Chapter 1

Canine Parvovirus Type 2

Chao-Nan Lin and Shu-Yun Chiang

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Abstract

Canine parvovirus (CPV) enteritis is characterized by intestinal hemorrhage with severe bloody diarrhea. The causative agent, CPV-2, was first identified in the late 1970s. CPV is a nonenveloped, linear, single-stranded DNA virus with a genome of approximately 5 kb, and it belongs to the genus *Parvovirus*, together with feline panleukopenia virus, mink enteritis virus, raccoon parvovirus, and porcine parvovirus. An antigenic variant, CPV-2a, identified within a few years after the emergence of CPV-2, and another variant, CPV-2b, began appearing in the canine population in 1984. In 2000, a novel antigenic variant, CPV-2c, was first detected in Italy. This chapter focuses on the history, viral evolution, epidemiology, pathogenesis, clinical signs, diagnosis, vaccination, and prevention of CPV-2.

Keywords: canine parvovirus type 2, CPV-2, viral evolution, antigenic variants, epidemiology, pathogenesis

1. Introduction

Canine parvovirus (CPV) infection is characterized by clinical gastroenteritis with severe hemorrhagic diarrhea and is a common infectious disease in younger dogs [1]. Gastroenteritis caused by CPV type 2 (CPV-2) infection, especially that caused by the newer variants of CPV-2, may progress rapidly [2, 3]. Dehydration is the rapid onset of the loss of bodily fluids caused by severe vomiting, diarrhea, or hemorrhagic diarrhea. Death occurs in as early as a few days after disease onset. This chapter documents the history, viral evolution, epidemiology, pathogenesis, clinical signs, diagnosis, vaccination, and prevention of CPV-2.

1.1. History

Canine parvoviral enteritis is characterized by intestinal hemorrhage with severe bloody diarrhea [4]. The causative agent, CPV-2, was first identified in the late 1970s [5]. CPV is a nonenvel-

oped, linear, single-stranded DNA virus with a genome of approximately 5 kb, and it belongs to the genus *Parvovirus,* together with feline panleukopenia virus (FPV), mink enteritis virus, raccoon parvovirus, and porcine parvovirus [6]. CPV-2 is distinct from CPV-1, also known as canine minute virus, which belongs to the genus *Bocavirus*. Indeed, CPV-2 is believed to have originated from FPV or a closely related FPV-like parvovirus of wild carnivores (**Figure 1**) [7, 8]. Various hypotheses for how this may have occurred have been suggested, including direct mutation from FPV and contact between cats and dogs kept as companion animals within the same home [8].

1.2. Viral evolution

Shortly after CPV was first identified in 1978, the original virus, CPV-2, was subsequently replaced in the dog population by strains carrying small antigenic variations (termed 2a, 2b, and 2c) of the VP2 protein that could be distinguished by monoclonal antibodies and genetic analysis. An antigenic variant, CPV-2a, identified within a few years after the emergence of CPV-2 [9, 10], and another variant, CPV-2b, began appearing in the canine population in 1984 [11]. A novel antigenic variant, Glu-426 mutant (now termed CPV-2c), was first detected in Italy in 2000 [12]. New antigenic variants of CPV-2 have been observed in epidemics around the world and are soon replacing the original CPV-2. CPV-2a variant shows several substitutions within the VP2 protein, including Met87Leu, Ile101Thr, Ala300Gly, and Asp305Tyr. Furthermore, CPV-2b variant has been identified to contain an additional amino acid change, Asn426Asp [13, 14]. These two antigenic variants further evolved into new CPV-2a and -2b

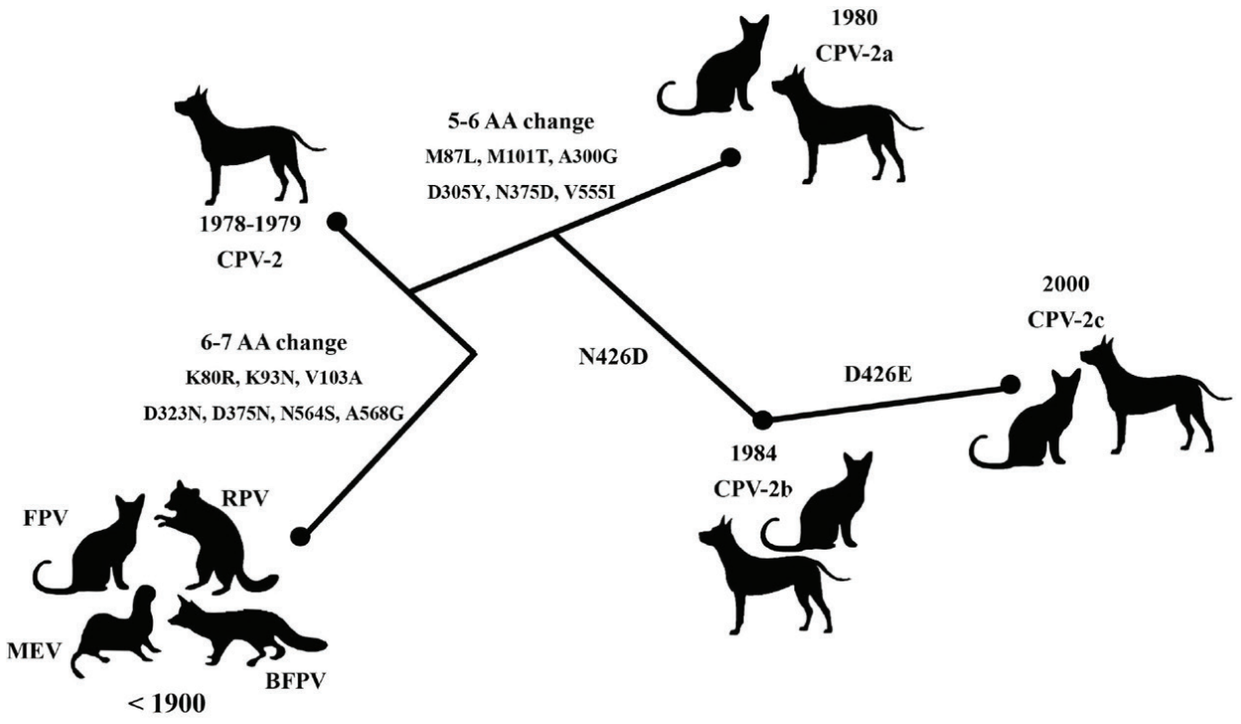

Figure 1. Cartoon of the evolution of canine parvovirus type (CPV-2). CPV-2 is believed to have originated from FPV or a closely related FPV-like parvovirus of wild carnivores (modified from Truyen [8]).

types, with amino acid substitutions at residue 297 (Ser to Ala), during the 1990s [15]. Antigenic variant CPV-2c was identified only one residue substitution (Asp426Glu) as differ from CPV-2a and -2b [12].

In addition to the amino acid substitution described above, amino acid substitutions Tyr324Ile, Gln370Arg, and Thr440Ala in the surface of the VP2 were also noted in the recent year [16]. Review of CPV-2 sequences from GenBank showed that this Ile324 variant of CPV-2a is also found in several countries, including Korea [17, 18], China [19–25], Thailand [26], Uruguay [27, 28], Japan [29], Taiwan [30, 31], and India [32, 33]. Surprisingly, aside from the Uruguayan strains, this Ile324 CPV-2a variant is only distributed in Asian countries. Previous study has shown that residue 324 of VP2 is subject to positive selection among all carnivore parvoviruses [34]. This residue is adjacent to the residue 323, which together with residue 93 is known to be affected in host range and tropism of canine transferrin receptor binding [35]. The mutation of VP2 residue 323 may affect interactions between residues in neighboring loops of either the same VP2 molecule or the threefold-related VP2, greatly reducing replication in canine cells [36]. The Gln370Arg change is unique in the Taiwanese [85] and Chinese CPV-2c strains [22, 25]. This substitution is also observed in Chinese panda parvovirus [37]. Residue 370 is located between residues 359 and 375, which constitutes a flexible surface loop of the capsid protein that is adjacent to a double Ca^{2+}-binding site. They were found to be essential for virus infectivity. Changes in them are correlated with the ability of the virus to hemagglutinate erythrocytes [38]. In addition, VP2 position 440 is located near a major antigenic site. The Thr440Ala change was found in China, the USA [39], Italy [14], Argentina [40], Uruguay [27], India [33], and Taiwan [85].

1.3. Epidemiology

According to the epidemiology surveillance of CPV-2, the distribution of these three antigenic variants (-2a, -2b, and -2c) is summarized in **Table 1**. Previous study has revealed that the oldest CPV-2c variant was isolated in 1996 in Germany [41]. Epidemiological surveillance in

Country	Positive of strain detected			Reference
	CPV-2a	CPV-2b	CPV-2c	
Europe				
Italy	+	+	+	[2]
Portugal	+	+	+	[16]
Spain	+	+	+	[78]
France	+	+	+	[79]
UK	+	+	+	[41]
Belgium	+	-	+	[79]
Germany	+	+	+	[79]
Greece	+	+	+	[43]

Country	Positive of strain detected			Reference
	CPV-2a	CPV-2b	CPV-2c	
Switzerland	+	+	+	[41]
Czech public	+	+	-	[79]
Romania	+	-	-	[79]
Hungary	+	-	-	[80]
Bulgaria	+	+	+	[81]
Turkey	+	+	+	[82]
Africa				
Tunisia	+	+	+	[47]
Morocco	+	+	+	[53]
North America				
USA	+	+	+	[39]
South America				
Uruguay	+	+	+	[83]
Argentina	+	+	+	[50]
Brazil	+	+	+	[84]
Ecuador	+	+	+	[51]
Mexico	-	-	+	[52]
Asia				
India	+	+	+	[55]
Taiwan	+	+	+	[85]
Korea	+	+	-	[18]
Japan	+	+	-	[15]
China	+	+	+	[19]
Thailand	+	+	-	[26]
Vietnam	+	+	+	[54]
Oceania		+	+	-
Australia	+	+	-	[86]

Table 1. Detection of the canine parvovirus variants in the world.

Europe shows that CPV-2c is predominant currently in Italy, Germany, and Spain and is also extensively co-distributed with CPV-2a or -2b in Portugal [42], Belgium, France, Greece [43], Bulgaria [44], Sweden [45], Turkey [46], and the United Kingdom. In recent years, CPV-2c has also been widespread in Tunisia [47], the USA [39], Uruguay [48], Brazil [49], Argentina [50],

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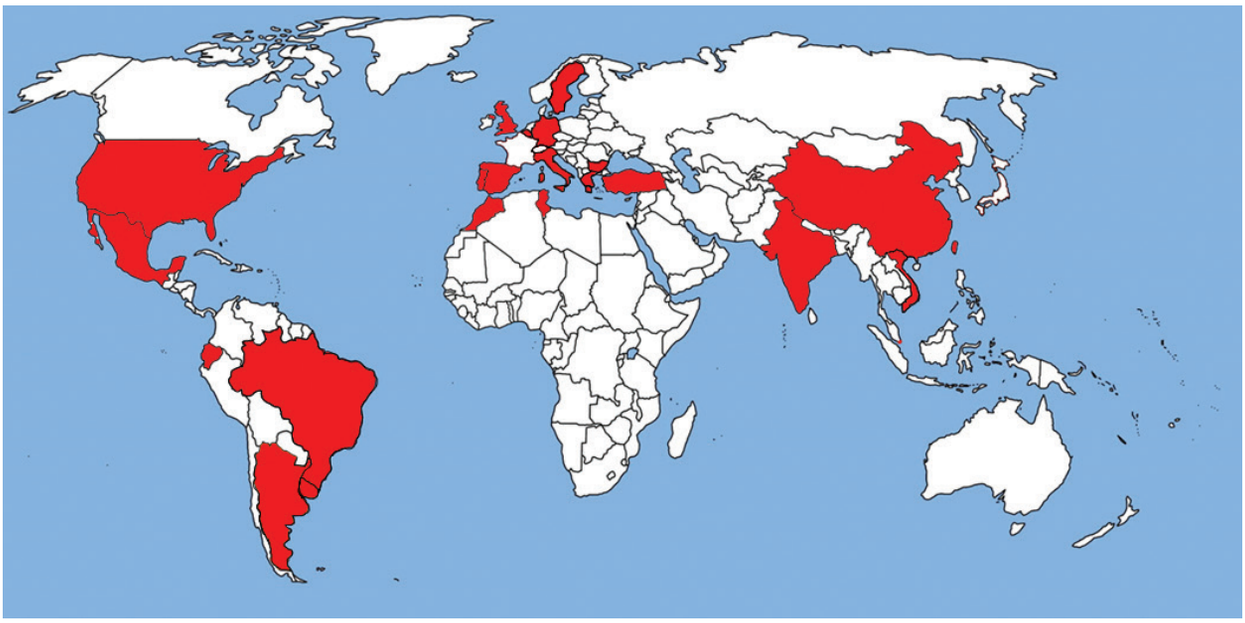

Figure 2. Distribution of canine parvovirus type 2c (CPV-2c) variants around the world. Red color represents that countries reporting CPV-2c case.

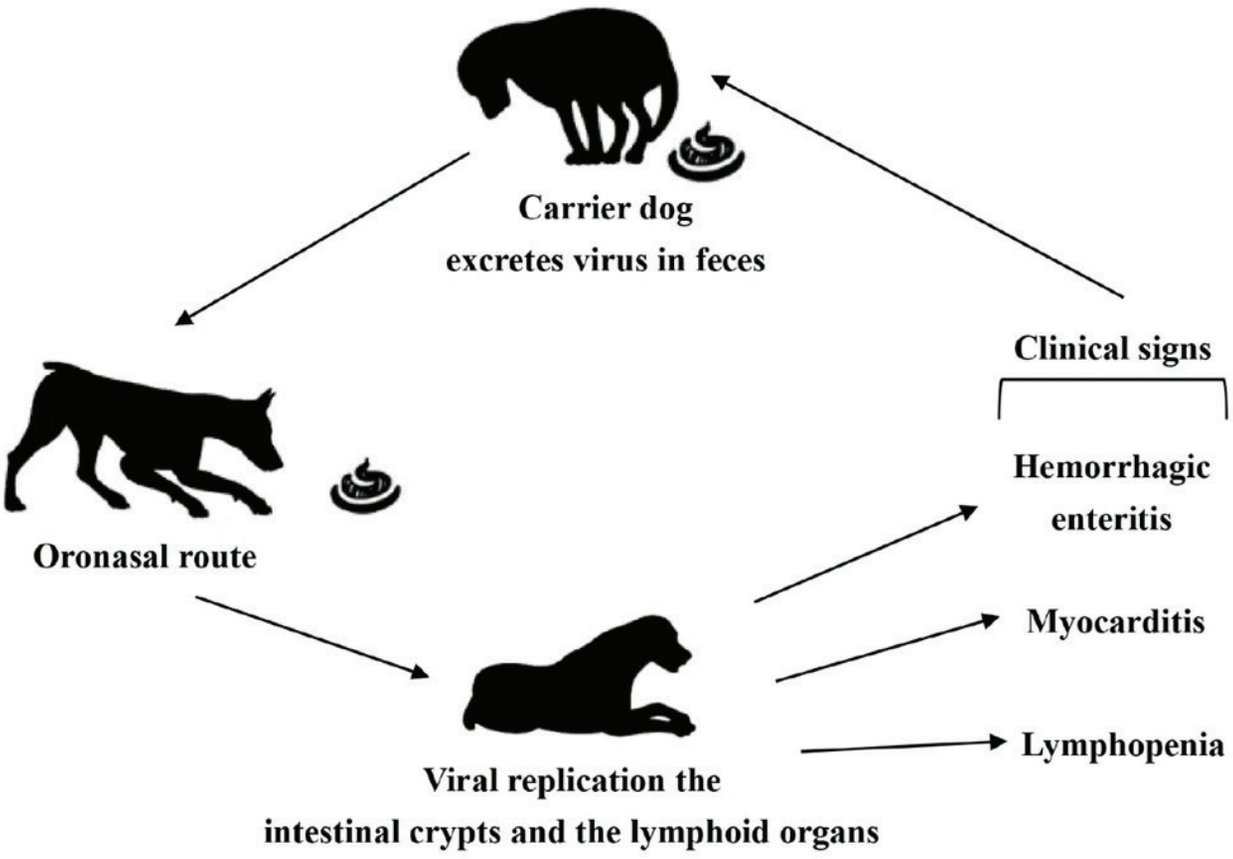

Figure 3. Transmission and clinical symptoms of canine parvovirus type 2 (CPV-2). Transmission of CPV-2 occurred by the fecal-oral route, after exposure to CPV-2 in feces and/or vomit, or viral-contaminated fomites.

Ecuador [51], Mexico [52], and Morocco [53]. Surprisingly, the CPV-2c variant has not been prevalent in Asia since the first identified in Vietnam in 2004 [54]. Only a few CPV-2c strains have been reported in India [55], China [19, 22, 25], and Taiwan [85]. To date, either CPV-2a or -2b has been prevalent in Asian countries [15, 17–19, 22, 25, 26, 29–33, 55–59]. Phylogenetic analysis demonstrated that the recent CPV-2c isolate from Taiwan shares a common evolutionary origin with Chinese strains of CPV-2c, as classified into novel Asian CPV-2c variants (Phe267Tyr, Tyr324Ile, Gln370Arg, and Asp426Glu) [85]. **Figure 2** summarizes the distribution of the CPV-2c variant around the world.

1.4. Pathogenesis

Transmission of CPV-2 occurred by the fecal-oral route, after exposure to CPV-2 in feces and/or vomit, or viral-contaminated fomites (**Figure 3**). The severity of clinical symptoms depends on the factors such as viral strain, host immunity, and the presence of the coinfection with other pathogens. In naturally [60] or experimentally [61] infected dogs, many dogs never develop overt clinical symptoms, especially when the dogs have high level of the maternally derived antibodies (MDAs) [61]. Higher titers of MDA in young dogs are protective against infection by CPV-2. Infected dogs with severe clinical symptoms of disease had lower levels of hemagglutination inhibition (HI) titers than did animals without clinical signs following

Figure 4. Mucosal hemorrhage in canine parvovirus type 2 (CPV-2)-infected dog. A 4-month-old puppy suffered from CPV-2 which showed lethargy, inappetence, and bloody diarrhea (from Professor Ming-Tang Chiou, Department of Veterinary Medicine, National Pingtung University of Science and Technology, Taiwan).

CPV-2 infection [61]. In the lowest HI titers group, CPV-2 shedding was noted up to 45 days post infection [61]. The incubation period of CPV-2 infection is 1–2 weeks. The affected gastrointestinal tissues include epithelium of the tongue, oral cavity, esophagus, and intestinal tract. CPV-2 replicates and destroys epithelial cells of the intestinal crypts causing malabsorption and increased intestinal permeability. CPV-2 shedding in feces was detected up to 45 and 54 days in experimentally [61] and naturally infected dogs [60], respectively. The period could also potentially correlate with the severity of the clinical status of the animals [62]. Viral shedding from infected dogs with bloody diarrhea was observed up to 63 days compared to 54 days in infected dogs with diarrhea (no dogs with hemorrhagic diarrhea or vomiting were tested) [60].

1.5. Clinical signs

The clinical signs of CPV-2 infection include fever, lethargy, inappetence, vomiting, diarrhea or bloody diarrhea (**Figure 4**), and dehydration. Myocarditis usually occurs up to the first 4 weeks of age or infected in utero, which may result in signs of sudden death

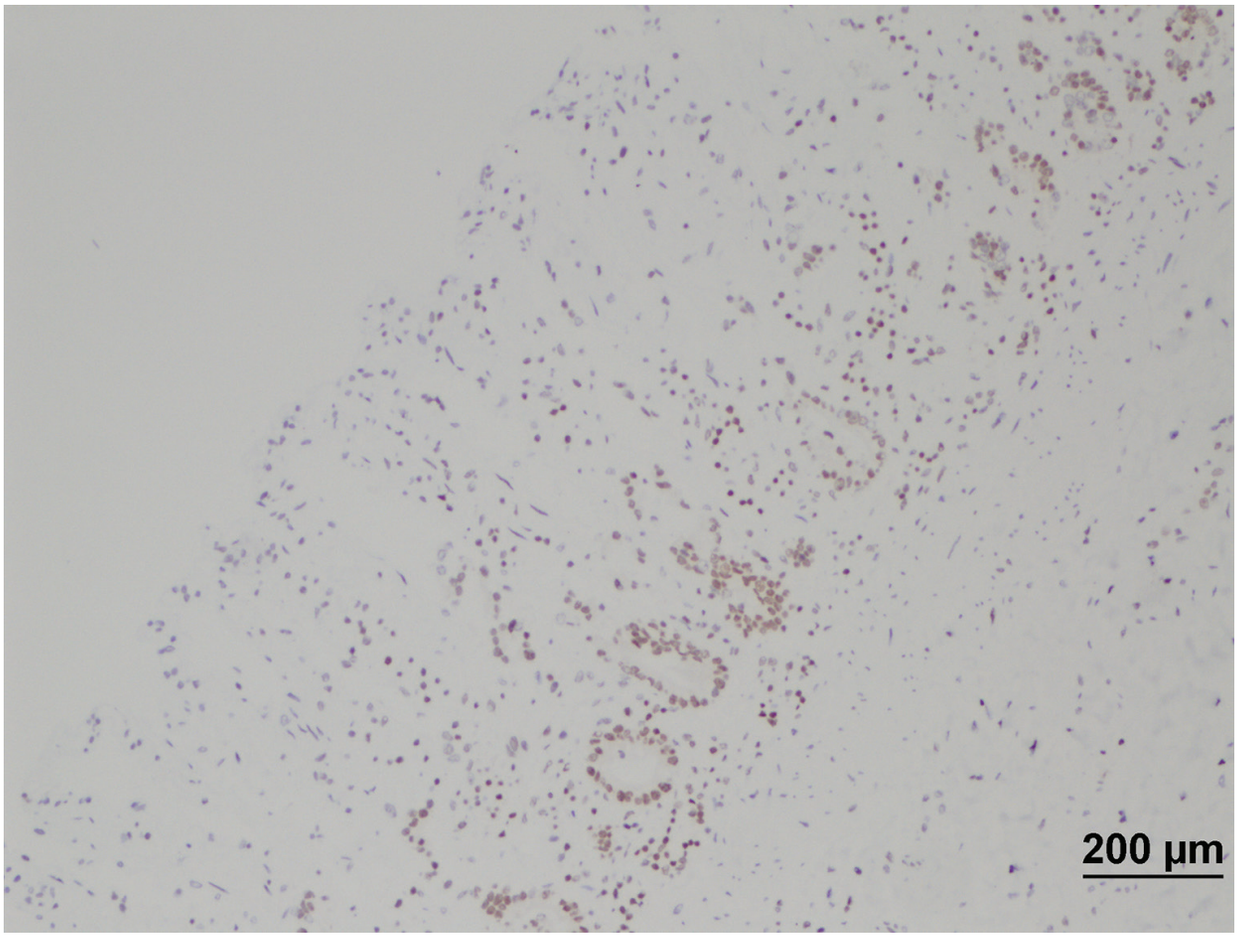

Figure 5. Detection of canine parvovirus type 2 (CPV-2) antigens in intestinal tract using in situ hybridization. CPV-2 immunolabeling is seen in the crypt epithelium (from Professor Ming-Tang Chiou, Department of Veterinary Medicine, National Pingtung University of Science and Technology, Taiwan).

or congestive heart failure. Cerebellar hypoplasia has been rarely reported in dogs with utero infection. CPV-2c shows almost the same clinical signs as CPV-2a and CPV-2b, such as anorexia, vomiting, acute gastroenteritis, and hemorrhagic diarrhea. However, CPV-2c infection has been reported to be indicative of a more severe disease induced by this variant [51, 63].

1.6. Diagnosis

The most common abnormalities found on the CBC are leukopenia, lymphopenia, and neutropenia. Some disease dogs develop anemia as a result of gastrointestinal blood loss. Electrolyte and coagulation abnormalities have been reported in dogs with parvoviral enteritis. The diagnosis of CPV-2 infection has relied on probe-based real-time polymerase chain reaction (PCR) [64–69], SYBR green-based real-time PCR [62, 70–72], conventional PCR [47, 68], electron microscopy [73], and methods provided as commercial kits [74]. CPV–2 antigens were found in crypt epithelium (**Figure 5**) or affected tissues such as spleen (**Figure 6**) using in situ hybridization.

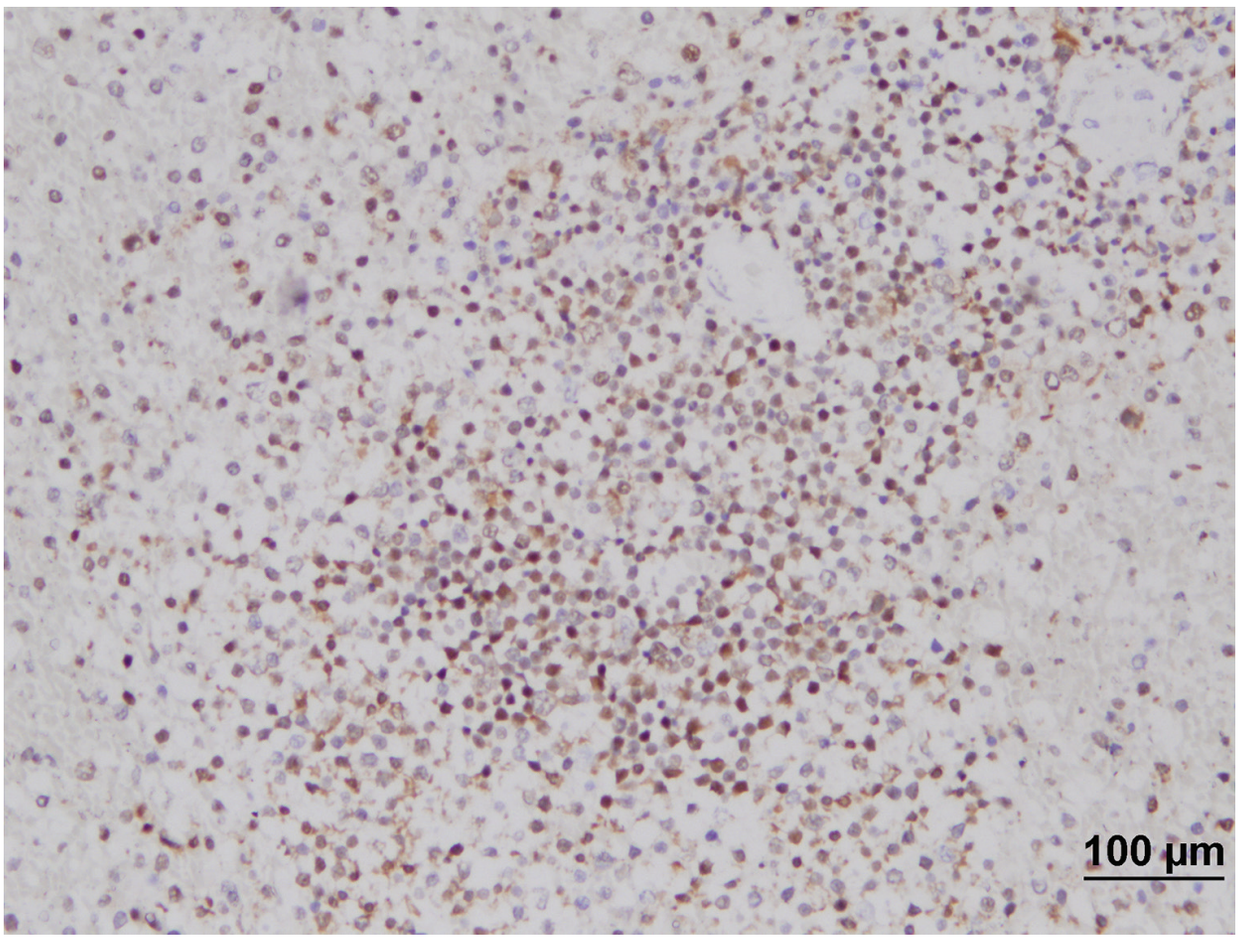

Figure 6. Detection of canine parvovirus type 2 (CPV-2) antigens in spleen using in situ hybridization. CPV-2 immunolabeling is seen in lymphocyte (from Professor Ming-Tang Chiou, Department of Veterinary Medicine, National Pingtung University of Science and Technology, Taiwan).

1.7. Vaccination and prevention

Immunization is the most effective method for the prevention of CPV-2 enteritis. However, the initial immunization should be of concern regarding the interference of the MDA. The second concern is whether the currently available CPV-2 vaccine provides adequate protection against CPV-2c infection. VP2 encodes a viral capsid protein that is the major structural protein of CPV-2 and is involved in the host-immune response [75]. Therefore, a small number of mutations may result in increased pathogenicity [51]. Several studies have demonstrated the efficacy of the current CPV-2 vaccine against CPV-2c infection [76, 77]. By contrast, some evidence suggests that dogs with the complete vaccination program still suffer from CPV-2c [63]. Therefore, the efficacy of the current vaccine against prototype CPV-2c and/or novel CPV-2c variant remains to be evaluated, especially in regard to the amino acid substitutions observed in the novel CPV-2c variant as compared to the prototype of CPV-2c. Parvoviruses are extremely stable in the environment and can be transmitted via indirect contact, an important factor in their maintenance in populations. Several disinfectants had been reported that parvoviruses can be inactivated with a 1:30 dilution of household bleach, potassium peroxymonosulfate, and accelerated hydrogen peroxide. These disinfectants will also inactivate other viruses.

2. Conclusion

CPV-2 is most likely one of the most common infectious diseases in younger dogs. CPV-2 is constantly mutating, leading to the evolution of novel variants. All countries should continue surveillance and monitor the events associated with CPV-2 disease. The need to update current vaccines remains to be assessed.

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References

[1] Yesilbag K, Yilmaz Z, Ozkul A, Pratelli A: Aetiological role of viruses in puppies with diarrhoea. Vet Res 2007, **161**:169–170.

[2] Buonavoglia C, Martella V, Pratelli A, Tempesta M, Cavalli A, Buonavoglia D, Bozzo G, Elia G, Decaro N, Carmichael L: Evidence for evolution of canine parvovirus type 2 in Italy. J Gen Virol 2001, **82**:3021–3025.

[3] Martella V, Cavalli A, Pratelli A, Bozzo G, Camero M, Buonavoglia D, Narcisi D, Tempesta M, Buonavoglia C: A canine parvovirus mutant is spreading in Italy. J Clin Microbiol 2004, **42**:1333–1336.

[4] MacLachlan NJ, Dubovi EJ: Parvoviridae. In *Fenner's Veterinary Virology*. 4th edn. Edited by MacLachlan NJ, Dubovi EJ. London: Academic Press; 2011: 507.

[5] Appel MJ, Scott FW, Carmichael LE: Isolation and immunisation studies of a canine parco-like virus from dogs with haemorrhagic enteritis. Vet Res 1979, **105**:156–159.

[6] Hoelzer K, Parrish CR: The emergence of parvoviruses of carnivores. Vet Res 2010, **41**:39–51.

[7] Allison AB, Harbison CE, Pagan I, Stucker KM, Kaelber JT, Brown JD, Ruder MG, Keel MK, Dubovi EJ, Holmes EC, Parrish CR: Role of multiple hosts in the cross-species transmission and emergence of a pandemic parvovirus. J Virol 2012, **86**:865–872.

[8] Truyen U: Evolution of canine parvovirus-a need for new vaccines? Vet Microbiol 2006, **117**:9–13.

[9] Parrish CR, O'Connell PH, Evermann JF, Carmichael LE: Natural variation of canine parvovirus. Science 1985, **230**:1046–1048.

[10] Parrish CR, Have P, Foreyt WJ, Evermann JF, Senda M, Carmichael LE: The global spread and replacement of canine parvovirus strains. J Gen Virol 1988, **69(Pt 5)**: 1111–1116.

[11] Parrish CR, Aquadro CF, Strassheim ML, Evermann JF, Sgro JY, Mohammed HO: Rapid antigenic-type replacement and DNA sequence evolution of canine parvovirus. J Virol 1991, **65**:6544–6552.

[12] Buonavoglia C, Martella V, Pratelli A, Tempesta M, Cavalli A, Buonavoglia D, Bozzo G, Elia G, Decaro N, Carmichael L: Evidence for evolution of canine parvovirus type 2 in Italy. J Gen Virol 2001, **82**:3021–3025.

[13] Martella V, Decaro N, Buonavoglia C: Evolution of CPV-2 and implication for antigenic/genetic characterization. Virus Genes 2006, **33**:11–13.

[14] Decaro N, Desario C, Parisi A, Martella V, Lorusso A, Miccolupo A, Mari V, Colaianni ML, Cavalli A, Di Trani L, Buonavoglia C: Genetic analysis of canine parvovirus type 2c. Virology 2009, **385**:5–10.

[15] Ohshima T, Hisaka M, Kawakami K, Kishi M, Tohya Y, Mochizuki M: Chronological analysis of canine parvovirus type 2 isolates in Japan. J Vet Med Sci 2008, **70**:769–775.

[16] Miranda C, Thompson G: Canine parvovirus: the worldwide occurrence of antigenic variants. J Gen Virol 2016, **97**: 2043-2057..

[17] Jeoung SY, Ahn SJ, Kim D: Genetic analysis of VP2 gene of canine parvovirus isolates in Korea. J Vet Med Sci 2008, **70**:719–722.

[18] Yoon SH, Jeong W, Kim HJ, An DJ: Molecular insights into the phylogeny of canine parvovirus 2 (CPV-2) with emphasis on Korean isolates: a Bayesian approach. Arch Virol 2009, **154**:1353–1360.

[19] Zhang R, Yang S, Zhang W, Zhang T, Xie Z, Feng H, Wang S, Xia X: Phylogenetic analysis of the VP2 gene of canine parvoviruses circulating in China. Virus Genes 2010, **40**:397–402.

[20] Yi L, Tong M, Cheng Y, Song W, Cheng S: Phylogenetic analysis of canine parvovirus VP2 gene in China. Transbound Emerg Dis 2016, 63:e262-e269.

[21] Zhong Z, Liang L, Zhao J, Xu X, Cao X, Liu X, Zhou Z, Ren Z, Shen L, Geng Y, et al: First isolation of new canine parvovirus 2a from Tibetan mastiff and global analysis of the full-length VP2 gene of canine parvoviruses 2 in China. Int J Mol Sci 2014, **15**:12166–12187.

[22] Geng Y, Guo D, Li C, Wang E, Wei S, Wang Z, Yao S, Zhao X, Su M, Wang X, et al: Co-circulation of the rare CPV-2c with unique Gln370Arg substitution, new CPV-2b with unique Thr440Ala substitution, and new CPV-2a with high prevalence and variation in Heilongjiang Province, Northeast China. PLoS One 2015, **10**:e0137288.

[23] Han SC, Guo HC, Sun SQ, Shu L, Wei YQ, Sun DH, Cao SZ, Peng GN, Liu XT: Full-length genomic characterizations of two canine parvoviruses prevalent in Northwest China. Arch Microbiol 2015, **197**:621–626.

[24] Xu J, Guo HC, Wei YQ, Shu L, Wang J, Li JS, Cao SZ, Sun SQ: Phylogenetic analysis of canine parvovirus isolates from Sichuan and Gansu provinces of China in 2011. Transbound Emerg Dis 2015, **62**:91–95.

[25] Zhao H, Wang J, Jiang Y, Cheng Y, Lin P, Zhu H, Han G, Yi L, Zhang S, Guo L, Cheng S: Typing of canine parvovirus strains circulating in North-East China. Transbound Emerg Dis 2015. doi:10.1111/tbed.12390.

[26] Phromnoi S, Sirinarumitr K, Sirinarumitr T: Sequence analysis of VP2 gene of canine parvovirus isolates in Thailand. Virus Genes 2010, **41**:23–29.

[27] Perez R, Bianchi P, Calleros L, Francia L, Hernandez M, Maya L, Panzera Y, Sosa K, Zoller S: Recent spreading of a divergent canine parvovirus type 2a (CPV-2a) strain in a CPV-2c homogenous population. Vet Microbiol 2012, **155**:214–219.

[28] Perez R, Calleros L, Marandino A, Sarute N, Iraola G, Grecco S, Blanc H, Vignuzzi M, Isakov O, Shomron N, et al: Phylogenetic and genome-wide deep-sequencing analyses of canine parvovirus reveal co-infection with field variants and emergence of a recent recombinant strain. PLoS One 2014, **9**:e111779.

[29] Soma T, Taharaguchi S, Ohinata T, Ishii H, Hara M: Analysis of the VP2 protein gene of canine parvovirus strains from affected dogs in Japan. Res Vet Sci 2013, **94**:368–371.

[30] Chou SJ, Lin HT, Wu JT, Yang WC, Chan KW: Genotyping of canine parvovirus type 2 VP2 gene in southern Taiwan in 2011. Taiwan Vet J 2013, **39**:81–92.

[31] Lin CN, Chien CH, Chiou MT, Chueh LL, Hung MY, Hsu HS: Genetic characterization of type 2a canine parvoviruses from Taiwan reveals the emergence of an Ile324 mutation in VP2. Virol J 2014, **11**:39.

[32] Mukhopadhyay HK, Matta SL, Amsaveni S, Antony PX, Thanislass J, Pillai RM: Phylogenetic analysis of canine parvovirus partial VP2 gene in India. Virus Genes 2013, **48**:89–95.

[33] Mittal M, Chakravarti S, Mohapatra JK, Chug PK, Dubey R, Narwal PS, Kumar A, Churamani CP, Kanwar NS: Molecular typing of canine parvovirus strains circulating from 2008-2012 in an organized kennel in India reveals the possibility of vaccination failure. Infect Genet Evol 2014, **23**:1–6.

[34] Hoelzer K, Shackelton LA, Parrish CR, Holmes EC: Phylogenetic analysis reveals the emergence, evolution and dispersal of carnivore parvoviruses. J Gen Virol 2008, **89**:2280–2289.

[35] Hueffer K, Parrish CR: Parvovirus host range, cell tropism and evolution. Curr Opin Microbiol 2003, **6**:392–398.

[36] Chang SF, Sgro JY, Parrish CR: Multiple amino acids in the capsid structure of canine parvovirus coordinately determine the canine host range and specific antigenic and hemagglutination properties. J Virol 1992, **66**:6858–6867.

[37] Guo L, Yang SL, Chen SJ, Zhang Z, Wang C, Hou R, Ren Y, Wen X, Cao S, Guo W, et al: Identification of canine parvovirus with the Q370R point mutation in the VP2 gene from a giant panda (*Ailuropoda melanoleuca*). Virol J 2013, **10**:163.

[38] Simpson AA, Chandrasekar V, Hebert B, Sullivan GM, Rossmann MG, Parrish CR: Host range and variability of calcium binding by surface loops in the capsids of canine and feline parvoviruses. J Mol Biol 2000, **300**:597–610.

[39] Hong C, Decaro N, Desario C, Tanner P, Pardo MC, Sanchez S, Buonavoglia C, Saliki JT: Occurrence of canine parvovirus type 2c in the United States. J Vet Diagn Invest 2007, **19**:535–539.

[40] Calderon MG, Romanutti C, Wilda M, D'Antuono A, Keller L, Giacomodonato MN, Mattion N, La Torre J: Resurgence of canine parvovirus 2a strain in the domestic dog population from Argentina. J Virol Methods 2015, **222**:145–149.

[41] Decaro N, Desario C, Addie DD, Martella V, Vieira MJ, Elia G, Zicola A, Davis C, Thompson G, Thiry E, et al: The study molecular epidemiology of canine parvovirus, Europe. Emerg Infect Dis 2007, **13**:1222–1224.

[42] Miranda C, Parrish CR, Thompson G: Epidemiological evolution of canine parvovirus in the Portuguese domestic dog population. Vet Microbiol 2016, **183**:37–42.

[43] Ntafis V, Xylouri E, Kalli I, Desario C, Mari V, Decaro N, Buonavoglia C: Characterization of Canine parvovirus 2 variants circulating in Greece. J Vet Diagn Invest 2010, **22**:737–740.

[44] Filipov C, Desario C, Patouchas O, Eftimov P, Gruichev G, Manov V, Filipov G, Buonavoglia C, Decaro N: A ten-year molecular survey on parvoviruses infecting carnivores in Bulgaria. Transbound Emerg Dis 2016, 63:460–464.

[45] Sutton D, Vinberg C, Gustafsson A, Pearce J, Greenwood N: Canine parvovirus type 2c identified from an outbreak of severe gastroenteritis in a litter in Sweden. Acta Vet Scand 2013, **55**:64.

[46] Muz D, Oguzoglu TC, Timurkan MO, Akin H: Characterization of the partial VP2 gene region of canine parvoviruses in domestic cats from Turkey. Virus Genes 2012, **44**:301–308.

[47] Touihri L, Bouzid I, Daoud R, Desario C, El Goulli AF, Decaro N, Ghorbel A, Buonavoglia C, Bahloul C: Molecular characterization of canine parvovirus-2 variants circulating in Tunisia. Virus Genes 2009, **38**:249–258.

[48] Perez R, Francia L, Romero V, Maya L, Lopez I, Hernandez M: First detection of canine parvovirus type 2c in South America. Vet Microbiol 2007, **124**:147–152.

[49] Pinto LD, Streck AF, Goncalves KR, Souza CK, Corbellini AO, Corbellini LG, Canal CW: Typing of canine parvovirus strains circulating in Brazil between 2008 and 2010. Virus Res 2012, **165**:29–33.

[50] Calderon MG, Romanutti C, D'Antuono A, Keller L, Mattion N, La Torre J: Evolution of canine parvovirus in Argentina between years 2003 and 2010: CPV2c has become the predominant variant affecting the domestic dog population. Virus Res 2011, **157**:106–110.

[51] Aldaz J, Garcia-Diaz J, Calleros L, Sosa K, Iraola G, Marandino A, Hernandez M, Panzera Y, Perez R: High local genetic diversity of canine parvovirus from Ecuador. Vet Microbiol 2013, **166**:214–219.

[52] Pedroza-Roldan C, Paez-Magallan V, Charles-Nino C, Elizondo-Quiroga D, De Cervantes-Mireles RL, Lopez-Amezcua MA: Genotyping of canine parvovirus in western Mexico. J Vet Diagn Invest 2015, **27**:107–111.

[53] Amrani N, Desario C, Kadiri A, Cavalli A, Berrada J, Zro K, Sebbar G, Colaianni ML, Parisi A, Elia G, et al: Molecular epidemiology of canine parvovirus in Morocco. Infect Genet Evol 2016, **41**:201–206.

[54] Nakamura M, Tohya Y, Miyazawa T, Mochizuki M, Phung HT, Nguyen NH, Huynh LM, Nguyen LT, Nguyen PN, Nguyen PV, et al: A novel antigenic variant of canine parvovirus from a Vietnamese dog. Arch Virol 2004, **149**:2261–2269.

[55] Nandi S, Chidri S, Kumar M, Chauhan RS: Occurrence of canine parvovirus type 2c in the dogs with haemorrhagic enteritis in India. Res Vet Sci 2010, **88**:169–171.

[56] Chang WL, Chang AC, Pan MJ: Antigenic types of canine parvoviruses prevailing in Taiwan. Vet Rec 1996, **138**:447.

[57] Wang HC, Chen WD, Lin SL, Chan JP, Wong ML: Phylogenetic analysis of canine parvovirus VP2 gene in Taiwan. Virus Genes 2005, **31**:171–174.

[58] Kang BK, Song DS, Lee CS, Jung KI, Park SJ, Kim EM, Park BK: Prevalence and genetic characterization of canine parvoviruses in Korea. Virus Genes 2008, **36**:127–133.

[59] Mohan Raj J, Mukhopadhyay HK, Thanislass J, Antony PX, Pillai RM: Isolation, molecular characterization and phylogenetic analysis of canine parvovirus. Infect Genet Evol 2010, **10**:1237–1241.

[60] Decaro N, Desario C, Campolo M, Elia G, Martella V, Ricci D, Lorusso E, Buonavoglia C: Clinical and virological findings in pups naturally infected by canine parvovirus type 2 Glu-426 mutant. J Vet Diagn Invest 2005, **17**:133–138.

[61] Decaro N, Campolo M, Desario C, Elia G, Martella V, Lorusso E, Buonavoglia C: Maternally-derived antibodies in pups and protection from canine parvovirus infection. Biologicals 2005, **33**:261–267.

[62] Lin CN, Chien CH, Chiou MT, Wang JW, Lin YL, Xu YM: Development of SYBR green-based real-time PCR for the detection of canine, feline and porcine Parvoviruses. Taiwan Vet J 2014, **40**:1–9.

[63] Decaro N, Desario C, Elia G, Martella V, Mari V, Lavazza A, Nardi M, Buonavoglia C: Evidence for immunisation failure in vaccinated adult dogs infected with canine parvovirus type 2c. New Microbiol 2008, **31**:125–130.

[64] Decaro N, Elia G, Martella V, Desario C, Campolo M, Trani LD, Tarsitano E, Tempesta M, Buonavoglia C: A real-time PCR assay for rapid detection and quantitation of canine parvovirus type 2 in the feces of dogs. Vet Microbiol 2005, **105**:19–28.

[65] Decaro N, Elia G, Desario C, Roperto S, Martella V, Campolo M, Lorusso A, Cavalli A, Buonavoglia C: A minor groove binder probe real-time PCR assay for discrimination between type 2-based vaccines and field strains of canine parvovirus. J Virol Methods 2006, **136**:65–70.

[66] Decaro N, Elia G, Martella V, Campolo M, Desario C, Camero M, Cirone F, Lorusso E, Lucente MS, Narcisi D, et al: Characterisation of the canine parvovirus type 2 variants using minor groove binder probe technology. J Virol Methods 2006, **133**:92–99.

[67] McKnight CA, Maes RK, Wise AG, Kiupel M: Evaluation of tongue as a complementary sample for the diagnosis of parvoviral infection in dogs and cats. J Vet Diagn Invest 2007, **19**:409–413.

[68] Mochizuki M, San Gabriel MC, Nakatani H, Yoshida M, Harasawa R: Comparison of polymerase chain reaction with virus isolation and haemagglutination assays for the detection of canine parvoviruses in faecal specimens. Res Vet Sci 1993, **55**:60–63.

[69] Chen HY, Li XK, Cui BA, Wei ZY, Li XS, Wang YB, Zhao L, Wang ZY: A TaqMan-based real-time polymerase chain reaction for the detection of porcine parvovirus. J Virol Methods 2009, **156**:84–88.

[70] Kumar M, Nandi S: Development of a SYBR Green based real-time PCR assay for detection and quantitation of canine parvovirus in faecal samples. J Virol Methods 2010, **169**:198–201.

[71] Perez LJ, Perera CL, Frias MT, Nunez JI, Ganges L, de Arce HD: A multiple SYBR Green I-based real-time PCR system for the simultaneous detection of porcine circovirus type 2, porcine parvovirus, pseudorabies virus and Torque teno sus virus 1 and 2 in pigs. J Virol Methods 2012, **179**:233–241.

[72] Zheng LL, Wang YB, Li MF, Chen HY, Guo XP, Geng JW, Wang ZY, Wei ZY, Cui BA: Simultaneous detection of porcine parvovirus and porcine circovirus type 2 by duplex real-time PCR and amplicon melting curve analysis using SYBR Green. J Virol Methods 2013, **187**:15–19.

[73] Finlaison DS: Faecal viruses of dogs: an electron microscope study. Vet Microbiol 1995, **46**:295–305.

[74] Decaro N, Desario C, Beall MJ, Cavalli A, Campolo M, Dimarco AA, Amorisco F, Colaianni ML, Buonavoglia C: Detection of canine parvovirus type 2c by a commercially available in-house rapid test. Vet J 2010, **184**:373–375.

[75] Lopez de Turiso JA, Cortes E, Ranz A, Garcia J, Sanz A, Vela C, Casal JI: Fine mapping of canine parvovirus B cell epitopes. J Gen Virol 1991, **72(Pt 10)**:2445–2456.

[76] Larson LJ, Schultz RD: Do two current canine parvovirus type 2 and 2b vaccines provide protection against the new type 2c variant? Vet Ther 2008, **9**:94–101.

[77] Spibey N, Greenwood NM, Sutton D, Chalmers WS, Tarpey I: Canine parvovirus type 2 vaccine protects against virulent challenge with type 2c virus. Vet Microbiol 2008, **128**:48–55.

[78] Decaro N, Desario C, Billi M, Mari V, Elia G, Cavalli A, Martella V, Buonavoglia C: Western European epidemiological survey for parvovirus and coronavirus infections in dogs. Vet J 2011, 187:195-199.

[79] Decaro N, Buonavoglia C: Canine parvovirus-a review of epidemiological and diagnostic aspects, with emphasis on type 2c. Vet Microbiol 2012, 155:1-12.

[80] Csagola A, Varga S, Lorincz M, Tuboly T: Analysis of the full-length VP2 protein of canine parvoviruses circulating in Hungary. Arch Virol 2014, 159:2441-2444.

[81] Filipov C, Decaro N, Desario C, Amorisco F, Sciarretta R, Buonavoglia C: Canine parvovirus epidemiology in Bulgaria. J Vet Diagn Invest 2011, 23:152-154.

[82] Muz D, Oguzoglu TC, Timurkan MO, Akin H: Characterization of the partial VP2 gene region of canine parvoviruses in domestic cats from Turkey. Virus Genes 2012, 44:301-308.

[83] Maya L, Calleros L, Francia L, Hernandez M, Iraola G, Panzera Y, Sosa K, Pérez R: Phylodynamics analysis of canine parvovirus in Uruguay: evidence of two successive invasions by different variants. Arch Virol 2013, 158:1133-1141.

[84] Castro TX, Costa EM, Leite JP, Labarthe NV, Cubel Garcia RC: Partial VP2 sequencing of canine parvovirus (CPV) strains circulating in the state of Rio de Janeiro, Brazil: detection of the new variant CPV-2c. Braz J Microbiol 2010, 41:1093-1098.

[85] Chiang SY, Wu HY, Chiou MT, Chang MC, Lin CN: Identification of a novel canine parvovirus type 2c in Taiwan. Virol J 2016, 13:160.

[86] Meers J, Kyaw-Tanner M, Bensink Z, Zwijnenberg R: Genetic analysis of canine parvovirus from dogs in Australia. Aust Vet J 2007, 85:392-396.

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