

RESEARCH ARTICLE

Development and Application of an ELISA for the Detection of Porcine Deltacoronavirus IgG Antibodies

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Abstract

Porcine deltacoronavirus (PDCoV), also known as porcine coronavirus HKU15, was first detected in North America in early 2014 and associated with enteric disease in pigs, resulting in an urgent need to further investigate the ecology of this virus. While assays detecting nucleic acids were implemented quickly, assays to detect anti-PDCoV antibodies have not been available. In this study, an indirect anti-PDCoV IgG enzyme-linked immunosorbent assay (ELISA) based on the putative S1 portion of the spike protein was developed and utilized to determine the prevalence of anti-PDCoV IgG in U.S. pigs. The diagnostic sensitivity of the PDCoV ELISA was 91% with a diagnostic specificity of 95%. A total of 968 serum samples were tested including samples with confirmed infection with PDCoV, porcine epidemic diarrhea virus (PEDV), transmissible gastroenteritis virus or porcine respiratory coronavirus. There was no cross-reactivity with any of the other coronaviruses. Among 355 arbitrarily selected serum samples collected in 2014 and originating from 51 farms across 18 U.S. states, anti-PDCoV IgG antibodies were detected in 8.7% of the samples and in 25.5% of the farms whereas anti-PEDV IgG was detected in 22.8% of the samples and in 54.9% of the farms. In addition, anti-PDCoV IgG antibodies were detected in archived samples collected in 2010, perhaps indicating an earlier undetected introduction into the U.S. pig population. Overall, the obtained data suggest that PDCoV seroprevalence in U.S. pigs is lower compared to PEDV and PDCoV may have been introduced to the U.S. prior to PEDV.

Introduction

Porcine deltacoronavirus (PDCoV) was first identified in a fecal sample collected in 2009 from a pig in Hong Kong, China, and isolated by Xiao and Alai et al. [1]. PDCoV was first identified in apparently healthy adult animals [1–3]. Recently, PDCoV has been described in a association with diarrhea in piglets of all production age in North America [4–6]. Specifically, in February 2014, the Ohio Department of Agriculture identified a previously unrecognized

PDCoV was detected in nine fecal fomites from a pig farm in Ohio, with clinical signs of a very diarrheal in onset and endemic diarrhea associated with increased mortality in piglets [4]. The presence of an immunizable gastroenteric virus (TGEV) also led to a portion of the sample and also possibly for porcine epidemic diarrhea virus (PEDV) [4]. In response to the impact of the new emerging porcine coronavirus PEDV [7,8] and PDCoV [4] in the U.S. pig population, the USDA initiated a federal order requiring reporting of all novel cases associated with all porcine endemic coronavirus and effective June 5, 2014 [9]. In contrast to PEDV [10–12], the epidemiology is still pathogenic and clinically symptomatic associated with PDCoV infection is still largely unknown. Nevertheless, preliminary studies obtained after experimental infection of gnotobiotic piglets with HIV-1 indicate very few clinical signs (diarrhea, vomiting, dehydration) and microscopical lesions consistent with coronavirus infection in the small intestine [13]. However, serological assays could make field-based epidemiological studies available to date. Sequencing of the complete genome of U.S. PDCoV strains from different

prior to the e₁m collection ($n = 60$ /farm). The last 30 samples came from PDCoV negative farm D. The PDCoV infection was determined based on real-time RT-PCR for PDCoV on fecal sample. PEDV, PRCV and TGEV RNA were not detected in the feces. All RT-PCR results were confirmed by qPCR in the reference laboratory (ISU-VDL). Farm A sample collected at the first time point and sample from the negative farm D were classified as negative ($n = 60$). Farm A sample collected at the second time point and sample from the positive Farm B and C were classified as positive ($n = 150$). For the paired sample from Farm A, PDCoV seroconversion was defined as a four-fold increase in the antibody titer when comparing the first and second sample collection point.

Geographic distribution of PDCoV antibody positive samples. A total of 355 e₁m samples were analyzed during 2014 from U.S. pig farms identified by geographic origin as part of a national diagnostic study of the ISU-VDL. Five e₁m samples were collected from each of 71 independent farms from 51 different farms ($n = 5$ to 25 samples per farm) located in 18 different states across the U.S. (Colorado, Iowa, Illinois, Indiana, Kansas, Kentucky, Michigan, Minnesota, Missouri, Montana, Nebraska, New Jersey, North Carolina, Ohio, Oklahoma, Pennsylvania, South Dakota, and Wisconsin). All 355 samples were tested for presence of an anti-PDCoV IgG and for an anti-PEDV IgG antibody using an indirect ELISA described [25].

A hundred e₁m samples ($n = 403$) collected from 2006 to 2013 prior to initial recognition of PDCoV from 25 different farms from 18 different states in the U.S. (Iowa, Illinois, Nebraska, North Carolina, Missouri, Texas) [25–27] were also included and tested for presence of an anti-PDCoV IgG.

Antibody titration of PDCoV antibody positive samples. A total of 52 pooled liquid porcine plasma samples collected in 2010 as part of a previous study [28] were tested for titration. Each porcine plasma sample consisted of pooled plasma originating from a single animal of approximately 10,000 piglets housed on the same day. The samples were collected from 14 different farms located in the eastern part of the Midwestern U.S. [28]. Based on real-time RT-PCR testing, all samples obtained in 2010 were negative for PDCoV RNA.

PDCoV S1 ELISA development

Antigen selection. The region encoding the predicted S1 domain (amino acid 1–573) of the PDCoV strain PDCoV-IA2014-1 (GenBank accession number KM613173) was synthesized in a high combinatorial library sequence followed by a human IgG Fc domain, which was subsequently cloned into a eukaryotic expression vector and subcloned [25]. The S1-Fc fusion protein was expressed in a transfection of HEK-293T cells, purified using protein A column purification, cleaved in the high combinatorial library of the Fc tag, and tested for endotoxin removal.

Antibody titration. The optimal antigen concentration and the e₁m dilution for the S1-PDCoV ELISA were determined using a checkerboard titration. Microtiter plates (Nunc; The Molecular Sciences, Acton, MA, USA) were coated with the S1 protein peptide diluted in coating buffer (50 mM carbonate buffer, pH 9.6) at a concentration of 0.95 ng per well and incubated overnight at 4°C. After washing with PBS containing 0.05% Tween 20 (PBST), the plates were blocked with 1% bovine serum albumin (Jackson ImmunoResearch, West Grove, PA, USA) for 2 hours at 22°C and then incubated with the e₁m or plasma sample diluted 1:100 in PBS containing 10% goat serum (Gibco; Life Technologies, Grand Island, NY, USA) for 30 minutes at 37°C. After washing, a 1:10,000 diluted peroxidase-conjugated anti-human IgG (Jackson ImmunoResearch) was added and incubated at 37°C for 30 minutes. The peroxidase reaction was visualized by adding a 5-benzidine-tetramine hydrogen peroxide solution to the

ab (KPL, Gaithersburg, MD, USA) for 10 min at room temperature and stopped by adding 50 μ L of 2 M hydrochloric acid to each well. Optical density (OD) was measured at 450 nm using an ELISA plate reader (BioTek, Winooski, VT, USA). Serum dilution has given the geometric mean between the positive and the negative sample (P/N) was elected a control for blank, negative and positive, negative and blank (negative) sample were tested in duplicate and included on each plate.

Specificity of the PDCoV S1 ELISA. The specificity of the PDCoV S1 ELISA was evaluated using a mixture of positive and high antibody titer against TGEV ($n = 30$), PRCV ($n = 30$) or PEDV ($n = 30$) which were obtained through the ISU-VDL. The cutoff calculated by receiver operating characteristic (ROC) analysis for maximum diagnostic sensitivity and specificity using samples classified a PDCoV positive ($n = 150$) or negative ($n = 60$ samples). The cutoff value was elected to maximize sensitivity and specificity while minimizing the number of false negative and false positive results. The obtained value was the value added during the calculation of all of the samples. The ROC was defined to determine the cutoff of the PDCoV S1 ELISA using MedCalc for Windows, version 13.3.0.0. (MedCalc Software, Ostend, Belgium).

Reproducibility of the PDCoV S1 ELISA. The reproducibility of the PDCoV S1 ELISA was evaluated by including eight samples with different antibody titer. The coefficient of variation (CV) was calculated over five replicates in intra- and inter-assay variation. Each sample was tested on each of the plates on different occasions to determine the intra-assay CV, and the replicability within the same plate was evaluated to calculate the intra-assay CV.

Results

PDCoV S1 ELISA development

The ROC analysis based on 210 samples with known PDCoV exposure was used for the cutoff determination (Fig 1). The optimal cutoff for the PDCoV S1 ELISA was a 1:100 diluted sample OD value of 0.34 for which the sensitivity and specificity values were higher than 90%. Sensitivity was 90.6% and the specificity was 94.8%. The diagnostic accuracy of PDCoV S1 ELISA was considered to be high as the area under the curve (AUC) index was 0.98 with a standard deviation of 0.01. Intra- and inter-assay coefficient of variation (CV) of eight control samples in the PDCoV S1 ELISA was less than 10%. The intra-assay CV ranged from 2.6% to 4.2% while the inter-assay CV ranged from 5.2% to 9.4%, indicating that the results were reproducible. The assay specificity was determined by using samples positive for antibody to TGEV, PRCV or PEDV. The obtained PDCoV S1 ELISA OD values ranged from 0.04 to 0.33 (average SD, 0.12 \pm 0.06), indicating a lack of cross-reaction with other porcine coronaviruses. Among the 90 samples positive for antibody against TGEV, PRCV or PEDV, only one had an OD value higher than 0.3 for PDCoV. Specifically, PDCoV OD values ranged from 0.04 to 0.33 (average SD, 0.12 \pm 0.08) for TGEV; 0.05 to 0.291 (average SD, 0.10 \pm 0.06) for PRCV; and 0.07 to 0.244 (average SD, 0.13 \pm 0.05) for PEDV.

Presence of anti-PDCoV IgG antibodies in pig serum during an acute outbreak and four weeks later

Anti-PDCoV IgG antibody positive samples were detected in 7 (23.3%) of the 30 samples affected by diarrhea and in 28 (93.3%) samples four weeks after PDCoV RT-PCR diagnosis (Fig 2). To observe the seronegative behavior collection time. Serosurvey, characteristic of the sample was a four-fold increase in the OD value was detected in 16 (53.3%) of . Among the positive samples identified during the first collection, 1/7 had a serosurvey

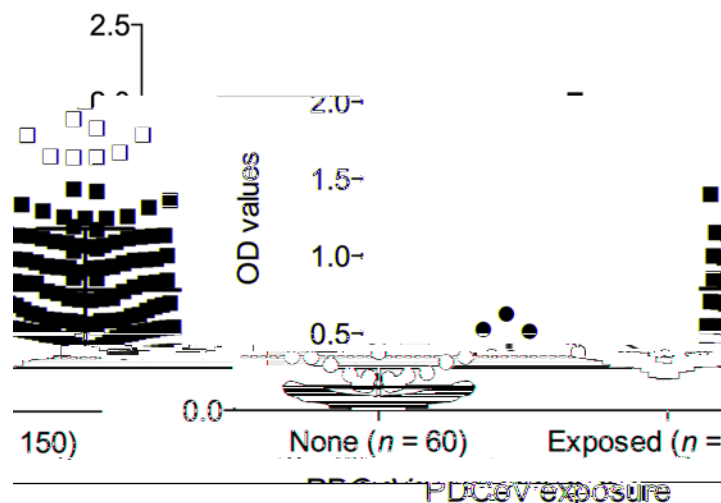


Fig 1. Distribution of serum anti-PDCoV IgG antibodies obtained from farms with known PDCoV exposure. Serum samples were classified as negative or positive based on viral RNA detection on fecal samples at the farm. Data presented as ELISA OD values \pm SEM. The assay cut-off (OD value of 0.34) is indicated by the dashed line.

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(4.4-fold increase in the OD₅₀₀); 3/7 had a least a 2-fold increase in the OD₅₀₀ (average \pm SD 2.46 \pm 0.74); and 3/7 had OD₅₀₀ increase more than 1.5-fold.

Presence of anti-PDCoV and -PEDV IgG antibodies in pig serum samples with unknown PDCoV exposure collected during 2014

An anti-PDCoV and -PEDV IgG antibody prevalence was determined in 355 serum samples collected during 2014 and summarized in Table 1. Thirty-one serum samples (8.7%) were anti-PDCoV IgG antibody positive which were identified in 13/51 (25.5%) farms. Positive detection was in

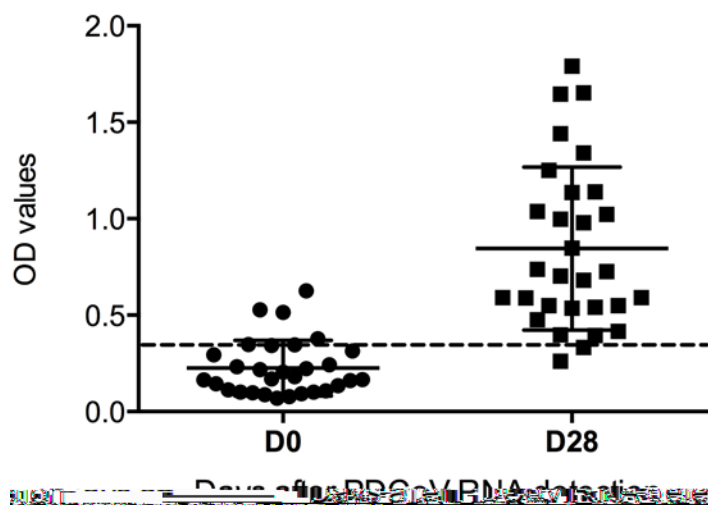


Fig 2. Distribution of serum anti-PDCoV IgG antibodies during an acute outbreak and four weeks later. An acute outbreak was defined as presence of clinical disease and demonstration of PDCoV RNA in feces. Data presented as ELISA OD values \pm SEM. The assay cut-off (OD value of 0.34) is indicated by the dashed line.

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Table 1. Detection rate of anti-PDCoV and anti-PEDV IgG antibodies in pig sera samples collected during 2014.

State	Number of positive samples/number samples tested	
	(Number of positive farms/number of farms tested)	
	PDCoV	PEDV
Colorado	0/5 (0/1)	3/5 (1/1)
Iowa	12/145 (7/20)	21/145 (11/20)
Illinois	1/15 (1/3)	4/15 (2/3)
Indiana	3/20 (1/4)	7/20 (2/4)
Kansas	0/5 (1/1)	0/5 (1/1)
Kentucky	0/5 (0/1)	0/5 (0/1)
Michigan	0/5 (0/1)	0/5 (0/1)
Minnesota	0/5 (0/1)	0/5 (0/1)
Missouri	3/20 (1/3)	20/20 (3/3)
Montana	0/5 (0/1)	0/5 (0/1)
North Carolina	0/30 (0/2)	1/30 (1/2)
Nebraska	8/10 (2/2)	7/10 (2/2)
New Jersey	0/5 (0/1)	0/5 (0/1)
Ohio	0/5 (0/1)	0/5 (0/1)
Oklahoma	0/35 (0/4)	15/35 (2/4)
Pennsylvania	4/20 (1/3)	3/20 (1/3)
South Dakota	0/5 (0/1)	0/5 (0/1)
Wisconsin	0/5 (0/1)	0/5 (0/1)
Total	31/355 (13/51)	81/355 (28/51)

All serum samples were obtained from commercial pig farms in 18 different states across the U.S.A.

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individual PDCoV farms ranged from 20 to 100%. An anti-PEDV IgG antibody was detected in 81/355 (22.81%) of the samples and in 28/51 (54.9%) of the investigated farms. Concurrent detection of an anti-PEDV and an anti-PDCoV IgG antibody occurred in 8/51 farms (15.7%) and 23/355 (6.5%) of the samples.

Presence of anti-PDCoV IgG antibodies in pig serum and plasma samples with unknown PDCoV exposure collected prior to 2014

Among the 403 archived samples collected between 2006 and 2013, 44 (10.9%) of the samples were found to be positive for an anti-PDCoV IgG antibody by the S1 ELISA (Table 2). The majority of positive samples were collected in 2013 (40/44, 90.9%). On positive farms, 20 to 60% of the samples were found to be positive. In the entire sample set collected in 2010; specifically, the samples originated on a farm in Illinois and one sample from a farm in Iowa. The OD values on the samples were 0.38, 0.39, 0.42, and 1.27. Due to the limited availability of the respective reagents and of the confirmation finding, 52 porcine pooled plasma samples from 2010 were analyzed. Two of 52 (3.8%) pooled plasma samples were positive for an anti-PDCoV IgG antibody; the OD values were 0.34 and 0.38. The overall OD value of negative samples ranged from 0.05 to 0.15 (mean \pm SD, 0.08 \pm 0.01).

Table 2. Detection rate of anti-PDCoV IgG antibodies from 2006 to 2014 in the U.S.A.

Year	PDCoV positive samples/number of samples tested (PDCoV positive farms/number of farms tested)
2006	0/19 (0/1)
2007	0/16 (0/1)
2010	4/58 (2/4)
2011	0/9 (0/2)
2012	0/91 (0/9)
2013	40/210 (6/10)
2014	31/355 (13/51)
Total	75/758 (21/78)

All serum samples were obtained from commercial pig farms.

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Discussion

PDCoV was initially discovered in U.S. pig in 2014 [4] leading to major infection on basic infection dynamics and time of introduction of this emerging pig virus. The objective of this study was to develop a serological assay to evaluate the 2014 prevalence rate of PDCoV in U.S. pig and to determine evidence for PDCoV infection in previous years.

In order to accomplish this goal, a recombinant PDCoV S1 protein peptide-based ELISA was developed and the S1 protein was selected as coating antigen. The amino acid identity of the PDCoV S1 protein and the corresponding PEDV conserved peptide (IA1 strain, GenBank accession number KF468753) is 20.2%, for TGEV (Paderborn strain, GenBank accession number AJ271965) is 20.7% and for PRCV (ISU-1 strain, GenBank accession number DQ811787) is 22.1% [5]. Therefore, the PDCoV S1 protein used in the present study was a novel one compared to PEDV, PRCV or TGEV and as expected, cross-reactivity was not observed. Furthermore, the molecular identification of the PDCoV epitope targeted for detection and evaluation compared with the alphacoronavirus PEDV, TGEV and PRCV. As expected, the S1 protein contained the major epitopes of the mapped epitope within the conserved protein non-elasticity motif (E, M, N and S). In addition, a comparison of the amino acid identity between the expected PDCoV S1 antigen for the developed ELISA and the other 19 PDCoV sequences in the GenBank indicated a similarity higher than 99% for the S1 protein peptide, which suggests high homogeneity in conserved epitopes of the molecular epitope detected.

A preliminary study generated ample material for a gold standard for PDCoV antibody detection and was available at the time the study was conducted, field samples in which known PDCoV exposure and from previously negative pig pens were obtained to gain information on basic PDCoV occurrence. An anti-PDCoV antibody and occurrence were detected within four weeks of initial observation of clinical diarrhea and detection of PDCoV RNA in fecal samples. Ideally, the cross-sectional study should be developed by using a panel of samples obtained from different animal health status and infection status, allowing the detection of [29]. Due to difficulties in classifying pig farm as negative, i.e. no previous exposure to PDCoV which would have required observation of fecal samples over time from an adequate number of pig pens on the farm, samples from the affected PDCoV outbreak (PDCoV real-time RT-PCR positive pig pens) were considered to be negative for the development purposes. Although this was a less efficient confirmation diagnosis of acute infection as occurrence was detected in paired samples from PDCoV outbreak, the lack of a second serological assay and known negative samples did not permit a precise estimation of the diagnostic sensitivity and specificity of the test. Selecting a single antibody cross-sectional study on the basis of field samples and

association in clinical history and RT-PCR could be in a lot of environments and/or specificity. To further add to this, the established cut-off value of 0.34 was used, giving the maximum value data of 573 samples originating from the negative farm (classified as negative due to absence of any PDCoV ELISA positive pig among the pig tested) by calculating the average OD (data not shown). It was determined that the adoption of this method obtained low cut-off value (0.24; OD average \pm SD; average SD 0.09 \pm 0.05), and provided a greater sensitivity. Therefore, samples with an OD value between 0.24 and 0.34 would probably be considered inconclusive. The lack of a gold standard for PDCoV antibody detection further complicates the problem in establishing an appropriate cut-off and accuracy of measurement in environments and specificity of the ELISA developed herein.

Based on maximum value data from the National Animal Health Laboratory Network (NAHLN) laboratory on September 17, 2014, 6.6% (382) of 5827 cattle obtained from 17 of 31 active epidemiological PDCoV RNA [30]. In the present study, 8.7% (31/355) of the maximum sample collected from 7/18 active epidemiological PDCoV IgG which is in agreement with the Animal and Public Health Information System (APHIS) surveillance data and PDCoV RNA detection by RT-PCR. In contrast, the percentage of PEDV RNA positive cattle was 26.0% (8386/32211) obtained from a total of 31/42 U.S. state according to the most recent NAHLN survey [30]. In the agreement, in this study, 22.8% (81/355) of the sample antibody was detected in 2014 epidemiological PEDV IgG.

It has been determined previously that co-infection of PDCoV with the enterovirus is a common [9]. In the present investigation, 38% of PEDV ELISA positive pig were also positive for an i-PDCoV antibody (data not shown). This is in agreement with previously reported findings that 78% of PDCoV RNA positive samples were also positive for PEDV RNA, coronavirus A RNA, coronavirus B RNA, coronavirus C RNA and 33% were co-infected with PEDV as determined by RT-PCR [14]. Experimental trials are needed to be conducted and the comparative surveillance of PDCoV on the enteric pathogen.

PDCoV was first identified in U.S. pig in 2014 [4] and subsequently the age of detection of RNA has been able to identify horses in late 2013 [30]. Access to a clinical sample can be limited and otherwise come from a clinical population sample collected in this study. While the PEDV was a novel validated on plasma, evidence in the literature suggests that the degree of antibody detection in serum and plasma is essentially identical [31–34]. Overall, the obtained data suggests that PDCoV has been circulating in the North American pig population prior to 2013, likely being recognized. Specifically, an antibody to PDCoV was detected in a clinical serum and plasma sample from 2010, the earliest i-PDCoV IgG antibody was not detected in serum sample collected in 2011 or 2012. This could be due to the limited number of available epidemiological samples in combination with an overall low PDCoV prevalence. Alternatively, the positive sample collected in 2010 could be false positive; however, a least one sample presented a high OD value. Upon availability of another PDCoV serological test in the future, the results will need to be confirmed.

In conclusion, overall data indicated that PDCoV RT-PCR surveillance is likely, the obtained an i-PDCoV IgG prevalence data further confirm an overall population prevalence rate of PDCoV infection in the U.S. pig population.

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Author Contributions

Conceived and designed the experiments: TO. Performed the experiments: AT CTX. Analyzed the data: PFG. Contributed reagents/materials/analysis tools: YWH. Wrote the paper: AT PFG CTX YWH TO. Carried out the statistical analysis and created the figure: PFG.

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