

Canine coronavirus: Current understanding of etiology, pathogenesis, clinical impact, and control strategies

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ABSTRACT

Canine coronavirus (CCoV) is an enveloped positive-sense RNA virus belonging to the family *Coronaviridae*. It commonly infects dogs and is primarily associated with gastrointestinal and respiratory diseases of variable severity. This review provides an updated knowledge regarding the etiology, epidemiology, genetic diversity, pathogenesis, clinical presentation, diagnostic approaches, and preventive strategies associated with CCoV infection. Two major genotypes, CCoV-I and CCoV-II, including pantropic variants, exhibit distinct biological characteristics that contribute to disease progression and clinical outcomes in dogs. Frequent mutation and recombination events particularly within the spike gene drive viral evolution and may alter host range and virulence. Although clinical disease is often mild and self-limiting in adult dogs, severe or fatal cases may occur in young puppies, immunocompromised dogs, or in the presence of co-infections with other pathogens. Recent advances in molecular diagnostics, such as qRT-PCR and multiplex PCR assays, have significantly improved the accuracy of strain differentiation and enhanced epidemiological surveillance efforts. Preventive measures rely on strict hygiene practices, targeted vaccination programs for high-risk populations, and implementation of biosecurity protocols. Ongoing genomic monitoring and research are essential to detect emerging variants with potential changes in virulence or zoonotic potential, supporting more effective control and management strategies for CCoV infection.

Introduction

Canine coronavirus (CCoV) belongs to the *Coronaviridae* family, which has an envelope with a positive single-stranded RNA (ssRNA) genome measuring 27-32 kb. Based on genomic and phylogenetic analysis, Coronavirus are classified into four genera in the *Coronaviridae* family, namely Alphacoronavirus, Betacoronavirus, Gamma coronavirus, which is known to have the largest RNA genome among the others, and Delta coronavirus, which has been identified in birds, bats, and mice as natural reservoirs (Decaro *et al.*, 2020). CCoV is one of the viruses from the Alphacoronavirus family, which includes viruses such as Feline coronavirus (FCoV), Mink coronavirus (MinkCoV), Ferret coronavirus (FRCoV), Alpaca coronavirus, and infectious gastrointestinal viruses (Adams *et al.*, 2016).

Canine coronavirus can attack the digestive system, known as Canine Enteric Coronavirus (CECoV), and the upper respiratory tract (CRCoV). The recent pandemic caused by the Severe Acute Respiratory Syndrome Coronavirus (Adams *et al.*, 2016). SARS CoV-2 has had a severe impact on global public health and illustrates the threat that new coronaviruses can pose to humans and other animals (Khamassi Khbou *et al.*, 2021). Coronaviruses continue to mutate and evolve, leading to cross-species infections between animals and humans, thereby expanding the spread of CoVs (Daron and Bravo, 2021). In recent decades, several coronaviruses have been discovered in dogs, known as CCoV. This is due to the high mutation frequency and wide host range of these viruses (Nova, 2021). Based on their antigenic and genetic characteristics, CoVs are classified into three main groups. The first group includes TGEV, FCoV, CCoV, HCoV-229E, and PED (Yang *et al.*, 2020). The second group consists of MHV, BCoV, HCoV-OC43, HEV, RtCoV, and ECoV. The third group comprises IBV, TCov, and Pheasant Coronavirus (Alluwaimi *et al.*, 2020).

CECoV strains are identified with different properties, including pantropic strains of enteric viruses that cause fatal multisystemic diseases.

Continuous evolution and mutation in CCoV occur through the accumulation of point mutations (He *et al.*, 2020). These mutations occur in the genome when a single base pair is added, altered, or deleted. Although most point mutations are harmless, they can have various functional consequences, including changes in gene expression or changes in the proteins encoded in the genome, as well as genetic insertions or deletions, which cause the emergence of viruses with altered properties, including tropism and virulence (Olarde-Castillo *et al.*, 2025). Most infectious diseases in humans are caused by pathogens that first spread in non-human animal species—a process known as ‘zoonotic spillover.’ Evidence suggests that CCoV itself may have undergone zoonotic spillover, as nearly identical CCoV strains were detected in human samples from Malaysia and Haiti, suggesting a recent cross-species transmission event (Nova, 2021; Zehr *et al.*, 2022).

Etiology

Coronaviruses, particularly α CoVs, can infect multiple host species and cause a range of clinical diseases, highlighting their complex evolutionary patterns. Widespread distribution and high genetic variability of bat coronaviruses related to human SARS-CoVs, new viruses are expected to emerge in the future (Cui *et al.*, 2019). Despite this significant risk, no definitive measures have been taken to minimize close contact or cohabitation between animals especially wildlife and humans. With urbanization increasing, the world may soon face new severe health crises (Dema *et al.*, 2023; Poonsin *et al.*, 2023).

The identification of a probable novel human pathogen exhibiting close genetic relatedness to canine coronavirus (CCoV), together with reports of a swine-origin coronavirus infecting children in Haiti, highlights an important emerging public health concern (Lednicky *et al.*, 2022; Matthew-Belmar *et al.*, 2025). Notably, the recently characterized recombinant

strain CCoV-HuPn-2018, isolated from a patient with pneumonia, may represent the eighth recognized human-infecting coronavirus (Vlasova *et al.*, 2022). Moreover, although domestic dogs have not been confirmed as transmission vectors for SARS-CoV-2, evidence indicates that they are susceptible to infection, emphasizing their potential role within the human-animal interface. Given the close companionship and frequent physical interaction between humans and domestic dogs, opportunities for viral adaptation and cross-species transmission may be enhanced (Sit *et al.*, 2020; Shi *et al.*, 2024b). Therefore, compiling epidemiological data on CCoV infections is crucial for effective monitoring and prevention efforts.

History

Since its initial identification in 1971 during an outbreak within a canine military unit in Germany, canine coronavirus (CCoV) has spread quickly across the globe and is now considered enzootic, with prevalence rates reported to vary widely from 6.25% to 72.5% (Wang *et al.*, 2016). Historically, CCoV has been largely underestimated in its significance, and vaccinations against it are not commonly recommended due to the lack of a reliable challenge model to test vaccine efficacy. Despite this, CCoV plays a notable role in causing enteritis ranging from moderate to severe severity. Over the past few decades, CCoV has experienced genetic changes through mutation and recombination processes that have altered its tissue targeting (tropism) and virulence. These evolutionary events have led to the emergence of new, genetically distinct strains, some of which have increased pathogenic capabilities. The majority of CCoV strains detected belong to type II viruses, which are able to grow readily in canine and feline cell cultures. In contrast, type I CCoV strains have not been isolated by traditional culture methods but have only been identified through molecular techniques such as reverse transcription polymerase chain reaction (RT-PCR) and quantitative PCR (qPCR) (Pratelli *et al.*, 2022).

A remarkable discovery is that some CCoV strains detected in humans possess extensively recombinant spike genes originating from both feline and canine coronavirus lineages. These have been classified as human CCoV strains Z19 and HuPn-2018, which appear to show respiratory tract tropism rather than enteric (Zehr *et al.*, 2022). Furthermore, recent full genome sequencing of the CCoV-UCD-1 strain [PP526172], originally isolated in the 1970s and thought to contain a transmissible gastroenteritis virus (TGEV)-like N-terminal domain (NTD) revealed near-identical sequences to the human CCoV-HuPn-2018 strain. This genetic similarity heightens interest in the zoonotic potential of these viruses, raising concerns about cross-species transmission and the emergence of novel infectious agents (Zehr *et al.*, 2022; Olarte-Castillo *et al.*, 2025).

Epidemiology

Recent international epidemiological studies on canine coronavirus (CCoV) provide updated insights into its prevalence, genotypes, and disease spread among dog populations. A study in 2024 revealed that CCoV has two main genotypes circulating globally: CCoV type I and type IIa, with a higher prevalence of CCoV-I (approximately 10.2%) compared to CCoV-IIa (6.0%). Mixed infections with both genotypes were also detected (Nguyen and Pham Thi, 2021). The virus mainly infects the intestinal tract but pantropic (systemic spread) variants are less common. These findings confirm that CCoV remains endemic in dog populations worldwide, particularly affecting puppies and dogs in shelters (Mira *et al.*, 2024).

Another systematic review and meta-analysis in 2024 emphasized the global dissemination of canine enteric coronavirus and raised concerns about co-infections and variant emergence, highlighting the need for routine molecular screening and epidemiological surveillance to control outbreaks effectively. The review underscores persistence of CCoV despite vaccination efforts and variations in strain virulence and spread

depending on regional and environmental factors (Odigie *et al.*, 2024). Lastly, an epidemiological investigation in southwestern China enhanced understanding of genetic diversity and transmission dynamics of CCoV, which is critical for vaccine development and disease management strategies in dogs (Dong *et al.*, 2022).

Pathogenesis

The pathogenesis of enteric canine coronavirus begins with viral attachment and entry into susceptible intestinal epithelial cells, particularly mature enterocytes located at the tips and lateral surfaces of the small-intestinal villi. Viral entry is primarily mediated by the spike (S) glycoprotein, which determines receptor recognition, membrane fusion, cellular tropism, and consequently, pathogenicity. For CCoV-II, canine aminopeptidase N (cAPN/CD13) functions as an entry receptor, whereas the cellular receptor used by CCoV-I has not yet been conclusively identified. Importantly, CCoV-I and CCoV-II also differ in the proteolytic architecture of their spike proteins. CCoV-I possesses basic cleavage motifs at both the S1/S2 boundary and the S2' region, whereas CCoV-II generally lacks a prominent multibasic S1/S2 motif but contains a conserved basic S2' cleavage motif, commonly represented as R-K-R-Y/F-R-S. Proteolytic activation at or near S2' facilitates exposure of the fusion peptide and subsequent fusion between viral and cellular membranes (Licitra *et al.*, 2014; Licitra *et al.*, 2015). Although trypsin- and cathepsin-like proteases have been proposed to activate CCoV spike proteins, the specific contribution of the cell-surface serine protease TMPRSS2 to classical enteric CCoV-I or CCoV-II infection has not been established. Indeed, studies of the related CCoV-HuPn-2018 showed that TMPRSS2 did not enhance spike-mediated entry, whereas the endosomal proteases cathepsin B and cathepsin L contributed to pH-dependent viral entry (Liu *et al.*, 2023).

Following entry, viral replication within mature enterocytes disrupts cellular homeostasis and induces cytopathic injury. Infection may promote degeneration and death of infected epithelial cells, including apoptosis and necrosis, followed by loss of the apical brush border and exfoliation of damaged enterocytes into the intestinal lumen. As mature enterocytes are progressively lost, villi become shortened and atrophic, reducing the functional absorptive surface of the small intestine. Consequently, impaired membrane-associated digestion and nutrient absorption, together with altered epithelial permeability and fluid transport, contribute to maldigestion, malabsorption, and diarrhea (Afonso *et al.*, 2025; Sabyrzhah *et al.*, 2025). Thus, villous atrophy should be regarded not simply as a histological lesion but as the structural consequence of virus-induced enterocyte loss and insufficient replacement of differentiated absorptive cells.

Severe intestinal disease may occur when epithelial injury becomes extensive or is accompanied by damage to crypts and gut-associated lymphoid tissue. Cases of severe CCoV-associated enteritis in puppies have demonstrated hemorrhagic enteritis, villous shortening, crypt necrosis, lymphoplasmacytic intestinal inflammation, lymphoid depletion, and, in some animals, ileocecal intussusception (Santos *et al.*, 2023). Intussusception is likely a secondary consequence rather than a direct cytopathic effect of CCoV. Severe intestinal inflammation altered intestinal motility, bowel-wall edema, and disruption of normal peristalsis may create conditions that favor telescoping of one intestinal segment into another. Therefore, the occurrence of intussusception should be interpreted as a complication of severe enteric disease rather than a primary molecular effect of viral replication.

The pathogenesis of pantropic CCoV-IIa differs substantially from that of conventional enterotropic infection because these variants can disseminate beyond the intestinal tract. Experimental infection with the prototype pantropic strain CB/05 has demonstrated viral involvement of lymphoid and parenchymal tissues, accompanied by leukopenia, marked lymphopenia, and systemic lesions. A transient or low-level viremia has been proposed as one possible route through which the virus reaches

lymphoid tissues and internal organs. Viral antigen or RNA has been detected in tissues including the thymus, spleen, mesenteric lymph nodes, lung, liver, and kidney, indicating an expanded cellular and tissue tropism (Decaro *et al.*, 2008; Marinaro *et al.*, 2010). In addition, coronavirus antigen has been reported within macrophage-like cells in affected tissues, while experimental *in vitro* studies suggest that pantropic CCoV can replicate in canine macrophages and promote a pro-inflammatory M1-like phenotype. These observations provide a potential cellular mechanism linking infection with systemic dissemination and inflammatory tissue injury, although the exact contribution of infected monocytes or macrophages to *in vivo* dissemination remains incompletely defined.

Immune dysregulation appears to be an important component of pantropic CCoV-IIa pathogenesis. Experimental CB/05 infection causes an early reduction in circulating CD4+ and CD8+ T lymphocytes and a smaller decline in B-cell populations, together with acute CD14+ monocytosis. CD8+ T-cell and B-cell numbers may recover relatively rapidly, whereas CD4+ T-cell depletion can persist for several weeks and, in experimental infections, has required up to approximately 60 days for complete recovery (Marinaro *et al.*, 2010). Infection and depletion of lymphoid tissues may therefore impair both cell-mediated immunity and coordination of antiviral humoral responses, potentially increasing susceptibility to secondary or concurrent infections. However, a classical cytokine storm or specific hyper-inflammatory cytokine profile has not yet been conclusively demonstrated for pantropic CCoV *in vivo*. Accordingly, systemic lesions should not currently be attributed to uncontrolled cytokine release without additional evidence. Instead, available data support a combination of expanded viral tissue tropism, lymphoid injury, altered leukocyte populations, and inflammatory responses as contributors to systemic disease.

The immune mechanisms controlling enteric and pantropic CCoV infection also differ according to the anatomical distribution of viral replication. In conventional enteric infection, mucosal immunity is particularly important because viral replication is concentrated at the intestinal surface. CCoV-specific secretory IgA produced at the intestinal mucosa can inhibit viral attachment and limit infection of enterocytes, and higher fecal IgA concentrations have been associated with increased protection against enteric CCoV challenge. In contrast, high serum antibody titers alone do not necessarily provide sterilizing protection at the intestinal mucosa (Decaro *et al.*, 2008). Current evidence does not establish completely distinct clearance mechanisms for CCoV-I and CCoV-II enteric infections, particularly because both genotypes frequently occur as coinfections and CCoV-I remains less experimentally characterized. Therefore, it is more accurate to state that mucosal IgA is a major correlate of protection against enteric CCoV infection rather than assigning mucosal clearance exclusively to CCoV-I.

Systemic immune responses become more relevant for pantropic CCoV-IIa because viral replication extends beyond the intestinal mucosa. Neutralizing serum antibodies, T-cell-mediated responses, and innate immune cells are expected to contribute to control of extraintestinal infection. Nevertheless, naturally acquired immunity against enteric CCoV does not provide complete cross-protection against pantropic CCoV-IIa. Dogs with pre-existing high serum antibody titers against enteric CCoV remain susceptible to experimental CB/05 infection and developed viral shedding, gastrointestinal signs, lymphopenia, and viral involvement of lymphoid tissues. This finding indicates that systemic antibody concentrations alone do not reliably predict protection against pantropic infection and suggests that differences in viral tropism and antigenic properties can allow pantropic CCoV-IIa to partially evade immunity induced by conventional enteric strains.

Canine respiratory coronavirus (CRCoV) follows a distinct pathogenic pathway because it is a betacoronavirus with predominant tropism for the respiratory tract rather than the intestinal epithelium. Infection occurs mainly following exposure to respiratory secretions and is associated with viral replication in the nasal and tracheal epithelium. The CRCoV spike protein interacts with cell-surface sialic acids as attachment factors, while

experimental evidence suggests that additional protein receptors are required for productive entry. Following attachment and internalization, including caveolin-dependent endocytosis in susceptible cell systems, viral replication damages ciliated respiratory epithelial cells. The resulting ciliary loss, epithelial desquamation, inflammation, and impairment of mucociliary clearance facilitate accumulation of respiratory secretions and may increase susceptibility to secondary respiratory pathogens. These effects contribute to the role of CRCoV as one component of the multifactorial Canine Infectious Respiratory Disease Complex rather than as the sole etiological agent of the syndrome (Haake *et al.*, 2020).

Clinical manifestations

Canine coronavirus infection is difficult to differentiate from other infectious causes of enteritis. CCoV infection is generally less severe than infection with Canine Parvovirus type 2. Clinical signs can vary widely, and the disease can affect dogs of any age, in contrast to CPV infections, where affected dogs are usually under 2 years old. Dogs infected with CCoV often experience sudden onset of diarrhea, sometimes preceded by vomiting. Other common signs are loss of appetite and lethargy (Tesfaye *et al.*, 2024).

Signs can be more severe in infections with particularly virulent strains or in very young canine puppies. In severe cases, diarrhea may become watery and be followed by dehydration and electrolyte imbalances (Buonavoglia *et al.*, 2023). Most affected dogs recover spontaneously after 8 to 10 days. When secondary complicating factors arise (parasites, bacteria, or other viruses), the disease can be prolonged significantly. In pantropic Coronavirus infections, there are more severe symptoms, including fever (39.5 to 40°C), lethargy, anorexia, vomiting, hemorrhagic diarrhea, leukopenia, and neurological signs (ataxia, seizures) followed by death within 2 days (Rowland *et al.*, 2021).

Diagnosis

Molecular detection by reverse transcription quantitative PCR (RT-qPCR) is currently one of the most sensitive and practical laboratory approaches for confirming canine coronavirus (CCoV) infection, particularly through the detection of viral RNA in fecal or rectal-swab samples. The selection of the genomic target depends on the diagnostic purpose. For broad detection of enteric CCoV, the conserved ORF5 region encoding the membrane (M) protein is commonly targeted. An early TaqMan RT-qPCR assay targeting the CCoV M gene showed a detection limit of approximately 10 copies of standard viral RNA and a linear quantitative range from 10 to 10⁸ copies, demonstrating substantially greater analytical sensitivity than conventional RT-PCR targeting the same region (Decaro *et al.*, 2008). More recent multiplex RT-qPCR assays have retained ORF5 as a diagnostic target. For example, Thieulent *et al.* (2023) reported a 95% limit of detection (LOD95) of approximately 4 genome copies/μL in singleplex format and 6 genome copies/μL in multiplex format for canine enteric coronavirus, with high amplification efficiency and reproducibility. Similarly, a recently developed quadruplex RT-qPCR targeting a conserved region of the CCoV M gene detected both CCoV-I and CCoV-II with an LOD of approximately 1.0×10² copies per reaction and showed more than 99% agreement with reference molecular assays (Zhao *et al.*, 2024).

Although the M gene is suitable for broad CCoV screening because of its relative conservation, additional genomic regions may be required for strain or genotype characterization. In particular, sequence variation within the spike (S) gene can be used to differentiate CCoV genotypes and subtypes, including CCoV-I, CCoV-IIa, and recombinant CCoV-IIb strains, while genotype-specific fluorogenic RT-PCR assays can also discriminate CCoV-I from CCoV-II (Decaro *et al.*, 2008). Therefore, positive screening results may be followed by genotype-specific PCR or sequencing of the S gene when epidemiological characterization, investigation

of pantropic strains, or identification of recombinant variants is required.

Analytical specificity is particularly important because CCoV belongs to Alphacoronavirus 1 and is genetically and antigenically related to feline coronavirus (FCoV) and transmissible gastroenteritis virus (TGEV). Earlier PCR assays targeting conserved regions of the M gene demonstrated amplification of closely related alphacoronaviruses, including TGEV and, with some primer combinations, feline infectious peritonitis virus, illustrating the potential for cross-reactivity when primers are directed toward highly conserved sequences (Pratelli *et al.*, 1999). Modern probe-based RT-qPCR assays reduce this problem through sequence-specific primers and fluorogenic probes and should be analytically validated against closely related coronaviruses as well as other common canine enteric pathogens. Recent multiplex assays have demonstrated high target specificity without detectable cross-amplification among the viral targets included in their validation panels (Thieulent *et al.*, 2023; Zhao *et al.*, 2024).

Accordingly, RT-qPCR results should be interpreted together with clinical findings, epidemiological information, sample type, and the timing of sample collection. Detection of CCoV RNA confirms viral shedding but does not by itself establish that CCoV is the sole cause of gastrointestinal disease, because asymptomatic infection, prolonged fecal shedding, and coinfection with other enteric pathogens may occur. Serological assays can provide evidence of previous exposure or immune responses but are less useful for confirming acute enteric infection, whereas virus isolation is technically demanding and generally less sensitive than molecular detection. Therefore, RT-qPCR of fecal samples, followed when necessary, by genotype-specific PCR or sequencing, provides a more appropriate molecular framework for the diagnosis and epidemiological characterization of CCoV infection.

Differential diagnosis

Canine coronavirus (CCoV) has two main types, namely Canine Enteric Coronavirus (CECoV), which attacks the digestive system, infects the intestinal epithelium, causing gastrointestinal disorders such as acute diarrhea and vomiting, and Canine Respiratory Coronavirus (CRCoV), which attacks the upper respiratory tract and is one of the pathogens that causes Canine Infectious Respiratory Disease Complex (CIRDC) (Haake *et al.*, 2020; Zhou *et al.*, 2024). Different infection sites and clinical symptoms lead to differences in differential diagnosis. CCoV has symptoms similar to Canine Parvovirus (CPV) or bacterial gastrointestinal infections, while CRCoV needs to be distinguished from pathogens causing CIRDC such as Canine Adenovirus type 2 (CAV-2), Canine Parainfluenza Virus (CPIV), and *Bordetella bronchiseptica* (Shi *et al.*, 2024a; Zhou *et al.*, 2024).

CECoV and CPV have clinical symptoms that can cause acute gastroenteritis in puppies and are difficult to distinguish clinically. The difference lies in CPV, which generally causes more severe symptoms such as severe dehydration and significant leukopenia. To confirm the diagnosis, fecal antigen testing or qPCR can be performed (Sabyrzhah *et al.*, 2025; Thieulent *et al.*, 2025). Enteric bacteria such as *Salmonella* spp., *Campylobacter* spp., and *Clostridium perfringens* should be considered in the diagnosis of CCoV in cases of acute diarrhea, especially if the dog has a history of consuming raw food or contact with a virus-contaminated environment (Loor-Giler *et al.*, 2025). Intestinal protozoa such as *Giardia duodenalis* can also cause acute diarrhea, therefore parasitological examination and specific PCR testing can be performed to confirm the diagnosis (Kurnosova *et al.*, 2024; Zong Minko *et al.*, 2024). Co-infection between CCoV and CPV or other enteric agents can worsen the clinical condition. The ideal diagnostic approach in cases of canine enteritis is to combine rapid tests and PCR with genetic sequencing to confirm the causative agent (Kurnosova *et al.*, 2024).

One of the pathogens causing CIRDC is CRCoV, which needs to be distinguished from other respiratory viruses such as CPIV and CAV-2 because all three of these viruses can cause upper respiratory tract disorders in dogs. *Bordetella bronchiseptica* infection is often found concurrently

with these viruses, therefore bacteriological examination or PCR is required for definitive diagnosis (Chamorro *et al.*, 2023). Infections in CIRDC cases indicate multipathogen infections, especially if dogs kept in densely populated environments (Chen *et al.*, 2024).

Transmission

CECoV is primarily spread via the fecal-oral route, typically through contact with contaminated feces from infected dogs, whereas CRCoV is transmitted through the respiratory route, via droplets expelled by infected dogs (Zhou *et al.*, 2024; Walz *et al.*, 2025). Transmission most frequently occurs in environments with high dog density, such as shelters and kennels (Sha *et al.*, 2022). Dogs with subclinical CCoV infections may shed the virus in feces for several days to weeks after clinical onset, contributing to environmental contamination and transmission from asymptomatic carriers (Haake *et al.*, 2020; Santos *et al.*, 2023). Epidemiological analysis indicates that environmental factors such as kennel hygiene, feed management, and feces disposal may influence transmission (Zhang *et al.*, 2023).

Dogs infected with CCoV can excrete the virus in their feces for several days to weeks after clinical onset, with inter-individual variation depending on age and immune status (Thibault *et al.*, 2022). CRCoV is shed in respiratory secretions for a short period but contact between dogs in enclosed spaces can prolong the transmission period (Zhou *et al.*, 2024). Molecular investigations show that healthy dogs can still be detected for viral RNA in fecal or nasopharyngeal swab samples (Zhang *et al.*, 2023). Puppies are more susceptible to CCoV because their immune systems are not yet fully developed (Shi *et al.*, 2024b).

The CCoV virus can survive for long periods on contaminated surfaces and in contaminated environments such as kennels, feeding areas, or cleaning equipments (Thibault *et al.*, 2022). Inadequate cleaning and disinfection can lead to the spread of CCoV. Poor ventilation can increase the risk of CRCoV spread through surfaces contaminated with droplets from infected dogs (Zhou *et al.*, 2024). Epidemiological analysis shows that recurrent outbreaks often occur in high-density environments and in facilities that fail to implement thorough sanitation procedures after animal rotation (Odigie *et al.*, 2024). Emerging recombinant CCoV variants pose a risk of uncontrolled spread (Lednický *et al.*, 2022).

CCoV is often found alongside other pathogens such as CPV or *Bordetella bronchiseptica*. These co-infections can affect the severity of symptoms and the amount of virus shed, thereby increasing transmission (Thieulent *et al.*, 2025). CRCoV combined with other bacteria can accelerate spread in closed environments (Zhou *et al.*, 2024). Dogs with dual infections heal slower than those with single infections. This underscores the importance of comprehensive diagnosis in cases of diarrhea or contagious cough in dogs (Zhang *et al.*, 2023; Chen *et al.*, 2024).

Recent studies have identified genetic recombination in CCoV, which may influence viral characteristics and transmission patterns. Recombinant strains have been detected in several regions and exhibit distinct transmission patterns (Shi *et al.*, 2024b). Genome sequencing analysis shows partial gene similarity with other coronaviruses that infect humans and animals. Although there is no strong evidence that CCoV can be transmitted to humans, the possibility of cross-species transmission needs to be watched (Zhang *et al.*, 2023; Chen *et al.*, 2024).

Risk factors

CECoV and CRCoV show a pattern of spread that is highly influenced by host factors, causative agents, and the living environment of dogs (Wu *et al.*, 2023). Puppies are at high risk due to declining maternal immunity and an immune system that is not yet fully developed (Jacot *et al.*, 2021; Poonsin *et al.*, 2023). Dogs with poor nutrition or compromised immune systems show more severe infections and symptoms. A history of chronic or systemic disease can also be a factor that increases suscep-

tibility to CCoV infection (Sha *et al.*, 2022; Mira *et al.*, 2024). Genetic factors between dogs can influence susceptibility levels, although evidence still requires further study (Li *et al.*, 2023). Environmental factors such as outdoor group interactions or shared grooming areas can increase opportunities for close contact and enhance the risk of viral transmission (Corman *et al.*, 2020).

Animal density in shared animal facilities such as pet shops, pet hotels, shelters, or farms can accelerate the spread of CCoV through feces or droplets from infected dogs (Corman *et al.*, 2020; Odigie *et al.*, 2024). Poor care and sanitation correlate with higher infection prevalence in field surveillance (Mira *et al.*, 2024). Interregional animal transportation can increase the risk of spreading recombinant CCoV strains (Shi *et al.*, 2024b). Season and climatic conditions have also been reported to influence infection prevalence, with increased cases in spring and fall (Chen *et al.*, 2024). Kennel management practices such as mixing litters without quarantine increase CCoV cross-exposure. Exposure to wild animals or other reservoirs can lead to genetic recombination and the emergence of new strains (Zehr *et al.*, 2022; Afonso *et al.*, 2025).

Some CCoV strains show zoonotic potential in humans who are in close contact with (Silva Filho *et al.*, 2023; Vlasova *et al.*, 2022). Close contact with owners or frequent direct contact with dogs increases the likelihood of cross-species exposure (Decaro *et al.*, 2021; Wu *et al.*, 2023). The movement of pets across regions can spread new strains to other environments. Limited coordination across sectors can reduce the early detection of potential spillovers (Shi *et al.*, 2024b). Weak biosecurity practices at points of contact between humans and animals facilitate reverse transmission and opportunities for adaptation of recombinant CCoV viruses (Del Sorbo *et al.*, 2025).

Public health importance

CCoV exhibits the potential for recombination and genetic variation that may enhance its ability to cross species barriers and subsequently pose a zoonotic risk (Shi *et al.*, 2024b). Genetic similarities in CCoV have been found with several other strains of carnivore coronaviruses that have the potential to affect humans (Zhou *et al.*, 2024). Field studies report that CCoV has been found in domestic dogs and stray dogs, suggesting that direct contact with infected dogs may increase the risk of exposure (Yang *et al.*, 2022). Genetic changes in CCoV isolates documented by studies in Asia and Europe have the potential to alter the tropism of the virus, which is an important basis for understanding the potential for cross-species infection (Pandit *et al.*, 2023). New genetic detections in various regions indicate the possibility of wider virus spread. Research cases examining the CCoV genome have noted the existence of recombinant clusters, with the discovery of new isolates associated with public health risks (Shi *et al.*, 2024b; Del Sorbo *et al.*, 2025).

CCoV infection in dogs is a public health concern because dogs are pets that frequently interact with humans. Pet dogs are mostly infected with CCoV with subclinical symptoms, but they can still transmit the virus, making its spread difficult to control (Shi *et al.*, 2024b). Stray dogs and pet dogs living in the same environment with high density can increase the risk of CCoV infection. Although evidence of CCoV transmission and infection in humans is still limited, there are reports indicating that CCoV has undergone unusual changes that need to be watched out for (Mira *et al.*, 2024). The potential for zoonosis creates public concern and impacts animal welfare, as some owners may abandon or neglect infected dogs (Odigie *et al.*, 2024; Del Sorbo *et al.*, 2025).

Treatment

Treatment of CCoV infection is primarily aimed at reducing clinical morbidity, preventing dehydration, and minimizing secondary complications. The mainstay of therapy is supportive care, as most enteric and respiratory infections are self-limiting in adult (Pratelli *et al.*, 2022; Dong

et al., 2022). Hydration stabilization, electrolyte correction, and nutritional management are initial interventions to prevent malnutrition in puppies affected by CCoV. Clinical monitoring is performed to detect deterioration in the condition of infected dogs, such as severe dehydration, secondary sepsis, or the development of systemic disease, which may alter the planned therapy (Chen *et al.*, 2024). Antibiotics are ineffective against viruses but may be considered if there is a secondary bacterial infection or risk of aspiration in severe cases (Corman *et al.*, 2020; Pratelli *et al.*, 2022).

The focus of enteral therapy is on oral or parenteral rehydration, adjusted according to the degree of dehydration and drinking ability, with treatment administered according to body weight. In anorexic puppies, regular and easily digestible nutrition is recommended because early enteral nutrition can reduce morbidity. Intravenous fluid administration for rehydration in dogs should consider electrolyte loss and acidosis due to severe diarrhea with serum electrolyte monitoring (Chen *et al.*, 2024). Therapy for respiratory CCoV involves supportive care such as oxygen therapy, nebulization, and treatment to keep the airways clear (Corman *et al.*, 2020; Haake *et al.*, 2020). Symptomatic therapy may include bronchodilators and mucolytics in cases showing obstruction or excessive mucus production. In cases of CIRDC where CCoV is identified alongside companion pathogens such as Bordetella, Influenza, or Mycoplasma, selective antibiotics are administered if a dual infection occurs. Dogs infected with CCoV undergo ventilation monitoring, and animal density is reduced to minimize transmission to other dogs (Corman *et al.*, 2020). Antivirals for CCoV are not yet officially registered for the treatment of this virus in dogs. Recent research shows that nucleoside analogs such as molnupiravir and GS-441524 derivatives have activity against coronaviruses in feline coronavirus (FCoV), making them potential candidates for development in dogs. Data on the safety and efficacy of GS-441524 specifically in dogs infected with CCoV are still very limited (Černá *et al.*, 2025).

Vaccination

Vaccination against CCoV aims to induce protective immune responses in dogs, enhancing resistance to viral infections affecting the digestive and respiratory systems (Zappulli *et al.*, 2020). Diseases caused by CCoV infection are mild, so this vaccine is not considered a top priority in routine vaccinations. CCoV cases are subclinical, so vaccination is still being considered in terms of cost (Chen *et al.*, 2024). Different infection rates in different regions mean that vaccination decisions are tailored to local conditions (Odigie *et al.*, 2024). An inactivated CCoV vaccine has been developed and is used on a limited scale. However, CCoV vaccination is not included in routine vaccinations (Hossain *et al.*, 2022).

The CCoV vaccine used is generally an inactivated vaccine that is injected into dogs and can help release the virus through feces after infection (Hossain *et al.*, 2022). This vaccine has limitations in producing a mucosal IgA response, which is considered important for protection against enteric infections. CCoV vaccines can use live-attenuated vaccines that have been tested orally or intranasally and can potentially induce immunity in mucosal epithelial tissue. The immune system expected to be formed in the body from the administration of the CCoV vaccine involves IgA and neutralizing antibodies in the blood. Genetic variation of CCoV can affect vaccine effectiveness (Shi *et al.*, 2024b). Vaccination success is influenced by the dog's age, maternal antibodies, and animal health history (Hossain *et al.*, 2022).

Vaccinated dogs that contract CCoV generally exhibit milder clinical signs compared to unvaccinated animals. Vaccination guidelines from the World Small Animal Veterinary Association (WSAVA) stated that the CCoV vaccine is not a routine vaccine because the symptoms it causes are not particularly fatal. CCoV vaccination is recommended for puppies because they are at high risk of infection (Dong *et al.*, 2022). In puppies, vaccination is performed after maternal antibodies have subsided to ensure an optimal immune response (Hossain *et al.*, 2022). Circulation levels, sani-

tation conditions, or transportation stress are indicators for assessing the administration of CCoV vaccination (Chen *et al.*, 2024).

Control strategies

CCoV control in dog populations focuses on early detection, biosecurity, population management, and appropriate clinical interventions. Control programs are implemented to reduce morbidity in susceptible dogs, decrease transmission, and prevent outbreaks in collective facilities (Odigie *et al.*, 2024). CCoV can play a complex role in CIRDC and gastrointestinal diseases, therefore control strategies must adopt a cross-pathogen approach that addresses both respiratory and enteric pathogens. Continuous monitoring enables the detection of new variants of CCoV and helps assess whether these strains can alter virulence and vaccine response (Shi *et al.*, 2024a). Screening animals with molecular or antigen tests can help identify subclinical reservoirs that pose a risk of transmitting the virus (Corman *et al.*, 2020). Coordination of reporting between diagnostic laboratories, clinicians, and animal health authorities can improve rapid response to disease outbreaks (Buonavoglia *et al.*, 2023).

Proper disinfection and cleaning of the environment are key steps in controlling the virus because CCoV can survive on surfaces under certain conditions. Effective fecal management, increased cleaning frequency, and the use of easily sanitized equipment and materials can significantly reduce the risk of viral transmission (Odigie *et al.*, 2024; Corman *et al.*, 2020). Good air circulation and ventilation can reduce the risk of CCoV transmission through droplets from infected dogs. Reducing density and separating sick dogs from healthy dogs can lower the potential for transmission within a population. Improving environmental conditions, enhancing nutrition, and reducing excessive handling can reduce the severity of the disease and viral shedding in infected dogs (Chen *et al.*, 2024).

Conclusion

Canine coronavirus (CCoV) remains an important pathogen in dog populations worldwide, primarily causing gastrointestinal, Canine Enteric Coronavirus (CECoV) and respiratory diseases, Canine Respiratory Coronavirus (CRCoV). Genetic diversity and recombination between CCoV subtypes and related coronaviruses have led to new variants with altered virulence and tissue tropism. Although most infections are mild, the presence of pantropic and recombinant strains indicates the virus's capacity for adaptation and potential zoonotic risk. Effective control requires a multifaceted approach combining molecular surveillance, vaccination in susceptible populations, strict biosecurity, and public awareness. Continuous genomic monitoring and application of the One Health framework are essential to anticipate cross-species spillover events and strengthen preparedness for emerging coronavirus threats.

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Conflict of interest

The authors have declared no conflict of interest.

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