates display mild hemolytic zones on blood agar depending on the strain (Kasprzak *et al*., 1994). Certain mutations result in changes in colony morphology (e.g., domed versus smooth), which are associated with altered expression of surface antigens and toxins, making colony observation a useful tool in phenotypic characterization (Nagano *et al*., 1988). Under electron microscopy, flagella, pili, and outer membrane vesicles (OMVs) are visible; the OMVs have been described as bilayered membranous particles containing OMPs and lipopolysaccharides (LPS) with potential roles in host interaction (Richter, 1967; Bottero *et al*., 2018). Antigenic variation in OMPs and LPS among isolates contributes to measurable immunological heterogeneity in the field, influencing serological detection and vaccine efficacy (Preston *et al*., 2006). The Gram-negative cell wall structure with an LPS-rich outer membrane also explains the endotoxin-mediated responses observed during severe in vivo infections (Vinogradov *et al*., 2000).

The interaction of *B. bronchiseptica* with respiratory epithelial cells shows strong adhesion to ciliated surfaces and occasional invasion or uptake visible under transmission electron microscopy (TEM), reflecting the bacterium's capacity to colonize mucosal layers (Gueirard *et al*., 2005). During colonization, the release of OMVs carrying surface antigens and virulence factors can modulate local immune responses, and these OMVs have been investigated as potential adjuvants or vaccine antigens (Bottero *et al*., 2018). Ultrastructural observations of biofilms using scanning electron microscopy (SEM) on in vitro substrates reveal a three-dimensional architecture dependent on surface adhesins and exopolysaccharide components, with community morphology distinct from planktonic cells (Nicholson *et al*., 2012). Genetic regulators such as diguanylate cyclases and c-di-GMP effectors modify surface phenotypes and biofilm-forming ability, influencing both colony morphology and the microscopic biofilm structure (Belhart *et al*., 2023). The presence of type III secretion systems (T3SS) in some isolates affects cell-surface interactions and cellular phenotypes during infection, producing ultrastructural differences in T3SS-producing cells (Nicholson *et al*., 2014).

Morphological differences among strains, including variations in flagellar expression, adhesins, OMPs, and LPS composition, have significant functional consequences for colonization, inflammatory encephalopathy, and environmental persistence, making morphological analysis relevant for epidemiological studies and vaccine development (Chamorro *et al*., 2023). Clinical isolates with strong biofilm-forming capacity display distinctive colony morphology and surface structures, often associated with increased resistance to antimicrobials and immune clearance (Yi *et al*., 2024). Modern studies combining TEM/SEM, OMP proteomic analyses, and genomic sequencing have enabled detailed correlations between cellular morphology, genotype, and virulence profiles, making morphology an integral component of comprehensive phenotypic characterization (Thieulent *et al*., 2025). Because cellular morphology and surface structure influence diagnostic detection and antigen design, morphological descriptions of *B. bronchiseptica* should always be supported by microscopic, biochemical, and molecular data in each study (Sisti *et al*., 2002).

## Epidemiology

*Bordetella bronchiseptica* is a primary pathogen in the Canine Infectious Respiratory Disease Complex (CIRDC), which can independently

cause disease or act as part of a coinfection with other pathogens. The prevalence of *B. bronchiseptica* coinfection in dogs with CIRDC reaches 47%, with *Mycoplasma* and canine respiratory coronavirus being the most commonly co-detected pathogens. This highlights the importance of developing combination vaccines and comprehensive prevention strategies to control the disease across different regions and age groups. Informatively, *B. bronchiseptica* is not limited to respiratory infections but has also been identified in cases of urinary tract infections in dogs. A molecular study in Iraq reported a prevalence of 13.92% among dogs with urinary tract infections, and serological testing revealed antibodies against *B. bronchiseptica* in 32.91% of dogs tested. Phylogenetic analysis showed a high similarity with global strains, indicating potential cross-regional transmission (Kadhim *et al*., 2025).

Research in China reported that *B. bronchiseptica* is a major cause of respiratory disease in dogs and cats, with a PCR-positive prevalence of 22.94%. More than 90% of isolates carried four key virulence genes, and all isolates exhibited multidrug resistance. This underscores the challenges in infection control and the urgent need for the development of new, effective vaccines. *B. bronchiseptica* is transmitted via aerosols, contact with contaminated feces or urine, and fomites. All dog breeds and age groups are susceptible, and the infection is highly contagious. Prevention through isolation, quarantine, and vaccination is strongly recommended to reduce transmission risks, particularly in high-density environments such as kennels (Rose *et al*., 2025).

A study in Kerala, India, found that 20% of dogs showing CIRDC symptoms tested positive for *B. bronchiseptica* via PCR, with most cases occurring in dogs under one year old and those living in multi-dog households. This finding emphasizes the importance of vaccination and environmental management in preventing disease spread (Sariga *et al*., 2022). A seroepidemiological survey in Sweden reported a 22% seroprevalence of *B. bronchiseptica* antibodies among pet dogs. No correlation was found between dog population density and *B. bronchiseptica* seroprevalence, in contrast to the canine parainfluenza virus, which was more commonly detected among group-housed dogs (Englund *et al*., 2003). Research in Turkey indicated that serum amyloid A (SAA) levels were significantly elevated in dogs infected with *B. bronchiseptica*, suggesting that SAA could serve as a diagnostic and monitoring biomarker for the disease. The serological prevalence in the region was 12% (Akar *et al*., 2025).

Histopathologically, *B. bronchiseptica* is frequently found adhering to the cilia of the respiratory tract and can cause fatal pneumonia, although it more commonly results in non-fatal tracheobronchitis. Specific diagnosis is crucial to distinguish primary pneumonia from aspiration pneumonia and to prevent transmission between animals (Taha-Abdelaziz *et al*., 2016). Real-time PCR methods are more sensitive than culture techniques for detecting *B. bronchiseptica* in bronchoalveolar fluid from dogs with persistent lower respiratory symptoms. However, PCR results must be carefully interpreted, as they can detect DNA from non-viable organisms or colonization; thus, combining molecular, microbiological, and clinical data is essential (Atencia *et al*., 2025). Lung microbiota analysis in dogs infected with *B. bronchiseptica* has revealed dysbiosis, characterized by reduced microbial diversity and increased bacterial load compared to healthy dogs. The 16S rDNA sequencing technique provides highly informative and reliable identification of pathogens in infectious pulmonary diseases.

## Pathogenesis

The initial colonization of *Bordetella bronchiseptica* begins with adhesion to the respiratory epithelium through surface adhesins such as filamentous hemagglutinin and fimbriae, which facilitate attachment to ciliated cells of the nasopharyngeal tract (Mattoo and Cherry, 2005). The two-component BvgAS regulatory system controls the expression of adhesins and toxins during the virulent ($bvg^+$) phase, enabling phenotypic switching between persistent colonization and the non-virulent, more motile phase (Groathouse *et al*., 2003). Following attachment, *B. bronchiseptica* produces adenylate cyclase-hemolysin (*Cya*A), which disrupts phagocytic function and alters intracellular signaling by increasing cAMP levels, thereby contributing to the evasion of the host's innate immune response (Harvill *et al*., 1999).

Biofilm formation on mucosal surfaces enables long-term persistence by protecting the bacteria from mucociliary clearance and antimicrobial activity, making biofilm a key strategy for chronic infection (Cattelan *et al*., 2016). Extracellular polymeric substances and surface components such as Bps polysaccharides and matrix-associated proteins facilitate the development of structured communities that resist environmental stress and local immune responses (Medhekar *et al*., 2009). In addition to structural factors, secretion of effectors such as BteA via the Type III Secretion System (T3SS) enhances cytotoxicity toward epithelial cells and modifies the mucosal microenvironment to support prolonged colonization (Kamanova *et al*., 2020). *B. bronchiseptica* also modulates immune cell responses by altering macrophage polarization and suppressing $CD4^+$ T-cell proliferation, thereby skewing immune responses toward a Th17 phenotype and promoting bacterial survival in the respiratory tract (Siciliano *et al*., 2006). Experimental studies have demonstrated that genetic variation in toxin-related loci (e.g., *cya*A or T3SS-associated genes) affects virulence and persistence among strains, emphasizing the role of strain-to-strain variability in clinical outcomes (Buboltz *et al*., 2008). Metabolic adaptation and the ability of *B. bronchiseptica* to interact with or disrupt the host nasal microbiota also influence whether colonization progresses to symptomatic infection or remains asymptomatic and chronic (Luczó *et al*., 2023).

At the cellular level, T3SS effectors and toxin products induce non-apoptotic cell death or phagocytic dysfunction, reducing the host's cellular clearance capacity against bacteria adhering to the respiratory epithelium (French *et al*., 2009). The dermonecrotic toxin (*Dnt*) exerts broader effects beyond local lesions. Animal studies indicate that *Dnt* can influence tissue maturation and humoral immune responses at infection sites, correlating with specific clinical lesions (Brockmeier *et al*., 2002). In vivo experiments using animal models have shown that mutants lacking *Cya*A or T3SS exhibit altered persistence capacity, confirming the combinatorial role of toxins and secretion systems in modulating long-term colonization (Harvill *et al*., 1999). Phase variation ($bvg^+/bvg^-$) allows *Bordetella* to shift from an adhesive/virulent phenotype to a motile, environmentally resistant phenotype, meaning that phase dynamics contribute to infection distribution and inter-host transmission (Groathouse *et al*., 2003). Ultimately, an integrative understanding of *B. bronchiseptica* pathogenesis, linking adhesion, toxin secretion, biofilm formation, and immune modulation, forms the foundation for developing therapeutic and vaccine strategies targeting multiple virulence factors (Jeron *et al*., 2018). Recent genomic and molecular studies mapping virulence determinants and secreted effectors have identified potential new therapeutic targets (e.g., T3SS inhibitors or antibiofilm agents) that may reduce the persistence and transmission capacity of *B. bronchiseptica* (Hegerle *et al*., 2013).

## Clinical manifestations

Clinical signs in *Bordetella bronchiseptica* infected dogs are generally associated with the upper respiratory tract and can range from mild to moderately severe. Most infected dogs exhibit symptoms such as coughing (approximately 83.33%), ocular/nasal discharge (58.33%), fever (41.66%), dyspnea (16.67%), and gagging or retching (33.33%) (Rose *et al*., 2024). In more chronic or complicated cases, as reported in a study in 2020, dogs diagnosed with *B. bronchiseptica* presented with a productive daily cough lasting for one month or longer, mucopurulent discharge in the trachea/bronchi, broncho-interstitial or alveolar radiographic changes, and increased neutrophil counts in bronchoalveolar lavage fluid (Fastres *et al*., 2020).

Other studies indicated that many dogs develop clinical signs typically 3 to 4 days after exposure, and symptoms may persist for up to two weeks. The most frequently reported symptoms include coughing, gagging or retching, and serous ocular and nasal discharge. Most infected dogs remain clinically active and do not develop fever, although some cases may show more severe signs depending on immune status and the presence of coinfections. Coinfection with other pathogens such as *Mycoplasma* and canine respiratory coronavirus often exacerbates clinical signs, increases the risk of pneumonia, and prolongs disease duration. The prevalence of coinfection in CIRDC cases reaches 47%, emphasizing the importance of developing combination vaccines and comprehensive preventive strategies (Wagener *et al*., 1984). Furthermore, chronic infections may lead to complications such as bronchiolitis obliterans and progressive pulmonary fibrosis (Jaffey *et al*., 2019).

## Diagnosis

Diagnosis of *Bordetella bronchiseptica* infection in dogs requires a combination of clinical, bacteriological, and molecular approaches. Common clinical samples include nasopharyngeal or oropharyngeal swabs, tracheal secretions, bronchoalveolar lavage fluid (BALF), and lung tissue in pneumonia cases (Chamorro *et al*., 2023). Bacterial culture on selective media such as MacConkey agar or Bordet-Gengou agar remains a conventional method for *B. bronchiseptica* identification, although its sensitivity decreases in cases with low bacterial loads or prior antibiotic administration (Fastrès *et al*., 2020). Culture isolation remains important as it allows antimicrobial susceptibility testing and biotype identification, however, results require longer processing time compared to molecular methods (Chalker *et al*., 2003). Therefore, successful diagnosis depends heavily on appropriate sample collection, storage conditions, and rapid transportation to the laboratory to maintain bacterial viability (Jeon *et al*., 2023).

Molecular methods such as conventional PCR, real-time PCR, and multiplex PCR have become the primary tools for detecting the DNA of *B. bronchiseptica* in various sample types, including nasopharyngeal swabs, BALF, and respiratory secretions (Thieulent *et al*., 2025). Studies have shown that PCR demonstrates higher sensitivity than culture, particularly in dogs that are newly infected or have received antibiotic therapy (Fastrès *et al*., 2020). Multiplex PCR enables simultaneous detection of *B. bronchiseptica* along with other respiratory pathogens, such as *Mycoplasma cynos* and canine parainfluenza virus, facilitating the identification of co-infections (Jeon *et al*., 2023). However, PCR results must be interpreted with caution, as the method detects genetic material rather than active infection, which may yield positive results in dogs that have recovered or are asymptomatic carriers (Tabatabaei *et al*., 2022).

Serological assays such as ELISA, agglutination, and neutralization tests are also used to detect antibodies against *B. bronchiseptica*, particularly for population surveillance and vaccine efficacy evaluation (Akar *et al*., 2025). However, serology cannot differentiate between natural infection, active disease, or post-vaccination immune responses (Chalker *et al*., 2003). The correlation between serological and molecular detection is reported to be weak to moderate, thus combining methods is recommended for accurate diagnosis. Paired serum samples (acute and convalescent phases) can help confirm active infection through rising antibody titers, while measuring antibodies against specific antigens such as filamentous hemagglutinin (*Fha*) and pertactin enhances diagnostic specificity (Chamorro *et al*., 2023).

Cytological analysis of BALF and bacterial culture provides additional diagnostic value. Cytology may reveal neutrophilic inflammation and small rod-shaped bacteria within a dense mucous background (Fastrès *et al*., 2020). Culture from BALF allows confirmation of *B. bronchiseptica* presence and antimicrobial susceptibility testing to guide appropriate therapy (Canonne *et al*., 2018). Quantitative PCR is also useful for distinguishing between mild colonization and clinically significant infection when combined with cytological findings and clinical data (Jeon *et al*., 2023). Recent methods such as next-generation sequencing (NGS) have been employed to detect a broad range of respiratory pathogens, including *B. bronchiseptica*, although their use remains limited due to high cost and complex data interpretation (Thieulent *et al*., 2025).

Several diagnostic challenges are commonly encountered, including delayed sampling, prior antibiotic use, and limited laboratory facilities, which may lead to false-negative results (Kadhim *et al*., 2025). Field isolates with strong biofilm-forming capacity and antibiotic resistance also complicate culture-based identification (Shang *et al*., 2024). In clinical practice, the ideal diagnostic approach includes early sample collection, PCR for rapid screening, culture for confirmation and antimicrobial testing, and serology for surveillance purposes (Jeon *et al*., 2023; Chamorro *et al*., 2023). Laboratory results must always be interpreted within the clinical context, considering factors such as clinical signs, vaccination status, and animal contact history, to differentiate between colonization, subclinical infection, and active disease (Thieulent *et al*., 2025; Fastrès *et al*., 2020).

## Differential diagnosis

Viral infections such as canine parainfluenza virus (CPiV) often cause dry cough and upper respiratory signs that closely resemble bordetellosis, therefore should be considered first in dogs with a history of exposure in kennels or group settings (Cordisco *et al*., 2022). Molecular surveys in canine populations have shown that CPiV is frequently dominant in the canine infectious respiratory disease complex (CIRDC), and clinical suspicion should be followed by specific viral diagnostic testing when available (Yondo *et al*., 2023). Canine influenza virus (CIV; e.g., H3N2/H3N8) can produce clinical signs ranging from mild to severe pneumonia, making epidemiological differences, vaccination history, and laboratory testing essential for distinguishing it from *Bordetella* infection (Ge *et al*., 2024). Given the genotypic and epidemiological diversity of CIV among different geographic areas, influenza outbreaks may exhibit overlapping clinical presentations. Accordingly, RT-PCR testing should be considered, particularly in severe or clustered cases (Wasik *et al*., 2025). Canine respiratory coronavirus (CRCoV) is another CIRDC agent producing similar clinical signs such as cough and rhinorrhea and is often detected concurrently with other pathogens, thus multiplex testing for CRCoV improves differential diagnosis accuracy (Poonsin *et al*., 2023). Rapid diagnostic panels that include multiplex PCR/RT-PCR for CRCoV, CPiV, CIV, and *Bordetella* increase diagnostic precision in dogs with acute respiratory signs (Zhou *et al*., 2024).

Other bacterial pathogens frequently implicated as primary or coinfecting agents in CIRDC include *Mycoplasma cynos*, which is strongly associated with pneumonia cases and should be considered in dogs exhibiting progressive lower respiratory signs (Chalker *et al*., 2004). Molecular diagnostic techniques such as real-time PCR for *M. cynos* enhance detection and help clarify its role as a primary pathogen or coinfection in *Bordetella*-positive dogs (Tallmadge *et al*., 2019). Case reports and molecular identification studies confirm that *M. cynos* can be found in laboratories and shelter dogs with respiratory disease, emphasizing that the absence of this organism should not be overlooked in differential evaluation (Hong *et al*., 2012). Aspiration pneumonia, typically related to inhalation of oropharyngeal material or regurgitation, may produce radiographic and clinical features similar to secondary bacterial pneumonia due to *Bordetella*, making a thorough history of aspiration risk crucial (Howard *et al*., 2021). Reviews of aspiration pneumonia highlighted that secondary bacterial flora often differ from those in primary infections, and culture testing from tracheal wash or BALF is essential to differentiate aspiration etiology from primary *Bordetella* infection (Sherman, 2017). Canine adenovirus type 2 (CAV-2) may also present with laryngotracheitis and a cough resembling kennel cough, therefore, vaccination history and serologic or virologic testing are needed to rule out CAV-2 in differential diagnosis (Chander *et al*., 2021).

Non-infectious disorders such as tracheal collapse frequently cause paroxysmal "honking" cough and can be misinterpreted as upper respiratory infection if radiographic or endoscopic evaluation is not performed (Kim *et al*., 2024). Systematic analyses have shown that tracheal collapse and dynamic airway collapse disorders should always be considered in small-breed dogs with chronic cough, as management differs significantly from anti-infective therapy (Robin *et al*., 2024). *Streptococcus equi subsp. zooepidemicus* has been implicated in outbreaks of acute hemorrhagic pneumonia and can cause more severe clinical presentations than *Bordetella*, making detection of this bacterium important, particularly in fatal or outbreak cases (Velineni *et al*., 2014). Epidemiological studies have emphasized its ability to cause severe respiratory disease requiring rapid antibiotic intervention and isolation, thus it must be differentiated from *Bordetella* infection in susceptible populations (Mangano *et al*., 2024). Respiratory diagnostic panels incorporating PCR for viruses, bacterial culture, and nasal microbiota analysis assist in distinguishing CIRDC agents and identifying asymptomatic carriers that act as reservoirs (Santos *et al*., 2023). In practice, a comprehensive differential diagnostic approach should integrate patient history (vaccination and exposure), clinical examination, thoracic radiography, and specific laboratory testing (PCR, culture, serology) to differentiate *Bordetella* from other infectious and non-infectious agents (Wasik *et al*., 2025).

## Transmission

*Bordetella bronchiseptica* in dogs is primarily transmitted through respiratory droplets and aerosols, leading to rapid spread within closely housed populations (Reagan *et al*., 2019). In addition to aerosol transmission, infection can occur via direct contact and contaminated fomites, factors that often explain outbreaks in boarding facilities or kennels (Keil *et al*., 1998). Experimental and epidemiological studies have shown that aerosol exposure or direct contact with infected dogs can result in very high transmission rates within a few days (Shang *et al*., 2024). Infected dogs may shed bacteria for weeks to months, and asymptomatic carriers play a critical role in maintaining transmission chains (Chalker *et al*., 2003). Although primarily an animal disease, zoonotic transmission to humans has been reported, particularly in immunocompromised individuals, emphasizing the importance of One Health approach (Kraai *et al*., 2023). Coinfection with other respiratory pathogens, both viral and bacterial, enhances spread and clinical severity, making canine infectious respiratory disease complex (CIRDC) a multifactorial condition (Mitchell *et al*., 2015).

Mucosal immunization, such as intranasal vaccination, has been shown to reduce bacterial colonization and shedding, thereby decreasing transmission potential compared to some parenteral regimens (Ellis, 2015). Population density and environmental factors in shelters, kennels, or dog shows are consistently associated with increased risk of *B. bronchiseptica* transmission (Englund *et al*., 2003). Effective control strategies include early identification and isolation of cases, improved ventilation, thorough cleaning and disinfection of fomites, and structured animal management to minimize close contact between individuals (Stull *et al*., 2016).

## Animal and public health considerations

Infection with *Bordetella bronchiseptica* in dogs and cats carries public health implications, as this bacterium can be transmitted to humans, particularly to individuals with compromised immune systems (Moore *et al*., 2022). Several reports have confirmed that live vaccine strains of *B. bronchiseptica* administered to pets can be transmitted to humans and cause infection, emphasizing the need for zoonotic awareness (Kraai *et al*., 2023). Studies have shown that infected or live-vaccinated animals can shed bacteria and act as potential reservoirs for cross-species transmission within close human environments (Chamorro *et al*., 2023). From the animal health perspective, the prevalence of *B. bronchiseptica* among dog populations is relatively high in several surveys, and many isolates demonstrate resistance to multiple classes of antibiotics, indicating that infection control in animals is essential to mitigate public health risks (Zhou *et al*., 2024).

Thus, One Health approach is highly relevant: controlling infection in animals through proper vaccination, population management, and environmental hygiene directly reduces the risk of human transmission (Day *et al*., 2020). Many dogs infected with *B. bronchiseptica* remain subclinical carriers and can disseminate the bacterium into their surroundings without exhibiting symptoms, making detection difficult without active surveillance (Zhou *et al*., 2024). High-density environments such as kennels and animal shelters pose an increased risk for animal-to-animal transmission, subsequently elevating the likelihood of human exposure within these settings (Day *et al*., 2020). Interventions such as intranasal vaccination in dogs have been shown to reduce bacterial colonization and shedding, highlighting that vaccination management in companion animals plays a key role in zoonotic risk mitigation (Ellis, 2015). Since immunocompromised individuals have been reported to acquire *B. bronchiseptica* infection from animals. Although such cases remain rare, pet owners and animal facility personnel should be educated about potential risks and protective measures (Moore *et al*., 2022). Therefore, routine surveillance of pet infections and monitoring of immunologically vulnerable owners represent critical strategies to minimize cross-species transmission (Kraai *et al*., 2023).

## Treatment

The management of *Bordetella bronchiseptica* infection in dogs depends on the severity of clinical signs and the immune status of the animal, with most mild cases resolving through supportive care without the need for systemic antibiotics (Collins *et al*., 2022). Supportive therapy includes adequate rest, hydration, and cough control to maintain mucociliary function (Fastrès *et al*., 2020). However, in cases presenting with systemic signs such as fever or lethargy, antibiotics like doxycycline are often used due to their strong activity against *B. bronchiseptica* isolates (Zhang *et al*., 2021). Increasing resistance to fluoroquinolones and β-lactam antibiotics has been reported in several regions, highlighting the importance of performing antimicrobial susceptibility testing (Yi *et al*., 2024). In severe cases such as pneumonia, fluid therapy, oxygen supplementation, and parenteral antibiotics guided by culture results are required to reduce mortality (Kraai *et al*., 2023).

Empirical antibiotic selection should consider local resistance patterns, as *B. bronchiseptica* isolates exhibit variable susceptibility profiles (Shang *et al*., 2024). Doxycycline remains the first-line treatment due to its proven efficacy and excellent penetration into pulmonary tissues (Lappin *et al*., 2020). In refractory cases, macrolides such as azithromycin may be considered for their activity against respiratory pathogens (Scott-Garrard *et al*., 2020). Combination antibiotic therapy might be warranted in cases with confirmed biofilm formation or secondary bacterial infections (Rodriguez *et al*., 2023).

## Vaccination

Vaccination against *Bordetella bronchiseptica* in dogs has demonstrated significant clinical efficacy, with long-term studies showing that a single oral administration of a live avirulent vaccine provides protection for up to one year against aerosol challenge with *B. bronchiseptica* (Hainer *et al*., 2021). Different routes of administration have been compared; randomized studies indicate that intranasal vaccination yields better clinical outcomes than oral vaccination in reducing cough and nasal discharge in young dogs, although oral vaccines still offer measurable benefits (Ellis *et al*., 2016). In adult dogs previously vaccinated, both parenteral (subcutaneous) and intranasal vaccines stimulate systemic (IgG) and local (IgA) antibody responses, with the intranasal route showing superior induction

of local mucosal immunity (Ellis *et al*., 2017). Immunological onset is also critical: studies show that both oral and intranasal vaccines can induce protection within seven days post-vaccination, an important feature for high-risk populations such as kennel dogs (Scott-Garrard *et al*., 2018). Safety evaluations have confirmed that intranasal and oral vaccines do not significantly impair olfactory thresholds in working or detection dogs, which is essential for maintaining their operational performance.

Booster frequency remains under discussion, but many facilities recommend revaccination every 6–12 months, particularly for socially active dogs or those frequently exposed to other dogs (Collins *et al*., 2022). Development of next-generation vaccines is ongoing, including subunit formulations based on outer membrane proteins (OMPs), which in laboratory models have shown strong TH1 responses and over 90% protection with minimal adverse effects, representing a promising future approach for veterinary immunization (Jang *et al*., 2024). It is important to note that vaccination does not completely prevent infection but rather reduces the severity of clinical disease and the duration of bacterial shedding, emphasizing that immunization should be integrated with biosecurity, sanitation, and environmental management practices (Ellis *et al*., 2016).

## Conclusion

*Bordetella bronchiseptica* remains an important bacterial pathogen associated with canine infectious respiratory disease complex, particularly in high-density environments such as kennels, shelters, and dog daycare facilities. Its ability to colonize the respiratory tract, persist in carriers, interact with other respiratory pathogens, and exhibit antimicrobial resistance complicates disease control and clinical management. Effective prevention therefore requires an integrated strategy involving vaccination, early detection, isolation of infected animals, proper ventilation, hygiene control, and antimicrobial stewardship. From a One Health perspective, reducing bacterial circulation in companion animals is also important to minimize zoonotic risks, especially for immunocompromised individuals. In addition, biosecurity protocols in kennels should extend beyond routine surface disinfection by considering environmental reservoirs, including standing water and biofilm-prone areas, that may facilitate the persistence and transmission of *Bordetella bronchiseptica*.

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## Conflict of interest

The authors declare no conflict of interest.

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