The present invention also provides infectious DNA clones, biologically functional plasmid or viral vector containing the infectious nucleic acid genome molecule of Torque teno sus virus (TsuV). The present invention also provides methods for diagnosing TsuV infection via immunological methods, e.g., enzyme-linked immunosorbent assay (ELISA) and Western blot using PTTV specific antigens for detecting serum PTTV specific antibodies which indicate infections TsuV1, TsuV2, and individual TsuV1 genotypes.

12 Claims, 27 Drawing Sheets

Specification includes a Sequence Listing.
References Cited

OTHER PUBLICATIONS


References Cited

OTHER PUBLICATIONS


Huang, Y.W., et al. “Expression of the putative ORF1 capsid protein of Torque teno sus virus 2 (TTSuV2) and development of Western blot and ELISA serodiagnostic assays: correlation between TTSuV2 viral load and IgG antibody level in pigs,” Virus Res 158, pp. 79-88, 2011.

* cited by examiner
**FIG. 2D**

Graph showing temperature versus $\frac{d(RU)/dt}{dt}$.

**FIG. 2E**

Genetic analysis results for different markers and standards.


TTSuV1

TTSuV2
**Fig. 3A**

- pSC-TTV2-#471942
- pSC-2PTTV2b-RR
- pSC-PTTV2c
- M

4.9 Kb
2.8 Kb
2.1 Kb

**Fig. 3B**

- High-copy-number circular DNA
- Two-copy circular DNA
- Linear DNA
- One-copy circular DNA

- Linear TTsuV2 genomic DNA
- Ligation mixture

- 10 Kb
- 5 Kb
- 4 Kb
- 3 Kb
- 2.5 Kb
- 2 Kb
- 1.5 Kb
- 1 Kb
- 0.8 Kb
- 0.6 Kb
- 0.4 Kb
Fig. 6

- - pSC-TTV2-US pSC-TTV2-ΔAA
Fig. 8A  Fig. 8B  Fig. 8C
**Fig. 9A**

<table>
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<tr>
<th>KDa</th>
<th>M</th>
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</tr>
</tbody>
</table>

**Fig. 9B**

**Fig. 9C**

Gnotobiotic pigs

Conventional pigs from Wisconsin
**Fig. 10A**

TTSuV1 viremia  | Anti-TTSuV1a IgG  | Anti-TTSuV1b IgG  | No. of diagnosed samples
--- | --- | --- | ---
Positive rate (Positive No./Total No.) | 31.9% (44/138) | 92.8% (128/138) | 87.7% (121/138) |
+ | + | + | 40 |
+ | + | - | 2 |
+ | - | + | 2 |
+ | - | - | 0 |
- | + | + | 77 |
- | + | - | 9 |
- | - | + | 2 |
- | - | - | 6 |

**Fig. 10B**

![Fig. 10B](image)

**Fig. 10C**

![Fig. 10C](image)
**Fig. 11A**

Graph showing the virus titer (copies/ml) over time from Arrival to Two Months After Arrival.

**Fig. 11B**

Graph showing the antibody level to TTSV1a ORF 1 (S/N) from Arrival to Two Months After Arrival.

**Fig. 11C**

Graph showing the antibody level to TTSV1b ORF 1 (S/N) from Arrival to Two Months After Arrival.
Fig. 12A

TTSuV1a Antibody Level (S/N)

Unaffected  Affected

P > 0.05

n=30

Fig. 12B

TTSuV1b Antibody Level (S/N)

Unaffected  Affected

P > 0.05

n=30
Fig. 12C

Viral Loads (copies/ml)

$\rho > 0.05$

Fig. 12D

Viral Loads (copies/ml)

$P < 0.05$
### Fig. 13A

<table>
<thead>
<tr>
<th>Positive rate (Positive No./Total No.)</th>
<th>Anti-TTSuV1a IgG</th>
<th>Anti-TTSuV1b IgG</th>
<th>Anti-TTSuV2b IgG</th>
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</tbody>
</table>

### Fig. 13B

![Graph showing TTSuV1a S/N vs. TTSuV1b S/N](image)
Fig. 15A

Antibody staining  Merge with DAPI

Fig. 15B

Fig. 15C
Fig. 16

PTTV1a-VA

aa 317 > 635

Hydrophilicity

PTTV1b-VA

aa 322 > 639

346 IDRWRKKQT

348 LNRWRKQA

578 EERESETSFTSAESSSEGDSDDQAE

581 TEETASSSITSAESSTEGDGSDDDEET
FIG. 18B
FIG. 19
1

INFEKTIONS GENOMIC DNA CLONE AND SEROLOGICAL PROFILE OF TORQUE TENO SUS VIRUS 1 AND 2

REFERENCE TO RELATED APPLICATION

This application is a divisional of U.S. patent application Ser. No. 13/840,805, filed Mar. 15, 2013, which is a continuation-in-part of U.S. patent application Ser. No. 12/861,378, which claims the benefit of U.S. Provisional Patent Application No. 61/235,833, filed on Aug. 21, 2009, and U.S. Provisional Patent Application No. 61/316,519, filed on Mar. 23, 2010. The disclosures of the above mentioned priority applications are hereby incorporated by reference in their entirety into the present disclosure.

FIELD OF INVENTION

The present invention relates to infectious DNA clones of Torque teno sus virus (TTSuV), also known as porcine Torque teno virus (PTTV), and diagnosis of Torque teno sus virus (TTSuV) infection, particularly diagnosis of species- or type-specific TTSuV infection, and simultaneous infection of multiple strains from different genotypes.

BACKGROUND OF THE INVENTION


Due to the lack of a cell culture system to propagate anelloviruses, little is known regarding the molecular biology and pathogenesis of anelloviruses. In order to definitively characterize diseases associated with anellovirus infection, an appropriate animal model is needed. Since multiple infections of different genotypes or subtypes of human TTV or TTSuV are common events (Gallei, A., et al. 2010. J Clin Microbiol 48:507-14), it is important to construct a pathological study of a single phenotype. Although infectious DNA clones of human TTV in cultured cells have been reported (de Villiers, E. M., et al. 2011. The diversity of torque teno viruses: in vitro replication leads to the formation of additional replication-competent subviral molecules. J Virol 85:7284-95; Kakkola, L., et al. 2007. Construction and biological activity of a full-length molecular clone of human Torque teno virus (TTN) genotype. FEBS J 274:4719-30; Leppik, L., et al. 2007. In vivo and in vitro intragenomic rearrangement of TT viruses. J Virol 81:9346-56), it is important to construct an infectious TTSuV DNA clone so that TTSuV can be used as a useful model to study the replication and transcription mechanisms and to dissect the structural and functional relationships of anellovirus genomes. More importantly, the availability of a TTSuV infectious DNA clone will afford us an opportunity to use the pig as a model system to study the replication and pathogenesis of TTSuV or even human TTV.


The inventors have previously developed and validated serum Western blot (WB) and indirect ELISA assays for detection of the IgG antibody against TTSuV2 in porcine sera using the purified recombinant TTSuV2-ORF1 protein expressed in E. coli (Huang, Y. W., et al. 2011. Virus Res 158:79-88). By using TTSuV2-specific real-time quantitative PCR (qPCR) and ELISA, the inventors were able to detect the combined virological and serological profile of TTSuV2 infection under natural or diseased conditions using 160 porcine sera collected from different sources (Huang, Y. W., et al. 2011. Id.). In the present invention, the inventors initially aimed to assess the serological profiles of the two TTSuV1 genotypes (TTSuV1a and TTSuV1b) in pigs, respectively. Subsequently, the inventors aimed to compare the virological and serological profiles of TTSuV1a and TTSuV1b with that of TTSuV2, and to determine the degree of correlation of IgG antibody levels between anti-TTSuV1a and -TTSuV1b and between anti-TTSuV1a or -1b and anti-TTSuV2. Finally, for the first time, the inventors assessed the antigenic relationships between two TTSuV1 genotypes (TTSuV1a and TTSuV1b), between two species (TTSuV1 and TTSuV2), and between porcine and human genogroup 1 anelloviruses using ELISA and immunofluorescence assay with antibody cross-reactions in PK-15 cells transfected with recombinant plasmids expressing the ORF1s from TTSuV1a, TTSuV1b and TTSuV2, respectively.

**SUMMARY OF THE INVENTION**

The present invention provides an infectious nucleic acid molecule of porcine Torque teno virus (PTTV), also known as, and referred to herein interchangeably as, Torque teno sus virus (TTSuV) comprising a nucleic acid molecule encoding an infectious TTSuV which contains at least one copy of genomic sequence having at least 85% homology to a genomic sequence of TTSuV2.
The present invention provides an infectious nucleic acid molecule ("infectious DNA clone") of porcine Torque teno virus (PTTV) comprising a nucleic acid molecule encoding an infectious PTTV which contains at least one copy of genomic sequence having at least 80% homology to a genomic sequence selected from the group consisting of genotypes of PTTV1a-VA, PTTV1b-VA, PTTV2b-VA, and PTTV2c-VA.

According to one aspect of the present invention, the infectious DNA clones of PTTV of set forth in claim 1, wherein the genomic sequence is selected from sequences set forth in SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:12.

The present invention provides a biologically functional plasmid or viral vector containing the infectious PTTV genomes.

The present invention provides a suitable host cell transfected with the infectious clone DNA plasmid or viral vector. The present invention provides an infectious PTTV produced by cells transfected with the PTTV infectious DNA clones.

The present invention also provides a viral vaccine comprising a nontoxic, physiologically acceptable carrier and an immunogenic amount of a member selected from the group consisting of (a) a nucleic acid molecule containing at least one copy of genomic sequence having at least 80% homology to a genomic sequence selected from the group consisting of PTTV genotypes or subtypes PTTV1a-VA, PTTV1b-VA, PTTV2b-VA, and PTTV2c-VA, or its complementary strand, (b) a biologically functional plasmid or viral vector containing a nucleic acid molecule containing at least one copy of genomic sequence having at least 80% homology to a genomic sequence selected from the group consisting of PTTV genotypes or subtypes PTTV1a-VA, PTTV1b-VA, PTTV2b-VA, and PTTV2c-VA, or its complementary strand, and (c) an avirulent, infectious nonpathogenic PTTV which contains at least one copy of genomic sequence having at least 80% homology to a genomic sequence selected from the group consisting of PTTV genotypes or subtypes PTTV1a-VA, PTTV1b-VA, PTTV2b-VA, and PTTV2c-VA.

According to one aspect of the present invention, the vaccine contains live PTTV virus derived from the PTTV infectious clones. According to another aspect of the present invention, the vaccine contains killed PTTV virus derived from the PTTV infectious clones.

The present invention provides purified recombinant proteins expressed from the ORF1 capsid genes of PTTV genotypes or subtypes PTTV1a-VA, PTTV1b-VA, and PTTV2c-VA in bacterial expression system, and the use of these recombinant capsid proteins as subunit vaccines against PTTV infections. In one embodiment of the present invention, the recombinant capsid proteins for the use as subunit vaccines are expressed in baculovirus expression system and other expression vector systems.

According to a further aspect of the present invention, further contains an adjuvant.

The present invention further provides a method of immunizing a pig against PTTV viral infection, comprising administering to a pig an immunologically effective amount of the viral vaccine.

According to one aspect of the present invention, the method comprising administering the recombinant subunit capsid protein, the infectious nucleic acid molecule or live PTTV virus to the pig.

According to another aspect of the present invention, the method comprising administering the vaccine parenterally, intranasally, intradermally, or transdermally to the pig. According a further aspect of the present invention, the method comprising administering the vaccine intralymphoidly or intramuscularly to the pig.

The present invention also provides an isolated polynucleotide consisting of the sequence of the nucleotide sequence of PTTV1a-VA set forth in SEQ ID NO:9.

According to one aspect of the present invention, the polynucleotide sequence is ORF1 of PTTV genotype PTTV1a-VA. According to another aspect of the present invention, the polynucleotide sequence is ORF1 of PTTV genotype PTTV1b-VA. According to yet another aspect of the present invention, the polynucleotide sequence is ORF1 of PTTV subtype PTTV2c-VA.

According to one aspect of the present invention, the polynucleotide sequence is selected from the group consisting of ORF1 of PTTV genotypes or subtypes PTTV1a-VA, PTTV1b-VA, PTTV2b-VA, and PTTV2c-VA, or its complementary strand, and an avirulent, infectious nonpathogenic PTTV genotype set forth in SEQ ID NO:16. According to yet another aspect of the present invention, the polynucleotide sequence is ORF1 of PTTV subtype PTTV2c-VA.

According to one aspect of the present invention, the polypeptide sequence is selected from the group consisting of polypeptides set forth in SEQ ID NO:13 to SEQ ID NO:28. According to an additional aspect of the present invention, the polypeptide sequence is set forth in SEQ ID NO:13. According to another aspect of the present invention, the polypeptide sequence is set forth in SEQ ID NO:16. In one specific embodiment of the present invention, the polypeptide sequence is C-terminal region (aa 310-625) of SEQ ID NO:16. According to yet another aspect of the present invention, the polypeptide sequence is set forth in SEQ ID NO:20.

According to an additional aspect of the present invention, the vaccine further contains an adjuvant.

The present invention further provides a method of immunizing a pig against PTTV viral infection, comprising administering to a pig an immunologically effective amount of the vaccine comprising an immunogenic fragment of a polypeptide sequence or a complete protein translated according to a polynucleotide sequence selected from the group consisting of ORF1, ORF2, ORF1/1, and ORF2/2 of PTTV genotypes or subtypes PTTV1a-VA, PTTV1b-VA, PTTV2b-VA, and PTTV2c-VA, particularly the ORF1 encoding the capsid protein.
According to one aspect of the present invention, the method comprises administering the immunogenic fragment or recombinant capsid protein to the pig.

According to another aspect of the present invention, the method comprises administering the vaccine parenterally, intramuscularly or intranasally to the pig.

According to a further aspect of the present invention, the method comprises administering the vaccine intralymphonically or intramuscularly to the pig.

The present invention additionally provides a method for diagnosing PTTV infection and quantification of PTTV load, comprising extracting DNA from a sample suspected of PTTV infection, performing polymerase chain reaction (PCR) using primers comprising the sequences set forth in SEQ ID NO:29 and SEQ ID NO:30, and detecting PTTV specific amplification. According to one aspect of the present invention, the polymerase chain reaction is a SYBR green real-time PCR.

The present invention further provides a method for diagnosing PTTV2 infection and quantification of PTTV2 load, comprising extracting DNA from a sample suspected of PTTV2 infection, performing polymerase chain reaction (PCR) using primers comprising the sequences set forth in SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31 and SEQ ID NO:32, and detecting PTTV2 specific amplification. According to one aspect of the present invention, the polymerase chain reaction is a SYBR green real-time PCR.

The present invention also provides a method for simultaneously detecting and diagnosing PTTV1 and PTTV2 infection, comprising extracting DNA from a sample suspected of PTTV infection, performing polymerase chain reaction (PCR) using primers comprising the sequences set forth in SEQ ID NO:31 and SEQ ID NO:32, and detecting PTTV1 and PTTV2 specific amplification. According to one aspect of the present invention, the polymerase chain reaction is a SYBR green real-time PCR.

The present invention, in addition, provides a method for simultaneously detecting and diagnosing PTTV1a and PTTV1b infection, comprising extracting DNA from a sample suspected of PTTV1 infection, performing a first polymerase chain reaction (PCR) using primers comprising the sequences set forth in SEQ ID NO:31 and SEQ ID NO:32, and detecting PTTV1 and PTTV2 specific amplification. According to one aspect of the present invention, the polymerase chain reaction is a SYBR green real-time PCR.

The present invention provides a method for diagnosing PTTV infection, comprising immobilizing an immunogenic fragment of a polypeptide sequence translated according to a polynucleotide sequence selected from the group consisting of ORF1, ORF2, ORF1/1, and ORF2/2 of PTTV genotypes or subtypes PTTV1a-VA, PTTV1b-VA, and PTTV2c-VA; contacting a serum sample from a pig suspected of PTTV infection with the immobilized immunogenic fragment, and detecting captured antibody specific to the immunogenic fragment.

According to one aspect of the present invention, the polynucleotide sequence is set forth in SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, and SEQ ID NO:28. According to another aspect of the present invention, the polypeptide sequence is set forth in SEQ ID NO:13. According to another aspect of the present invention, the polypeptide sequence is set forth in SEQ ID NO:14. According to one embodiment of the present invention, the polypeptide sequence is set forth in SEQ ID NO:16. According to a further embodiment of the present invention, the immunogenic fragment is C-terminal region (aa 310-625) of ORF1.

The present invention provides a method for diagnosing PTTV infection, comprising immobilizing an immunogenic fragment of a polypeptide sequence translated according to a polynucleotide sequence selected from the group consisting of ORF1, ORF2, ORF1/1, and ORF2/2 of PTTV genotypes or subtypes PTTV1a-VA, PTTV1b-VA, and PTTV2c-VA; contacting a serum sample from a pig suspected of PTTV infection with the immobilized immunogenic fragment, and detecting captured antibody specific to the immunogenic fragment.

According to one aspect of the present invention, the polynucleotide sequence is set forth in SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, and SEQ ID NO:28. According to another aspect of the present invention, the polypeptide sequence is set forth in SEQ ID NO:13. According to another aspect of the present invention, the polypeptide sequence is set forth in SEQ ID NO:14. According to another embodiment of the present invention, the polypeptide sequence is set forth in SEQ ID NO:16. According to yet another embodiment of the present invention, the polypeptide sequence is set forth in SEQ ID NO:20.

The present invention provides three standardized enzyme-linked immunosorbent assays (ELISA) to diagnose PTTV infections and detect antibodies in serum of pigs infected by PTTV genotypes PTTV1a-VA, PTTV1b-VA, and all known subtypes in PTTV species 2.

The ELISA diagnostic tests are based on the bacterial-expressed or baculovirus-expressed recombinant ORF1 capsid protein of PTTV genotypes PTTV1a-VA, PTTV1b-VA, and PTTV2c-VA.

According to another aspect of the present invention, the detecting captured antibody is via Western blot. According to another aspect of the present invention, the detecting captured antibody is via enzyme-linked immunosorbent assay (ELISA).

According to one embodiment, the at least one copy of genomic sequence has at least 95% homology to the genomic sequence of TTSuV2.

According to another embodiment, the genome of TTSuV2 is a genomic clone of PTTV2c-VA. In one specific example, the genomic sequence is selected from sequences set forth in SEQ ID NO: 12.

According to a further embodiment, the genomic sequence of TTSuV2 is of genomic clone of TTV2-#471942. In a specific example, the genomic sequence is selected from sequences set forth in SEQ ID NO: 62.

According to an additional embodiment, the genomic sequence of TTSuV2 comprising at least one genetic marker in intron 1. In a specific example, the genetic marker in intron 1 is an artificially introduced restriction site.

The present invention provides a method for diagnosing PTTV infection, comprising immobilizing an immunogenic fragment of a polypeptide sequence translated according to a polynucleotide sequence selected from the group consisting of ORF1, ORF2, ORF1/1, and ORF2/2 of PTTV genotypes or subtypes PTTV1a-VA, PTTV1b-VA, and PTTV2c-VA; contacting a serum sample from a pig suspected of PTTV infection with the immobilized immunogenic fragment, and detecting captured antibody specific to the immunogenic fragment.

According to one aspect of the present invention, the polynucleotide sequence is set forth in SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, and SEQ ID NO:28.
from a pig suspected of TTSuV infection with the immobilized immunogenic fragment or complete protein, and detecting antibody specific to the immunogenic fragment.

According to one embodiment, the polypeptide sequence is selected from the group consisting of ORF1 proteins of TTSuV genotypes or subtypes TTSuVla or TTSuVlb.

According to another embodiment, the polypeptide sequence is selected from the group consisting of N-terminal truncated ORF1 proteins of TTSuV genotypes or subtypes TTSuVla, TTSuVlb or TTSuV2. In a specific example, the polypeptide sequence is amino acid No. 317-635 of ORF1 protein of TTSuVla. In another example, the polypeptide sequence is amino acid No. 322-639 of ORF1 protein of TTSuVlb.

**BRIEF DESCRIPTION OF THE DRAWINGS**

The above-mentioned features of the invention will become more clearly understood from the following detailed description of the invention read together with the drawings in which:

**FIG. 1(A)-FIG. 1(G) represent schematic diagrams of TTSuV2 constructs containing full-length TTSuV2 genomic DNA. FIG. 1(A) pSC-PTTV2c (from the U.S. TTSuV2 isolate PTTV2c-VA; GenBank accession no. GU456386). FIG. 1(B) pSC-2PTTV2c-RR (tandem-dimerized PTTV2c-VA genomes). FIG. 1(C) pSC-PTTV2c-#471942 (from the German TTSuV2 isolate PTTV2c-#471942; GenBank accession no. GUI 88046). FIG. 1(D) pSC-2PTTV2c-RR (tandem-dimerized PTTV2c-#471942 genomes). FIG. 1(E) pSC-PTTV2-EU (derived from pSC-PTTV2c-#471942). A Hpal site as the silent genetic marker was introduced in this clone. FIG. 1(F) pSC-PTTV2-US (derived from pSC-PTTV2c). PsiI and Msel sites as the silent genetic markers were introduced in this clone. FIG. 1(G) pSC-PTTV2-AAA. A 104-bp deletion as the silent genetic marker was introduced in this clone.**

**FIG. 2(A)-FIG. 2(E) illustrate detection of TTSuV1 or TTSuV2 contamination in live different cell lines (PCV1-free PK-15, 3D4/31, IPEC-J2, BHK-21 and MARC-145) and an cHE disease-free porcine serum by real-time qPCR. Fluorescence curves (FIG. 2(A) and FIG. 2(C)) and melting curves (FIG. 2(B) and FIG. 2(D)) of TTSuV1 (FIG. 2(A) and FIG. 2(B)) or TTSuV2 (FIG. 2(C) and FIG. 2(D)) qPCR products are shown after 40 cycles of amplifications of the standard template with the minimum dilution limit (10⁻⁴ pg indicated by red), five different cell lines (blue) and the porcine serum (green). For each sample, duplicate determinations were made. FIG. 2(E) Detection of specific TTSuV1 or TTSuV2 qPCR products (marked by black arrowheads) by agarose gel electrophoresis.**

**FIG. 3(A) and FIG. 3(B) illustrate identification and quality assessment of linear or circular TTSuV2 genomic DNA. FIG. 3(A) Comparisons of the HindIII single-digestion patterns between clones pSC-PTTV2c-#471942 and pSC-2PTTV2c-RR (left panel) and AflIII single-digestion patterns between clones pSC-PTTV2c and pSC-2PTTV2c-RR (right panel) by agarose gel electrophoresis. M: DNA markers. The results were consistent to the predicted patterns of the digested fragments (shown by black arrowheads). The 2.8-Kb fragments indicate the intact single TTSuV2 genomic DNA from the clone pSC-2PTTV2b-RR or pSC-2PTTV2c-RR. FIG. 3(B) Quality assessment of concatemerized ligation products of the BamH1-digested and purified PTTV2c genomic DNA. The samples were electrophoresed in a 1% agarose gel before (linear DNA) and after (ligation mixture) T4 DNA ligase treatment. Linear DNA (~2.8 Kb) and formations of the putative one-copy (monomer), two-copy (dimer) and high-copy-number circular DNA are indicated by arrowheads.**

**FIG. 4(A)-FIG. 4(E) illustrate Immunofluorescence assay (IFA) results on PCV1-free PK-15 cells transfected with the ligation mixtures of linear TTSuV2 genomic DNA derived from clones pSC-PTTV2c FIG. 4(A) or pSC-PTTV2c-#471942 FIG. 4(C), with plasmids pSC-2PTTV2c-RR FIG. 4(B) or pSC-2PTTV2b-RR FIG. 4(D), or with Lipofectamine LTX only FIG. 4(E). Cells were stained with a rabbit anti-TTSuV2 ORF1 polyclonal antibody (Ab) and a Texas Red-conjugated goat anti-rabbit IgG (red) at 5 days post-transfection (the left panels), DAPI (blue) was used to stain the cell nucleus (the middle panels). The Ab and DAPI stainings are merged (right panels). Magnification=200x.**

**FIG. 5(A)-FIG. 5(C) illustrate the putative transcription profile and protein expression of TTSuV2 based on the PTTV2c-VA genome (a fragment of nucleotides which correspond to nucleotides 1-2500 of SEQ ID NO:12). FIG. 5(A) Schematic diagram of three putative viral mRNAs and six viral proteins. The TATA box, splicing sites (SD: splicing donor; SA: splicing acceptor) and the positions of primers TTV2-448F (SEQ ID NO:66) and TTV2-2316R (SEQ ID NO:6) were indicated at the top. The three open reading frames (ORFs) are depicted by colored boxes. The sizes of the six ORFs and two introns are also shown. FIG. 5(B) Sequencing of the RT-PCR products amplified by primers TTV2-448F and TTV2-2316R verified the splicing of the putative intron 1. FIG. 5(C) Sequencing of the RT-PCR products amplified by primers TTV2-448F and TTV2-2316R identified an additional intron (intron 2). Arrows and numbers indicate the joint site of the exons.**

**FIG. 6 illustrates IFA results of PCV1-free PK-15 cells transfected with the ligation mixtures of linear TTSuV2 genomic DNA derived from clones pSC-PTTV2c-EU or pSC-PTTV2b-US or pSC-PTTV2-AAA. Cells were stained with an anti-TTSuV2 ORF1 antibody (Ab) and an Alexa fluor 488-conjugated goat anti-rabbit IgG (green) at 3 days post-transfection. DAPI (blue) was used to stain the cell nucleus. Only merge of Ab and DAPI stainings are shown. Magnification=200x.**

**FIG. 7 illustrates transfection of nine different cell lines with the ligation mixture of linear TTSuV2 genomic DNA derived from the clone pSC-PTTV2-US, Alexa fluor 488-conjugated goat anti-rabbit IgG (green) merged with nuclear staining using DAPI (blue) are shown. Magnification=200x.**

**FIG. 8(A)-FIG. 8(C) illustrate expression and purification of the amino-terminally truncated TTSuVla and TTSuVlb ORF1 proteins, respectively. FIG. 8(A) SDS-PAGE analysis of unpurified and purified TTSuV1a-ORF1 products. FIG. 8(B) SDS-PAGE analysis of unpurified and purified TTSuV1b-ORF1 products. An amino- and carboxyl-terminally double-truncated TTSuV1b-ORF1 products of smaller protein size served as the control. FIG. 8(C) Near-infrared fluorescent WB analysis of purified 1a- and 1b-ORF1 products using an anti-His-tagged mAb. Open arrowheads indicate the truncated ORF1 protein of the expected size whereas filled arrowheads show the presumably homodimers of the expected proteins. M: protein markers.**
FIG. 9(A)-FIG. 9(C) illustrate TTSuV1a or TTSuV1b serum WB and ELISA. FIG. 9(A) WB analyses using the gnotobiotic pig serum samples from Virginia and a commercial OIE disease-free porcine serum as the positive control reference serum (pos). FIG. 9(B) Representative results of TTSuV1a WB analyses of conventional pig sera from a farm in Wisconsin. Purified 1a-ORF1 protein was used as the antigen. Sera tested negative for both TTSuV1a and TTSuV1b antibodies by WB were pooled and used as the negative control reference serum. Open arrowheads indicate the truncated ORF1 protein of expected size. Only the bands in green color were considered as positive. M: protein markers. FIG. 9(C) TTSuV1a or TTSuV1b ELISA results of the seven Virginia gnotobiotic pig serum samples, positive and negative control reference sera.

FIG. 10(A)-FIG. 10(C) illustrate serological and virological profiles of TTSuV1 infection in 138 sera of pigs from three different herds. FIG. 10(A) Distribution of TTSuV1 viremia, anti-TTSuV1a and anti-TTSuV1b IgG among 138 serum samples. Box-and-Whisker-plots of TTSuV1a FIG. 10(B) and TTSuV1b FIG. 10(C) serum antibody level by TTSuV1 viral DNA load. N: Negative. The detection limit of the TTSuV1 real-time qPCR was 4 log_{10} copies/ml in this study.

FIG. 11(A)-FIG. 11(C) illustrate a retrospective evaluation of TTSuV1 viral loads FIG. 11(A), antibody levels to the ORF1 protein of TTSuV1a FIG. 11(B) and TTSuV1b FIG. 11(C) in 10 pigs in group A from the time of their arrival at the research facility to two months after arrival.

FIG. 12(A)-FIG. 12(D) illustrate box plots showing the comparisons of anti-TTSuV1a FIG. 12(A) or anti-TTSuV1b FIG. 12(B) ORF1 antibody levels and TTSuV1 antibody FIG. 12(C) or PCV2 FIG. 12(D) viral loads between the PCVAD-affect ed and -unaffected pigs.

FIG. 13(A) and FIG. 13(B) illustrate a high correlation between anti-TTSuV1a and anti-TTSuV1b IgG in 138 serum samples. FIG. 13(A) Distribution of anti-TTSuV1a, -TTSuV1b and -TTSuV2 IgG. FIG. 13(B) Scatter plots showing a good linear relationship of antibody level between anti-TTSuV1a and anti-TTSuV1b (p<0.0001).

FIG. 14(A)-FIG. 14(C) illustrate reactivity of the three purified TTSuV ORF1 antigens: TTSuV1a FIG. 14(A), TTSuV1b FIG. 14(B) and TTSuV2 FIG. 14(C) with rabbit antisera against ORF1s of TTSuV1a, TTSuV1b or TTSuV2 or with pre-bled rabbit serum with 2-fold serial dilutions by ELISAs. Each antigen was tested in duplicate against each serum sample. Mean OD values are presented.

FIG. 15(A)-FIG. 15(C) illustrate Immunofluorescence assay (IFA) results of PCV1-free PK-15 cells transfected with the plasmids pTri-1aORF1 FIG. 15(A), pTri-1bORF1 FIG. 15(B) or pTri-2cORF1 FIG. 15(C) at 3 days post-transfection. pTri-1aORF1- or pTri-1bORF1-transfected cells were stained with the rabbit anti-TTSuV1a and -TTSuV1b ORF1 antisera, respectively, whereas pTri-2cORF1-transfected cells were stained with the rabbit anti-TTSuV2 ORF1 antisera. The Alexa Fluor 488-conjugated goat anti-rabbit IgG was used as the secondary Ab in IFA (all the left panels). Ab staining merged with nuclear staining using DAPI (blue) are shown in the right panels. Magnification=200×.

FIG. 16 illustrates comparison of hydrophilicity profiles of TTSuV1a (PITTV1a-VA strain) (SEQ ID NO:13) and TTSuV1b (PITTV1b-VA strain (SEQ ID NO:14) ORF1 and identification of two putative common antigenic domains in ORF1 of TTSuV1. The C-terminal region used for the expression of the truncated 1a- or 1b-ORF1 is indicated by a box. The corresponding alignment of amino acid (aa) sequences and aa positions of the two domains are also shown. Favorable mismatches of the aa were displayed as colons whereas neutral mismatches are depicted as periods.

FIG. 17(A)-FIG. 17(D) represent the schematic diagram of genomic structures, strategies for genomic cloning and assemblies of four prototype U.S. strains of porcine TTV virus group 1 (species 1) and group 2 (species 2) strains. FIG. 17(A) represents a schematic diagram of genomic structures and strategies for genomic cloning of porcine TTV virus group 1 strains. FIG. 17(B) represents a schematic diagram of genomic structures and strategies for genomic cloning of porcine TTV virus group 2 strains. FIG. 17(C) illustrates differentiation and assembly of full-length genomic sequences of PITTV1 strains PITTV1a-VA and PITTV1b-VA with PCR fragments Band C that were subsequently cloned. (PTTV1a-VA=SEQ ID NO: 9, Sd-1TVV31=SEQ ID NO: 53, PITTV1b-VA=SEQ ID NO: 10, TVT-1p=SEQ ID NO: 56). FIG. 17(D) genomic sequences of PITTV2 strains PITTV2b-VA and PITTV2c-VA with PCR fragments E and F that were subsequently cloned. (TVT2p=SEQ ID NO: 59, PITTV2b-VA=SEQ ID NO: 11, and PITTV2c-VA=SEQ ID NO: 12).

FIG. 18(A)-FIG. 18(C) represent an alignment of the full-length amino acid sequences of ORF1 among seven PITTV strains. (PTTV1a-VA=SEQ ID NO:13, Sd-1TVV31=SEQ ID NO:54, PITTV1b-VA=SEQ ID NO: 14, TVT-1p=SEQ ID NO: 57, TTV-2p=SEQ ID NO:60, PITTV2b-VA=SEQ ID NO:15, and PITTV2c-VA=SEQ ID NO: 16).

FIG. 19 represents an alignment of the full-length amino acid sequences of ORF2 among seven PITTV strains. (PTTV1a-VA=SEQ ID NO:17, Sd-1TVV31=SEQ ID NO:55, PITTV1b-VA=SEQ ID NO:18, TVT-1p=SEQ ID NO: 58, TTV-2p=SEQ ID NO:61, PITTV2b-VA=SEQ ID NO:19, and PITTV2c-VA=SEQ ID NO:20).

FIG. 20 represents an alignment of nucleotide sequences located at the N-terminal part of the putative ORF1 among seven PITTV strains. (PTTV1a-VA=SEQ ID NO:9, Sd-1TVV31=SEQ ID NO:53, PITTV1b-VA=SEQ ID NO:10, TVT-1p=SEQ ID NO:56, TTV-2p=SEQ ID NO:59, PITTV2b-VA=SEQ ID NO:11, and PITTV2c-VA=SEQ ID NO:12).

FIG. 21A-FIG. 21F represent the schematic diagrams of construction of full-length genomic DNA clones of porcine TTVs. FIG. 21A: pSC-PTTV1a (from the US PITTV isolate PITTV1a-VA; GenBank accession no. GU456383). FIG. 21B: pSC-PTTV1b (from the US PITTV isolate PITTV1b-VA; GenBank accession no. GU456384). FIG. 21C: pSC-PTTV2c (from the US PITTV isolate PITTV2c-VA; GenBank accession no. GU456386). FIG. 21D: pSC-PTTV2c-RR (tandem-dimerized genomes). FIG. 21E: TVT2-#471942-full (from the Germany PITTV isolate TVT2-#471942; a gift from Dr. Andreas Gallei, not generated by the applicants). FIG. 21F: pSC-2PTTV2c-RR (tandem-dimerized genomes; generated by the applicants based on the clone TVT2-#471942-full). The plasmid back-bone used for the cloning of (A)-(D), and (E) was the pSCB-amp/kan vector (indicated in black). Grey arrows indicated the PITTV genomic copies.

FIG. 22A-FIG. 22D represent the determination of the in vivo infectivity of the two porcine TVT2 DNA clones, pSC-2PTTV2b-RR and pSC-2PTTV2c-RR, in conventional pigs, respectively. FIG. 22A shows changes of viremia or virus titers (copies/ml) as determined by PITTV2-specific real-time PCR for pSC-2PTTV2b-RR. FIG. 22B shows changes of viremia or virus titers (copies/ml) as determined by PITTV2-specific real-time PCR for pSC-2PTTV2c-RR. FIG. 22C shows seroconversion to IgG anti-porcine TVT2 ORF1 antibodies in pigs infected with TVT2 DNA clone.
pSC-2PTTV2b-RR. FIG. 22D shows seroconversion to IgG anti-porcine TTV2 ORF1 antibodies in pigs infected with TTV2 DNA clone pSC-2PTTV2c-RR. Anti-PTTV2 antibody is plotted as the ELISA optical density (A405). The ELISA cutoff value, indicated by a dashed line in each panel, is 0.4.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the present invention, in one specific example, the aforementioned four novel porcine TTV subtypes are isolated from a single boar in Virginia.

In FIG. 17A and FIG. 17B respectively, both the PTTV1 and PTTV2 genomes are shown in bold and the sizes and directions of the four putative ORFs (ORF1, ORF2, ORF1/1 and ORF2/2) are indicated by arrows. The GC-rich regions are also shown. Dashed-line arcs A and D represent the regions used for detection of PTTV1 and PTTV2 from serum and semen samples by nested PCR, respectively. Dashed-line arcs B and C represent the two overlapping PCR fragments for genomic cloning of PTTV1 whereas dashed-line arcs E and F represent the two overlapping PCR fragments for genomic cloning of PTTV2. The locations of the primers used in the study (see Table I) are also shown in the corresponding positions.

One boar serum sample (SR#5) that was shown to be positive for both PTTV1 and PTTV2 in the first-round PCR, thus indicative of higher virus load, was used for subsequent full-length genomic cloning of PTTV. Surprisingly, initial attempts to utilize two primer sets (NG372/NG373 and NG384/NG385) of an inverse PCR (Okamoto et al., 2002, supra) designed for cloning of the first PTTV strain Sd-TTV31 to amplify the virus genomic DNA were not successful. No PCR product was obtained after several trials. Based upon the initial sequence of the region A of PTTV1 and the region D of PTTV2, two new pairs of primers (TTV1-IF (SEQ ID NO:1)/TTV1-2340R (SEQ ID NO:2) and TTV1-2311F (SEQ ID NO:3)/TTV1-IR (SEQ ID NO:4)) were subsequently designed to amplify regions B and C spanning the assumed PTTV1 genome, and two additional pairs of primers (TTV2-IF (SEQ ID NO:5)/TTV2-2316R (SEQ ID NO:6) and TTV2-GCF (SEQ ID NO:7)/TTV2-IR (SEQ ID NO:8)) to amplify regions E and F spanning the assumed PTTV2 genome, respectively (FIG. 17A-17D and Table I). Primers TTV1-2340R (SEQ ID NO:2) and TTV1-2311F (SEQ ID NO:3) were deduced from a common sequence in PTTV1 stains Sd-TTV31 (Okamoto et al., 2002, supra) and TTV-1p (Niel et al., 2005) that is absent in PTTV2 strain TTV-2p (Niel et al., 2005, supra), whereas primers TTV2-2316R (SEQ ID NO:6) and TTV2-GCF (SEQ ID NO:7) were deduced from a sequence in PTTV1 stains Sd-TTV31 (Okamoto et al., 2002, supra) and TTV-1p (Niel et al., 2005) that is absent in the two PTTV1 strains. The resulting four different PCR products with expected sizes were each inserted into a blunt-end cloning vector, and the resulting recombinant plasmids were transformed into *Escherichia coli*. Eight to fifteen positive (with white color) bacterial clones for each construct representing fragments B, C, E and F were identified and subsequently sequenced.

<table>
<thead>
<tr>
<th>Primer ID</th>
<th>Sequence (5’ to 3’)</th>
<th>Used for:</th>
</tr>
</thead>
<tbody>
<tr>
<td>TTV1-mF</td>
<td>TACACTTCCGCGGTTCAGGAGGCT</td>
<td>Detection of porcine TTV1</td>
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<tr>
<td>(SEQ ID NO: 45)</td>
<td></td>
<td></td>
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<tr>
<td>TTV1-mR</td>
<td>ACTCAGCATTCCGAACTCAGCA</td>
<td>Detection of porcine TTV1</td>
</tr>
<tr>
<td>(SEQ ID NO: 46)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TTV1-nF</td>
<td>CAATTTGGCTCGCTTCGCTCGC</td>
<td>Detection of porcine TTV1</td>
</tr>
<tr>
<td>(SEQ ID NO: 47)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TTV1-nR</td>
<td>TACTTATATTGCTTTCGCTGCGAC</td>
<td>Detection of porcine TTV1</td>
</tr>
<tr>
<td>(SEQ ID NO: 48)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TTV2-mF</td>
<td>AGTTACACATAACACACACACAAACCC</td>
<td>Detection of porcine TTV2</td>
</tr>
<tr>
<td>(SEQ ID NO: 49)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TTV2-mR</td>
<td>ATTACCGCCTGCGCGATAGGCA</td>
<td>Detection of porcine TTV2</td>
</tr>
<tr>
<td>(SEQ ID NO: 50)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TTV2-nF</td>
<td>CCAAACCAACAGAAGAAGCTGG</td>
<td>Detection of porcine TTV2</td>
</tr>
<tr>
<td>(SEQ ID NO: 51)</td>
<td></td>
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<tr>
<td>TTV2-nR</td>
<td>CCTGACTCCGCTCTCAGGAG</td>
<td>Detection of porcine TTV2</td>
</tr>
<tr>
<td>(SEQ ID NO: 52)</td>
<td></td>
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<tr>
<td>TTV1-IF</td>
<td>CATAGGCGTGATACACATCGAGGCTT</td>
<td>Genomic cloning (fragment B)</td>
</tr>
<tr>
<td>(SEQ ID NO: 1)</td>
<td></td>
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</tr>
<tr>
<td>TTV1-2340R</td>
<td>GGTCATCAGACGATCCATCTCCCTCAG</td>
<td>Genomic cloning (fragment B)</td>
</tr>
<tr>
<td>(SEQ ID NO: 2)</td>
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</tr>
<tr>
<td>TTV1-2311F</td>
<td>TTCTGAGGAGATAGATCGTCGAGA</td>
<td>Genomic cloning (fragment C)</td>
</tr>
<tr>
<td>(SEQ ID NO: 3)</td>
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<tr>
<td>TTV1-IR</td>
<td>TGGAGCTCCGACGATACTCAGGACT</td>
<td>Genomic cloning (fragment C)</td>
</tr>
<tr>
<td>(SEQ ID NO: 4)</td>
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</table>
Unexpectedly, two groups of sequence data from each construct were identified, indicating that there exist two types of PTTVs in genogroup 1 and genogroup 2 from the same pig. In order to differentiate and assemble the four PTTV strains, sequence comparisons were performed together with the three known PTTV strains, Sd-TTV31, TTV-1p and TTV-2p (FIGS. 17C and 17D).

FIG. 17C illustrates differentiation and assembly of full-length genomic sequences of PTTV1 strains PTTV1a-VA and PTTV1b-VA with PCR fragments B and C that were subsequently cloned. The initiation codons of ORF1 and ORF2 in the fragment B as well as the termination codons of ORF1 in the fragment C are marked by “*” or “**”. The corresponding sequences of two known PTTV1 strains, Sd-TTV31 and TTV-1p, are also shown. Conserved sequences are shaded, and dashes indicate nucleotide deletions.

For PTTV1, the initiation codon ATG and the termination codon TGA of the putative ORF1 were located in fragments B and C, respectively (FIG. 17C). The positions of the codons were differed in two PTTV1 groups, the first one identical to Sd-TTV31 and the second one identical to TTV-1p (FIG. 17C). In addition, the ORF2 initiation codons in the two groups were also located at different positions consistent with that of ORF1. Moreover, phylogenetic analyses using four different sequences of the region B (two from the sequencing data and two from strains Sd-TTV31 and TTV-1p) and four different sequences of the region C supported that the first sequence was clustered with Sd-TTV31 and the second was clustered with TTV-1p (data not shown). Therefore, we were able to differentiate and assemble two groups of sequence data from both fragments B and C into two full-length PTTV1 genomes that were designated as strains PTTV1a-VA (SEQ ID NO:9) and PTTV1b-VA (SEQ ID NO:10), respectively (FIG. 17C).

FIG. 17D illustrates differentiation and assembly of full-length genomic sequences of PTTV2 strains PTTV2a-VA and PTTV2c-VA with PCR fragments E and F that were subsequently cloned. The corresponding sequence of TTV-2p strain is included and the conserved sequences are shaded. Dashes indicate nucleotide deletions. The unique nucleotides within the overlapping region (boxed with dashed-line) for each strain (a continuous “AG” nucleotides for PTTV2b-VA (SEQ ID NO:11) and two single “A” and “G” nucleotides for PTTV2c-VA (SEQ ID NO:12)) are shown, respectively.

Differentiation of the two PTTV2 strains was easier. A unique continuous “AG” nucleotides located in the overlapping region of two PCR fragments was shared by two groups of sequence data from fragments E and F, respectively (FIG. 17D). The assembled full-length genomic sequence represented a PTTV2 strain and was designated as PTTV2b-VA (SEQ ID NO:11). Similarly, the complete genomic sequence of a second strain designated as PTTV2c-VA (SEQ ID NO:12) was assembled based upon two unique single “A” and “G” nucleotides shared in the overlapping region by another set of sequence data from fragments E and F, respectively (FIG. 17D). Phylogenetic analyses using four sequences from fragments E and F together with the two corresponding sequences from TTV-2p also supported this assignment (data not shown).

The present invention provides four isolated porcine TTV virus genotypes or subtypes that are associated with viral infections in pigs. This invention includes, but is not limited to, porcine TTV virus genotypes or subtypes PTTV1a-VA, PTTV1b-VA, PTTV2a-VA, and PTTV2c-VA, the virus genotypes or subtypes which have nucleotide sequences set forth in SEQ ID NO:9 (PTTV1a-VA), SEQ ID NO:10 (PTTV1b-VA), SEQ ID NO:11 (PTTV2a-VA), and SEQ ID NO:12 (PTTV2c-VA), their functional equivalent or complementary strand. It will be understood that the specific nucleotide sequence derived from any porcine TTV will have slight variations that exist naturally between individual viruses. These variations in sequences may be seen in deletions, substitutions, insertions and the like.

The proposed genomic structure for each of the four PTTV strains was analyzed in detail and summarized in Table 2, together with the three known PTTV strains, Sd-TTV31, TTV-1p and TTV-2p. All the four U.S. strains of PTTV have a similar genomic size of 2,878 by (PTTV1a-VA SEQ ID NO:9), 2,875 by (PTTV1b-VA SEQ ID NO:10), 2,870 by (PTTV2b-VA SEQ ID NO:11), and 2,803 by (PTTV2c-VA SEQ ID NO:12), respectively. Both PTTV1a-VA (SEQ ID NO:9) and Sd-TTV31 have the same genomic length. The published sequences of the strains TTV-1p and TTV-2p all have many undetermined nucleotides in the GC-rich region of the UTR. After artificial filling of these nucleotides with the consensus sequences corresponding to PTTV1 and PTTV2, it was shown that the TTV-1p is more closely-related to PTTV1b-VA (SEQ ID NO:10), and that TTV-2-p is more closely-related to PTTV2b-VA (SEQ ID NO:11) in genomic length, respectively (data not shown).

The assembled genomic sequences of porcine TTV virus genotypes or subtypes PTTV1a-VA (SEQ ID NO:9), PTTV1b-VA (SEQ ID NO:10), PTTV2a-VA (SEQ ID NO:11), and PTTV2c-VA(SEQ ID NO:12) are submitted to Genbank® (Nucleic Acids Research, 2008 January; 36(Da-
Two recent studies have identified the transcribed viral mRNAs and the expression of at least six viral proteins during human TTV replication (Mueller et al., 2008, supra; Qiu et al., 2005, supra), which is more than the predicted number of ORFs encoded by human TTV (Okamoto, H., et al. (2000b). TT virus mRNAs detected in the bone marrow cells from an infected individual. Biochem Biophys Res Commun 279(2), 700-703), therefore we included the new human TTV genomic information for comparison with the PTTV sequences. The 5'-endsof the mRNA transcripts of human TTV strain P/1C1 were mapped to an “A” that is 25 nt downstream of the TATA-box (Mueller et al., 2008, supra). This starting point, its adjacent sequence (CGAATG-GCTGAGTTTATGCCGC (SEQ ID NO:39); the starting point was underlined) and the distance to the upstream TATA-box (24 nt; Table 2) are very conserved in all seven PTTV strains, suggesting that PTTV and human TTV may utilize a common 5'-end of mRNA for translation.

Five additional completely-conserved regions were identified in the vicinity of the TATA-box among all seven PTTV strains. Two regions of 11 nt each (AGTCCTCATTT (SEQ ID NO:40) and AACCAATCAGA (SEQ ID NO:41)) are located in the upstream of the TATA-box, whereas the remaining three regions (CTGGGCGGGTGCCGGAG of 17 nt (SEQ ID NO:42); CGGAGTCAAGGGGC of 14 nt (SEQ ID NO:43); TATCGGGCAGG of 11 nt (SEQ ID NO:44)) are located between the proposed 5'-end of mRNA and the initiation codon of ORF2. These conserved PTTV-specific sequences may contain the common elements regulating the viral gene expression.

Previously, three ORFs (ORFs 1-3) were proposed in the genome of the three known PTTV strains, respectively (Niel et al., 2005, supra; Okamoto et al., 2002, supra). The four prototype U.S. strains of PTTV identified in this study possess this structure. The corresponding ORF3 in human TTV has been renamed as ORF2/2 since it initiates at the same ATG in ORF2 and remains in the same ORF (extending ORF2) after the splicing (FIG. 17A-17B) (Mueller et al., 2008, supra; Qiu et al., 2005, supra). We follow the nomenclature of human TTV for revising PTTV classification in this study. Human TTV ORF1/1 is a newly identified viral protein that is encoded by two exons in ORF1 (Qiu et al., 2005, supra). ORF1/1 shares the identical N- and C-terminal part with ORF1. The PTTV ORF1/1 counterpart was readily identified in all seven PTTV strains (FIG. 17A-17B and Table 2).

The ORF1 and ORF2 are encoded by a ~2.8 kb viral mRNA whereas the ORF1/1 and ORF2/2 are encoded by a spliced viral mRNA with ~about.1.2 kb in human TTV (Mueller et al., 2008, supra; Qiu et al., 2005, supra). Since these four ORFs were also deduced in PTTV genomes, and since the sequences and positions of the putative splice
donor and acceptor sites in the seven PTTV strains are very conserved (Table 2), it is speculated that porcine TTV probably also encodes the two corresponding mRNAs. Most of the human TTV strains share a genetics similarity with the CAV, encoding a TTV apoptosis-inducing protein (TAIP) in which its CAV counterpart was named apoptin (de Smit, M. H., and Noteborn, M. H. (2009). Apoptosis-inducing proteins in chicken anemia virus and TT virus. Curr Top Microbiol Immunol 331, 131-49). The ORF of TAIP is embedded within the ORF2. However, the corresponding TAIP does not exist in porcine TTV. A recent study showed that the expression of apoptin or TAIP was required for CAV replication in cultured cells (Prasetyo, A. A., et al. (2009). Replication of chicken anemia virus (CAV) requires apoptin and is complemented by VP3 of human torque teno virus (TTV). Virology 385(1), 85-92).

Pairwise sequence comparisons (PASC) is a useful method that plots the frequency distribution of pairwise nucleotide sequence identity percentages from all available genomic sequence of viruses in the same family (Bao, Y., Kapustín, Y., and Tatusova, T. (2008). Virus Classification by Pairwise Sequence Comparison (PASC). In “Encyclopedia of Virology, 5 vols.” (B. W. J. Mahy, and M. H. V. Van Regenmortel, Eds.), Vol. 5, pp. 342-8. Elsevier, Oxford). The different peaks generated by the PASC program usually represent groups of virus genera, species, types, subtypes and strains. In this study, we performed PASC analyses of TTV using 121 full-length genomic sequences of human and animal TTV-related strains available in GenBank database. Assuming that TTV members are classified into a separate family, Anelloviridae, the two major peaks, at 36-55% and 55-67% nucleotide sequence identities, represent groups of genera and species, respectively. Accordingly, a TTV type is defined as a group of TTV having 67-85% nucleotide sequence identity whereas a TTV subtype may be defined as a group of TTV sequences sharing 85-95% nucleotide sequence identity. TTV strains sharing more than 95% nucleotide sequence identity may be further classified into variants. A similar classification has been proposed using sequences of 103 TTV isolates by Jelčić et al. (Jelčić, I., et al. (2004). Isolation of multiple TT virus genotypes from spleen biopsy tissue from a Hodgkin’s disease patient: genome reorganization and diversity in the hypervariable region. J Virol 78(14), 7498-507).

This proposed criteria of TTV classification were applied to phylogenetic analyses of the genomic sequences of the 4 prototype U.S. strains of PTTV and the 3 other known PTTV strains. Pairwise comparison of full-length nucleotide sequences among these strains showed that the four PTTV1 strains have 54.0-56.4% nucleotide sequence identity compared to the three PTTV2 strains (Table 3). Therefore, the previously designated “genogroup” of PTTV in the literature will probably be more appropriate to designate as “species”, and PTTV1 and PTTV2 probably should represent porcine TTV species 1 and species 2, respectively. PTTV species 1 consists of two types of viruses designated as type 1a (including Sd-TTV31 and PTTV1a-VA (SEQ ID NO:9)) and type 1b (including TTV-1p and PTTV1b-VA (SEQ ID NO:10)), respectively, since the nucleotide sequence identity between these two types of viruses is between 69.8-70.7% (Table 3). Sd-TTV31 and PTTV1a-VA (SEQ ID NO:9) are recognized as variant strains of the same species due to their higher sequence identity (95.1%). However, the two type 1b strains, TTV-1p and PTTV1b-VA (SEQ ID NO:10), may belong to two different subtypes (nucleotide sequence identity: 86.4%). For PTTV species 2, three strains are likely to be classified into separate subtypes (TTV-2p for subtype 2a, PTTV2b-VA (SEQ ID NO:11) for subtype 2b, and PTTV2c-VA (SEQ ID NO:12) for subtype 2c, respectively) based upon their 86.5-90.9% nucleotide sequence identity. This proposed new classification system for PTTV was clearly evident in the phylogenetic tree. Phylogenetic trees constructed based upon the deduced amino acid sequences of ORF1, ORF1/1, ORF2 and ORF2/2 of PTTV were also consistent with this proposed classification.

### Table 3

| Pairwise sequence comparison of the full-length genomic sequence of the seven porcine TTV strains |
|-------------------------------------------------|-----------------|-----------------|-----------------|-----------------|
| Porcine TTV species 1                             | Porcine TTV species 2                             |
| Type 1a                                        | Type 1b                                        | Subtype 2a     | Subtype 2b     | Subtype 2c     |
| PTTV1a-VA                                       | Sd-TTV31                                       | TTV-1p         | TTV-2p         | PTTV2b-VA      | PTTV2c-VA      |
|                                                   |                                               |                |                |                |
| Type 1b                                        |                                               |                |                |                |
| PTTV1a-VA                                       | —                                             | 95.1           | 70.5           | 69.8           |
| Sd-TTV31                                       | —                                             | 70.7           | 70.1           |                |
| Type 1b                                        |                                               |                |                |                |
| PTTV1b-VA                                       | —                                             | 86.4           | 54.0           | 54.7           |
| TTV-1p                                         | —                                             | 55.2           | 54.7           | 55.4           |
| Subtype 2a                                     |                                               |                |                |                |
| TTV-2p                                         | —                                             | 86.5           | 86.8           |                |
| Subtype 2b                                     |                                               |                |                |                |
| PTTV2b-VA                                      | —                                             |                |                | 90.9           |
| Subtype 2c                                     |                                               |                |                |                |
| PTTV2c-VA                                      | —                                             |                |                |                |

The data were generated by using the PASC program, and the values indicate % nucleotide sequence identities.

Unique mutations and deletions and/or insertions are scattered throughout the genomes between PTTV species, types and subtypes. For example, the location of ORF1 initiation and termination codons and the ORF2 initiation codons between PTTV type 1a and 1b, which was shown in
FIG. 17C as mentioned above, are different. The two PTTV1b strains also have a 2-codon deletion after the ORF2 initiation compared to PTTV1a (FIG. 17C).

Remarkably, both TTV-2p and PTTV2b-VA have a large 52-nucleotide deletion, which is 39 nt upstream of the first 11-nucleotide conserved sequence (AGTCCCTCATT; SEQ ID NO:40) in the UTR, compared to PTTV2c-VA. Due to this deletion, the genomic size of PTTV2b-VA (probably TTV-2p as well) was significantly smaller than that of PTTV2c-VA (Table 2).

A number of “subviral” human TTV clones have been isolated from serum samples that are considered as full-length TTV genomes since the ORFs in a majority of these subviral molecules usually remain intact (de Villiers et al., 2000; Leppik et al., 2007). They have variable lengths in the UTR that are completely or partially deleted. The situation of TTV-2p and PTTV2b-VA appears to resemble that of the human TTV subviral molecules, implying that subtypes PTTV2a and PTTV2b-VA might be the subviral molecules derived from subtype PTTV2c. Of note, the 3′-terminal sequence of a nested-PCR primer TTV2-nt (Table 1) that is commonly used for detection of the PTTV2 from field samples by other groups (Ellis et al., 2008, supra; Kekarainen et al., 2007, supra; Kekarainen et al., 2006, supra; Krakowka et al., 2008, supra) is located at both sides of the deletion. Therefore, the current nested-PCR assay for PTTV2 detection is likely not sufficient to identify the genetically diverse strains of PTTV2c subtype.

The source of the isolated virus strain is serum, fecal, saliva, semen and tissue samples of pigs having the porcine TTV viral infection. However, it is contemplated that recombinant DNA technology can be used to duplicate and chemically synthesize the nucleotide sequence. Therefore, the scope of the present invention encompasses the isolated polynucleotide which comprises, but is not limited to, a nucleotide sequence set forth in SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:12, or its complementary strand; a polynucleotide which hybridizes to and binds to at least 67% complementary to the nucleotide sequence set forth in SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:12, preferably 85% complementary, or more preferably 95% complementary; or an immunogenic fragment selected from the group consisting of an amino acid sequence of ORF1 protein set forth in SEQ ID NO:13 (PTTV1a-VA), SEQ ID NO:14 (PTTV1b-VA), SEQ ID NO:15 (PTTV2b-VA), SEQ ID NO:16 (PTTV2c-VA), an amino acid sequence of ORF2 protein set forth in SEQ ID NO:17 (PTTV1a-VA), SEQ ID NO:18 (PTTV1b-VA), SEQ ID NO:19 (PTTV2b-VA), and SEQ ID NO:20 (PTTV2c-VA), an amino acid sequence of ORF1 protein set forth in SEQ ID NO:21 (PTTV1a-VA), SEQ ID NO:22 (PTTV1b-VA), SEQ ID NO:23 (PTTV2b-VA), SEQ ID NO:24 (PTTV2c-VA), an amino acid sequence of ORF2 protein set forth in SEQ ID NO:25 (PTTV1a-VA), SEQ ID NO:26 (PTTV1b-VA), SEQ ID NO:27 (PTTV2b-VA), SEQ ID NO:28 (PTTV2c-VA). The immunogenic or antigenic coding regions or fragments can be determined by techniques known in the art and then used to make monoclonal or polyclonal antibodies for immunoreactivity screening or other diagnostic purposes. The invention further encompasses the purified, immunogenic protein encoded by the isolated polynucleotides. Desirably, the protein may be an isolated or recombinant ORF1 protein or an ORF2 protein of at least one of the above isolated porcine TTV subtypes, more desirably ORF1 protein.

The ORF1 of porcine TTV is believed to encode a structural and replication-associated protein (Maggi, F. and Bendinelli, M. (2009). Immunobiology of the Torque teno viruses and other anelloviruses. Curr Top Microbiol Immunol 331, 65-90). The ORF1-encoding products of seven PTV strains have 624-635 aa in length and possess a high number of arginine residues at the N-terminals that are thought to have the DNA-binding activity (FIG. 18A-18C).

In FIG. 18A-C, conserved sequences are shaded. Dashes indicate amino acid deletions. The RCR motifs are boxed with solid lines. Three HVRs (PTTV1-HVRs 1, 2 and 3) of PTTV1 strains and two HVRs (PTTV2-HVRs 1 and 2) of PTTV2 strains are boxed with dashed lines. The connection boundaries of ORF1/1 are indicated by arrows. The predicted rolling-circle replication (RCR) motifs (Ilyina, T. V., and Koonin, E. V. (1992). Conserved sequence motifs in the initiator proteins for rolling circle DNA replication encoded by diverse replisomes from eubacteria, eucaryotes and archaea-bacteria. Nucleic Acids Res 20(13), 3279-85) are presented at different positions in different PTTV types and subtypes that may be type- or subtype-specific. RCR motif-III (YxxK) is conserved in the PTTV type 1a (aa position 14-17 of PTTV1a-VA SEQ ID NO:13) and type 1b strains (aa position 379-382 of PTTV1b-VA SEQ ID NO:14), respectively, whereas the same conserved motif identified in all three PTTV2 strains is located at aa position 482-485 of PTTV2b-VA SEQ ID NO:15 (FIG. 4). Both PTTV2b-VA SEQ ID NO:15 and PTTV2c-VA SEQ ID NO:16 also have a conserved RCR motif-II (HxQ) at aa position 331-333 of PTTV2b-VA that is absence in TTV-2p (FIG. 18A-C).

The ORF1 proteins of PTTV strains between species 1 and species 2 share very low aa sequence identity with only 22.4 to 25.8%, which makes it difficult to identify significantly conserved aa sequences between the two species (FIG. 18A-C). In PTTV species 1, the aa identity of ORF1 between type 1a and 1b strains are 50.3-52.7%. Three major hypervariable regions (HVR), PTTV1-HVRs 1 to 3, with a relatively high number of aa substitutions, were identified among the four PTTV1 strains, whereas two HVRs (PTTV2-HVRs 1 and 2) were observed among the three PTTV2 strains (FIG. 18A-C). The three PTTV2 strains have an approximately 20-aa deletion in the corresponding PTTV1-HVR1 region. Moreover, the two HVRs of PTTV2 are within the corresponding PTTV1-HVR3 region (FIG. 18A-C). These HVRs are located only in the ORF1 but not in the truncated ORF1/1. They likely play a role in evading the host immune surveillance and helping PTTV to establish a persistent infection, as suggested by studies of human TTV.

The aa sequences of ORF2 differed considerably between the four PTTV1 (PTTV1a-VA SEQ ID NO:17; PTTV1b-VA SEQ ID NO:18) and three PTTV2 (PTTV2b-VA SEQ ID NO:19; PTTV2c-VA SEQ ID NO:20) strains (FIG. 19). However, they share a conserved protein-tyrosine phosphatase (PTPase)-like motif (WxHx(Cx)xH) at the N-terminus (FIG. 18A-C). This motif is also conserved among all human TTV, TTMV and TMMDV strains as well as CAV. The TTMV or CAV ORF2 protein also exhibited a serine/threonine phosphatase (S/T Pphase) activity (Peters, M. A., Jackson, D. C., Crabb, B. S., and Browning, G. F. (2002). Chicken anemia virus VP2 is a novel dual specificity protein phosphatase. J Biol Chem 277(42), 39566-73). The dual specificity of the ORF2 protein is thought to regulate host gene transcription, signal transduction and cytokine responses during viral replication. Recently, mutagenesis analyses of two conserved basic aa residues before the last histidine residue of the motif in CAV revealed that the two residues affect virus replication, cytopathology in vitro and attenuation in vivo (Peters, M. A., Crabb, B. S., Washington, E. A., and Browning, G. F. (2006). Site-directed mutagenesis
of the VP2 gene of Chicken anemia virus affects virus replication, cytopathology and host-cell MHC class I expression. J Gen Virol 87(Pt 4), 823-31; Peters, M. A., Crabb, B. S., Tivendale, K. A., and Browning, G. F. (2007). Attenuation of chicken anemia virus by site-directed mutagenesis of VP2. J Gen Virol 88(Pt 8), 2168-75. The two basic aa residues ("KK") are conserved in the three PTTV2 strains. However, only the first basic residue ("R") is retained in the two PTTV1a strains whereas both basic residues are substituted in the PTTV1b strains (FIG. 19). In FIG. 19, dashes indicate amino acid deletions.

In summary, the present invention has determined the full-length genomic sequences of four porcine TTV strains representing different genotypes or subtypes in a serum sample from a single boar in Virginia. The findings from this study clearly indicates that, similar to human TTV, multiple PTTV infections with distinct genotypes or subtypes exist and probably are common in pigs. We have also provided new information regarding the genomic organization, the degree of variability and the characteristics of conserved nucleotide and amino acid motifs of PTTV, which will improve the current PCR detection assay, aid in developing reagents for serological diagnostics and help initiate the structural and functional study of PTTV. A new classification of PTTV is also proposed in this study based upon the phylogenetic and genetic analyses of the genomic sequences of seven known PTTV strains.

The present invention also provides methods for diagnostics of porcine TTV infection by detecting viral DNA in samples of porcine TTV infected pigs or other mammals. One preferred embodiment of the present invention involves methods for detecting porcine TTV nucleic acid sequences in a porcine or other mammalian species using oligonucleotide primers for polymerase chain reaction (PCR) to further aid in the diagnosis of viral infection or disease. The diagnostic tests, which are useful in detecting the presence or absence of the porcine TTV viral nucleic acid sequence in the porcine or other mammalian species, comprise isolating viral DNA from samples of porcine TTV infected pigs, or pigs suspected of infection of TTV, and performing SYBR green real-time quantitative PCR using PTTV1-specific (SEQ ID NO:29) and PTTV2-specific (SEQ ID NO:31) primers or PTTV2-specific primers TTV2F4 (SEQ ID NO:31) and TTV2R4 (SEQ ID NO:32) were designed based upon two conserved genomic regions immediately before the putative ORF2 across six PTTV1 genomes, whereas PTTV2-specific primers TTV2F4 (SEQ ID NO:31) and TTV2R4 (SEQ ID NO:32) were designed based upon two conserved genomic regions immediately after the putative ORF2/ across four PTTV2 genomes (Table 4). Primers showed no potentials for self- and cross-dimerization. The expected amplicon sizes were a 118-bp fragment from the PTTV1 primers corresponding to the PTTV1b-VA genome and a 200-bp fragment from the PTTV2 primers corresponding to the PTTV2c-VA genome, respectively.

### TABLE 4

<table>
<thead>
<tr>
<th>Primer ID</th>
<th>Sequence (5' to 3')</th>
<th>Purpose</th>
</tr>
</thead>
<tbody>
<tr>
<td>TTV1F</td>
<td>TCCGAATGGCGTGAATTTAGC</td>
<td>PTTV1-specific real-time PCR</td>
</tr>
<tr>
<td>SEQ ID NO: 29</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TTV1R</td>
<td>TCCGAATGGCGTGAATTTAGC</td>
<td>PTTV1-specific real-time PCR</td>
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<tr>
<td>SEQ ID NO: 30</td>
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<td></td>
</tr>
<tr>
<td>TTV2F4</td>
<td>GUTGATGAAGAGAGAGATGAA</td>
<td>PTTV2-specific real-time PCR</td>
</tr>
<tr>
<td>SEQ ID NO: 31</td>
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<td></td>
</tr>
<tr>
<td>TTV2R4</td>
<td>AATGATTGGACACAGGAG</td>
<td>PTTV2-specific real-time PCR</td>
</tr>
<tr>
<td>SEQ ID NO: 32</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Plab-mF</td>
<td>TACGGGCTACGGCTCAGCT</td>
<td>Duplex nested PCR</td>
</tr>
<tr>
<td>SEQ ID NO: 33</td>
<td></td>
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<tr>
<td>Plab-nF</td>
<td>TACGGGCTACGGCTCAGCT</td>
<td>Duplex nested PCR</td>
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<tr>
<td>SEQ ID NO: 34</td>
<td></td>
<td></td>
</tr>
<tr>
<td>P1a-nF</td>
<td>CCTACATGAGAAGAGAGAG</td>
<td>Duplex nested PCR</td>
</tr>
<tr>
<td>SEQ ID NO: 35</td>
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Oligonucleotide primers used for real-time PCR and duplex nested PCR detections of porcine TTVs.

In another embodiment of the present invention, the diagnostic method may employ duplex nested PCR. The method comprises isolating viral DNA from samples of porcine TTV infected pigs or pigs suspected of infection of TTV, performing a first round of PCR using one pair of primers Plab-mF (SEQ ID NO:33)/Plab-mR (SEQ ID NO:34), and performing a second round of PCR using a mixture of two pairs of primers, P1a-nF (SEQ ID NO:35)/P1a-nR (SEQ ID NO:36) for detection of PTTV1a, and P1b-nF (SEQ ID NO:37)/P1b-nR (SEQ ID NO:38) for detection of PTTV1b, and visualizing the PCR products.

The above diagnostics methods maybe optimized by one skilled in the art according to well known methods in the art. Accordingly, an embodiment of the present invention develops two novel singleplex SYBR green real-time PCR assays to quantify the viral loads of two porcine TTV species, respectively; PTTV1- and PTTV2-specific primers were designed to target the extremely conserved regions across six PTTV1 and four PTTV2 full-length genomes available to date, respectively. Another embodiment of the present invention combines the two singleplex assays into a duplex real-time PCR assay followed by MCA of the viral amplicons that can be identified by their distinct melting temperatures for simultaneous detection of the two porcine TTV species, PTTV1a and PTTV1b. In a third embodiment, a duplex nested PCR assay for simultaneous amplification of the viral DNAs from two types of PTTV1 in the first round PCR and differential detection of types 1a and 1b in the second round PCR was developed for the identification of two types of porcine TTV species, PTTV1a and PTTV1b, in a single sample. These assays represent simple and practical tools for diagnosis of species- or type-specific porcine TTVs.

Potential primers sequences were identified by multiple sequence alignments of 10 available porcine TTV full-genome sequences. PTTV1-specific primers TTV1F (SEQ ID NO:29) and TTV1R (SEQ ID NO:30) were designed based upon two conserved genomic regions immediately before the putative ORF2 across six PTTV1 genomes, whereas PTTV2-specific primers TTV2F4 (SEQ ID NO:31) and TTV2R4 (SEQ ID NO:32) were designed based upon two conserved genomic regions immediately after the putative ORF2/ across four PTTV2 genomes (Table 4). Primers showed no potentials for self- and cross-dimerization. The expected amplicon sizes were a 118-bp fragment from the PTTV1 primers corresponding to the PTTV1b-VA genome and a 200-bp fragment from the PTTV2 primers corresponding to the PTTV2c-VA genome, respectively.
TABLE 4 -continued

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<th>Sequence (5' to 3')</th>
<th>Purpose</th>
</tr>
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<tr>
<td>P1a-nR</td>
<td>CCAGGCTCTCCAGGCTG</td>
<td>Duplex nested PCR</td>
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<tr>
<td>SEQ ID NO: 36</td>
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</tr>
<tr>
<td>P1b-nF</td>
<td>AAGCCTACCAAGGGCTG</td>
<td>Duplex nested PCR</td>
</tr>
<tr>
<td>SEQ ID NO: 37</td>
<td></td>
<td></td>
</tr>
<tr>
<td>P1b-nR</td>
<td>GCGTCT(G/T)GTAGCGGTAGT</td>
<td>Duplex nested PCR</td>
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</table>

According to one specific embodiment of the present invention, SYBR green simplex real-time PCR using PTTV1- and PTTV2-specific primers can be used specifically to detect porcine TTV1 and TTV2 DNA, respectively. For PTTV1, a standard curve was established over a range of target DNA concentrations per 25 μl. The linear range was shown to span 4.4x10^4 to 4.4x10^7 copies. The minimum detection limit (44 copies) corresponded to a threshold cycle (Ct) of 37.57. For PTTV2, standard curve was also generated and used to detect DNA concentration ranging from 8.6x10^5 to 8.6x10^7 copies per 25 μl reaction. The corresponding Ct of minimum detection limit (8.6 copies) was 36.53.

According to another specific embodiment of the present invention, SYBR green duplex real-time PCR is utilized for the simultaneous detection of porcine TTV1 and TTV2 DNA. The 7-degree difference of Tm value between PTTV1 (87.0°C) and PTTV2 (80.0°C) made it feasible to distinguish them from one another by the MCA. Therefore, two singleplex assays can be coupled into a duplex real-time PCR assay for the simultaneous detection of PTTV1 and PTTV2. A positive sample was one that had a symmetrical melt peak within the known Tm for that product. This new assay was first validated by using a 10-fold dilution of PTTV1 and PTTV2 standards mixture. The non-template negative control using sterile water as the template showed a non-specific amplification caused by cross-dimerization between the PTTV1 and PTTV2 primers not seen in the singleplex assays. This produced a distinct melt peak between 72.0°C and 76.0°C.

The inventors of the present invention demonstrated the existence of two distinct genotypes, tentatively named PTTV1a and PTTV1b, in porcine TTV species 1. To further determine whether the co-infection of PTTV1a and PTTV1b is common in pigs, a novel duplex nested PCR assay to quickly distinguish between the two was developed. Alignment of porcine TTV genomic DNA sequences identified a conserved genomic region located at the N-terminal part of the putative ORF1 encoding the viral capsid protein (FIG. 20). This region also contains the entire ORF2 and the partial UTR in the upstream. Primers P1ab-nf (SEQ ID NO:33)/P1ab-nr (SEQ ID NO:34) were designed to simultaneously amplify both PTTV1a and PTTV1b DNAs in the first-round PCR. A mixture of PTTV1a-specific primers P1a-nF (SEQ ID NO:35)/P1a-nR (SEQ ID NO:36) and PTTV1b-specific primers P1b-nF (SEQ ID NO:37)/P1b-nR (SEQ ID NO:38) was used to differentially amplify each genotype in the second-round PCR. The final PCR products of PTTV1a and PTTV1b were 162 by and 96 by in sizes, respectively, which could be easily distinguished by gel electrophoresis on a 1% agarose gel stained with ethidium bromide. This assay was not expected to detect PTTV2 DNA due to the specificity of primers (FIG. 20). In FIG. 20, conserved sequences were indicated by dots and shaded. Dashes indicated nucleotide deletions. The locations and directions of three pairs of primers used for duplex nested PCR were marked by arrows.

In one example, the 20 serum samples from adult boars that were subjected to the duplex nested PCR assay were all found to be positive for both PTTV1a and PTTV1b, as determined by visualizing two bands of the expected sizes and subsequent sequencing confirmation of PCR products (data not shown). No PCR products were amplified in the 19 semen samples, which was consistent with the results of PTTV1 conventional nested PCR and real-time PCR assays described above.

Infection of pigs with the two species of porcine TTV has been found back to 1985 in Spanish pig farms according to a retrospective investigation (Segales et al., 2009, supra). However, whether porcine TTVs are associated with any particular pig diseases remains elusive. Since both of porcine TTV species have a high prevalence in domestic pigs, determination of TTV viral loads is presumably more important than assessing the presence of TTV DNA. The level of viral loads in serum and semen samples has been indicated as an important marker for PCVAD in PCV2 infection (Opriessnig et al., 2007, supra). Therefore, establishment of quantitative PTTV-specific real-time PCR assays would help identify potential disease conditions associated with porcine TTVs.

Two TaqMan probe-based real-time PCR assays have recently been described. The singleplex assay developed by a Canadian group was not species-specific and was only designed to quantify the total viral loads of two PTTV species (Brassard et al., 2009, supra). The duplex assay established by a German group allowed the specific and simultaneous detection of both species (Gallei et al., 2009, supra). The target sequences of primers used in those two assays were determined by alignment of the three porcine TTV genomic sequences (Sd-TTV31, TTV-1p and TTV-2p) and were located in the UTR. In the present study, with 7 additional complete PTTV genomic sequences available (4 PTTV1 and 3 PTTV2 sequences), we analyzed and re-determined the conserved regions across the 10 full-length PTTV genomes. Based upon the updated alignment result from this study, two species-specific singleplex SYBR green-based real-time PCR assays were developed to quantify the viral loads of PTTV1 and PTTV2, respectively. The primers used in our assays were designed to bind to conserved genomic regions distinct from the previous studies, which may increase the accuracy of quantification. Our assays showed a considerable species-specificity and sensitivity of detection with 44 genomic copies for PTTV1 and 8.8 genomic copies for PTTV2 per 25-μl reaction, whereas the detection limit of 10 genomic copies per reaction was reported in the TaqMan probe-based duplex real-time PCR (Gallei et al., 2009, supra). In addition, the SYBR green-based real-time PCR assay is a flexible and inexpensive approach that can be directly carried out without the need to use fluorescently labeled probes. Finally, considering porcine TTVs exhibit a high degree of genetic diversity, the results from SYBR green-based assays are unlikely affected by the different genetic background of porcine TTV variants that likely contain mutations in the probe-binding sequences in the TaqMan probe-based assays.

In spite of the presence of TTV DNA, all serum samples from healthy pigs tested in this study had low amounts of PTTV1 and PTTV2 that were less than 2x10^7 copies/ml. Moreover, only an extremely low titer of PTTV2 DNA was detected in three semen samples. Most of the tested serum
plex assays, we developed and validated a quick, inexpensive and reliable approach to the simultaneous detection and quantification of porcine TTVs. In addition, semen PCV2 DNA positivity is also a notable marker of diseases status (Opiressaig et al., 2007, supra). In addition, semen PCV2 DNA positivity is also a notable marker of diseases status (Opiressaig et al., 2007, supra).

The purpose of this study was to develop a simple, practical and valuable tool for the detection of both PTTV species and the simultaneous detection of multiple porcine TTVs. The conventional nested PCR assay for porcine TTVs detection is time-consuming (requiring total 4 rounds of PCR), laborious and prone to sample contamination occurring during multiple rounds of PCR processing. Due to the difference of Tsub in value between PTTV1 and PTTV2 species, an MCA following duplex PCR amplification is able to ensure distinct reaction specificity. Another advantage of this duplex real-time PCR assay is that inclusion of PTTV1 and PTTV2 standards is dispensable when performing the described protocol, which makes it easier for much wider use in any diagnostic labs equipped with an automated real-time PCR instrument. Multiple infection of porcine TTVs with distinct genotypes or subtypes of the same species has been demonstrated (Gallei et al., 2009, supra). In particular, our previous study showed that porcine TTV species 1 consists of two distinct types, PTTV1a (including strains Sd-1TV31 and PTTV1a-VA) and PTTV1b (including strains TT1-1p and PTTV1b-VA). The two newly published PTTV1 isolates with full-length genomes, swSTHY-TT27 (GQ120664) from Canada and FTV1 #471819 (GU188045) from Germany, were both classified into type 1b based upon the phylogenetic analysis (data not shown). The duplex nested PCR described in this study confirmed that dual infection of two PTTV1 genotypes frequently occurred in pigs. This novel assay is the first diagnostic PCR approach developed to distinguish between PTTV1a and 1b so far. Since it is currently not known whether one or both of PTTV1a and PTTV1b infection represents a relevant factor associated with diseases, our differential PCR assay should be of great value for future potential disease associations of these two PTTV types.

According to another aspect of the invention, porcine TTV ORF proteins were expressed and validated using Western blot and ELISA assays based on recombinant antigens were developed and validated using porcine serum samples from different sources. In particular, serological testing using the PTTV1a-, PTTV1b- and PTTV2-specific ELISA provides an accurate and simple tool for revealing the association of porcine TTV infection with diseases.

According to a further aspect of the invention, porcine TTV ORF1 proteins were expressed and purified as recombinant ORF1 capsid protein in an E. coli expression system. Three truncated and His-tagged ORF1 capsid proteins of PTTV1a, PTTV1b and PTTV2, were expressed and purified in Escherichia coli (E. coli), respectively, and served as recombinant capsid subunit vaccines against PTV infection.

Four porcine TTV2 strains, TTV2-p, TTV2#472142, PTTV2-VA and PTTV2c-VA, had available complete genomic sequences to date. Although they are phylogenetically classified into three putative subtypes, a comparative analysis of hydrophilicity profiles of the ORF1 encoding amino acids from four PTV2 showed that they shared three hydrophilic regions, an arginine-rich region from aa 1-49 at the N-terminal and two particular domains (I and II) located at the middle and C-terminal part, respectively. The C-terminal region used for truncated PTTV2c-VA ORF1 expression and the corresponding regions shared in other three PTV2 strains were predicted as a deleted box. Alignments of the amino acid sequences demonstrated high levels of sequence conservation of domains I (aa 322-349) and II (aa 536-625) across the four PTV2 strains.

Since hydrophilic domains are believed to be important for the antigenicity of many proteins, the C-terminal region (aa 310-625) of the PTTV2c-VA ORF1 was constructed and expressed in E. coli. The recombinant protein was insoluble and expressed within the bacterial inclusion bodies. SDS-PAGE of purified 2c-ORF1 products, purified 2c-ORF1 products and Western blot analysis of purified 2c-ORF1 products using an anti-His-tagged mAb was undertaken. The ORF1 protein with the expected size and its truncated product and the putative dimers of the expected and truncated proteins were observed. A band of ~40 KD was consistent with the expected size of 2c-ORF1 whereas the ~30 KD polypeptide was probably an N-terminally truncated product from the former. After purification with a nickel-affinity column, four polypeptides including the two described significant bands were shown in SDS-PAGE. They were also detected by western blot using an anti-His-tagged mAb. Two high-molecular-mass bands were the homodimers formed by the two polypeptides of ~40 KDa and ~30 KDa, respectively, based on the predicted sizes ~80 KDa and ~60 KDa. The results demonstrated that the purified C-terminal PTTV2c-ORF1 was successfully produced and could be used for porcine TTV2 antibody detection in porcine sera.

According to another aspect of the present invention, porcine TTV2 antibodies in various porcine serum samples can be detected by Western blot using purified C-terminal PTTV2c-ORF1. A total of more than 200 serum samples of conventional pigs (healthy or diseased), CD/CD pig’s and gut/diabetic pigs from different sources were collected.
Samples were randomly selected for detection of anti-PTTV2c-ORF1 IgG antibodies using the purified C-terminal PTTV2c-ORF1 as antigen. Western blot analyses of selected porcine serum samples of conventional pigs, CD/CD pigs, and gnotobiotic pigs was undertaken. Purified PTTV2c-ORF1 products were used as the antigens. The two marked ~40 KDa and ~30 KDa bands were detected in most samples of the conventional pigs and CD/CD pigs, indicating widely PTTV2 infection in these pigs. However, all the gnotobiotic pigs from two different sources (Blacksburg, Va. and Ames, Iowa) had no detectable PTTV2 antibody. Additional low-molecular-mass bands were also observed. They were likely from the necrotic reactivity in the Western blot.

According to yet another aspect of the present invention, PTTV2-specific ELISA can be used as a porcine TTV serological test. Seronegative results were also shown in a few samples from both gnotobiotic pigs or the farm. These negative samples were pooled and used as a negative reference in the development of a PTTV2-specific ELISA. The remaining samples from this source were positive. In addition, porcine sera from a commercial company used in cell culture (supposed to be free of diseases-only) also displayed strong anti-PTTV2-ORF2 positivity, which was used as a positive control for ELISA. The concentrations of purified 2c-ORF1 antigen, porcine sera and IgG conjugate were determined by checkboard titration to present low background signal and give the highest difference of OD405 value between the positive and negative controls. The optimal antigen amount was 69 ng per well, and the optimal ELISA results were obtained by a 1:1 dilution of serum samples and a 1:4000 dilution of IgG conjugates. The ELISA cutoff values ranged from 0.25 to 0.5 in each trial.

138 conventional pig sera samples from 3 herds were chosen to analyze the correlation between PTTV2 viral load and anti-PTTV2 antibody levels of their sera from their arrival in the new facility to two months after arrival. Nine of the 10 pigs had decreased viral loads (three had no detectable virus) after 2 months whilst the anti-PTTV2 antibody titers increased in nine of 10 pigs. The results suggested that the pigs with undetectable or higher PTTV2 viral load (10^6 copies/ml) were more likely to have a lower serum PTTV2 antibody titer than pigs with middle values of PTTV2 viral load.

In particular, sera from 10 pigs in the same herd were also analyzed by comparing the PTTV2 viral loads and anti-PTTV2 antibody levels of their sera from their arrival in the new facility to two months after arrival. Nine of the 10 pigs had decreased viral loads (three had no detectable virus) after 2 months whilst the anti-PTTV2 antibody titers increased in nine of 10 pigs. The results suggested that the pigs acquired PTTV2 infection at early stage, which induced humoral response and produced anti-ORF1 capsid IgG antibody progressively. The PTTV2-ORF1 IgG antibody was able to neutralize or even clear the virus, indicating the ORF1 indeed encode a viral capsid protein and may contain neutralizing epitopes against PTTV2.

According to one embodiment of the present invention, the C-terminal PTTV1a- and PTTV1b-ORF1 proteins were expressed and purified in E. coli system, respectively. SDS-PAGE and western blot analysis using an anti His-tagged mAb showed that both 1a- and 1b-ORF products had two polypeptides, one with expected size ~40 KDa and another as the putative homodimer ~80 KDa. Compared to 2c-ORF1 expression, no truncated polypeptide was observed. As a comparative control, expression of a C-terminal-truncated 1 b-ORF1 region (1 b-ORF1true) resulted in a lower-molecular-mass polypeptide compared to its C-terminal-non-truncated counterpart 1b-ORF1.

According to one embodiment of the present invention, the purified C-terminal PTTV1a- and PTTV1b-ORF1 proteins were used to develop genotype-specific serum Western blots and ELISA as described for PTTV2 above.

Additionally, the present invention provides a useful diagnostic reagent for detecting the porcine TTV infection which comprise a monoclonal or polyclonal antibody purified from a natural host such as, for example, by inoculating a pig with the porcine TTV or the immunogenic composition of the invention in an effective immunogenic quantity to produce a viral infection and recovering the antibody from the serum of the infected pig. Alternatively, the antibodies can be raised in experimental animals against the natural or synthetic polypeptides derived or expressed from the amino acid sequences or immunogenic fragments encoded by the nucleotide sequence of the isolated porcine TTV. For example, monoclonal antibodies can be produced from hybridoma cells which are obtained from mice such as, for example, Balb/c, immunized with a polypeptide antigen derived from the nucleotide sequence of the isolated porcine TTV. Selection of the hybridoma cells is made by growth in hypoxanthine, thymidine, and aminopterin in a standard cell culture medium like Dulbecco’s modified Eagle’s medium (DMEM) or minimal essential medium. The hybridoma cells which produce antibodies can be cloned according to procedures known in the art. Then, the discrete colonies which are formed can be transferred into separate wells of culture plates for cultivation in a suitable culture medium. Identification of antibody secreting cells is done by conventional screening methods with the appropriate antigen or immunogen. Cultivating the hybridoma cells in vitro or in vivo by obtaining ascites fluid in mice after injecting the hybridoma produces the desired monoclonal antibody via well-known techniques.

For another alternative method, porcine TTV capsid protein can be expressed in a baculovirus expression system or E. coli expression system according to procedures known in the art. The expressed recombinant porcine TTV capsid protein can be used as the antigen for diagnosis in an enzyme-linked immunosorbent assay (ELISA). The ELISA assay based on the recombinant capsid antigen, for example, can be used to detect antibodies to porcine TTV in porcine and mammalian species. Although the ELISA assay is preferred, other known diagnostic tests can be employed such as immunofluorescence assay (IFA), immunoperoxidase assay (IPA), etc.

Desirably, a commercial ELISA diagnostic assay in accordance with the present invention can be used to diagnose porcine TTV infection in pigs. The examples illustrate using purified ORF1 and ORF2 proteins of porcine TTV to develop an ELISA assay to detect anti-TTV antibodies in pigs. Sera collected from pigs infected with porcine TTV and negative sera from control pigs was used to validate the assay. PTTV2 specific, PTTV1a specific, and PTTV1b specific antibodies were demonstrated to specifically recognize PTTV ORF proteins. Further standardization of the test by techniques known to those skilled in the art may optimize the commercialization of a diagnostic assay for porcine TTV.

Another aspect of the present invention is the unique immunogenic composition comprising the isolated porcine TTV or an antigenic protein encoded by an isolated polynucleotide described hereinabove and its use for raising or producing antibodies. The composition contains a nontoxic, physiologically acceptable carrier and, optionally, one or more adjuvants. Suitable carriers, such as, for example, water, saline, ethanol, ethylene glycol, glycerol, etc., are easily selected from conventional excipients and co-formu-
the second copy of PTTV2b genome was presented in this study. BamH1 is the unique site on the three PTTV genomes, which was engineered at both ends of the three plasmid DNA of each clone clearly resulted in two different fragments of 4.3-Kb and 2.8-Kb in size. The 4.3-Kb fragments represented the backbone vector whereas 2.8-Kb fragments represented the inserted PTTV genomic DNA. The empty vector pSC-B-amp/kan digested with the same enzyme only showed a 4.3-Kb band. The resulting PTTV clones were designated pSC-PTTV1a, pSC-PTTV1b and pSC-PTTV2c, respectively (FIG. 21A-C).

Furthermore, two copies of the full-length PTTV2c-RR genome derived from the clone pSC-PTTV2c were ligated in tandem into the pSC-B-amp/kan vector to generate the clone pSC-2PTTV2c-RR (FIG. 21D). Comparison of the Afl II single digestion patterns between pSC-PTTV2c and pSC-2PTTV2c-RR showed that the latter plasmid had an additional 2.8-Kb fragment representing the second copy of PTTV2c genome. Subsequently, we utilized the same cloning strategy to produce a tandem-dimerized PTTV2b DNA clone derived from the Germany TTV clone TTV2-#471942-full. An additional 2.8-Kb fragment representing the second copy of PTTV2b genome was presented in this construct, designated pSC-2PTTV2b-RR (FIG. 21F), which was digested with the Hind III alone when compared to its one-genome-copy counterpart, confirming the successful construction.

The replication competencies of the constructed PTTV infectious clones were tested by in vitro transfection of PK-15 cells. IFA using the commercially generated rabbit polyclonal antibodies against PTTV2c ORF1 confirmed that both the concatenomers of clones TTV2-#471942-full and pSC-PTTV2c were replication competent, respectively. Passageing of the transfected cells did not eliminate or reduce the fluorescent signals, suggesting that the expression of ORF1 proteins was resulted from the PTTV2 concatenomers that mimicked the natural PTTV2b or PTTV2c circular molecules. No fluorescent signals was observed in mock-transfected cells or DNA-transfected cells using pre-immune rabbit serum as the antibody for IFA detection (data not shown). The concatenomers of the clone pSC-PTTV1a also showed to be replication-competent using an anti-PTTV1a ORF1 antibody. The positive fluorescent signals were located in the nucleus of transfected or passaged cells, indicating that porcine TTVs likely replicate in the cell nucleus. It is not unexpected because porcine circovirus (PCV) has a similar expression pattern in vitro.

Direct transfection of the tandem-dimerized clone pSC-2PTTV2b-RR or pSC-2PTTV2c-RR in PK-15 cells resulted in viral replication and produces the ORF1 capsid antigen. IFA using antibodies against PTTV2 ORF1 confirmed that both clones were also replication-competent and the positive ORF1 antigens were localized in the nuclei.

According to one embodiment of the present invention, infectious clones of porcine TTV can be used to inoculate pigs, which will then elicit an immune response of the host animal and stimulate production of neutralizing antibodies. In one particular embodiment of the present invention, the two tandem-dimerized PTTV2 clones were infectious when injected into the lymph nodes and muscles of conventional pigs.

To test the in vivo infectivity of PTTV2 molecular clones, conventional pigs were inoculated with the clone pSC-2TTV2b-RR or pSC-2TTV2c-RR. Serum samples were collected from animals at 0, 7, 14, 21 and 28 days post-inoculation (DPI). PTTV DNA was detected in pSC-2TTV2c-RR-inoculated pigs beginning at 7 DPI (#92), 14 DPI (#188 and #191) and 21 DPI (#180), respectively (FIG. 22A-D). PTTV viremia appeared late for pigs inoculated with the clone pSC-2TTV2b-RR: two began at 14 DPI (#189 and #192), one at 21 DPI (#181) and one at 28 DPI (#193) (FIG. 22A). The viral loads increased during the course in all inoculated pigs that had the highest viral loads at 28 DPI before necropsy, as determined by PTTV2-specific real-time PCR (FIG. 22A and FIG. 22B). The real-time PCR products amplified from selected pigs were sequenced and found to have identical sequences to the corresponding regions of pSC-2TTV2b-RR or pSC-2TTV2c-RR (data not shown). All inoculated pigs were negative for PTTV2 ORF1 antibodies at 0 and 7 DPI. At 14 DPI, all the four pSC-2TTV2b-RR-inoculated pigs seroconverted to anti-PTTV2 ORF1 IgG, whereas pigs in pSC-2TTV2c-RR-inoculated group seroconverted at 14 (#92 and #180), 21 (#191) and 28 (#188) DPI, respectively (FIG. 22B and FIG. 22D). The results indicated that active porcine TTV2b or TTV2c infection had occurred.

FIG. 1 is a schematic diagram of TTSuV2 constructs containing full-length TTSuV2 genomic DNA. FIG. 1(A) pSC-PTTV2c (from the U.S. TTSuV2 isolate PTTV2c-VA: GenBank accession no. GU456386; SEQ ID NO:12). FIG. 1(B) pSC-2PTTV2c-RR (tandem-dimerized PTTV2c-VA genomes). FIG. 1(C) pSC-PTTV2-#471942 (from the German TTSuV2 isolate TTV2-#471942; GenBank accession no. GU88046; SEQ ID NO:62). FIG. 1(D) pSC-2PTTV2b-RR (tandem-dimerized TTV2-#471942 genomes). FIG. 1(E) pSC-2PTTV2-EU (derived from pSC-PTTV2-#471942). A Hpal site as the silent genetic marker was introduced in this clone.
The inventors selected five commonly-used cell lines including PK-15, 3D4/31 and IPEC-J2, and two other cell lines including BHK-21 and MARC-145. These cell lines are known to be permissive for a wide variety of animal virus infections. In order to rule out the possibility of endogenous contamination of TTSuV1 or TTSuV2 in cultured cell lines, both viral DNA and ORF1 protein expression were subjected to TTSuV1 or TTSuV2 real-time qPCR and IFA detections, respectively. An OIE diseases-free porcine serum, which had been shown to have a high level of anti-TTSuV ORF1 antibody, was also included as a control (Huang, Y. W., et al. 2011. Virus Res 158:79-88). The results obtained with the qPCR analysis showed that none of the five cell lines tested in the study were positive for TTSuV1 or TTSuV2 DNA, as determined by the analyses of fluorescence curves, melting curves and agarose gel electrophoresis, since their fluorescence curves were below the minimum detection limit, their melting curves did not overlap with that of the standards, and there were no detectable specific bands corresponding to the expected PCR products (Fig. 2). In contrast, as expected, the commercial porcine serum was positive for TTSuV1 and TTSuV2 DNA (Fig. 2).

Neither the viral DNA nor the expression of the putative ORF1 capsid protein of TTSuV1 or TTSuV2 was endogenously present in five representative cell lines tested in this study. The present study first aimed to identify potential permissive cell lines supporting the TTSuV propagation. The inventors selected five commonly-used cell lines including three that are of pig origin: PCV1-free PK-15, 3D4/31 and IPEC-J2, and two other cell lines including BHK-21 and MARC-145. These cell lines are known to be permissive for a wide variety of animal virus infections. In order to rule out the possibility of endogenous contamination of TTSuV1 or TTSuV2 in cultured cell lines, both viral DNA and ORF1 protein expression were subjected to TTSuV1 or TTSuV2 real-time qPCR and IFA detections, respectively. An OIE diseases-free porcine serum, which had been shown to have a high level of anti-TTSuV ORF1 antibody, was also included as a control (Huang, Y. W., et al. 2011. Virus Res 158:79-88). The results obtained with the qPCR analysis showed that none of the five cell lines tested in the study were positive for TTSuV1 or TTSuV2 DNA, as determined by the analyses of fluorescence curves, melting curves and agarose gel electrophoresis, since their fluorescence curves were below the minimum detection limit, their melting curves did not overlap with that of the standards, and there were no detectable specific bands corresponding to the expected PCR products (Fig. 2). In contrast, as expected, the commercial porcine serum was positive for TTSuV1 and TTSuV2 DNA (Fig. 2).

To develop cell-based serological methods such as IFA or immunoperoxidase monolayer assay (IPMA) for TTSuV detection, the inventors raised three specific antisera against the putative ORF1 capsid protein of TTSuV1a, TTSuV1b (Huang, Y. W., et al. 2012. Serological profile of Torque teno sus virus species 1 (TTSuV1) in pigs and antigenic relationships between two TTSuV1 genotypes (a and b), between two species (TTSuV1 and 2), and between porcine and human anelloviruses. J. Virol. Submitted Manuscript) or TTSuV2 in rabbits. When the five cell lines were stained with each of the three virus-specific antisera, respectively, no positive fluorescence signals were detected, indicating the absence of endogenous TTSuV1 or TTSuV2 ORF1 expression (data not shown). The IFA results were consistent with the qPCR analysis, which demonstrated that the five selected cell lines were not contaminated with TTSuV1 or TTSuV2 and thus can be used for testing the susceptibility of TTSuV infection or replication by transfection with TTSuV2 DNA clones.

Construction and characterization of full-length TTSuV2 DNA clones in porcine kidney PK-15 cells. The inventors were particularly interested in characterizing the infectivity of TTSuV full-length DNA clone since TTSuV2 has been reported to be associated with PMWS or PCVAD at a high prevalence rate of viral DNA (Kekarainen, T., et al. 2006. J
Gen Virol 87:833-7), a high viral load (Aramouni, M., et al. 2011. Vet Microbiol 153:377-81) and a low antibody level in disease-affected pigs with an unknown mechanism (Huang, Y. W., et al. 2011. Virus Res 158:79-88). The inventors first generated two monomeric full-length TTSuV2 DNA clones, pSC-PTTV2c and pSC-PTTV2-#471942, derived from a prototype U.S. isolate PTTV2c-VA and a German isolate TTV2-#471942, respectively (FIGS. 1A & 1C) (Gallei, A., et al. 2010. Vet Microbiol 143:202-12; Huang, Y. W., et al. 2010. Virology 396:287-97). Each of the full-length TTSuV2 genomic DNA was inserted into a cloning vector pSC-B-amp/kan that does not contain an eukaryotic promoter. The restriction site BamHI or EcoRV is the unique site on the PTTV2c-VA or TTV2-#471942 genome, which was engineered at both ends of genomic DNA to facilitate the generation of concatamers and thus to mimic the TTSuV circular DNA genome. BamHI or EcoRV single digestion of the plasmid DNA of each clone clearly resulted in two different fragments of 4.3-Kb and 2.8-Kb in size. The 4.3-Kb fragment represented the backbone vector whereas the 2.8-Kb fragment represented the inserted monomeric TTSuV2 genomic DNA (data not shown).

Subsequently, two copies of the full-length PTTV2c-VA genome from the clone pSC-PTTV2c were ligated in tandem into the pSC-B-amp/kan vector to generate the clone pSC-2PTTV2c-RR (FIG. 1B). Comparison of the AlfI single digestion patterns between pSC-PTTV2c-RR and pSC-2PTTV2c-RR showed that the latter clone had an additional 2.8-Kb fragment representing the intact single TTSuV2 genomic DNA (FIG. 3A, right panel). The inventors utilized the same cloning strategy to produce a tandem-dimerized TTSuV2 DNA clone, pSC-2PTTV2b-RR, derived from pSC-PTTV2-#471942 (FIG. 1D). Similarly, when digested with HindIII alone, an additional 2.8-Kb fragment representing the intact single TTSuV2 genome was presented in this construct, compared to its monomeric parent clone (FIG. 3A, left panel), thus confirming the successful construction of the clone.

Circular TTSuV2 DNA was generated by tandem ligation of the purified linear TTSuV2 genomic DNA excised from the clone pSC-PTTV2c or pSC-PTTV2-#471942. Typical monomer, dimer and high-copy-molecules of concatemer genomic DNA (data not shown). BamHI or EcoRV single digestion of the plasmid DNA of each clone clearly resulted in two different fragments of 4.3-Kb and 2.8-Kb in size. The 4.3-Kb fragment represented the backbone vector whereas the 2.8-Kb fragment represented the inserted monomeric TTSuV2 genomic DNA (data not shown).

The continuous mRNA1 encodes ORF1 and ORF2 whereas the 2.8-Kb fragment representing the intact single TTSuV2 genome was presented in this construct, compared to its monomeric parent clone (FIG. 3A, left panel), thus confirming the successful construction of the clone.

Circular TTSuV2 DNA was generated by tandem ligation of the purified linear TTSuV2 genomic DNA excised from the clone pSC-PTTV2c or pSC-PTTV2-#471942. Typical monomer, dimer and high-copy-molecules of concatemer TTSuV2 DNA were observed in the ligation products (FIG. 3B). The ligation mixture from PTTV2c-VA or TTV2-#471942 was transfected into PCV1-free PK-15 cells. IFA conducted at five days post-transfection, using the rabbit antiserum against PTTV2c-VA ORF1, indicated that TTSuV2 ORF1 antigen was expressed in the nuclei of the transfected cells with approximately 5% positive rate (FIG. 4A & 4C). No fluorescent signal was observed in mock-transfected cells stained with the same anti-PTTV2 serum (FIG. 4E) or in circular TTSuV2 DNA-transfected cells stained with the anti-TTSuV1a ORF1, anti-TTSuV1b ORF1 (Huang, Y. W., et al. 2012. Serological profile of Torque teno sus virus species 1 (TTSuV1) in pigs and antigenic relationships between two TTSuV1 genotypes (1a and 1b), between two species (TTSuV1 and 2), and between porcine and human anelloviruses. J. Virol. Submitted Manuscript) or pre-bleed rabbit serum (data not shown). Passage of the transfected cells for two times did not eliminate but reduced the fluorescent signal (data not shown). When the transfected cells were continuously passed for up to 20 passages, no positive signal was detectable, suggesting that TTSuV2 infection did not occur (data not shown).

The inventors next tested whether direct transfection of plasmid DNA of the tandem-dimerized clone pSC-2PTTV2c-RR or pSC-2PTTV2b-RR into PK-15 cells resulted in the synthesis of TTSuV2 ORF1. The tandem-dimerized double-stranded DNA does not represent genomic anellovirus DNA but might represent an infectious replicative intermediate. IFA at five days post-transfection using the same anti-TTSuV2 ORF1 antiserum confirmed that both DNA clones also expressed ORF1 in transfected PK-15 cells (FIGS. 4B & 4D). Again, the ORF1 was expressed in cell nuclei. However, the fluorescent intensity and positive rate were lower than that in circular TTSuV2 DNA-transfected cells (FIGS. 4B & 4D). The inventors did not observe the localization of ORF1 antigen in the cytoplasm of the transfected cells.

Experimental identification of two introns in the TTSuV genome. Although the transcriptional profile using cloned TTSuV full-length genomic DNA has not been reported, we previously speculated that TTSuV likely expresses two essential viral mRNA transcripts, mRNA1 and mRNA2, to produce the four known ORF counterparts of human TTV (FIG. 5A) (Huang, Y. W., et al. 2010. Virology 396:287-97). The continuous mRNA1 encodes ORF1 and ORF2 whereas removal of the putative intron of 1341 nt (designated intron 1 here), corresponding to nt positions 649-1998 in PTTV2c-VA genome, generates the putative mRNA2 that encodes two discontinuous ORFs, ORF 1/1 and ORF 2/2 (Huang, Y. W., et al. 2010. J Virol 79:6505-10). To verify whether the splicing of the putative intron 1 in TTSuV2 occurred, total RNA was extracted in PK-15 cells transfected with circular PTTV2c-VA DNA followed by DNase I treatment and RT-PCR analysis. Two PCR product bands of approximately 500 bp and 600 bp in sizes were visualized by agarose gel electrophoresis. Sequencing of the cloned PCR fragments resulted in the identification of two sequences. As expected, the large cDNA fragment of 585 bp was exactly the intron 1-spliced product (FIG. 5B), whereas the small cDNA product of 492 bp contained two splicing regions including the intron 1 and an additional 91-nucleotide intron, corresponding to nt positions 2103-2193 in PTTV2c-VA genome, which was designated intron 2 in this study (FIG. 5C). The splicing sites are conserved among all published TTSuV2 sequences (data not shown). Therefore, in this study for the first time the inventors experimentally demonstrated the existence of splicing of intron 1 and the viral mRNA2 transcripts. The inventors also identified a novel viral mRNA transcript, termed mRNA3, which encodes two putative proteins, ORF1/1/2 and ORF2/2/3, and which switches reading frames from 1 to 2, and 2 to 3, respectively, due to splicing of intron 2 (FIG. 5A). The mRNA3 transcript contains at least three exons on the TTSuV2 genome. Since the inventors failed to determine the 5'- and 3'-ends of the viral mRNA transcripts by rapid amplification of cDNA ends (RACE)-PCR, it is possible that there exists an additional TTSuV2 intron in the upstream of ORF2, as known in human TTV transcripts (Mueller, B., et al. 2008. Virology 381:36-45; Qiu, J., et al. 2005. J Virol 79:6505-10). Nevertheless, transfection of PK-15 cells with circularized TTSuV2 genomic DNA resulted in the synthesis of viral mRNA transcripts and the expression of ORF1 protein, indicating that the TTSuV2 concatamers mimicked the transcription and protein expression from the natural circular genome of TTSuV2.

A tandem-dimerized TTSuV2 clone, pSC-2PTTV2c-RR, is infectious when inoculated in the CD pigs. To test the
infectivity of TTSuV2 DNA clones in pigs, the inventors first performed a pilot study with three groups of CD pigs with two pigs per group. The pigs were inoculated with PBS buffer (pig nos. 1 and 2) in group 1, the tandem-dimerized clone pSC-2TTV2c-RR (pig nos. 3 and 4) in group 2, and pSC-2PTTV2b-RR (pig nos. 5 and 6) in group 3, respectively. Serum samples were collected from animals at 0, 7, 14, 21, 28, 35 and 42 days post-inoculation (DPI). Pig no. 2 died of septicaemia due to an unidentified bacterial infection shortly after inoculation.

TTSuV2 DNA was detected in two pigs inoculated with pSC-2TTV2c-RR beginning at 28 DPI by real-time qPCR. The viral loads, although very low, increased weekly until 42 DPI before necropsy at 44 DPI in both pigs. The viral loads in serum of pig no. 3 increased from 1.93x10^6 at DPI 28 to 5.59x10^6 at DPI 35 and 4.36x10^6 at DPI 42 whereas the serum viral loads in pig no. 4 elevated from 5.07x10^6 at DPI 28 to 4.49x10^6 at DPI 35 and 8.87x10^6 at DPI 42. Moderate microscopic lesions in brain (lymphoplasmacytic encephalitis mainly perivascular), liver (lymphohistiocytic hepatitis) and kidney (lymphoplasmacytic interstitial nephritis) were observed in pig no. 3 but not in no. 4. The remaining three pigs including pigs inoculated with the clone pSC-2TTV2b-RR did not develop viremia throughout the study. However, pig no. 5 had mild lymphohistiocytic multifocal hepatitis.

The results from this pilot pig experiment indicated that the clone pSC-2PTTV2c-RR originated from a U.S. strain of TTSuV2 is infectious. Characterization of two TTSuV2 full-length DNA clones with engineered genetic markers and a derived mutant clone in vitro. To further rule out the possible contamination of other indigenous TTSuV2 infections in the pilot animal study, it is critical to introduce tractable genetic markers in the TTSuV2 genome so that the cloned virus and potential indigenous contaminating virus in pigs can be discriminated in inoculated animals. The inventors introduced a unique HpaI restriction site and two unique restriction sites, PsI and MfeI, into two TTSuV2 monomeric DNA clones pSC-TTV2-471942 and pSC-PTTV2c to produce two new clones pSC-2TTV2-EU and pSC-2TTV2-US, respectively (FIGS. 1E and 1F). The positions of these sites, located in the intron 1, were expected to not change the putative ORF1 capsid amino acid sequence. PK-15 cells were transfected with ligation mixtures of the linear TTSuV2 genomic DNA excised from these two marker clones, respectively. The ORF1 expression in nuclei of the transfected cells was detected by IFA at 3 days post-transfection, similar to the patterns of their parental clones (FIG. 6), indicating that the clones with introduced genetic markers are replication competent.

A mutant clone pSC-2TTV2-AAA with a 104-bp deletion (nt positions 332-437) from the putative TATA box (nt positions 283-289; FIG. 5A) to the ORF1 (nt 528) and ORF2 (nt 445) start codons was generated based on the clone pSC-2TTV2-US (FIG. 1G). When transfected into the PK-15 cells, the circularized DNA from this mutant clone did not express the ORF1 antigen (FIG. 6), suggesting that the deleted region likely contains a cis-acting element important for viral mRNA transcription or TTSuV2 ORF1 translation. The result of the deletion mutant clone also implied that the observed expression of ORF1 is likely driven by the replication-competent TTSuV2 DNA since the tandem-dimerized clone and concatenated ligation products from the parental PTTV2c-VA genome were both infectious in pigs (see below).

Expression of the TTSuV2 ORF1 protein in various cell lines transfected with the circularized TTSuV2 DNA from the clone pSC-2TTV2-US. From the in vitro transfection experiments described above, it appeared that, although the TTSuV2 putative ORF1 capsid protein is expressed, the PK-15 cells do not support the cell-to-cell spread of TTSuV2 recovered from the introduced TTSuV2 DNA clones. Alternatively, it is possible that the assembly of TTSuV2 virions in the transfected PK-15 cells may be deficient. To search for another cell line that may be permissive for TTSuV2 infection, the inventors subsequently transfected eleven other different cell lines with the circularized TTSuV2 DNA from the clone pSC-2TTV2-US, respectively. These cell lines included the four cell lines (3D4131, IPEC-J2, BHK-21 and MARC-145) that were tested negative for TTSuV1 or TTSuV2 at both the DNA and protein levels. The clone pSC-2TTV2-US ORF1 as determined by IFA (data not shown).

After transfection, all the eleven cell lines expressed the ORF1 protein at 3 days post-transfection (FIG. 7; the results of BHK-21 and CHO-K1 not shown). The percentages of transfected cells with positive IFA signals were subjectively categorized into three levels: IPEC-J2, ST, PCV1-free PK-15, Huh-7, and HepG2 with a high level of positive rates (>5%); 3D4/31, Vero, MARC-145 and 293TT with a middle level of positive rates (between 2-5%); HeLa, BHK-21 and CHO-K1 with a low level of positive rates (<2%). In general, TTSuV2-specific antibody staining patterns of individual positive cells by IFA could be divided into three different types: (i) cells displaying dense nuclear staining; (ii) cells displaying large nuclear inclusion staining; and (iii) cells displaying punctate nuclear staining. The last two patterns indicated the localization of ORF1 antigen in cell nuclei. No cytoplasmic staining was observed in the transfected cells.

To test if some of these IFA-positive cells were susceptible to TTSuV2 infection, supernatants collected from cell lysates of PK-15, ST, and 293TT cells transfected with the circularized TTSuV2 DNA were inoculated into all cell lines with high level positive rates and some with middle level positive rates including the 293TT cell line, respectively. The inoculated cells were cultured for 3 to 5 days and examined by IFA. No fluorescent signal was detected in these cells (data not shown), indicating that none of the tested cell lines are susceptible to productive TTSuV2 infection.

Rescue of TTSuV2 from concatamerized TTSuV2 DNA of the clone pSC-2TTV-US in CD/CD pigs. With the introduced genetic markers in the full-length DNA clones that can be used to distinguish between infections caused by the cloned virus and potential indigenous contaminating virus, the inventors performed an additional study in CD/CD pigs to further verify the in vivo infectivity of the TTSuV2 genomic DNA clones. Twelve CD/CD pigs were assigned to three groups with four pigs each. Pigs in each group were inoculated with PBS buffer, concatamerized “TTV2-EU DNA”, and “TTV2-US DNA”, respectively. Pre-inoculation serum samples for all pigs (collected at 30 days prior to inoculation) were tested negative for TTSuV1 or TTSuV2 DNA by real-time qPCR. Serum samples were collected from all animals at 0, 7, 14, 21, 28 and 35 DPI.

TTSuV2 DNA was detected in all eight inoculated pigs, but unfortunately, it was also detected in two negative control pigs, indicating contamination by other indigenous strains of TTSuV2 in the research facility or the source pigs, which is not uncommon. One pig (no. 133) inoculated with the concatamerized “TTV2-US DNA” had a detectable viremia even at 0 DPI, whereas the other pigs developed...
viremia at 14 or 21 DPI. Except for pig no. 133, the seven TTSuV2-DNA inoculated pigs and the two TTSuV2-positive pigs in negative control group had an increased viral load until necropsy, indicating active virus infection. The inventors speculated that the source of the TTSuV2 contamination was likely due to the 1-month waiting period between the date of pre-inoculation serum sample testing (for which all animals were all negative) and 0 DPI.

However, thanks to the introduced genetic markers in the TTSuV DNA clones used in this study, the inventors were still able to determine if the TTSuV2 DNA clones were infectious in pigs, which was the main objective of our study. Since the inventors have previously demonstrated that a single pig can be infected by multiple strains of TTSuV2 and TTSuV1 (9, 17), then prior infection or concurrent infection of an indigenous TTSuV strain should not interfere with the infection of pigs by the TTSuV2 DNA clones the inventors intended to test in this study. To determine if the genetic markers of TTV2-EU or TTV2-US were present only the serum samples from pigs experimentally inoculated with the TTSuV2-US full-length DNA clone is infectious in pigs. The results also experimentally verified, for the first time, that pigs can be co-infected by different strains of TTSuV2.

Little is known about the etiology and molecular biology of anelloviruses due to the lack of a cell culture system to propagate human TTV or TTSuV and the lack of a suitable animal model combined with reverse genetics systems for anellovirus studies. Reports of TTSuV DNA sequences detected in commercial porcine vaccine products, porcine-derived human drugs and in porcine-derived trypsin by nested PCR suggested a widespread contamination of TTSuV (Kekearnains, T., L., et al. 2009). Swine torque teno virus detection in pig commercial vaccines, enzymes for laboratory use and human drugs containing components of porcine origin. J Gen Virol 90:648-53; Krakowka, S., et al. 2011. Production of infectious human hepatocellular carcinoma cells by porcine circovirus type 1. Vaccine 29:7303-6; Huttermann, K., et al. 2004. Infection studies on human cell lines with porcine circovirus type 1 and porcine circovirus type 2. Xenotransplantation 11:284-94; Ma, H., et al. 2011. Investigations of porcine circovirus type 1 (PCV1)-related and other cell lines. Vaccine 29:8429-37; Tischer, I., et al. 1982. A very small porcine virus with circular single-stranded DNA. Nature 295:64-6). Theoretically, the possibility of TTSuV contamination in cell cultures is very low, since anellovirus has been shown to be extremely difficult to propagate in vitro. The present study utilized the (i) more sensitive qPCR assay (compared to the one-round PCR in the Teixeira et al study); (ii) the IFA; and (iii) transfection of circular TTSuV genomic DNA into the cells as the positive control (see below) to demonstrate the absence of TTSuV at both the DNA and amino acids levels in 12 representative cell lines including four of pig origin (PK-15, ST, 3D4/31 and IPEC-J2). Therefore, based on the results from this study, the inventors conclude that, contrary to what some may believe, there is very little, if any, endogenous TTSuV contamination in well-established continuous cell lineages. Instead, detection of contaminating TTSuV DNA sequences in biological products reported by other groups may come from the porcine-derived trypsin or serum (Kekearnains, T., L., et al. 2009. J Gen Virol 90:648-53; Teixeira, T. F., et al. 2011. PLoS One 6:e17501). The latter was actually confirmed in the present study for the first time (FIG. 2).

Subsequently, the inventors demonstrated that all of these TTSuV-free cell lines supported TTSuV ORF1 expression by transfection with the circular TTSuV2 genomic DNA or the tandem-dimerized TTSuV2 plasmids (FIG. 4, FIG. 6 and Fig. 7). The TTSuV2 ORF1 protein was expressed in cell nuclei, especially in nucleoli, which is consistent with the localization of human TTV ORF1 in Huh-7 cells transfected with the circular full-length TTV genomic DNA by immunoblotting with the ORF1-specific antibody (Mueller, B., et al. 2008. Virology 381:36-45). Most recently, it was also reported that TTSuV1 or TTSuV2 ORF1-GPP fusion protein expressed from the recombinant construct was accumulated in nucleoli of the PK-15 cells (Martinez-Guino, L., et al. 2011. Expression profile and subcellular localization of Torque teno sus viruses proteins. J Gen Virol 92:2446-57).

In that study, the five cell lines that were also used here in our study, including PK-15, ST, BHK-21, Vero and MA-104 cells (from which the MARC-145 cell line is derived) had been shown to have detectable TTSuV1 and/or TTSuV2 sequences by using a one-round duplex PCR assay (Teixeira, T. F., Id.). It is unclear why there is such a major discrepancy between our results in this study and those by the Brazilian group. A reliable approach to prove the presence of a contaminating virus in cell cultures used in biological products is to determine its susceptibility to virus infection, which has been exemplified by PCV1 (Beach, N. M., et al. 2011. Productive infection of human hepatocellular carcinoma cells by porcine circovirus type 1. Vaccine 29:7303-6; Huttermann, K., et al. 2004. Infection studies on human cell lines with porcine circovirus type 1 and porcine circovirus type 2. Xenotransplantation 11:284-94; Ma, H., et al. 2011. Investigations of porcine circovirus type 1 (PCV1)-related and other cell lines. Vaccine 29:8429-37; Tischer, I., et al. 1982. A very small porcine virus with circular single-stranded DNA. Nature 295:64-6). Theoretically, the possibility of TTSuV contamination in cell cultures is very low, since anellovirus has been shown to be extremely difficult to propagate in vitro. The present study utilized the (i) more sensitive qPCR assay (compared to the one-round PCR in the Teixeira et al study); (ii) the IFA; and (iii) transfection of circular TTSuV genomic DNA into the cells as the positive control (see below) to demonstrate the absence of TTSuV at both the DNA and amino acids levels in 12 representative cell lines including four of pig origin (PK-15, ST, 3D4/31 and IPEC-J2). Therefore, based on the results from this study, the inventors conclude that, contrary to what some may believe, there is very little, if any, endogenous TTSuV contamination in well-established continuous cell lineages. Instead, detection of contaminating TTSuV DNA sequences in biological products reported by other groups may come from the porcine-derived trypsin or serum (Kekearnains, T., L., et al. 2009. J Gen Virol 90:648-53; Teixeira, T. F., et al. 2011. PLoS One 6:e17501). The latter was actually confirmed in the present study for the first time (FIG. 2).

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In addition, in this study TTSuV2-specific rRNA splicing events were detected intransfected PK-15 cells by RT-PCR, indicating the synthesis of viral mRNA transcripts in the transfected cells. While the inventors experimentally demonstrated the existence of two viral mRNAs transcripts (mRNA2 and mRNA3) (FIG. 5), the putative mRNA 1 encoding the full-length ORF1 of TTSuV2 was not detected (data not shown), which may suggest a lower quantity and integrity of mRNA1 than that of mRNA2 and mRNA3. In accordance with the result described by Martinez-Guino et al., splicing of the 91-nl intron 2 sequence in mRNA3 also
occurred in the post-transcription of TTSuV2 ORF1-GFP fusion gene based on none-full-length viral clone (Martinez-Guinao, et al. 2011, id.).

The synthesis of viral mRNA transcripts and the subsequent expression of the ORF1 or ORF1-related viral proteins in transfected cells were driven by the endogenous TTSuV2 promoter. The processes were also regulated by the unidentiﬁed cis-acting elements, as we showed in this study that deletion of a 104-bp sequence downstream of the TATA box completely eliminated ORF1 expression (FIG. 6). To our knowledge, this is the first demonstration of porcine anellovirus viral mRNA and protein expression and mutagenesis analysis based on the viral DNA concatemers produced from circularized viral genomes or a tandem-dimerized full-length clone.

It appeared that both PTTV2c-VA and TTV2-#471942 DNA concatemers were replication-competent when transfected into cells since they mimicked the natural TTSuV2 circular genome. However, the rescue of PTTV2c-VA (“TTV2-US”), but not TTV2-#471942 (“TTV2-EU”), was only demonstrated in two in vivo animal experiments. The major sequence difference between these two TTSuV2 strains was in the GC-rich region. It has been proposed that the GC-rich region in anelloviruses forms unique stem-loop structures, which may play a signiﬁcant role in viral replication (Miyata, H., et al. 1999. Identiﬁcation of a novel GC-rich 113-nucleotide region to complete the circular, single-stranded DNA genome of TT virus, the ﬁrst human circovirus. J Virol 73:3582-6; Okamoto, H., et al. 1999. Id. The entire nucleotide sequence of a TT virus isolate from the United States (TUSO1; comparison with reported isolates and phylogenetic analysis, Virology 259:437-48). Further in-depth mutagenesis analysis, which was not the scope of the present study, is required to explain this discrepancy between the two clones.

The inventors also showed that, although the three cell lines (PK-15, ST and 293T) tested in the study supported a limited level of TTSuV2 replication, the infection of these cells by TTSuV2, if any, was non-productive since the supernatants of the transfected cells did not induce a second-round infection. Most recently, the 293T cell line was shown to be susceptible for human TTV propagation due to its expression of SV40 large T antigen at a high level (5). The authors proposed that the human TTV genome contains a conserved octanucleotide in the UTR forming a stem-loop as the putative origin of replication. Five 4-bp motifs (CGGG and GGGG) were found adjacent to the stem-loop, which may act as the recognition sites for the SV40 large T antigen to facilitate TTV replication (de Villiers, E. M., et al. 2011. J Virol 85:7284-95). However, when the inventors performed a sequence alignment analysis of the corresponding sequences among human TTV, TTSuV, Torque teno canis virus (dog anellovirus) and Torque teno felis virus (cat anellovirus), neither the conserved octanucleotide nor the 4-bp motif was identiﬁed in the latter three anelloviruses (data not shown). Therefore, the SV40 large T protein expressed in 293T cells likely does not provide the proposed helper effect on TTSuV replication. Further study is needed to screen whether additional cell lines are permissive to TTSuV2 infection.

Previous studies from our group and others have demonstrated that, even under strictly controlled experimental conditions in research facilities, TTSuV-negative pigs can easily acquire TTSuV infection due to the ubiquitous nature of this virus in pigs and environments (Gauger, P. C., et al. 2011. Vet Microbiol 153:229-39; Huang, Y. W., et al. 2011. Virus Res 158:79-88). Although our second in vivo experiment in the present study unfortunately “validated” these previous reports, our results did demonstrate the successful rescue of TTSuV2 in pigs inoculated with either the tandem-dimerized plasmids or circular TTSuV2 DNA with the introduced genetic markers. Unfortunately, due to the presence of indigenous TTSuV2 in the CD/CD pigs from the second animal study, the inventors could not analyze or correlate any pathological lesions in the inoculated pigs to TTSuV infection. Therefore, a future study using the germ-free gnotobiotic pig and the infectious DNA clone is warranted to characterize the pathological lesions solely attributable to TTSuV2 infection. The availability of the pig model combined with the reverse genetics system of anellovirus described in this study will facilitate future studies of porcine and even human anellovirus biology and pathogenesis.

The family Anelloviridae includes human and animal Torque teno viruses (TTV) with extensive genetic diversity. The antigenic diversity among anelloviruses has never been assessed. Using Torque teno sus virus (TTSuV) as a model, the inventors describe here the ﬁrst investigation on antigenic relationships among different anelloviruses. Using the TTSuV1a or TTSuV1b ELISA based on the respective recombinant ORF1 antigen and TTSuV1-speciﬁc real-time PCR, the combined serological and virological proﬁle of TTSuV1 infection in pigs was determined and compared with that of TTSuV2. TTSuV1 is likely not associated with porcine circovirus associated disease since both the viral loads and antibody levels were not diﬀerent between affected and unaffected pigs and since there was no synergistic eﬀect of concurrent PCV2/TTSuV1 infections. The inventors did observe a higher correlation of IgG antibody levels between anti-TTSuV1a and -TTSuV2b than between anti-TTSuV1a or -1b and anti-TTSuV2 in these serum samples, implying potential antigenic cross-reactivity. To conﬁrm this, rabbit antiserum against the putative ORF1 capsid proteins of TTSuV1a, TTSuV1b or TTSuV2 were raised and the antigenic relationships and diversity among these TTSuVs were analyzed by ELISA. Additionally, antibody cross-reactivity was analyzed using PK-15 cells transfected with one of the three TTSuV ORF1 constructs. The results demonstrate antigenic cross-reactivity between the two genotypes, TTSuV1a and TTSuV1b, but not between the two species, TTSuV1a or 1b and TTSuV2. In addition, an anti-genogroup 1 human TTV serum did not react with any of the three TTSuV antigens. The results add to the knowledge base on diversity among anelloviruses and have important implications for diagnosis, classiﬁcation and vaccine development of TTSuVs.

Expression and puriﬁcation of the N-terminally truncated TTSuV1a and TTSuV1b ORF1 proteins. Previously the inventors had successfully expressed a truncated TTSuV1 ORF1 protein in E. coli (Huang, Y. W., et al. 2011. Virus Res. 158:79-88). Using a similar strategy, the C-terminal region of the TTSuV1a-ORF1 or TTSuV1b-ORF1 gene with a C-terminally engineered 8xHis-tag was inserted into the tripeptide sequence vector pTrEx1.1-Neo, resulting in two recombinant constructs, pTri-1aORF1 and pTri-1bORF1. The inventors also constructed an ORF1 C-terminally truncated version of 1b-ORF1 as a control, termed pTri-1bORF1-ctrrc, which is 71-aa shorter than 1b-ORF1, to compare the size with that of pTri-1bORF1 in SDS-PAGE and WB analysis.

The three recombinant proteins, 1a-ORF1, 1b-ORF1 and 1bORF1-ctrrc were found to be insoluble and expressed within the bacteria as inclusion bodies. Puriﬁcation of the crude lysates from 1a-ORF1 products with a nickel-afﬁnity
column resulted in visualization of two bands of ~40 KDa (white arrowheads) and ~70 KDa (black arrowheads), as analyzed by Coomassie blue staining (FIG. 8A). The ~40 KDa band is the expected product of the truncated 1a-ORF1 protein, whereas the ~70 KDa polypeptide is an unknown product but should be derived from the former since it also reacted with an anti-His-tagged Mab (see below). Expression of 1b-ORF1 or 1bORF1-ctruc showed a smear in the crude lysates (FIG. 8B). After purification, two bands of ~40 KDa and ~70 KDa, similar to 1a-ORF1, were also identified in the purified 1b sample, whereas only a ~30 KDa polypeptide (white arrowheads) was detected in the purified 1b-ORF1 sample (FIG. 8B). The bands of ~40 KDa and ~30 KDa were consistent with the expected sizes of 1 b-ORF1 and 1 bORF1-ctruc proteins, respectively. All the identified polypeptides in the purified products were detected by WB using the anti-His-tagged Mab (FIG. 8C). The results indicated that both the truncated 1a-ORF1 and 1b-ORF1 proteins were successfully expressed in E. coli and thus can be used as antigens for TTSuV1a and TTSuV1b antibody detection in porcine sera.

Development of TTSuV1a- and TTSuV1b-based serum WB and indirect ELISAs. In order to identify reference positive and negative sera as controls, a total of 100 serum samples from different sources including those from the gnotobiotic pigs were collected. Samples were screened for anti-TTSuV1a or anti-TTSuV1b IgG seropositivity by serum WB analysis using the purified 1a-ORF1 or 1b-ORF1 as the antigens, respectively. A TTSuV2-seropositive and TTSuV1TTSuV2-DNA positive porcine serum (Huang, Y. W., et al. 2012. Rescue of a porcine anellovirus (Torque teno swine virus 2) from cloned genomic DNA in pigs. J Virol. Submitted Manuscript) showed reactivity with the 1a-ORF1 and the 1b-ORF1 antigen, as the ~40 KDa band was present in the WB analysis (FIG. 9A; two rightmost lanes). Therefore, this serum was considered to be TTSuV1a- and TTSuV1b-seropositive and thus was used as a reference positive control for the ELISAs. All the seven Virginia and 12 Iowa gnotobiotic pigs had no detectable TTSuV1a and TTSuV1b antibodies (FIG. 9A). Except for a few serum samples from conventional pigs from a Wisconsin swine farm (FIG. 9B; the two lanes on the left), the remaining samples were tested positive for both TTSuV1a and TTSuV1b antibodies by the WB analysis. The single-negative serum samples from Wisconsin conventional pigs were pooled and used as a negative control reference serum.

With the available positive and negative control reference sera, TTSuV1a- and TTSuV1b-based ELISAs were subsequently developed and standardized, respectively. The concentrations of the purified 1a-ORF1 or 1b-ORF1 antigen, porcine sera and IgG conjugate were determined by a checkerboard titration assay to ensure low background signal and to give the highest difference of OD450 values between the positive and negative controls. WB-negative gnotobiotic porcine sera showed very low OD values (<0.1) compared to the negative control reference serum (FIG. 9C), suggesting that these pig sera should not serve as a negative control reference for detection of Porcine field samples in the ELISA test.

Association of TTSuV1 viral DNA loads and anti-TTSuV1a and anti-TTSuV1b IgG antibody levels. A total of 160 serum samples were collected and evaluated for the prevalence and viral DNA load of TTSuV1 by real-time qPCR and for seroprevalence and antibody levels (represented by S/N values) of anti-TTSuV1a and anti-TTSuV1b IgG by the ELISAs. Among the 160 samples, 138 sera in groups A to C were collected from three herds under field conditions whereas the remaining 22 sera in groups D (gnotobiotic pigs) and E were collected from pigs raised and housed under strictly controlled experimental conditions in research facilities.

None of the 12 TTSuV1a/TTSuV1b-seronegative gnotobiotic pigs in group D had a detectable viremia. In group E pigs, only one pig was viremic whereas six were seropositive for TTSuV1a and among them, one pig was also seropositive for TTSuV1b.

In groups A and C, 44 of 138 pigs were viremic (31.9%) whereas 128 were TTSuV1a-seropositive (92.8%) and 121 were TTSuV1b-seropositive (87.7%) (FIG. 10A). The incidence of TTSuV1 viremia was much lower than the TTSuV1a or 1b seropositive rate, suggesting previous clearance of the virus by neutralizing antibodies during the post-TTSuV1 infection convalescent period. Similar to the previously obtained results for TTSuV2 (Huang, Y. W., et al. 2011. Virus Res 158:79-88), pigs with undetectable TTSuV1 viral DNA load were more likely to have lower levels of TTSuV1a and TTSuV1b antibody titers than pigs with TTSuV1a/1b antibodies, were found in 40 serum samples. Notably, the number of pigs that were TTSuV1a/ TTSuV1b-dually seropositive but viral DNA-negative (77 samples) was higher than that of pigs with TTSuV1a- or TTSuV1b-seropositivity only (FIG. 10A). In addition, the total number of porcine sera with both antibodies was 117 (40+77) among the 138 serum samples, implying that (i) co-infection rates of pigs with TTSuV1a and TTSuV1b are high, which was expected; and (ii) a certain degree of cross-reactivity may exist between anti-TTSuV1a and anti-TTSuV1b IgG antibodies.

The inventors had previously demonstrated that, over a two-month period, the 10 group-A pigs had decreasing TTSuV2 viral loads that were associated with elevated anti-TTSuV2 ORF1 IgG antibody levels (Huang, Y. W., et al. 2011. Virus Res 158:79-88). Whether an analogous situation for TTSuV1 in these ten pigs existed was subsequently analyzed in this study, by comparing the TTSuV1 viral DNA loads and the anti-TTSuV1a or anti-TTSuV1b antibody levels in sera from their arrival until two months later. Five of ten pigs were TTSuV1 DNA negative during the two months, and in four pigs (ID#4314, 4316, 4319 and 4321) the viral DNA loads decreased after two months, including in 3 pigs (ID#4314, 4319 and 4321) with no detectable TTSuV1 DNA (FIG. 11A). In contrast, both the anti-TTSuV1a and anti-TTSuV1b antibody titers increased in all 10 pigs (FIGS. 11B & 11C). These results were consistent with those of the TTSuV2 study, a TTSuV1 is likely not associated with PCVAD. The inventors had previously found that PCVAD-affected pigs had a significantly lower level of TTSuV2 antibody than PCVAD-unaffected pigs in group B (Huang, Y. W., et al. 2011. Virus Res 158:79-88). However, determination of the levels of anti-TTSuV1a and anti-TTSuV1b IgG antibodies in these serum samples did not reveal a difference between the PCVAD-affected and -unaffected pigs (FIGS. 12A & 12B). In addition, there was no statistically significant difference of TTSuV1 viral loads between the PCVAD-affected and -unaffected pigs (FIG. 12C). In contrast, PCV2 viral load was significantly higher (p<0.05) in PCVAD-affected pigs compared to PCVAD-unaffected pigs (FIG. 12D).

The inventors further analyzed whether there existed a PCV2 and TTSuV1 synergistic effect associated with PCVAD. Serum viral DNA prevalence rates (viremia) of
Comparison and correlations of seroprevalence and antibody levels among anti-TTSuV1a, anti-TTSuV1b and anti-TTSuV2. Mixed infections of TTSuV1 and TTSuV2 are common in pigs, as determined by the presence of viral DNA of both TTSuV1 and TTSuV2 in the same pig using PCR (Gallei, A., et al. 2010. Vet Microbiol 143:202-12; Huang, Y. W., et al. 2010. Development of SYBR green-based real-time PCR and duplex nested PCR assays for quantitation and differential detection of species- or type-specific porcine Torque teno viruses. J Virol Methods 170: 140-6; Huang, Y. W., et al. 2011. Virus Res 158:79-88; Huang, Y. W., et al. 2010. Virology 396:289-97). In this study, the inventors provided the serological evidence to support this conclusion by analyzing the seroprevalence distribution of anti-TTSuV1a, -TTSuV1b and -TTSuV2 IgG in the 138 serum samples in groups A-C. As shown in FIG. 6A, 82 of 138 serum samples were triple-seropositive, indicating that these pigs had been infected by TTSuV1 (TTSuV1a and/or TTSuV1b) and TTSuV2.

The distribution of dual seropositive samples was significantly different. A total of 117 (82+30+5) porcine sera were dual-seropositive for both anti-TTSuV1a and anti-TTSuV1b, which was consistent with the number calculated in FIG. 10A. In contrast, dual seropositivity to anti-TTSuV1a and anti-TTSuV2, or to anti-TTSuV1b and anti-TTSuV2, each occurred in only one sample (FIG. 13A). Furthermore, correlations of antibody levels between anti-TTSuV1a and anti-TTSuV1b, between anti-TTSuV1a and anti-TTSuV2, and between anti-TTSuV1b and anti-TTSuV2 were assessed in the 138 serum samples by using Spearman’s correlation coefficient. A good linear relationship was observed between the anti-TTSuV1a and anti-TTSuV1b (FIG. 13B; Spearman’s rank correlation coefficient=0.91, p<0.0001). When all the 160 samples were included, a better agreement was obtained (Spearman’s rank correlation coefficient=0.93, p<0.0001). A lesser degree of correlation between anti-TTSuV1a and anti-TTSuV2 or between anti-TTSuV1b and anti-TTSuV2 was found when compared to that between anti-TTSuV1a and anti-TTSuV1b (data not shown). The results further revealed an association of seroprevalence and antibody levels between anti-TTSuV1a and anti-TTSuV1b, and thus it is logical to hypothesize that there exists an antigenic cross-reactivity between the two TTSuV1a and TTSuV1b genotypes.

Identification of two putative antigenic sites on the ORF1 genes of TTSuV1a, TTSuV1b and TTSuV2 by ELISA. Three antisera against the truncated recombinant ORF1 s of TTSuV1a, TTSuV1b or TTSuV2 were raised by immunization of rabbits with the respective purified recombinant antigen. Cross-immunoreactivity studies were initially performed to assess whether one of these antigens could cross-react with antisera against the other two antigens in an ELISA format. The pre-bleed rabbit serum was used as the negative control. As expected, each of three TTSuV antigens reacted with its corresponding homologous antisera but not with the pre-bleed negative control serum (OD values<0.1) that were serially diluted from 1:200 to 1:1600 (FIG. 14A-14C).

The TTSuV2 antigen did not appear to cross-react with TTSuV1a or TTSuV1b antisera even at 1:200 dilution since the OD value was relatively low (FIG. 14C). In contrast, the TTSuV1b antigen did cross-react with the anti-TTSuV1a serum (as shown at 1:200 and 1:400 dilutions, both OD values<0.5) but not with the anti-TTSuV2 serum (FIG. 14B) whereas the TTSuV1a antigen likely cross-reacted against the anti-TTSuV1b serum (at 1:200 dilution) but not with the anti-TTSuV2 serum (FIG. 14A). The ELISA results strongly supported our hypothesis that there is an antigenic cross-reactivity between the two TTSuV1a and TTSuV1b genotypes but not between the two species TTSuV1a or 1b and TTSuV2.

Demonstration of antigenic relationships among TTSuV1a, TTSuV1b and TTSuV2, and between TTSuVs and a genogroup 1 human TTV by IFA. In order to definitely analyze the antigenic cross-reactivity among these viruses, an antibody cross-reactivity experiment was performed by using IFA staining. PK-15 cells were transfected with three plasmid constructs, pTri-IaORF1, pTri-IbORF1 and pTri-2cORF1, which harbor the truncated ORF1 capsid genes from TTSuV1a, TTSuV1b and TTSuV2, respectively. Three days post-transfection, cells were stained with anti-TTSuV1a, anti-TTSuV1b, anti-TTSuV2 and pre-bleed serum, respectively. As shown in FIG. 15, cells transfected with pTri-IaORF1 (FIG. 15A) or pTri-IbORF1 (FIG. 15B) stained positive with both anti-TTSuV1a and anti-TTSuV1b but not with the anti-TTSuV2 or the pre-bleed serum (data not shown), whereas cells transfected with pTri-2cORF1 only reacted with anti-TTSuV2 serum (FIG. 15C). Each TTSuV1 antisera reacted stronger with its own homologous antigen than the heterologous antigen based on comparison of the positive cell numbers and fluorescence intensity (FIGS. 15A and 15B). The truncated ORF1s were expressed in both nuclei and cytoplasm of the transfected cells (FIG. 15), which was different from what we found in cells transfected with full-length TTSuV DNA clones (15), probably due to the lack of most of the putative nuclear localization signals (NLS) located at the N-terminal part of the ORF1 in the truncated genes (computer analysis; data not shown). Table 1 summarizes the results of the cross-reactive immunostaining study. In addition, when transfected cells were each stained with an anti-human genogroup 1 TTV ORF1 antisera (AK47; raised in rabbits), no fluorescent signal was detected. Mock-transfected cells did not stain with any of the five antisera (Table 1). The IFA result further confirmed the presence of antigenic cross-reactivity between TTSuV1a and TTSuV1b as shown by the ELISA but not between the TTSuV1a or 1b and TTSuV2. The results also revealed that there was no antigenic cross-reactivity between genogroup 1 human TTV and porcine anelloviruses.
the common antigenic sites on the ORF1 between the genotypes TTSuV1a and TTSuV1b, the inventors performed a comparative analysis of hydrophilicity profiles of the ORF1 aa sequences between PTTV1a-VA and PTTV1b-VA. Two conserved hydrophilic regions located at the middle and C-terminal regions were identified (FIG. 16). The C-terminal antigenic domain appeared to be more antigenic than the domain in the middle region. Alignment of the two putative antigenic regions among all published TTSuV1 sequences revealed a high degree of sequence conservation (data not shown).


Detection of human TTV IgG antibodies in human populations based on the human TTV ORF1 as the antigen has been reported (Maggi, F. and M. Bendinelli, Id.). Handa et al reported a 38% prevalence of human TTV antibody among 100 American blood donors when using the N-terminal part (aa 1-411) containing the arginine-rich region of ORF1 of a human genotype 1b TTV isolate as the antigen (Handa, A., et al. 2000. Prevalence of the newly described human circovirus, TTV, in United States blood donors. Transfusion 40:245-51). In contrast, antibody reactivity in humans to the N-terminus of ORF1 (ORF1-N) of a human TTV genotype 6 was not detected by a Finnish group. After removal of the arginine-rich region (aa 1-62), the arginine-deleted constructs (ORF1AArg and ORF1-NAArg) as well as the C-terminal portion (ORF1-C; aa 344-737) were expressed, 48% human TTV IgG prevalence was detected in sera of 21 healthy Finnish adults using the three products as the antigens (Kakkola, L., et al. 2008. Virology 382:182-9).

Two groups also utilized similar strategies targeting the C-terminal region to successfully express human TTV ORF1. Muller et al demonstrated that an ORF1-specific antisera against the C-terminal part of ORF1 (aa 402-733) of the human TTV isolate P/1C1 generated in a rabbit was able to detect ORF1 expression in cell culture (21), whereas a French group reported the detection of anti-human TTV ORF1 IgG antibodies in 69 of 70 French subjects including 30 blood donors, 30 cryptogenic hepatitis patients and 10 healthy children using an ORF1 C-terminus-based WB analysis (Ort, C., et al. 2000. J Gen Virol 81:2940-58). Most recently, our group successfully used the C-terminal fragment of the ORF1 protein of a U.S. strain of TTSuV2 as the antigen to detect TTSuV2-specific IgG antibodies in pig sera by ELISA. Together with the present study for serological detections of the two porcine TTV species-1 genotypes TTSuV1a and TTSuV1b, the obtained data suggest that the C-terminal portion of ORF1 of anelloviruses is an appropriate target for the development of serodiagnostic assays. Indeed, based on the CAV virion structure determined by cryo-electron microscopic images, the C-terminal half portion of the ORF1 is proposed to form the outer part of the capsid that is exposed to the virion surface whereas the basic N-terminal part of the CAV ORF1 is proposed to be inside the capsid to bind the viral DNA, and the middle part of the ORF1 is proposed to form the inner shell of the capsid (Crowther, R. A., et al. 2003. Comparison of the structures of three circoviruses: chicken anemia virus, porcine circovirus type 2, and beak and feather disease virus. J Virol 77:13036-41). The ORF1 polypeptide of anellovirus has been suggested to be organized in the same way as that of CAV (Crowther, R. A., 2003. Id.). This proposed structure is consistent with the computer analysis of the ORF1 hydrophilicity profiles of TTSuV1 (FIG. 16) and TTSuV2 (Huang, Y. W., et al. 2011. Virus Res 158:79-88). In either case, there are two conserved major hydrophilic regions located at the middle and C-terminal regions that span the C-terminal half portion of the ORF1.

Reliability and specificity of the established ELISAs for differential TTSuVs antibody detections were guaranteed by screening of the positive and negative reference sera through a serum WB. It was further demonstrated by triple sero-positivity of TTSuV1a, TTSuV1b, and TTSuV2 in gnotobiotic pigs of group D (FIG. 9). A high seropositive rate of TTSuV1a (~92.8%) or TTSuV1b (87.7%) was revealed in the 138 groups A-C pigs (FIG. 10A), which was higher than that of TTSuV2 (~60%) (13), indicating a wider spread of actual TTSuV1 infection or the presence of long-persisting anti-TTSuV1 ORF1 antibodies in these pigs regardless of a low incidence of TTSuV1 viremia. Accordingly, these results, for the first time, provided serological evidence supporting multiple infections of TTSuV1a, TTSuV1b and TTSuV2 in the same pigs. To our knowledge, this is also the first study demonstrating multiple anellovirus infections in the same animals by using serological diagnosis in addition to the PCR assay. Therefore, the subsequent question raised was to determine the specificity of seropositivity and cross-antigenic reactivity among different TTSuV species and genotypes.

In this study, the inventors demonstrated by investigating four different aspects that indeed there exists antigenic cross-reactivity between the two TTSuV1a and TTSuV1b genotypes but not between the two TTSuV species (TTSuV1a or 1b and TTSuV2). First, when compared to the serum samples with single TTSuV1a- or TTSuV1b-seropositivity, the numbers of serum samples with TTSuV1a/1b-dual seropositivity was much higher (FIG. 10A), likely implying a certain degree of cross-antigenic reactivity between TTSuV1a and TTSuV1b antibodies. Secondly, the number of serum samples with dual TTSuV1a and TTSuV1b seropositivity was significantly higher than that of dual seropositivity to TTSuV1a and TTSuV2, or to TTSuV1b and TTSuV2 (FIG. 13A). In addition, a high correlation of antibody levels between anti-TTSuV1a and anti-TTSuV1b as assessed by Spearman’s correlation coefficient was observed (FIG. 13B). These analyses were conducted under the background of multiple TTSuV infections in field samples, which led us to propose a logical hypothesis regarding the presence of an antigenic cross-reactivity between TTSuV1a and TTSuV1b. Thirdly, this hypothesis was experimentally confirmed by analysis of the antigenic relationships among TTSuV1a, TTSuV1b and TTSuV2 through antigen-specific ELISAs (FIG. 14), and antibody cross-reactivity studies in PK-15 cells transfected with the three TTSuV ORF1 constructs, respectively (FIG. 15 and Table 1). Finally, sequence comparison of ORF1 of the TTSuV also supported the observed epidemiologic and experimental data in this study; while there was no significant sequence homology of TTSuV1a or 1b ORF1 with that of TTSuV2, the inventors identified two putative antigenic sites on the ORF1 that are shared by TTSuV1a and TTSuV1b (FIG. 16).
In addition, in this study the inventors also demonstrated the absence of antigenic cross-reactivity between TTSuVs and a human genogroup 1 TTV by IFA. Taken together, the results from this study have important implications in predicting the antigenic cross-reactivity among different anelloviruses based on the ORF1 aa sequence homology. Currently, anelloviruses are classified into nine genera according to the infected host species (human/ape, tamarin, dourocoului, tupaia, pig, dog and cat), nucleotide sequence identity and the genome size of primate anelloviruses (TTV, TTMV and TTMDV) (Biagini, P., et al. 2011. Anelloviridae, p. 331-341. In A. M. Q. King, M. J. Adams, E. B. Carstens, and E. J. Lefkowitz (ed.), Virus Taxonomy, 9th Report of the ICTV. Elsevier Academic Press, London). The ORF1 of the TTSuV (Genus Jotatorquevirus) share 15.6-22.3% aa sequence identity with the other eight genera based on multiple sequence alignment (data not shown), which is similar to that between TTSuVs and the human genogroup 1 TTV (19.1-21.0%). Therefore, it is reasonable to deduce that porcine anellovirus is not antigenically cross-reactive with other anelloviruses in the same animal species. The ORF1 aa sequence homologues among the nine genera range from 15.0% to 27.3% (data not shown), thus implying that antigenic diversity between different genera does exist.

The two TTSuV species (TTSuV1 and TTSuV2) do not share antigenicity in the ORF1 antigen since they only had 22.4-25.8% aa sequence identity, whereas the two TTSuV1 genotypes (TTSuV1a and 1b) were antigenically related and cross-reactive due to their higher aa sequence homology (49.4-52.4%). It is possible that the antigenic relationship of different anelloviruses in the same genus may depend on a threshold or a range of aa sequence homology. The available data using TTSuV as a model will provide insights into similar research of antigenic diversity on human anelloviruses (TTV, TTMV and TTMDV) in the future.

The present study on TTSuV1 together with our previous study on TTSuV2 (Huang, Y. W., et al. 2011. Virus Res 158:79-88) also revealed a broader picture of the nature of mixed TTSuVs infections under natural or clinically disease conditions by assessing the serological and virological profiles. It is not surprising to see in this study that several features of TTSuV1 infection were consistent with that of TTSuV2 (FIGS. 3 & FIG. 11). More importantly, the inventors provided new evidence to support the current opinion that TTSuV1 is likely not associated with PCVAD (1, 18, 23), by demonstrating that both viral loads and antibody levels were not significant different between PCVAD-affected and -unaffected pigs (FIG. 12), and that there was no significant PCV2/TTSuV1 synergetic effect. It is not known whether the presence of ORF1 antibody is protective against homologous TTSuV infection. However, since antibodies to TTSuV1 or TTSuV2 ORF1 do not cross-react with the heterologous TTSuV antigen, it appears that TTSuV1 infection and the consequent humoral immune response do not interfere with TTSuV2 infection. Therefore, this may make the development of a single vaccine against the two recognized TTSuV species difficult. Together, the results from the present study have important implications in understanding the diversity of anellovirus, and in diagnosis and vaccine development of TTSuVs.

Vaccines of the infectious viral and infectious molecular DNA clones, and methods of using them, are also included within the scope of the present invention. Inoculated pigs are protected from viral infection and associated diseases caused by TTV2 infection or coinfection. The novel method protects pigs in need of protection against viral infection by administering to the pig an immunologically effective amount of a vaccine according to the invention, such as, for example, a vaccine comprising an immunogen amount of the infectious TTSuV DNA, a plasmid or viral vector containing the infectious DNA clone of TTSuV, the recombinant TTSuV DNA, the polypeptide expression products, the bacterium-expressed or baculovirus-expressed purified recombinant ORF1 capsid protein, etc. Other antigens such as PRRSV, PPV, other infectious swine agents and immune stimulants may be provided concurrently to the pig to provide a broad spectrum of protection against viral infections.

The vaccines comprise, for example, the infectious viral and molecular DNA clones, the cloned TTSuV infectious DNA genome in suitable plasmids or vectors such as, for example, the pSC-B vector, an avirulent, live virus, an inactivated virus, expressed recombinant capsid subunit vaccine, etc. in combination with a nontoxic, physiologically acceptable carrier and, optionally, one or more adjuvants. The vaccine may also comprise the infectious TTSuV2 molecular DNA clone described herein. The infectious TTSuV DNA, the plasmid DNA containing the infectious viral genome and the live virus are preferred with the live virus being most preferred. The avirulent, live viral vaccine of the present invention provides an advantage over traditional viral vaccines that use either attenuated, live viruses which run the risk of reverting back to the virulent state or killed cell culture propagated whole virus which may not induce sufficient antibody immune response for protection against the viral disease.

Vaccines and methods of using them are also included within the scope of the present invention. Inoculated mammalian species are protected from serious viral infection, may also provide protection for disease related to coinfection of TTSuV, such as porcine dermatitis and nephropathy syndrome (PDNS), postweaning multisystemic wasting syndrome (PMWS), and other related illness. The vaccines comprise, for example, an inactivated or attenuated TTSuV virus, a nontoxic, physiologically acceptable carrier and, optionally, one or more adjuvants.

The adjuvant, which may be administered in conjunction with the vaccine of the present invention, is a substance that increases the immunological response of the pig to the vaccine. The adjuvant may be administered at the same time and at the same site as the vaccine, or at a different time, for example, as a booster. Adjuvants also may advantageously be administered to the pig in a manner or at a site different from the manner or site in which the vaccine is administered. Suitable adjuvants include, but are not limited to, aluminum hydroxide (alum), immunostimulating complexes (ISCOMS), non-ionic block polymers or copolymers, cytokines (like IL-1, IL-2, IL-7, IFNα, IFNβ, IFNγ, etc.), saponins, monophosphoryl lipid A (MLA), muramyl dipeptides (MDP) and the like. Other suitable adjuvants include, for example, aluminum potassium sulfate, heat-labile or heat-stable enterotoxin isolated from Escherichia coli, cholera toxin or the B subunit thereof, diphtheria toxin, tetanus toxin, pertussis toxin, Freund’s incomplete or complete adjuvant, etc. Toxin-based adjuvants, such as diphtheria toxin, tetanus toxin and pertussis toxin may be inactivated prior to use, for example, by treatment with formaldehyde.

The vaccines may further contain additional antigens to promote the immunological activity of the infectious TTSuV DNA clones such as, for example, porcine reproductive and respiratory syndrome virus (PRRSV), porcine parvovirus (PPV), other infectious swine agents and immune stimulants.

The new vaccines of this invention are not restricted to any particular type or method of preparation. The cloned
viral vaccines include, but are not limited to, infectious DNA vaccines (i.e., using plasmids, vectors or other conventional carriers to directly inject DNA into pigs), live vaccines, modified live vaccines, inactivated vaccines, subunit vaccines, attenuated vaccines, genetically engineered vaccines, etc. These vaccines are prepared by standard methods known in the art.

As a further benefit, the preferred live virus of the present invention provides a genetically stable vaccine that is easier to make, store and deliver than other types of attenuated vaccines.

Another preferred vaccine of the present invention utilizes suitable plasmids for delivering the nonpathogenic DNA clone to pigs. In contrast to the traditional vaccine that uses live or killed cell culture propagated whole virus, this invention provides for the direct inoculation of pigs with the plasmid DNA containing the viral genome.

Additionally genetically engineered vaccines, which are desirable in the present invention, are produced by techniques known in the art. Such techniques involve, but are not limited to, further manipulation of recombinant DNA, modification of or substitutions to the amino acid sequences of the recombinant proteins and the like.

Genetically engineered vaccines based on recombinant DNA technology are made, for instance, by identifying alternative portions of the viral gene encoding proteins responsible for inducing a stronger immune or protective response in pigs (e.g., proteins derived from ORF1, ORF1/1, ORF2, ORF2/2, etc.). Such identified genes or immunodominant fragments can be cloned into standard protein expression vectors, such as the baculovirus vector, and used to infect appropriate host cells (see, for example, O'Reilly et al., "Baculovirus Expression Vectors: A Lab Manual," Freeman & Co., 1992). The host cells are cultured, thus expressing the desired vaccine proteins, which can be purified to the desired extent and formulated into a suitable vaccine product. The recombinant subunit vaccines are based on bacteria-expressed (FIG. 10, FIG. 15) or baculovirus-expressed ORF1 capsid proteins of TTsuV1a, PTTsuV1b and TTSuV2.

If the clones retain any undesirably natural abilities of causing disease, it is also possible to pinpoint the nucleotide sequences in the viral genome responsible for any residual virulence, and genetically engineer the virus avirulent through, for example, site-directed mutagenesis. Site-directed mutagenesis is able to add, delete or change one or more nucleotides (see, for instance, Zoller et al., DNA 3:479-488, 1984). An oligonucleotide is synthesized containing the desired mutation and annealed to a portion of single stranded viral DNA. The hybrid molecule, which results from that procedure, is enveloped to transform bacteria. Then double-stranded DNA, which is isolated containing the appropriate mutation, is used to produce full-length DNA by ligation to a restriction fragment of the latter that is subsequently transfected into a suitable cell culture. Ligation of the genome into the suitable vector for transfer may be accomplished through any standard technique known to those of ordinary skill in the art. Transfection of the vector into host cells for the production of viral progeny may be done using any of the conventional methods such as calcium-phosphate or DEAE-dextran mediated transfection, electroporation, protoplast fusion and other well-known techniques (e.g., Sambrook et al., "Molecular Cloning: A Laboratory Manual," Cold Spring Harbor Laboratory Press, 1989). The cloned virus then exhibits the desired mutation. Alternatively, two oligonucleotides can be synthesized which contain the appropriate mutation. These may be annealed to form double-stranded DNA that can be inserted in the viral DNA to produce full-length DNA.

An immunologically effective amount of the vaccines of the present invention is administered to a pig in need of protection against viral infection. The immunologically effective amount or the immunogenic amount that inoculates the pig can be easily determined or readily titrated by routine testing. An effective amount is one in which a sufficient immunological response to the vaccine is attained to protect the pig exposed to the TTsuV virus. Preferably, the pig is protected to an extent in which one to all of the adverse physiological symptoms or effects of the viral disease are significantly reduced, ameliorated or totally prevented.

The vaccine can be administered in a single dose or in repeated doses. Dosages may range, for example, from about 1 microgram to about 1,000 micrograms of the plasmid DNA containing the infecting viral genome (dependent upon the concentration of the immuno-active component of the vaccine), preferably 100 to 200 micrograms of the TTsuV DNA clone, but should not contain an amount of virus-based antigen sufficient to result in an adverse reaction or physiological symptoms of viral infection. Methods are known in the art for determining or titrating suitable dosages of active antigenic agent to find minimal effective dosages based on the weight of the pig, concentration of the antigen and other typical factors. Preferably, the infectious viral DNA clone is used as a vaccine, or a live infectious virus can be generated in vitro and then the live virus is used as a vaccine. In that case, from about 50 to about 10,000 of the 50% tissue culture infective dose (TCID 50) of live virus, for example, can be given to a pig.

The new vaccines of this invention are not restricted to any particular type or method of preparation. The vaccines include, but are not limited to, modified live vaccines, inactivated vaccines, subunit vaccines, attenuated vaccines, genetically engineered vaccines, etc.

The advantages of live vaccines are that all possible immune responses are activated in the recipient of the vaccine, including systemic, local, humoral and cell-mediated immune responses. The disadvantages of live virus vaccines, which may outweigh the advantages, lie in the potential for contamination with live adventitious viral agents or the risk that the virus may revert to virulence in the field.

To prepare inactivated virus vaccines, for instance, the virus propagation and virus production can occur in cultured porcine cell lines such as, without limitation PK-15 cells. Serial virus inactivation is then optimized by protocols generally known to those of ordinary skill in the art or, preferably, by the methods described herein.

Inactivated virus vaccines may be prepared by treating the TTsuV with inactivating agents such as formalin or hydrophobic solvents, acids, etc., by irradiation with ultraviolet light or X-rays, by heating, etc. Inactivation is conducted in a manner understood in the art. For example, in chemical inactivation, a suitable virus sample or serum sample containing the virus is treated for a sufficient length of time with a sufficient amount or concentration of inactivating agent at a sufficiently high (or low, depending on the inactivating agent) temperature or pH to inactivate the virus. Inactivation by heating is conducted at a temperature and for a length of time sufficient to inactivate the virus. Inactivation by irradiation is conducted using a wavelength of light or other energy source for a length of time sufficient to inactivate the virus. The virus is considered inactivated if it is unable to infect a cell susceptible to infection.
The preparation of subunit vaccines typically differs from the preparation of a modified live vaccine or an inactivated vaccine. Prior to preparation of a subunit vaccine, the protective or antigenic components of the vaccine must be identified. In the present invention, antigenic components of TTsuV were identified as the ORF1a capsid proteins of TTsuV1a, TTsuV1b and TTsuV2, which were expressed and purified in *Escherichia coli* (*E. coli*) in this invention, and other expression systems, such as baculovirus expression system, for use as subunit recombinant capsid vaccines. Such protective or antigenic components include certain amino acid segments or fragments of the viral capsid proteins which raise a particularly strong protective or immunological response in pigs; single or multiple viral capsid proteins themselves, oligomers thereof, and higher-order associations of the viral capsid proteins which form virus substructures or identifiable parts or units of such substructures; oligosaccharides, glycolipids or glycoproteins present on or near the surface of the virus or in viral substructures such as the lipoproteins or lipid groups associated with the virus, etc. Preferably, the ORF1 protein is employed as the antigenic component of the subunit vaccine. Other proteins may also be used such as those encoded by the nucleotide sequence in the ORF2, ORF1/1, and ORF2/2 gene. These immunogenic components are readily identified by methods known in the art. Once identified, the protective or antigenic portions of the virus (i.e., the “subunit”) are subsequently purified and/or cloned by procedures known in the art. The subunit vaccine provides an advantage over other vaccines based on the live virus since the subunit, such as highly purified subunits of the virus, is less toxic than the whole virus.

If the subunit vaccine is produced through recombinant genetic techniques, expression of the cloned subunit such as the ORF1a, ORF2, ORF1/1, and ORF2/2 genes, for example, may be expressed by the method provided above, and may also be optimized by methods known to those in the art (see, for example, Maniatis et al., “Molecular Cloning: A Laboratory Manual,” Cold Spring Harbor Laboratory, Cold Spring Harbor, Mass. (1989)). On the other hand, if the subunit being employed represents an intact structural feature of the virus, such as an entire capsid protein, the procedure for its isolation from the virus must then be optimized. In either case, after optimization of the inactivation protocol, the subunit purification protocol may be optimized prior to manufacture.

To prepare attenuated vaccines, the live, pathogenic virus is first attenuated (rendered nonpathogenic or harmless) by methods known in the art or, preferably, as described herein. For instance, attenuated viruses may be prepared by the technique of the present invention which involves the novel serial passage through embryonated pig eggs. Attenuated viruses can be found in nature and may have naturally-occurring gene deletions or, alternatively, the pathogenic viruses can be attenuated by making gene deletions or producing gene mutations. The attenuated and inactivated virus vaccines comprise the preferred vaccines of the present invention.

Genetically engineered vaccines, which are also desirable in the present invention, are produced by techniques known in the art. Such techniques involve, but are not limited to, the use of RNA, recombinant DNA, recombinant proteins, live viruses and the like.

For instance, after purification, the wild-type virus may be isolated from suitable clinical, biological samples such as serum, fecal, saliva, semen and tissue samples by methods known in the art, preferably by the method taught herein using infected pigs or infected suitable cell lines. The DNA is extracted from the biologically pure virus or infectious agent by methods known in the art, and purified by methods known in the art, preferably by ultracentrifugation in a CsCl gradient. The cDNA of viral genome is cloned into a suitable host by methods known in the art (see Maniatis et al., id.), and the virus genome is then analyzed to determine essential regions of the genome for producing antigenic portions of the virus. Thereafter, the procedure is generally the same as that for the modified live vaccine, an inactivated vaccine or a subunit vaccine.

Genetically engineered vaccines based on recombinant DNA technology are made, for instance, by identifying the portion of the viral gene which encodes for proteins responsible for inducing a stronger immune or protective response in pigs (e.g., proteins derived from ORF1, ORF2, ORF1/1, and ORF2/2, etc.). Such identified genes or immuno-dominant fragments can be cloned into standard protein expression vectors, such as the baculovirus vector, and used to infect appropriate host cells (see, for example, O’Reilly et al., “Baculovirus Expression Vectors: A Laboratory Manual,” Freeman & Co. (1992)). The host cells are cultured, thus expressing the desired vaccine protein, which can be purified to the desired extent and formulated into a suitable vaccine product.

Genetically engineered proteins, useful in vaccines, for instance, may be expressed in insect cells, yeast cells or mammalian cells. The genetically engineered proteins, which may be purified or isolated by conventional methods, can be directly inoculated into a porcine or mammalian species to confer protection against TTsuV.

An insect cell line (like s9, sf21, or HIGH-FIVE) can be transformed with a transfer vector containing polynucleic acids obtained from the virus or copied from the viral genome which encodes one or more of the immuno-dominant proteins of the virus. The transfer vector includes, for example, linearized baculovirus DNA and a plasmid containing the desired polynucleotides. The host cell line may be co-transfected with the linearized baculovirus DNA and a plasmid in order to make a recombinant baculovirus.

Alternatively, DNA from the isolated TTsuV which encode one or more capsid proteins can be inserted into live vectors, such as a poxvirus or an adenovirus and used as a vaccine.

An immunologically effective amount of the vaccine of the present invention is administered to an porcine or mammalian species in need of protection against said infection or syndrome. The “immunologically effective amount” can be easily determined or readily titrated by routine testing. An effective amount is one in which a sufficient immunological response to the vaccine is attained to protect the pig or other mammal exposed to the TTsuV virus, or TTsuV co-infection, which may cause porcine dermatitis and nephropathy syndrome (PDNS), postweaning multisystemic wasting syndrome (PMWS) or related illness. Preferably, the pig or other mammalian species is protected to an extent in which one to all of the adverse physiological symptoms or effects of the viral disease are found to be significantly reduced, ameliorated or totally prevented.

The vaccine can be administered in a single dose or in repeated doses. Dosages may contain, for example, from 1 to 1,000 micrograms of virus-based antigen (dependent upon the concentration of the immuno-active component of the vaccine), but should not contain an amount of virus-based antigen sufficient to result in an adverse reaction or physiological symptoms of viral infection. Methods are known in the art for determining or titrating suitable dosages.
of active antigenic agent based on the weight of the bird or mammal, concentration of the antigen and other typical factors.

The vaccine can be administered to pigs. Also, the vaccine can be given to humans such as pig farmers who are at high risk of being infected by the viral agent. It is contemplated that a vaccine based on the TTSuV can be designed to provide broad protection against both porcine and human TTV. In other words, the vaccine based on the TTSuV can be preferentially designed to protect against TTV infection through the so-called “Jennerian approach” (i.e., cowpox virus vaccine can be used against human smallpox by Edward Jenner). Desirably, the vaccine is directly administered to a porcine or other mammalian species not yet exposed to the TTV virus. The vaccine can conveniently be administered orally, intrabucally, intramuscularly, transdermally, parenterally, etc. The parenteral route of administration includes, but is not limited to, intramuscular, intravenous, intraperitoneal and subcutaneous routes.

When administered as a liquid, the present vaccine may be prepared in the form of an aqueous solution, a syrup, an elixir, a tincture and the like. Such formulations are known in the art and are typically prepared by dissolution of the antigen and other typical additives in the appropriate carrier or solvent systems. Suitable carriers or solvents include, but are not limited to, water, saline, ethanol, ethylene glycol, glycerol, etc. Typical additives are, for example, certified dyes, flavors, sweeteners and antimicrobial preservatives such as thimerosal (sodium ethylmercurithiosalicylate). Such solutions may be stabilized, for example, by addition of partially hydrolyzed gelatin, sorbitol or cell culture medium, and may be buffered by conventional methods using reagents known in the art, such as sodium hydrogen phosphate, sodium dihydrogen phosphate, potassium hydrogen phosphate, potassium dihydrogen phosphate, a mixture thereof, and the like.

Liquid formulations also may include suspensions and emulsions which contain suspending or emulsifying agents in combination with other standard co-formulants. These types of liquid formulations may be prepared by conventional methods. Suspensions, for example, may be prepared using a colloid mill. Emulsions, for example, may be prepared using a homogenizer.

Parenteral formulations, designed for injection into body fluid systems, require proper isotonicity and pH buffering to the corresponding levels of mammalian body fluids. Isotonicity can be appropriately adjusted with sodium chloride and other salts as needed. Suitable solvents, such as ethanol or propylene glycol, can be used to increase the solubility of the ingredients in the formulation and the stability of the liquid preparation. Further additives which can be employed in the present vaccine include, but are not limited to, dextrose, conventional antioxidants and conventional chelating agents such as ethylenediamine tetracetic acid (EDTA). Parenteral dosage forms must also be sterilized prior to use.

The following examples demonstrate certain aspects of the present invention. However, it is to be understood that these examples are for illustration only and do not purport to be wholly definitive as to conditions and scope of this invention. It should be appreciated that when typical reaction conditions (e.g., temperature, reaction times, etc.) have been given, the conditions both above and below the specified ranges can also be used, though generally less conveniently. The examples are conducted at room temperature (about 23°C. to about 28°C.) and at atmospheric pressure. All parts and percents referred to herein are on a weight basis and all temperatures are expressed in degrees centigrade unless otherwise specified.

**EXAMPLES**

**Viral DNA Extraction, Nested PCR and Genomic PCR**

Convenient serum and semen samples from 20 conventional adult boars from a Virginia pig farm were used in the study. Total DNA was isolated from 20 serum and 19 semen samples using QIAamp DNA mini kit (Qiagen). To screen for the positive PTTV-containing samples, nested PCR amplifications of the conserved regions in the UTR of PTTV1 and PTTV2 were initially performed by using AmpliTag Gold polymerase (Applied Biosystems). The two primer pairs used to amplify the fragment A of PTTV1 were TTV1-mF (SEQ ID NO:45)/TTV1-mR (SEQ ID NO:46) (for the first-round PCR) and TTV1-nF (SEQ ID NO:47)/TTV1-nR (SEQ ID NO:48) (for the second-round PCR), whereas the two primer pairs used to amplify the fragment D of PTTV2 were TTV2-mF (SEQ ID NO:49)/TTV2-mR (SEQ ID NO:50) (for the first-round PCR) and TTV2-nF (SEQ ID NO:51)/TTV2-nR (SEQ ID NO:52) (for the second-round PCR) (FIGS. 17A and 17B, Table 1).

In order to amplify the full-length genomic sequences of both PTTV1 and PTTV2, we first performed an inverse genomic PCR using a pair of conserved gene-specific primes TTV1-IF (SEQ ID NO:1)/TTV1-IR (SEQ ID NO:4) located in region A for PTTV1 and another pair of gene-specific primes TTV2-IF (SEQ ID NO:5)/TTV2-IR (SEQ ID NO:8) located in region D for PTTV2, respectively, with Herculase II Fusion DNA Polymerase (Stratagene) according to the manufacturer’s instructions. No PCR products with expected sizes were detected. Subsequently we designed new sets of primers to amplify two regions covering the complete PTTV1 and PTTV2 genomes in the second-round PCR, respectively (FIG. 17A-17B). The primer pairs used to amplify fragments B and C of PTTV1 were TTV1-mF (SEQ ID NO:2) and TTV1-2311R (SEQ ID NO:8), respectively, whereas the primer pairs used to amplify fragments E and F of PTTV2 were TTV2-mF (SEQ ID NO:5) and TTV2-2316R (SEQ ID NO:9), respectively, whereas the primer pairs used to amplify fragments E and F of PTTV2 were TTV2-mF (SEQ ID NO:5) and TTV2-2316R (SEQ ID NO:9), respectively, whereas the primer pairs used to amplify fragments E and F of PTTV2 were TTV2-mF (SEQ ID NO:5) and TTV2-2316R (SEQ ID NO:9), respectively.

**Example 2**

Screening for Porcine TTV Positive Samples Collected from Boars in a Farm from Virginia

Porcine TTV DNA was previously detected from pigs in different geographic regions by nested-PCR based on the UTR sequence of a Japanese PTTV strain Sd-TTV31 (McKeeown et al., 2004, supra). With the recent identification of PTTV2, two different sets of nested-PCR primers have been used to amplify region A of PTTV1 and region D of PTTV2, respectively (FIG. 17A-17B) (Ellis et al., 2008,
supra; Kekarainen, T., et al (2006). J Gen Virol 87(Pt 4), 833-7; Krakowka et al., 2008, supra). A similar detection approach was also utilized in the present study to identify PTTV strains from pigs in the United States. In order to screen for indigenous PTTV1- or PTTV2-positive samples for subsequent use to determine the full-length genomic sequences, 20 sera (SR#1-20) and 19 semen samples (SM#1-18, and SM#20) collected from 20 boars in a farm of Virginia were subjected to nested-PCR analyses. Surprisingly, all the 20 serum samples were positive for PTTV1 and 19 were also positive for PTTV2 (except for SR#18). In contrast, only 1 semen sample (SM#6) was PTTV1-positive and 3 semen samples (SM#8, 9 and 20) were PTTV2-positive. The result was consistent with a recent study that in boar semen samples were shown to be positive for PTTV DNA in Spain (Kekarainen, T., Lopez-Sorin, S., and Segales, J. (2007). Detection of swine Torque teno virus genogroups 1 and 2 in boar sera and semen. Theriogenology 68(7), 966-71), and thus suggesting a potential vertical transmission of PTTV. However, the prevalence rates of both PTTV1 and PTTV2 in semen were much lower than that in sera, suggesting that there is no direct association for the presence of PTTV DNAs in sera and semen of the same pig.

Example 3

Sequence and Phylogenetic Analyses

Generic analyses and alignment of DNA and amino acid sequences were performed using Lasergene package (DNASTAR Inc., Madison, Wis.). The genomic sequences of three known PTTV strains and their corresponding GenBank accession numbers used for the alignment and comparison are Sd-TTV31 (AB076001), TTV-1p (AY823990) and TTV-2p (AY823991). Pairwise sequence comparisons (PASC) were performed using 121 full-length genomic sequences of human and animal TTV-related strains available in GenBank with an online program PASC (Pairwise Sequence Comparison) developed for analysis of pairwise identity distribution within viral families and available from the National Center for Biotechnology Information (NCBI) (Bao Y., Kapustin Y. & Tatusova T. (2008). Virus Classification by Pairwise Sequence Comparison (PASC). Encyclopedia of Virology, 5 vols. (B. W. J. Mahy and M. H. V. Van Regenmortel, Editors). Oxford: Elsevier. Vol. 5, 342-348).

Phylogenetic trees were constructed by the neighbor-joining method in the PAUP4.0 program (David Swofford, Smithsonian Institute, Washington, D.C., distributed by Sinauer Associate Inc.) based upon the full-length genomic sequences and the deduced amino acid sequences of 4 ORFs of seven PTTV strains. The data were obtained from 1000 re-sampling.

Example 4

Design of PCR Primers for Diagnosing Porcine PTTV Infection

Analyses and alignment of DNA sequences were performed using Lasergene package (DNASTAR Inc., Madison, Wis.). Full-length genomic sequences of ten porcine TTV strains and their corresponding GenBank accession numbers used for the alignment were as follows. Species PTTV1: Sd-TTV31 (AB076001), PTTV1a-VA (GU456383), TTV-1p (AY823990), PTTV1b-VA (GU456384), sWSTHY-I27 (GQ120664) and TTV1 #471819 (GU188045). Species PTTV2: PTTV2b-VA (GU456385), PTTV2c-VA (GU456386), TTV-2p (AY823991) and TTV2 #472142 (GU188046). The conserved sequences among the 6 PTTV1 and 4 PTTV2 genomes were identified, respectively, and subsequently used to guide real-time PCR primer selections using the Beacon Designer program (PREMIER Biosoft International, Palo Alto, Calif.). Primers used for the duplex nested PCR of PTTV1 were designed by the Lasergene package.

Example 5

Standard Curves of PTTV1 and PTTV2 Real-Time PCR

A region of 2091 bp corresponding to the PCR fragment B of PTTV1b-VA genome was re-amplified from the same PCR fragment using primers TTV1-IF (5'-CATAGGTTGTTAACCAATCAGAGTTAAAGCGGT-3') and TTV1-2340R (5'-GGTCATCAGACGATCCATCTCCCTGAC-3') as described previously (Huang et al., 2010). The resulting amplicon was gel-purified by QIAquick Gel Extraction Kit (Qiagen) and quantified by a NanoDrop spectrophotometer that was used for the real-time PCR standard template of porcine TTV species 1. A full-length DNA clone of PTTV2c-VA strain, pSC-PTTV2c, was constructed by assembling PCR fragments E and F from PTV2c-VA in the vector pSC-B-amp/kan (Huang et al., unpublished data). Plasmid pSC-PTTV2c (7082 bp) was used for the real-time PCR standard template of porcine TTV species 2 and the plasmid DNA concentration was measured by a NanoDrop spectrophotometer. A 10-fold dilution series of the two templates was used to generate the real-time PCR standard curves, respectively.

Example 6

Extraction of Viral DNA for PCR Assays

Total DNA was isolated from 20 serum and 19 semen samples collected from 20 conventional adult boars (with no clinical syndromes) from a Virginia pig farm using QIAamp DNA mini kit (Qiagen) as described previously (Huang et al., 2010). A sample volume of 400 µl for sera and semen was used to extract DNA with a final eluate of 50 µl sterile water. All extracted DNA samples were stored at −20°C until real-time PCR testing. Detection of porcine TTVs in these samples by conventional nested PCR had been described previously (Huang et al., 2010). Total DNA extracted from a goat serum sample with the same procedure was used as the negative control.

Example 7

SYBR Green Real-Time Quantitative PCR Assays

PTTV1- and PTTV2-specific real-time PCR were performed, respectively, using SensiMix SYBR & Fluorescein kit (Quanta c Ltd) and the Myiq iCYCLER Real Time PCR instrument (BIO-RAD Laboratories). Each 25-µl reaction contained 12.5 µl of SYBR green Master Mix, 4 µl of extracted DNA, 0.5 µl of each primer (10 nM) and 7.5 µl of sterile water. The PCR condition for PTTV1 was 10 min at 95°C followed by 40 cycles of amplification (15 sec at 95°C, 60 sec at 59.4°C, 10 sec at 72°C). This was immediately followed by a melting point analysis obtained by gradually increasing the temperature form 55°C to 95°C with the fluorescence signal being measured every 0.5°C. The PCR condition for PTTV2 was the same as PTTV1 except that the annealing temperature was 56°C. PTTV1 and PTTV2 standard templates were included as positive controls in every run. Amplification and data analysis were carried out using Myiq System software (BIO-RAD Laboratories). All samples were run in duplicate on the same plate.
Example 8

Specificity and Sensitivity of Two Singleplex Assays

The optimal annealing temperatures for amplification of PTTV1- and PTTV2-specific assays were 59.4°C and 56°C, respectively, as determined by a 10-fold dilution of amplifications using a gradient of annealing temperatures. Amplification of the 118-bp product using primers TTV1F/TTV1R was obtained only with PTTV1 template whereas amplification of the 200-bp product with PTTV2 template was only observed when primers TTV4/TTV4R were used. Neither assay yielded any cross-amplification from the other, confirming the specificity of the primers and targets (data not shown).

A PTTV1 standard curve was established over a range of target DNA concentrations per 25 µl. The minimum detection limit (44 copies) corresponded to a threshold cycle (Ct) of 37.57. Tested samples with Ct > 37.57 were considered as below the detection limit and were not quantifiable. Similarly, a PTTV2 standard curve was generated and used to detect DNA concentration ranging from 8.6x10^1 to 8.6x10^6 copies per 25 µl reaction. The corresponding Ct of minimum detection limit (8.6 copies) was 36.53. All samples that were considered as PTTV1- or PTTV2-positive had copy numbers lower than the respective maximum detection limit. Melting curves using a 10-fold dilution of PTTV1 or PTTV2 standard template, as well as 20 boar serum samples, displayed melting temperatures (Tm) of 87.0°C for PTTV1 and 80.0°C for PTTV2, respectively. No peaks were observed for the negative controls using sterile water or goat serum DNA as templates.

Example 9

Quantification of Porcine TTV1 and TTV2 in Boar Serum and Semen Samples

Viral load was expressed as copy numbers of PTTV1 or PTTV2 genomes per ml of original boar serum samples. PTTV1 DNA were detected in all 20 serum samples ranging from 1.91x10^5 to 3.25x10^5 copies/ml whereas PTTV2 DNA were detected in 19 serum samples (except #10) ranging from 3.59x10^5 to 1.39x10^6 copies/ml. The result was consistent to our previous study by using conventional nested PCR (Table 5). None of the semen samples were PTTV1-positive whereas three semen samples were PTTV2-positive with very low viral loads (230, 244 and 357 copies/ml, respectively).

TABLE 5

Comparison of porcine TTVs detection by different assays in 20 serum and 19 semen samples from adult boars in a Virginia Farm.

<table>
<thead>
<tr>
<th>Samples</th>
<th>PTTV1 real-time PCR</th>
<th>PTTV1 nested PCR</th>
<th>PTTV2 real-time PCR</th>
<th>PTTV2 nested PCR</th>
<th>PTTV1/PTTV2 duplex real-time PCR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Serum PTTV1</td>
<td>20/20</td>
<td>20/20</td>
<td>—</td>
<td>—</td>
<td>20/20</td>
</tr>
<tr>
<td>Serum PTTV2</td>
<td>—</td>
<td>—</td>
<td>19/20</td>
<td>19/20</td>
<td>19/20</td>
</tr>
<tr>
<td>Semen PTTV1</td>
<td>0/19</td>
<td>1/19</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>Semen PTTV2</td>
<td>—</td>
<td>—</td>
<td>3/19</td>
<td>3/19</td>
<td>—</td>
</tr>
</tbody>
</table>

Example 10

PTTV1/PTTV2 Duplex Real-Time PCR Assay

PTTV1/PTTV2 duplex real-time PCR assay was performed in a 25 µl PCR system containing 12.5 µl of SYBR green Master Mix, 0.5 µl of each PTTV1 primers, 0.5 µl of each PTTV2 primers, 4 µl of DNA and 6.5 µl of sterile water. The duplex PCR condition and melting point analysis were the same as PTTV1 except that the annealing temperature was 58°C. The melting peaks were analyzed to distinguish the PTTV1- and PTTV2-specific amplicons.

Example 11

Duplex Nested PCR

The first-round PCR was performed with a Platinum HiFi Supermix (Invitrogen) using 4 µl of extracted DNA in a total volume of 50 µl. The PCR condition was 30 cycles of 94°C for 30 sec, 55°C for 30 sec, 72°C for 30 sec with an initial denaturation of the template DNA at 94°C for 2 min. A 4-µl aliquot of the first-round PCR product was used for the second-round PCR with the same PCR reagents and condition. One pair of primers P1ab-mf/P1ab-mR was used in the first-round PCR whereas a mixture of two pairs of primers P1a-nf/P1a-nR for detection of PTTV1a, and P1b-nf/P1b-nR for detection of PTTV1b, were used in the second-round PCR (Table 1). The amplification products were visualized by gel electrophoresis on a 1% agarose gel stained with ethidium bromide and two bands specific for each type were differentiated by UV light.

Example 12

Construction of PTTV1 and PTTV2 ORF Expression Plasmids

The C-terminal parts of ORF1 of PTTV1a, PTTV1b and PTTV2c were amplified from the respective full-length DNA clones (pSC-PTTV1a, pSC-PTTV1b and pSC-PTTV2c; described elsewhere). The amplified fragments were expected to encode protein products with 319 aa for PTTV1a (ORF1 aa positions 317-635 (SEQ ID NO:13); GenBank accession no. GU456383), 318 aa for PTTV1b (ORF1 aa positions 322-639 (SEQ ID NO:14); GenBank accession no. GU456384), and 316 aa for PTTV2c (ORF1 aa positions 310-625 (SEQ ID NO:16); GenBank accession no. GU456386), respectively. A C-terminal truncated fragment of PTTV1b encoding 248 aa (ORF1 aa positions 322-569 (SEQ ID NO:14)) was also amplified and used as a comparison control for SDS-PAGE analysis. All the plas-
mids were constructed by cloning of the PCR products into an E. coli/baculovirus/mammalian cells triple expression vector pTrIEx1.1-Ne (Novagen) between the NcoI and XhoI restriction sites to generate C-terminally 8xHis-tagged fusion proteins. The four recombinant plasmids were designated pTri-PTTV1a-ORF1, pTri-PTTV1b-ORF1, pTri-PTTV1b-ORF1etruc and pTri-PTTV2c-ORF1. All cloned sequences were confirmed by DNA sequencing.

Example 13
Expression of Recombinant PTTV1 and PTTV2 Proteins

The four expression plasmids were transformed into Rosetta 2 (DE3) pLacI competent cells (Novagen), respectively, and the bacteria were plated on LB agar plates containing 100 ampicillin overnight at 37° C. A single transformation colony for each construct was used to inoculate 3 ml of LB medium containing 100 μg/ml of ampicillin (LB/amp), and grown 6-8 hours at 37° C. A 100-ml of Overnight Express TB Media (Novagen) was inoculated with the starter culture to induce protein expression, and was grown 16-18 hours at 37° C. The turbid 3 ml culture for each construct was then used to inoculate a 3 ml starter culture of LB/amp, and grown for 6-8 hours at 37° C. A 100-ml of Overnight Express TB Media (Novagen) was inoculated with the starter culture to induce protein expression, and was grown 16-18 hours at 37° C. After incubation, the autoinduction culture underwent centrifugation at 3400 rpm for 15 minutes at 4° C. The resulting supernatant for each construct was discarded, and each of the bacterial pellets was reserved at -20° C. until use.

Example 14
Purification and Dialysis of Recombinant Proteins

The recombinant proteins were insoluble and expressed within the bacterial inclusion bodies. Each of the bacterial pellets was treated with BugBuster and rLysosome according to the manufacturer’s protocol (Novagen), and Benzonase Nuclease (Novagen) was added for degradation of DNA and RNA. Each of the inclusion body pellets was subsequently resuspended with 840 μl of lysis buffer (6M Guanidine Hydrochloride, 0.1M sodium phosphate, 0.01M Tris-Chloride, 0.01M imidazole, pH 8.0), and frozen at -80° C. for at least 30 minutes. It was then thawed, diluted with an additional 2.5 ml of lysis buffer and gently rotated for 30 minutes at 20/0.1% SDS. It was transferred to the freshly washed PVDF membrane, and then the membrane was washed 3 times with tris buffered saline/0.05% tween 20 (TBS-T, Sigma). A Goat anti-rabbit IgG IRDye 800 (Li-Cor) antibody was diluted at 1:1000 in Odyssey blocking buffer (Li-Cor) at room temperature for 1 hour. The anti-6xHis-tagged MAb was diluted at 1:1000 in Odyssey blocking buffer/0.2% tween 20, and transferred to the membrane after the previous Odyssey blocking buffer was removed. The MAb was left on a rocker to incubate with the membrane for either 2 hours at room temperature or 4° C. overnight, and then the membrane was washed 3 times with tris buffered saline/0.05% tween 20 (TBS-T, Sigma). A Goat anti-rabbit IgG IRDye 800 (Li-Cor) antibody was diluted at 1:5000 in Odyssey blocking buffer/0.2% tween 20/0.1% SDS. It was transferred to the freshly washed PVDF membrane, and allowed to incubate for 1 hour at room temperature while gently rocking. The membrane was washed 3 times with TBS-T, 1 time with TBS and imaged with the Li-Cor Odyssey.

Example 15
SDS-PAGE and Anti-His-Tagged Western Blot

A western blot was developed to detect purified recombinant proteins by using an anti-6xHis-tagged monoclonal antibody (Rockland). Equal volumes of each of the purified truncated ORF1 proteins and LDS/10% B-ME were mixed, and boiled at 95° C. for 10 minutes. A 10μl of the boiled sample was added to each appropriate well of a 4-12% Bis-Tris Polyacrylamide Gel (Invitrogen), and was run at 200 volts for 43 minutes in 1xMES running buffer (Invitrogen). The proteins were transferred to a PVDF membrane (Bio-Rad) using a Trans blot semi dry transfer apparatus and 1xtransfer buffer (Invitrogen). Once transfer was complete, the PVDF membrane was incubated in Odyssey blocking buffer (Li-Cor) at room temperature for 1 hour. The anti-6xHis-tagged MAb was diluted at 1:1000 in Odyssey blocking buffer/0.2% tween 20, and transferred to the membrane after the previous Odyssey blocking buffer was removed. The MAb was left on a rocker to incubate with the membrane for either 2 hours at room temperature or 4° C. overnight, and then the membrane was washed 3 times with tris buffered saline/0.05% tween 20 (TBS-T, Sigma). A Goat anti-rabbit IgG IRDye 800 (Li-Cor) antibody was diluted at 1:5000 in Odyssey blocking buffer/0.2% tween 20/0.1% SDS. It was transferred to the freshly washed PVDF membrane, and allowed to incubate for 1 hour at room temperature while gently rocking. The membrane was washed 3 times with TBS-T, 1 time with TBS and imaged with the Li-Cor Odyssey.

Example 16
Serum Western Blot

A serum western blot was developed, and used to identify positive and negative serum controls for ELISA development. After SDS-PAGE as described above, the proteins were transferred to a PVDF membrane that was subsequently incubated in Odyssey blocking buffer (Li-Cor) at room temperature for 1 hour. A selected serum sample was diluted at 1:100 in Odyssey blocking buffer/0.2% tween 20, and transferred to the membrane after the previous Odyssey blocking buffer was removed. The serum sample was left on a rocker to incubate with the membrane for 2 hours at room temperature, and then the membrane was washed 3 times with tris buffered saline/0.05% tween 20 (TBS-T, Sigma). A goat anti-swine IgG IRDye 800 antibody (Rockland) was diluted at 1:2500 in Odyssey blocking buffer/0.2% tween 20/0.1% SDS. It was transferred to the freshly washed
Example 17

Indirect PTTV1a-, PTTV1b- and PTTV2-Specific ELISA

The optimal concentrations of the antigens used to coat the plates and dilutions of antiserum and conjugates were determined by checkerboard titration. The ELISA was initiated by diluting each of the purified recombinant His-tagged fusion proteins (PTTV1a, PTTV1b and PTTV2c, respectively) to 680 ng/ml in 1xCarbonate Coating Buffer (CCB) at a pH of 9.6, and coating medium binding ELISA plates (Greiner) with 100 µl/well. The plates were covered, and allowed to incubate at 37° C. for 2 hours. After coating, the diluted proteins were removed, and each well was washed 3 times with 300 µl of 1xTBS-T. Protein Free Blocking Buffer (Pierce) was then added at a volume of 300 µl/well, and the plates were allowed to incubate at 37° C. for 1 hour. Meanwhile, in a 96-well dilution block, the serum samples were diluted at 1:100 in 150 µl of protein free blocking buffer. The block was then removed, and 100 µl of each diluted serum sample was transferred to each corresponding well on the ELISA plates. The plates were allowed to incubate at 37° C. for 2 hours, after which each well was washed 3 times with 300 µl of TBS-T. Next, the HRP-conjugated anti-swine IgG antibody (Rockland) was diluted at 1:4000 in 12 ml of protein free block, and 100 µl was added to each well of the plates. This was incubated at 37° C. for 1 hour, and then each well was washed 3 times with 300 µl of TBS-T. In order to develop the ELISA, 100 µl of Sure Blue Reserve 1-Component (KPL) was added to each well of the plates. After 20 minutes, 100 µl of 1N HCl was added to each well to stop development. The plates were then read at 450 nm.

Example 18

Data Analyses

Porcine sera used in cell culture research from a commercial company (manufactured in New Zealand and considered free from all OIE diseases) were used as a positive control for the three ELISA protocols because the sera were all PTTV1a-, PTTV1b- and PTTV2-positive as detected by serum western blot and displayed high OD values (>2.0). We initially used pooled gnotobiotic pig sera as a negative control as they were negative in western blot detection. Subsequently, in comparison of the negative gnotobiotic pig sera, we screened some porcine sera collected from a conventional pig farm in Wisconsin. They were also negative in western blot detection and their OD values corresponded to that of negative gnotobiotic pig sera. These conventional porcine sera were pooled and used as a negative control. The cutoff value for each ELISA was calculated as the mean OD value of the negative control group (n=4) plus 3 times of the standard deviation.

Example 19

Construction of Full-Length Genomic DNA Clones of Porcine TTV1a, 1b and 2c

PCR Fragments B and C from the US isolate PTTV1a-VA (GenBank accession no. GU456383) were re-amplified from the constructs described previously, and were subsequently assembled into a full-length genomic DNA with a BamH I site at the both ends of the genome by overlapping PCR using the Herculase II Fusion DNA Polymerase (Stratagene) on the vector pSC-B-amp/kan (Stratagene). The resulting construct was designated pSC-PTTV1a (Fig. 21A). Using the same strategy, the clone pSC-PTTV1b (Fig. 17B) originated from the US isolate PTTV1b-VA (GenBank accession no. GU456384) and the clone pSC-PTTV2c (Fig. 21C) originated from the US isolate PTTV2c-VA (GenBank accession no. GU456386) were constructed with the same restriction sites (BamH1) on the same backbone vector. Plasmid TTV2-#471942-full (Fig. 21E) containing a full-length genomic DNA originated from a Germany pathogenic porcine TTV2 isolate. TTV2-#471942 was a gift from Dr. Andreas Gallei (BIVI, Germany). TTV2-#471942 was classified into the porcine TTV subtype 2b together with the US isolate PTTV1b-VA based upon the phylogenetic analysis (data not shown).

Example 20

Construction of Tandem-Dimerized DNA Clones of Porcine TTV2b and 2c

The full-length PTTV2c genome was excised from the clone pSC-PTTV2c by BamH I digestion, purified and ligated to form concatemers. Ligated concatemers were cloned into the BamH I-pre-digested pSC-B-amp/kan vector to produce a tandem-dimerized DNA clone, pSC-2PTTV2c-RR (FIG. 21D). Similarly, a tandem-dimerized DNA clone, pSC-2PTTV2b-RR, was generated from the clone TTV2-#471942-full using EcoR V restriction sites (FIG. 21F).

Example 21

Generation of PTTV1a-, PTTV1b- and PTTV2-Specific Anti-ORF1 Polyclonal Antibodies

The ORF1-encoding product is the putative capsid protein of TTV. To generate PTTV1a-, PTTV1b- and PTTV2-specific anti-ORF1 polyclonal antibodies to detect the expression of PTTV ORF1 proteins and to determine the infectivity of PTTV DNA clones, the three ORF1 proteins from PTTV1a, PTTV1b and PTTV2c were expressed in E. coli, purified and were subsequently used to immunize New Zealand white rabbits, respectively, as a custom antibody production service at Rockland Immunochemicals (Gilbertsville, Pa.). Each anti-ORF1 polyclonal antibody was produced from serum of immunized rabbits.

Example 22

In Vitro Transfection of PTTV Infectious Clones

PK-15 cells were seeded at 2x10^5 cells per well onto a 6-well plate and grown until 60%-70% confluency before transfection. The DNA clones pSC-2PTTV2b-RR and pSC-2PTTV2c-RR were directly transfected into PK-15 cells, respectively, using Lipofectamine LTX (Invitrogen) according to the manufacturer’s protocol. For clones pSC-PTTV1a, pSC-PTTV2c and TTV2-#471942-full, their ligated concatemers, produced as described above, were used for transfection, respectively. Cells were cultured for 3 to 5 days, and then were applied to an immunofluorescence assay (IFA) to detect the expression of ORF1 of porcine TTVs. Alterna-
tively, transfected cells were passaged into new 6-well plates and continued to culture for 3 days before the IFA detection.

Example 23

Immunofluorescence Assay (IFA)

Transfected or passaged cells were washed 2 times with PBS and fixed with acetone. Five hundred microliters of the antibodies, specific to pTTV1a or pTTV2 at 1:500 dilution in PBS, was added over the cells and incubated for 1 hour at room temperature. Cells were washed 3 times with PBS and 500 μl Texas red- or Alexa Fluor 488-labeled goat anti-rabbit IgG (Invitrogen) at 1:200 dilution was then added. After 1-hour incubation at room temperature and washed with PBS, the cells were stained with 500 μl DAPI (KPL, Inc.) at 1:1000 dilution and visualized under a fluorescence microscope.

Example 24

In Vivo Inoculation of Conventional Pigs with the Tandem-Dimerized Porcine TTV2 Clones

A pig inoculation study was performed to determine the infectivities of the two tandem-dimerized porcine TTV2 clones: pSC-2TTV2b-RR and pSC-2TTV2c-RR. Briefly, eight 4-week-old conventional pigs that were seronegative and viral DNA negative for porcine TTV2 were randomly assigned into two groups of four each. Each group of pigs was housed separately and maintained under conditions that met all requirements of the Institutional Committee on Animal Care and Use.

All pigs in each group were injected by a combination of the intra-lymph node route and intramuscular route. The four pigs (nos. 181, 189, 192 and 193) were each injected with 200 μg of the pSC-2TTV2b-RR plasmid DNA whereas another four pigs (nos. 92, 180, 188 and 191) were each inoculated with 200 μg of the pSC-2TTV2c-RR clone. Pigs were monitored daily for clinical signs of disease for a total of 28 days. All pigs were necropsied at 28 days postinoculation.

Example 25

Cell Lines and Cell Cultures

A total of twelve continuous cell lines were used in this study. A type 1 porcine circovirus (PCV1)-free porcine kidney epithelial cell line PK-15 (Fenaux, M., T. et al. 2004. In vitro replication of hepatitis E virus (HEV) genomes and of an HEV replicon expressing green fluorescent protein. J Virol 78:4838-46) and HepG2 (ATCC CRL-10741, passage 7) were each grown in DMEM medium. All samples were run in duplicate on the same plate. ATTSuV1 or TTSuV2 standard template and a porcine genome of the US. strain of TTSuV2 isolate PTTV2c-VA

To ensure that the porcine-derived cell lines used in the study were free of TTSuV contamination, five cell lines, PCV1-free PK-15, 3D4/31, IPEC-J2, BHK-21 and MARC-145, were tested for TTSuV1 or TTSuV2 DNA by using two singleplex SYBR green-based real-time qPCR assays (Huang, Y. W., et al. 2010. J Virol Methods 170:140-6). Briefly, total DNA was extracted from each cell line using the QIAamp DNA mini kit (Qiagen) and was subsequently subjected to TTSuV1 or TTSuV2 qPCR detection in a 25 μl PCR system using SensiMix SYBR & Fluorescein kit (QuanTice Ltd) as described previously (Huang, Y. W., et al. Id.). A TTSuV1 or TTSuV2 standard template and a porcine serum sample from a commercial company used in cell culture, which is supposed to be OIE (The World Organization for Animal Health) disease-free, were included as controls. All samples were run in duplicate on the same plate.

Example 27

Generation of a Rabbit Anti-TTSuV2 ORF1 Antiserum

The inventors have previously expressed and purified a recombinant truncated ORF1 protein of TTSuV2 (PTTV2c-VA strain) (Huang, Y. W., et al. 2011. Virus Res 158:79-88). The purified protein products were used to immunize New Zealand white rabbits as a custom antibody production service at Rockland Immunochemicals (Gilbertsville, Pa.). Serum samples from both rabbits were collected before immunization (pre-bleed) and at 45 days post-immunization.

Example 28

Construction of Full-Length Genomic DNA Clones of TTSuV2

Two PCR fragments (E and F) covering the full-length genome of the U.S. strain of TTSuV2 isolate PTTV2c-VA
The pSC-PTTV2c clone (FIG. 1F). The new clone, designed with two unique restriction sites, PstI (CIGCAG; SEQ ID NO:12) and BamHI (GATC; underlined), was excised from the clone pSC-PTTV2c using BamHI digestion, purified, and ligated head-to-tail to form concatemers. Two-copy concatemers were cloned into the BamHI-pre-digested pSC-B-amp/kan vector to produce a tandem-dimerized TTSuV2 DNA clone, pSC-2PTTV2c-RR (FIG. 1B). Similarly, two plasmids harboring monomeric and tandem-dimerized TTSuV2 genomic DNA originated from German TTSuV2 isolate TTV2-#471942 were cloned into the BamHI-pre-digested pSC-B-amp/kan vector to produce a tandem-dimerized TTSuV2 DNA clone, pSC-2PTTV2b-RR (FIG. 1C) and pSC-2PTTV2a-RR (FIG. 1D), respectively.

**Example 29**

**Introduction of Genetic Markers into the Two TTSuV2 Monomeric DNA Clones and Construction of a TTSuV2 Deletion Mutant**

An Hpal restriction enzyme site was engineered into the putative spliced region (intron) of TTSuV2 genome in the clone pSC-PTTV2-#472142 for introducing a genetic marker to discriminate between the cloned virus and the potential indigenous viruses in the subsequent animal study. To create the unique Hpal site (GTAAAC; mutations are underlined; SEQ ID NO:63), three point mutations, C to T, C to A and T to A at nucleotide (nt) positions 1817, 1819 and 1820 corresponding to the TTV2-#471942 genome were generated by a fusion PCR technique using two pairs of primers containing the desired mutations. The fusion PCR product replaced the corresponding region on the clone pSC-PTTV2-#471942 by using the cloning site KpnI at both ends. The mutations did not change the putative ORF1 capsid amino acid sequence. The resulting full-length DNA clone was named pSC-PTTV2-EU (FIG. 1E). Using the same strategy, two unique restriction sites, PstI (CTTCGAG; SEQ ID NO:64) and MfeI (CAATTG; SEQ ID NO:65), were introduced into the putative intron of the PTTV2c-VA genome in the pSC-PTTV2c clone (FIG. 1F). The new clone, designated pSC-PTTV2-US, contained three silent mutations at nt positions 1613 (A to T), 1784 (T to C) and 1787 (C to T) corresponding to the TTV2c-VA genome. A mutant clone pSC-PTTV2-AA, with a 104-bp deletion (at positions 332-437) from the putative TATA box to the ORF1/ORF2 start codon on the clone pSC-PTTV2-US, was also generated by removing the short deletion fragment with double-digestion with the AccI and Apal enzymes followed by formation of two blunt ends with a Klenow enzyme and self-ligation (FIG. 1G). All mutagenesis were confirmed by DNA sequencing.

**Example 30**

**In Vitro Transfection of TTSuV DNA Clones**

The PCV1-free PK-15 cells were seeded at 2x10⁵ cells per well onto a 6-well plate and grown until 60%-70% confluency before transfection. Two micrograms of the tandem-dimerized clones pSC-2PTTV2b-RR and pSC-2PTTV2c-RR were directly transfected into the cells, respectively, using Lipofectamine LTX (Invitrogen) according to the manufacturer’s protocol. For monomeric clones pSC-PTTV2c, pSC-PTTV2-#471942, pSC-PTTV2-EU, pSC-PTTV2-US and pSC-PTTV2-AAA, the respective genomic fragment was excised by BamHI or EcoRV enzyme, gel-purified, and re-ligated with the T4 DNA ligase overnight.

Transfection IFA detection were similar. The ligation mixtures (~2 μg) were used for transfection using Lipofectamine LTX, respectively. Cells were cultured for 3 to 5 days, and then subjected to an immunofluorescence assay (IFA) to detect the expression of ORF1. Alternatively, transfected cells were passaged into new 6-well plates and were cultured for 3 days before detection of ORF1 expression by IFA. Transfection of the other 11 cell lines and IFA detection were similar.

**Example 31**

**Immunofluorescence Assay (IFA)**

Transfected or passaged cells on 6-well plates were washed with PBS and fixed with acetone. Five hundred microliters of the anti-TTSuV ORF1 antiserum at a 1:500 dilution in PBS, was added to the cells for each well and incubated for 1 hour at room temperature. Cells were washed 3 times with PBS and 500 μl Texas Red- or Alexa Fluor 488-conjugated goat anti-rabbit IgG (Invitrogen) at a 1:300 dilution was subsequently added. After incubation for 1 hour at room temperature, the cells were washed with PBS, stained with 500 μl DAPI (KPL, Inc.) at a 1:1000 dilution and visualized under a fluorescence microscope.

**Example 32**

**RT-PCR**

Total RNA was extracted from PCV1-free PK-15 cells transfected with circular TTSuV2 DNA using the RNase-free DNase I treatment. cDNA synthesis was performed using Super-Script II reverse transcriptase (Invitrogen) with oligo-dT as the reverse primer. PCR was performed in a 50-μl reaction with the Advantage 2 PCR kit (Clontech) using primers TTV2-448F (5'-GAAGAAAGATGGCTGACGGTAGCG-3') and TTV2-2316R (5'-AGGTGAGGAGATCCTTGCGCTTG-3'; SEQ ID NO:66) and TTV2-2316R (5'-AGGTGAGGAGATCCTTGCGCTTG-3'; SEQ ID NO:66). The PCR products were gel-purified, cloned into a pCR2.1 vector (Invitrogen) by TA cloning strategy and sequenced.

**Example 33**

**In Vivo Transfection of Colostrum Deprived (CD) Pigs with the Tandem-Dimerized TTSuV2 Clones**

It has been previously demonstrated that the infectivity of infectious DNA clones for viruses with a circular genome can be tested by direct inoculation of dimerized full-length genomic DNA into animals (Fenaux, M., T. et al. 2004. A chimeric porcine circovirus (PCV) with the immunogenic
capsid gene of the pathogenic PCV type 2 (PCV2) cloned into the genomic backbone of the nonpathogenic PCV1 induces protective immunity against PCV2 infection in pigs. J Virol 78:6297-303). Therefore, in this study, a pilot animal study was initially conducted to determine the infectivity of the two tandem-dimerized TTSuV2 clones pSC-2TTV2c-RR and pSC-2TTV2b-RR. Briefly, six, 26-day old, CD pigs that were seronegative and viral DNA-negative for TTSuV1 and TTSuV2 were assigned into three groups of two each. Each group of pigs was housed separately and maintained under conditions that met all requirements of the Institutional Animal Care and Use Committee. The pigs in each group were injected by using a combination of intra-lymphoid (superficial inguinal lymph nodes) and intramuscular routes with the plasmid DNA of the full-length TTSuV2 clones. The two pigs (nos. 1 and 2) in group 1 were each given 1 ml of PBS buffer and used as the negative control. The two pigs (nos. 3 and 4) in group 2 were each injected with 200 μg of the pSC-2TTV2c-RR plasmid DNA whereas the remaining two pigs (nos. 5 and 6) in group 3 were each inoculated with 200 μg of the pSC-2TTV2b-RR clone.

Pigs were monitored daily for evidence of TTSuV2 infection for a total of 44 days. All pigs were necropsied at 44 days post-inoculation. Serum samples were collected from all pigs prior to inoculation and weekly thereafter until termination of the study. The samples were tested for the presence of TTSuV DNA and quantified for viral loads by a real-time qPCR (Huang, Y. W., et al. 2010. J Virol Methods 170:140-6). Samples of tissues including brain, lung, lymph nodes, liver, kidney, thymus, spleen, small intestines, large intestines, heart, tonsil, bone marrow were collected during necropsies and processed for microscopic examination. The tissues were examined in fashion blinded to the treatment status of the pigs and given a subjective score for severity of tissue lesions ranged from 0 (normal) to 3 (severe) (Fenaux, M., et al. A chimeric porcine circovirus (PCV) with the immunogenic capsid gene of the pathogenic PCV type 2 (PCV2) cloned into the genomic backbone of the nonpathogenic PCV1 induces protective immunity against PCV2 infection in pigs. J Virol 78:6297-303; Halbur, P. G., et al. 1995. Comparison of the pathogenicity of two US porcine reproductive and respiratory syndrome virus isolates with that of the Lelystad virus. Vet Pathol 32:648-60).

Example 34

In Vivo Transfection of Cesarean Derived, Colostrum Deprived (CD/CD) Pigs with the Circularized TTSuV2 Genomic DNA Containing Genetic Markers

To further verify the results from the initial pilot pig study, the inventors introduced tractable genetic markers into the full-length DNA clones and conducted another CD/CD pig study. Approximately 600 μg of circular or concatamerized TTSuV2 genomic DNA derived from the clone pSC-2TTV2/EU or pSC-2TTV2-US was generated by ligation of the linearized TTSuV2 genomic DNA. To determine the infectivity of the full-length DNA clones, the inventors inoculated four, 40-day-old, CD/CD pigs (nos. 127, 132, 136 and 142) in group 3 were each injected with 1.5 ml of PBS buffer and served as negative controls. All pigs were monitored for evidence of TTSuV2 infection for a total of 35 days, at which time they were necropsied. Viremia was tested by a TTSuV2 real-time qPCR (Huang, Y. W., et al. 2010. J Virol Methods 170:140-6). A TTSuV2 genomic region of 620 bp containing the engineered genetic markers in TTV2-EU or TTV2-US was amplified from the sera of inoculated pigs by PCR using primers TTV2-tagF (5’-TGACACAGGAACGCTAGGAAAATGCAGT-3’; SEQ ID NO: 67) and TTV2-tagR (5’-TGAAGTATTTAGGGTCATTTGTAGCA-3’; SEQ ID NO: 68) from selected serum samples of pigs with viremia. The PCR products were gel-purified and cloned into a pCR2.1 vector by using the TA cloning strategy. The white bacterial clones on the X-gal-containing agar plates were picked up for subsequent DNA extraction and sequencing.

Example 35

Sources of Porcine Sera

Porcine sera used in this study were described previously (Huang, Y. W., et al. 2011. Virus Res 158:79-88). Briefly, serum samples for serum Western blot (WB) analysis were collected from 20 conventional adult boars with no clinical symptoms from a Virginia pig farm, seven gnotobiotic pigs from Virginia (nos. 4 to 7, 224, 229 and 230; kindly provided by Drs. Lijuan Yuan and Guohua Li from Virginia Tech) and 12 from Iowa (group D), five cesarean-derived, colostrum-deprived (CD/CD) pigs and approximately 50 conventional piglets from a Wisconsin pig farm. A TTSuV2-seropositive porcine serum, which was manufactured in New Zealand and free of all known OIE (The World Organization for Animal Health) notifiable diseases, was also used in this study.

A hundred and sixty porcine serum samples were used for assessing the virological and serological profiles of TTSuV1a and TTSuV1b infection and were divided into five groups (A to E) as described previously (Huang, Y. W., et al. 2011. Virus Res 158:79-88): (i) Twenty group-A samples were from 10 specific-pathogen-free (SPF) pigs (60-80 days old at arrival) free of known pathogens and were collected at arrival in the facility and two months after arrival; (ii) Sixty group-B samples were collected from 105 days old pigs in a farm with an outbreak of porcine circovirus associated disease (PCVAD): 30 were from clinically affected pigs and 30 were clinically unaffected pigs; (iii) Fifty-eight group-C samples were collected from 28 days old pigs with unknown disease status; 28 were clinically affected and 30 were clinically unaffected; (iv) Twelve group-D samples were from 14-42 days old gnotobiotic pigs located in Iowa; (v) Ten group-E sera were from 21-30 days old SPF pigs used for an experimental PCV2 infection study.

Example 36

Construction of the TTSuV1a- and TTSuV1b-ORF1 Expression Plasmids

The C-terminal part of the ORF1 of two TTSuV1 strains, PTV1a-VA (GenBank accession no. GU456383; SEQ ID NO: 9) and PTV1b-VA (GenBank accession no. GU456384; SEQ ID NO: 10) was amplified, respectively, from the available PCR fragments reported previously. The amplicon was expected to encode a truncated PTV1a-VA ORF1 protein of 319 aa (positions 317-635 corresponding to...
PTTV1a-VA or a truncated PTTV1b-VA ORF1 protein of 318 aa (positions 322-639 corresponding to PTTV1b-VA). An additional methionine was introduced at the N-terminus of each amplified fragment. Two ORF1 expression plasmids, designated pTri-1aORF1 and pTri-1bORF1, were each constructed by cloning the respective PCR product into a bacterial/insect/mammalian-triple expression vector pTriEx1.1-Neo (Novagen) between the NcoI and XhoI restriction sites to generate two C-terminally 8xHis-tagged fusion proteins. The recombinant plasmids were confirmed by DNA sequencing. The TTSuV2 ORF1 expression construct, pTri-2cORF1, had been described previously (Huang, Y. W., et al. 2011. Virus Res 158:79-88).

Example 37

Expression and Purification of the Recombinant TTSuV1a- and TTSuV1b-ORF1 Proteins

The two plasmids were each transformed into Rosetta 2 (DE3) pLacI competent cells (Novagen). The bacteria were grown in 100-ml of Overnight Express TB Media (Novagen) for 16-18 hours at 37° C. and then the bacterial culture was harvested by centrifugation at 3,400 rpm for 15 minutes at 4° C. The resulting bacterial pellet was treated with BugBuster and rLysosome according to the manufacturer’s protocol (Novagen). Benzonase Nuclease (Novagen) was added to degrade DNA and RNA. The resulting inclusion bodies were lysed in 6M guanidine hydrochloride, 0.1 M sodium phosphate, 0.01 M Tris-Chloride, and 0.01 M imidazole with a pH value of 8.0. The lysate supernatants were collected by centrifugation and were used for His-tagged protein purification. The recombinant His-tagged TTSuV1a- or TTSuV1b ORF1 proteins used as the antigen for ELISA and rabbit immunization were quantified using a NanoDrop spectrophotometry and frozen at -80° C. until use.

Example 38

Generation of Anti-ORF1 Antiserum of TTSuV1a and TTSuV1b in Rabbits

The two ORF1 proteins of TTSuV1a and TTSuV1b expressed in E. coli were purified and used to immunize two New Zealand white rabbits, respectively, at a custom antibody production service at Rockland Immunochemicals (Gilbertsville, Pa.). Antisera were harvested at 50 days post-immunization.

Example 39

SDS-PAGE, Anti-His-Tagged WB and Serum WB Analysis

The unpurified or purified recombinant TTSuV1 ORF1 proteins were resolved on a 4-12% Bis-Tris Polyacrylamide Gel (Invitrogen) by electrophoresis and were subsequently transferred onto a polyvinylidene difluoride (PVDF) membrane. Proteins were detected on the PVDF membrane using an anti-6xHis-tagged Mab at a 1:1000 dilution at 4° C., followed by incubation with an IRDye 800CW conjugated goat anti-rabbit IgG (LI-COR Biosciences) at a 1:10,000 dilution at room temperature. After three washing steps using Tris buffered saline/0.05% Tween 20 (TBS-T; Sigma), the membrane was analyzed using the Odyssey Infrared Imaging System (LI-COR Biosciences).

For serum WB analysis, the purified TTSuV1a- and TTSuV1b-ORF1 proteins were incubated with individual porcine sera at a 1:200 dilution and with IRDye 800CW conjugated rabbit F(ab')2 anti-swine IgG (Rockland Immunochemicals, Inc.) at a 1:10,000 dilution at room temperature. The membrane was then analyzed using the Odyssey Infrared Imaging System.

Example 40

Indirect ELISAs

TTSuV1a- and TTSuV1b-based ELISAs were developed. The optimal concentration of the antigens and the optimal dilutions of sera and HRP conjugates were determined by checkerboard titrations. Similar to the TTSuV2-based ELISA reported previously, the optimal amount of the ORF1 antigen of TTSuV1a or TTSuV1b was 68 ng per well. The optimal ELISA results were obtained by using a 1:100 dilution of serum samples and a 1:4000 dilution of IgG conjugates.

The ELISA was initiated by diluting the purified ORF1 proteins in carbonate coating buffer (pH 9.6) that was used for coating 96-well ELISA plates (Greiner Bio-One) with 100 µl/well. After incubation at 37° C. for 2 hours, each well was washed 3 times with 300 µl of Tris-buffered saline-Tween 20 solution (TBS-T) and blocked with protein-free blocking buffer (Pierce) at a volume of 300 µl for 1 hour at 37° C. One hundred µl of each diluted serum sample was transferred to the corresponding well on the ELISA plates and incubated at 37° C. for 2 hours. After washing the wells three times with 300 µl of TBS-T buffer, the diluted HRP-conjugated rabbit anti-swine IgG (Rockland) was added to each well in a volume of 100 µl and the plate was incubated at 37° C. for 1 hour. A volume of 100 µl of Sure Blue Reserve 1-Component (KPL) was added to each well and incubated for 10 minutes at room temperature. The reaction was stopped by adding 100 µl/well of 1 N HCL. The plates were then read at 450 nm using a spectrophotometer. All serum samples were run in duplicates. Positive and negative controls run in quadruplicates were included on each plate. In general, the mean OD value of the negative control was less than 0.5 whereas the mean OD value of the positive control was greater than 1.5. The ELISA value was calculated as the S/N value that was expressed as a ratio of the mean OD value of a sample to the mean OD value of the negative control (n=4). A subjective cut-off S/N value of 1.2 was used to distinguish between positive and negative samples.

Example 41

Real-Time qPCR Assay for Quantitation of TTSuV1

A SYBR green-based TTSuV1-specific real-time quantitative PCR (qPCR) developed recently in our laboratory was used to measure the total TTSuV1 viral loads (both TTSuV1a and TTSuV1b) in the five groups of pig sera as described previously. The minimal detection limit was 1.0x 10^6 copies per ml in this study. The TTSuV1 qPCR assay does not cross-amplify TTSuV2 DNA (Huang, Y. W., et al. 2010. J Virol Methods 170:140-6). Quantitation of TTSuV2...
and PCV2 viral loads in group-B sera had been reported previously (Huang, Y. W., et al. 2011. Virus Res 158:79-88).

Example 42

Statistical Analyses

Data were analyzed using SAS software (version 9.2; SAS Institute Inc., Cary, N.C.) and GraphPad Prism software (version 5.0; San Diego, Calif.), respectively. Antibody levels (represented by S/N values) were compared between categories of log_{10} viral titers using the Kruskal-Wallis test followed by Dunn's procedure. For each group that contained clinically affected and non-affected pigs (groups B and C), log_{10} virus titers were compared between pigs with and without clinical signs using a Wilcoxon 2-sample test. Antibody levels were compared between pigs with and without disease using a 2-sample t-test. Using a cutoff point of 1.2, the proportion of pigs with antibodies was compared between affected and unaffected pigs using a Fisher's exact test.

Correlations between S/N values for TTSuV1a and S/N values for TTSuV1b, and between S/N values for TTSuV1a or TTSuV1b (separately) and TTSuV2 were assessed using Spearman's correlation coefficient. The correlations were separately generated for a combination of 3 groups (group-A to group-C).

To assess the synergistic effects between PCV2 and TTSuV1 on disease prevalence, the pigs in group B were categorized as follows: pigs positive for both PCV2 and TTSuV1, pigs only positive for PCV2, pigs only positive for TTSuV1, and pigs with neither PCV2 nor TTV1. Subsequently, the proportions of affected pigs were compared between the groups using Fisher’s exact test. Statistical significance was set to alpha=0.05.

Example 43

Transfection of PK-15 Cell with TTSuV Expression Constructs

PK-15 cells were seeded onto a 6-well plate and grown until 70%-80% confluency before transfection. Two micrograms of each of the three constructs pTri-la ORF1, pTri-b ORF1 and pTri-2c ORF1, mixed with 10 μl of Lipofectamine LTX (Invitrogen), were transfected into the cells, respectively. Cells were cultured for 3 days and were subjected to IFA to detect the ORF1 expression.

Example 44

Immunofluorescence Assay (IFA)

Five rabbit antisera were used for IFA staining, including anti-TTSuV1a, anti-TTSuV1b, anti-TTSuV2, pre-bleed rabbit negative control serum, and rabbit anti-human genogroup-1 TTV ORF1 antiserum (AK47; a generous gift from Dr. Annette Mankertz at the Robert Koch-Institute, Berlin, Germany). Transfected cells were fixed with acetone. Five hundred microliters of each of the five antisera, at a 1:500 dilution in PBS, was added on top of the cells in each well and incubated for 1 hour at room temperature. After three washing steps with PBS, the cells were incubated with 50 μl Alexa Fluor 488-labeled goat anti-rabbit IgG (Invitrogen) at a 1:200 dilution for 1 hour incubation at room temperature. Cells were stained with 500 μl DAPI (KPL, Inc.) at a 1:1000 dilution and visualized under a fluorescence microscope.

### TABLE 6

Reactivity of anti-TTSuV1a, anti-TTSuV1b, anti-TTSuV2, pre-bleed rabbit and anti-human TTV (AK47) sera in PCV1-free PK-15 cells transfected with plasmids encoding truncated ORF1s from TTSuV1a, TTSuV1b and TTSuV2, respectively, as determined by IFA. The intensity of the fluorescent signal was determined visually and expressed ranging from − to ++.

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<211> LENGTH: 2875
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 10

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agggcctatgt cggagactcag ggttgctgtaa ggggagctcaaa ggtgacgcaac 420
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gggtctggtct caggatcgag caaagacaccg cagtgcagatg ggtgtgctg 540
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<211> LENGTH: 2750
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 11
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<211> LENGTH: 2803
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 12
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    cccacacca ggaacactac aacaataccg ccaacaccgc gacacatca ccaacacac 180
    cagaaacactg tgcaaaaaag gggataaaa ttctatatggc gggatctgaa gttcacaat 240
    gaaataaaaa aacacaaact gaaacaacct cctctttttg aagttggcag taacatcaca 300
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<210> SEQ ID NO 13
<211> LENGTH: 635
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 13

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Lys Arg Arg Gly Gly Trp Arg Arg Arg Phe Arg Ile Arg Arg Arg Arg 20 25 30
Pro Trp Arg Arg Val Arg Arg Trp Arg Arg Ser Val Phe Arg 35 40 45
Arg Gly Gly Arg Ala Arg Ala Arg Phe Arg Ile Ser Ala Trp Asn Pro 50 55 60
Lys Val Leu Arg Asn Cys Arg Ile Thr Gly Trp Trp Pro Val Ile Gln 65 70 75 80
Cys Met Asp Gly Met Glu Trp Ile Lys Tyr Lys Pro Met Asp Leu Arg 85 90 95
Val Glu Ala Asn Trp Ile Phe Asn Lys Glu Asp Ser Lys Ile Glu Thr 100 105 110
Glu Gln Met Gly Tyr Leu Met Glu Tyr Gly Gly Gly Trp Ser Ser Gly 115 120 125
Val Ile Ser Leu Glu Gly Leu Phe Asn Glu Asn Leu Trp Arg Asn 130 135 140
Ile Trp Ser Lys Ser Asn Asp Gly Met Asp Leu Val Arg Phe Gly 145 150 155 160
Cys Arg Ile Arg Leu Tyr Pro Thr Glu Asn Glu Asp Tyr Leu Phe Trp 165 170 175
Tyr Asp Thr Glu Phe Asp Glu Gln Glu Arg Arg Met Leu Asp Glu Tyr 180 185 190
Thr Glu Pro Ser Val Met Leu Glu Ala Lys Asn Ser Arg Leu Ile Val 195 200 205
Cys Lys Glu Lys Met Pro Ile Arg Arg Arg Val Lys Ser Ile Phe Ile 210 215 220
Pro Pro Pro Ala Gin Leu Thr Thr Gin Trp Lys Phe Gin Gin Glu Leu 225 230 235 240
Cys Glu Phe Pro Leu Phe Asn Trp Ala Cys Ile Cys Ile Asp Met Asp 245 250 255
Thr Pro Phe Asp Tyr Asn Ala Trp Arg Asn Ala Trp Trp Leu Met 260 265 270
Arg Arg Leu Gin Asn Gin Met Glu Tyr Ile Glu Arg Trp Gly Arg 275 280 285
Ile Pro Met Thr Gly Asp Thr Glu Leu Pro Pro Asp Asp Phe Lys 290 295 300
Ala Gly Gly Val Asn Lys Asn Phe Lys Pro Thr Gly Ile Gin Arg Ile 305 310 315 320
Tyr Pro Ile Val Ala Val Cys Leu Val Glu Gly Asn Lys Arg Val Val 325 330 335
Lys Trp Ala Thr Val His Asn Gly Pro Ile Asp Arg Trp Arg Lys Lys 340 345 350
Gln Thr Gly Thr Leu Lys Leu Ser Asn Leu Arg Gly Leu Val Leu Arg 355 360 365
Val Cys Ser Glu Ser Glu Thr Tyr Lys Trp Thr Gly Ser Glu Phe 370 375 380
Thr Gly Ala Phe Gln Asp Trp Trp Pro Val Gly Gly Thr Gly Tyr 390 385 395 400
Pro Leu Cys Thr Ile Lys Met Asp Pro Glu Tyr Glu Asn Pro Thr Val 405 410 415 420
Glu Val Trp Ser Trp Lys Ala Asn Ile Pro Thr Ser Gly Thr Leu Lys 425 430 435
Asp Tyr Phe Gly Leu Ser Thr Gly Gln Gln Trp Lys Asp Thr Asp Phe 440 445
Ala Arg Leu Gln Leu Pro Arg Ser Ser His Asn Val Asp Phe Gly His 450 455 460
Lys Ala Arg Phe Gly Pro Phe Cys Val Lys Lys Pro Pro Val Glu Phe 470 465 475 480
Arg Asp Thr Ala Pro Asn Pro Leu Asn Ile Trp Val Lys Tyr Thr Phe 480 475 485 490 495
Tyr Phe Gln Phe Gly Gly Met Tyr Gln Pro Pro Thr Gly Ile Gln Asp 495 490 500 505 510
Pro Cys Thr Ser Asn Pro Thr Pro Val Met Val Gly Ala Val 510 515 520 525
Thr His Pro Lys Tyr Ala Gly Gln Gly Gly Ile Thr Thr Gln Ile Gly 530 535 540
Asp Gln Gly Ile Thr Ala Asl Ile Arg Ala Ile Ser Ala Pro Asp Asp Thr Tyr Thr Gln Ser Ala Phe Leu Lys Ala Pro Glu Thr Glu 550 545 550 550 555 555 560 565 570 575
Lys Glu Glu Glu Arg Glu Ser Glu Thr Ser Phe Thr Ser Ala Glu Ser 580 575 580 585 590
Ser Ser Glu Gly Asp Gly Ser Ser Asp Asp Gln Ala Glu Arg Arg Ala 595 590 600 600 605
Ala Arg Lys Arg Val Ile Lys Leu Leu Leu Lys Arg Leu Ala Asp Arg 600 605 610 615 620
Pro Val Asp Asn Lys Arg Arg Phe Ser Glu 625 630 635 640

<210> SEQ ID NO 14
<211> LENGTH: 639
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 14
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Arg Tyr Arg Lys Arg Arg Tyr Gly Trp Arg Arg Tyr Tyr Arg Tyr 20 25 30
Arg Pro Arg Tyr Tyr Arg Arg Arg Trp Leu Val Arg Arg Arg Arg 35 40 45
Ser Val Tyr Arg Arg Gly Arg Arg Ala Pro Tyr Arg Ile Ser 50 55 60
Ala Phe Asn Pro Lys Val Met Arg Val Val Ile Arg Gly Trp Trp 65 70 75 80
Pro Ile Leu Gln Cys Leu Lys Gly Gln Glu Ser Leu Arg Tyr Arg Pro 85 90 95
Leu Gln Trp Asp Thr Glu Lys Glu Trp Arg Val Lys Lys Asp Tyr Glu
Ala
Arg
Asn
Ala
Asp
Gln
His
Glu
Pro
Leu
465
Trp
Thr
385
Leu
Lys
305
Lys
Lys
225
Pro
Ser
Cys
225
Pro
Pro
Ser
Arg
Thr
Gln
Arg
Thr
Asp
Phe
225
230
235
240
Cys
Lys
Arg
Pro
Leu
Phe
Thr
Trp
Ala
Ala
Gly
Leu
Ile
Arg
Met
Gln
245
250
255
Lys
Pro
Phe
Asp
Ala
Asn
Gly
Ala
Phe
Arg
Asn
Ala
Trp
Trp
Leu
Glu
260
265
270
Thr
Arg
Asn
Asp
Gln
Gly
Glu
Leu
Trp
Gly
Arg
275
280
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Val
Pro
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Gln
Gly
Asp
Thr
Glu
Leu
Pro
Lys
Gln
Ser
Glu
Phe
Lys
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Lys
Glu
Asp
Asn
Pro
Asn
Tyr
Asn
Ile
Thr
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Gly
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Lys
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315
320
Asn
Ile
Tyr
Val
Ile
Val
Asp
Gln
Lys
Asp
Gln
Lys
Thr
325
330
335
Arg
Lys
Tel
Lys
Cys
Thr
Val
Thr
Leu
Asn
Arg
Trp
Arg
340
345
350
Lys
Ala
Gln
Ala
Ser
Thr
Leu
Ala
Gly
Asp
Leu
Gln
Gly
Leu
Val
355
360
365
Leu
Arg
Gln
Leu
Met
Asn
Gln
Glu
Met
Thr
Tyr
Thr
Trp
Lys
Ser
Gly
370
375
380
Glu
Phe
Ser
Ser
Pro
Phe
Leu
Gln
Arg
Trp
Lys
Gly
Thr
Arg
Leu
Ile
385
390
395
400
Thr
Ile
Asp
Ala
Arg
Lys
Ala
Asp
Thr
Glu
Asn
Pro
Lys
Val
Ser
Ser
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410
415
Trp
Glu
Trp
Gly
Gln
Arg
Trp
Asn
Thr
Ser
Gly
Thr
Val
Leu
Gln
Glu
420
425
430
Val
Phe
Asn
Ile
Ser
Leu
Asn
Thr
Gln
Ile
Arg
Gln
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Phe
435
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445
Ala
Lys
Leu
Thr
Leu
Pro
Lys
Ser
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Pro
His
Asp
Ile
Asp
Phe
Gly
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460
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Phe
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Pro
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Cys
Val
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Asn
Glu
Pro
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Glu
Phe
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Thr
Gly
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510
Pro
Cys
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Asp
Thr
Pro
Asp
Val
Pro
Gln
Ser
Gly
Ser
Val
515
520
525
Thr His Pro Lys Phe Ala Gly Lys Gly Gly Met Leu Thr Glu Thr Asp
530      535      540
Arg Trp Gly Ile Thr Ala Ala Ser Ser Arg Thr Leu Ser Ala Asp Thr
545      550      555      560
Pro Thr Glu Ala Ala Gln Ser Ala Leu Leu Arg Gly Asp Ala Glu Lys
565      570      575
Lys Gly Glu Glu Thr Glu Met Ala Ser Ser Ser Ile Thr Ser
580      585      590
Ala Glu Ser Ser Thr Glu Gly Ser Ser Asp Asp Glu Glu Thr
595      600      605
Ile Arg Arg Arg Arg Arg Thr Trp Lys Arg Leu Arg Met Val Arg
610      615      620
Gln Gln Leu Asp Arg Arg Met Asp His lys Arg Glu Arg Leu His
625      630      635

<210> SEQ ID NO 15
<211> LENGTH: 625
<212> TYPE: PRT
<213> ORGANISM: Torque teno virus

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Trp Arg His Arg Arg Thr Arg Tyr Phe Arg Tyr Arg Tyr Arg Arg
20      25     30
Ala Pro Arg Arg Arg Pro Lys Val Arg Arg Arg Arg Lys Ala
35      40     45
Pro Val Ile Gln Trp Phe Pro Pro Ser Arg Arg Thr Cys Leu Ile Glu
50      55     60
Gly Phe Trp Pro Leu Ser Tyr Gly His Trp Phe Arg Thr Cys Leu Pro
65      70     75    80
Met Arg Leu Asn Gly Leu Ile Phe Thr Gly Gly Gly Cys Asp Thr
85      90     95
Thr Glu Trp Ser Leu Gln Asn Leu Phe His Glu Lys Leu Asn Thr Arg
100     105    110
Asn Ile Thr Ala Ser Val Gly Met Glu Phe Ala Arg Phe Leu
115     120    125
Arg Gly Lys Phe Tyr Phe Arg Arg His Pro Trp Arg Ser Tyr Ile Val
130     135    140
Thr Trp Asp Gln Asp Ile Pro Cys Lys Pro Leu Pro Tyr Gln Asn Leu
145     150    155    160
Gln Pro Leu Leu Met Leu Leu Lys Glu His Lys Leu Val Leu Ser
165     170    175
Gln Lys Asp Cys Asn Pro Asn Arg Lys Glu Pro Val Thr Leu Lys
180     185    190
Phe Arg Pro Pro Pro Lys Leu Thr Ser Gln Trp Arg Leu Ser Arg Glu
195     200    205
Leu Ser Lys Ile Pro Leu Ile Leu Gly Ile Ser Leu Ile Asp Leu
210     215    220
Ser Glu Pro Trp Leu Glu Gly Trp Asp Ala Phe Tyr Ser Val Leu
225     230    235    240
Gly Tyr Glu Ala Ser Lys His Ser Ser Gly Arg Trp Ser Asn Thr Glu
245     250    255
Met Lys Tyr Phe Trp Ile Tyr Arg Thr Gly Val Gly Asn Ala Val Tyr

-continued
Thr Glu Met Val Asn Glu Gly Trp Pro Tyr Trp Leu Phe Phe Tyr Gly 305 310 315 320
Gln Ser Glu Gln Asp Ile Lys Leu Ala His Asp Gln Asp Ile Val 325 330 335
Arg Glu Tyr Ala Arg Asp Pro Lys Ser Lys Lys Leu Lys Ile Gly Val 340 345 350
Ile Gly Trp Ala Ser Ser Tyr Thr Thr Ala Gly Ser Asn Glu Asn 350 355 360 365
Ser Val Leu Gln Thr Pro Glu Ala Ile Gln Gly Tyr Val Ala Tyr 370 375 380
Ala Gly Ser Arg Ile Pro Gly Ala Gly Ser Ile Thr Asn Leu Phe Gln 385 390 395 400
Met Gly Trp Pro Gly Asp Gln Asn Trp Pro Pro Thr Asn Gln Asp Gln 405 410 415
Thr Asn Phe Asn Trp Gly Leu Arg Gly Leu Cys Val Leu Arg Asp Asn 420 425 430
Met Lys Leu Gly Ala Gln Leu Asp Asp Glu Cys Thr Met Leu Ser 435 440 445
Leu Phe Gly Pro Phe Val Glu Ala Asn Thr Ala Phe Ala Thr Asn 450 455 460
Asp Pro Lys Tyr Phe Arg Pro Glu Leu Lys Asp Tyr Asn Val Met 465 470 475 480
Lys Tyr Ala Phe Lys Phe Gln Trp Gly Gly His Gly Thr Glu Arg Phe 490 495
Lys Thr Thr Ile Gly Asp Pro Ser Thr Ile Pro Cys Pro Phe Glu Pro 500 505 510
Gly Glu Arg Tyr His His Gly Val Gln Asp Pro Ala Lys Val Glu Asn 515 520 525
Thr Val Leu Asn Pro Trp Asp Tyr Asp Cys Asp Gly Ile Val Arg Thr 530 535 540
Asp Thr Leu Lys Arg Leu Leu Glu Leu Pro Thr Glu Thr Glu Glu Thr 545 550 555 560
Glu Lys Ala Tyr Pro Leu Leu Gly Gln Lys Thr Glu Lys Glu Pro Leu 565 570 575
Ser Asp Ser Asp Glu Glu Ser Val Ile Ser Ser Thr Ser Ser Gly Ser 580 585 590
Ser Gln Glu Glu Glu Thr Gln Arg Arg Lys His His Lys Pro Ser Lys 595 600 605
Arg Arg Leu Leu Lys His Leu Gln Arg Val Val Lys Arg Met Lys Thr 610 615 620
Leu 625

<210> SEQ ID NO 16
<211> LENGTH: 625
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 16
Met Pro Tyr Arg Arg Tyr Arg Arg Arg Arg Arg Arg Arg Arg Arg Pro Thr Arg Arg 1 5 40 15
Trp Arg His Arg Arg Trp Arg Arg Phe Phe Arg Tyr Arg Arg Arg Arg 20 25 30
Ala Pro Arg Arg Arg Trp Thr Lys Val Arg Arg Arg Arg Arg Lys Ala 35 40 45
Pro Val Ile Gln Trp Phe Pro Pro Ser Arg Arg Thr Cys Leu Ile Glu 50 55 60
Gly Phe Trp Pro Leu Ser Tyr Gly His Trp Phe Arg Thr Cys Leu Pro 65 70 75 80
Met Arg Arg Leu Asn Gly Leu Ile Phe Thr Gly Gly Gly Cys Asp Trp 85 90 98
Thr Glu Trp Ser Leu Gln Asn Leu Tyr His Glu Lys Leu Asn Trp Arg 100 105 110
Asn Ile Trp Thr Ala Ser Asn Val Gly Met Glu Phe Ala Arg Phe Leu 115 120 125
Arg Gly Lys Phe Tyr Phe Arg His Pro Trp Arg Ser Tyr Ile Ile 130 135 140
Thr Trp Asp Gln Asp Ile Pro Cys Lys Pro Leu Pro Tyr Gln Asn Leu 145 150 155 160
His Pro Leu Leu Met Leu Leu Lys Gln His Lys Leu Val Leu Ser 165 170 175
Gln Lys Asp Cys Asn Pro Asn Arg Arg Gln Lys Pro Val Thr Leu Lys 180 185 190
Ile Arg Pro Pro Pro Lys Leu Thr Ser Glu Pro Leu Pro Ser Arg Glu 195 200 205
Leu Ala Lys Met Pro Leu Val Arg Leu Gly Val Ser Leu Ile Asp Leu 210 215 220
Ser Glu Pro Trp Leu Glu Gly Trp Gln Asn Ala Phe Tyr Ser Val Leu 225 230 235 240
Gly Tyr Glu Ala Ser Lys His Ser Gly Arg Trp Ser Asn Trp Thr Gln 245 250 255
Ile Lys Tyr Phe Trp Ile Tyr Asp Thr Gly Val Gly Asn Ala Val Tyr 260 265 270
Val Ile Leu Leu Lys Gln Glu Val Asp Asn Asn Pro Gly Ala Met Ala 275 280 285
Thr Lys Phe Val Thr Gly Pro Gly Gln His Pro Asp Ala Ile Asp Arg 290 295 300
Ile Glu Gln Ile Asn Glu Gly Trp Pro Tyr Trp Leu Phe Phe Tyr Gly 305 310 315 320
Gln Ser Glu Gln Asp Ile Lys Leu Ala His Asp Gin Glu Ile Ala 325 330 335
Arg Glu Tyr Ala Asn Asn Pro Lys Ser Lys Lys Leu Lys Ile Gly Val 340 345 350
Ile Gly Trp Ala Ser Ser Asn Phe Thr Thr Ala Gly Ser Ser Gin Asn 355 360 365 370
Gln Thr Pro Gln Pro Pro Glu Ala Ile Gln Gly Gly Gly Tyr Val Ala Tyr 370 375 380
Ala Gly Ser Lys Ile Gln Gly Ala Gly Ala Ile Thr Asn Leu Tyr Thr 385 390 395 400
Asp Ala Trp Pro Gly Asp Gln Asn Trp Pro Pro Leu Asn Arg Glu Gin 405 410 415
Thr Asn Phe Asn Trp Gly Leu Arg Gly Leu Cys Ile Met Arg Asp Asn
Met Lys Leu Gly Ala Gln Glu Leu Asp Asp Glu Cys Thr Met Leu Thr
420 425 430
Leu Phe Gly Pro Phe Val Glu Ala Asn Thr Ala Phe Ala Thr Asn
435 450 455 460
Asp Pro Lys Tyr Phe Arg Pro Glu Leu Lys Asp Tyr Asn Ile Val Met
465 470 475 480
Lys Tyr Ala Phe Lys Phe Gin Trp Gly Gly His Gly Thr Glu Arg Phe
485 490 495
Lys Thr Thr Ile Gly Asp Pro Ser Thr Ile Pro Cys Pro Phe Glu Pro
500 505 510
Gly Glu Arg Tyr His His Gly Val Gln Asp Pro Ala Lys Val Gln Asn
515 520 525
Thr Val Leu Asn Pro Trp Asp Tyr Asp Cys Asp Gln Ile Val Arg Thr
530 535 540
Asp Thr Leu Lys Arg Leu Leu Glu Leu Pro Thr Glu Thr Glu Thr
545 550 555 560
Glu Lys Ala Tyr Pro Leu Leu Gly Gln Thr Gln Leu Gly Glu Pro Leu
565 570 575
Ser Asp Ser Asp Glu Glu Ser Val Ile Ser Ser Thr Ser Ser Gly Ser
580 585 590
Ser Gln Glu Glu Thr Gln Arg Arg Gin His Lys Pro Ser Lys
595 600
Arg Arg Leu Leu Lys His Leu Gin Arg Val Val Lys Arg Met Lys Thr
610 615 620
Leu
625

<210> SEQ ID NO 17
<211> LENGTH: 73
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 17
Met Lys Glu Lys Asp Tyr Trp Glu Glu Ala Trp Leu Thr Ser Cys Thr
1 5 10 15
Ser Ile His Asp His His Cys Asn Cys Gin Ser Trp Arg Asp His Leu
20 25 30
Trp Thr Leu Cys Ala Leu Asp Asp Ala Asp Leu Ala Ala Ala Asp
35 40 45
Ile Ile Glu Arg Glu Glu Ala Asp Gly Glu Asp Phe Gly Phe Val
50 55 60
Asp Gly Asp Pro Gly Asp Ala Gly Gly
65 70

<210> SEQ ID NO 18
<211> LENGTH: 72
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 18
Met Pro Glu His Trp Glu Glu Ala Trp Leu Glu Ala Thr Lys Gly Trp
1 5 10 15
His Asp Leu Asp Cys Arg Cys Gin Trp Gin Asp His Leu Thr Leu
20 25 30
Leu Leu Ala Asp Gly Asp Ala Leu Ala Ala Ala Val Asp Ala Ile
Glu Arg Asp Ala Met Gly Gly Glu Asp Val Thr Thr Ala Thr Asp Arg
Val Thr Ile Gly Asp Arg Gly Trp

<210> SEQ ID NO 19
<211> LENGTH: 68
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 19
Met Glu Glu Arg Trp Leu Thr Val Ala Tyr Cys Ala His Gly Leu Phe
1 5 10 15
Cys Asp Cys Lys Asp Pro Lys Lys His Leu Glu Cys Leu Thr Asp
20 25 30
Ala Ile Ala Asp Ala Glu Gly Arg His Gly Asp Gly Gly Thr Gly
35 40 45
Gly Gly Asp Ala Thr Phe Asp Ile Gly Ile Asp Ala Leu Leu Ala Ala
50 55 60
Ala Ala Gln Arg
65

<210> SEQ ID NO 20
<211> LENGTH: 69
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 20
Met Glu Glu Arg Trp Leu Thr Val Ala Tyr Cys Ala His Gly Leu Phe
1 5 10 15
Cys Gly Cys Lys Asp Pro Lys Lys His Leu Glu Cys Leu Thr Asp
20 25 30
Ala Ile Ala Asp Ala Glu Gly Arg His Gly Asp Gly Gly Thr Gly
35 40 45
Gly Gly Asp Ala Ser Phe Asp Ile Gly Ile Asp Ala Leu Leu Ala Ala
50 55 60
Ala Ala Gln Arg
65

<210> SEQ ID NO 21
<211> LENGTH: 174
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 21
Met Arg Phe Arg Arg Arg Phe Gly Arg Arg Arg Arg Tyr Tyr Arg
1 5 10 15
Lys Arg Gly Gly Trp Arg Arg Arg Phe Arg Ile Arg Arg Arg Arg
20 25 30
Pro Trp Arg Arg Phe Gly Gly Met Tyr Gln Pro Thr Gly
35 40 45
Ile Gln Asp Pro Cys Thr Ser Asn Pro Thr Tyr Pro Val Arg Met Val
50 55 60
Gly Ala Val Thr His Pro Lys Tyr Ala Gly Gln Gly Gly Ile Thr Thr
65 70 75 80
Gln Ile Gly Asp Gin Gln Ile Thr Ala Ala Ser Ile Arg Ala Ile Ser
85 90 95
Ala Ala Pro Pro Asp Thr Tyr Thr Gln Ser Ala Phe Leu Lys Ala Pro 100 105 110
Glu Thr Glu Lys Glu Glu Glu Arg Ser Glu Thr Ser Phe Thr Ser 115 120 125
Ala Glu Ser Ser Ser Gly Asp Gly Ser Ser Asp Asp Gin Ala Glu 130 135 140
Arg Arg Ala Ala Arg Lys Arg Val Ile Lys Leu Leu Leu Lys Arg Leu 145 150 155 160
Ala Asp Arg Pro Val Asp Asn Lys Arg Arg Phe Ser Glu 165 170

<210> SEQ ID NO 22
<211> LENGTH: 182
<212> TYPE: PRT
<213> ORGANISM: Torque teno virus

<400> SEQUENCE: 22
Met Ala Pro Thr Arg Arg Trp Arg Arg Phe Gly Arg Arg Arg Arg 1 5 10 15
Arg Tyr Arg Lys Arg Arg Tyr Gly Trp Arg Arg Tyr Tyr Tyr Arg 20 25 30
Arg Pro Arg Tyr Tyr Arg Arg Trp Leu Phe Gly Gly Gly Tyr Gin 35 40 45
Pro Pro Thr Gly Ile Arg Asp Ile Asp Thr Pro Ala Tyr Pro 50 55 60
Val Pro Gln Ser Gly Ser Val Thr His Pro Lys Phe Ala Gly Lys Gly 65 70 75 80
Gly Met Leu Thr Glu Thr Asp Trp Gly Ile Thr Ala Ala Ser Ser 85 90 95
Arg Thr Leu Ser Ala Asp Thr Pro Thr Glu Ala Ala Gin Ser Ala Leu 100 105 110
Leu Arg Gly Asp Ala Glu Lys Gly Glu Glu Thr Glu Glu Thr Ala 115 120 125
Ser Ser Ser Ser Ile Thr Ser Ala Glu Ser Ser Ser Thr Gly Asp Gly 130 135 140
Ser Ser Asp Asp Glu Glu Thr Ile Arg Arg Arg Arg Arg Thr Trp Lys 145 150 155 160
Arg Leu Arg Met Val Arg Gin Glu Leu Asp Arg Arg Met Asp His 165 170 175
Lys Arg Glu Arg Leu His 180

<210> SEQ ID NO 23
<211> LENGTH: 178
<212> TYPE: PRT
<213> ORGANISM: Torque teno virus

<400> SEQUENCE: 23
Met Pro Tyr Arg Arg Tyr Arg Arg Arg Arg Arg Arg Pro Thr Arg Arg 1 5 10 15
Trp Arg His Arg Arg Arg Tyr Phe Arg Tyr Arg Tyr Arg Arg Arg 20 25 30
Ala Pro Arg Arg Arg Pro Lys Trp Gly Gin His Gly Thr Glu Arg 35 40 45
Phe Lys Thr Thr Ile Gly Asp Pro Ser Thr Ile Pro Cys Pro Phe Glu 50 55 60
Pro Gly Glu Arg Tyr His His Gly Val Gln Asp Pro Ala Lys Val Gln
65 70 75 80
Asn Thr Val Leu Asn Pro Trp Tyr Asp Cys Asp Gly Ile Val Arg
85 90 95
Thr Asp Thr Leu Lys Arg Leu Leu Glu Leu Pro Thr Glu Thr Glu Glu
100 105 110
Thr Glu Lys Ala Tyr Pro Leu Leu Gly Gln Lys Thr Glu Lys Glu Pro
115 120 125
Leu Ser Asp Ser Asp Glu Ser Val Ile Ser Ser Thr Ser Ser Gly
130 135 140
Ser Ser Gln Glu Glu Thr Gln Arg Arg Lys His His Lys Pro Ser
145 150 155 160
Lys Arg Arg Leu Leu Lys His Leu Gln Arg Val Val Lys Arg Met Lys
165 170 175
Thr Leu

<210> SEQ ID NO 24
<211> LENGTH: 178
<212> TYPE: Pratt
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 24
Met Pro Tyr Arg Tyr Arg Arg Arg Arg Arg Arg Pro Thr Arg Arg
1 5 10 15
Trp Arg His Arg Arg Arg Trp Arg Arg Phe Phe Arg Tyr Arg Arg
20 25 30
Ala Pro Arg Arg Arg Arg Thr Lys Trp Gly Gly His Gly Thr Glu Arg
35 40 45
Phe Lys Thr Thr Ile Gly Asp Pro Thr Ile Pro Cys Pro Phe Glu
50 55 60
Pro Gly Glu Arg Tyr His His Gly Val Gln Asp Pro Ala Lys Val Gln
65 70 75 80
Asn Thr Val Leu Asn Pro Trp Tyr Asp Cys Asp Gly Ile Val Arg
85 90 95
Thr Asp Thr Leu Lys Arg Leu Leu Glu Leu Pro Thr Glu Thr Glu Glu
100 105 110
Thr Glu Lys Ala Tyr Pro Leu Leu Gly Gln Lys Thr Glu Lys Glu Pro
115 120 125
Leu Ser Asp Ser Asp Glu Ser Val Ile Ser Ser Thr Ser Ser Gly
130 135 140
Ser Ser Gln Glu Glu Thr Gln Arg Arg Lys His His Lys Pro Ser
145 150 155 160
Lys Arg Arg Leu Leu Lys His Leu Gln Arg Val Val Lys Arg Met Lys
165 170 175
Thr Leu

<210> SEQ ID NO 25
<211> LENGTH: 224
<212> TYPE: Pratt
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 25
Met Lys Glu Lys Asp Tyr Trp Glu Glu Ala Trp Leu Thr Ser Cys Thr
1 5 10 15
Ser Ile His Asp His His Cys Asn Cys Gly Ser Trp Arg Asp His Leu
Trp Thr Leu Cys Ala Leu Asp Asp Ala Asp Leu Ala Ala Ala Ala Ala Ala Asp
Ile Ile Glu Arg Glu Glu Ala Asp Gly Gly Glu Asp Phe Gly Phe Val
Asp Gly Asp Pro Gly Asp Ala Gly Gly Ser Ala Ala Cys Thr Ser Leu
Pro Pro Glu Ser Lys Ile Pro Ala Leu Leu Thr Arg Pro Ile Leu Ser
Glu Trp Ser Glu Gin Leu His Thr Pro Asn Thr Pro Gly Lys Ala Glu
Ser Arg Pro Lys Leu Glu Ile Lys Val Ser Pro Leu Pro Leu Ser Val
Pro Ser Val Gin Leu His Gin Ile Pro Thr Arg Ser Arg Arg Ser Ser
Lys Pro Arg Lys Pro Arg Lys Gin Gin Arg Gin Gin Gin Gin Gin Gin
Ser Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
<210> SEQ ID NO 26
<211> LENGTH: 228
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 26
Met Met Lys Arg Gln Ser Asp Ala Glu Gly Gly Pro Gly Ser Asp Ser
180 185 190
Asp Gly Trp Ser Asp Ser Ser Leu Thr Asp Glu Trp Thr Thr Ser Asp
195 200 205
Ser Asp Phe Ile Asp Thr Pro Ile Arg Glu Arg Cys Leu Asn Lys Lys
210 215 220
Gln Lys Lys Arg
225

SEQ ID NO 27
LENGTH: 199
TYPE: PRT
ORGANISM: Torque teno virus

SEQUENCE: 27
Met Glu Glu Arg Trp Leu Thr Val Ala Tyr Cys Ala His Gly Leu Phe
1 5 10 15
Cys Asp Cys Lys Asn Pro Lys Lys His Leu Glu Lys Cys Leu Thr Asp
20 25 30
Ala Ile Ala Asp Ala Glu Asp Asp Gly Asp Gly Thr Gly
35 40 45
Gly Gly Asp Ala Thr Phe Asp Ile Gly Ile Asp Ala Leu Leu Ala Ala
50 55 60
Ala Ala Gln Ser Gly Asp Met Ala Pro Lys Leu Lys Cys Gly Thr Gly
65 70 75 80
Ser Glu Ile Pro Ala Pro Tyr His Val Pro Leu Asn Pro Gly Asn Gly
85 90 95
Thr Thr Thr Gly Tyr Lys Thr Pro Pro Arg Tyr Lys Thr Gin Ser Ser
100 105 110
Thr Leu Gly Thr Met Thr Val Thr Gly Leu Leu Gin Ile Leu Ser
115 120 125
Lys Asp Phe Ser Asn Ser Pro Gin Arg Arg Arg Arg Arg Arg Arg Arg
130 135 140
Thr His Ser Leu Asp Lys Gin Arg Lys Ser His Tyr Gin Thr Pro
145 150 155 160
Thr Lys Arg Ala Leu Ser Gin Ala Arg Ala Val Asp Pro Leu Lys Lys
165 170 175
Lys Arg Arg Arg Asp Gin Ser Thr Ser Gin Ala Ser Asp Ser Asp Ser
180 185 190
Ser Ser Thr Ser Ser Gly Trp
195

SEQ ID NO 28
LENGTH: 199
TYPE: PRT
ORGANISM: Torque teno virus

SEQUENCE: 28
Met Glu Glu Arg Trp Leu Thr Val Ala Tyr Cys Ala His Gly Leu Phe
1 5 10 15
Cys Gly Cys Lys Asp Pro Lys Lys His Leu Glu Lys Cys Leu Thr Asp
20 25 30
Ala Ile Ala Asp Ala Glu Asp Asp Gly Asp Gly Thr Gly
35 40 45
Gly Gly Asp Ala Ser Phe Asp Ile Gly Ile Asp Ala Leu Leu Ala Ala
50 55 60
Ala Ala Gln Ser Gly Glu Ala Thr Glu Pro Lys Asp Ser Lys Gln Pro
65 70 75 80
Ser Glu Ile Pro Ala Pro Tyr His Val Pro Leu Asn Pro Gly Asn Gly
85 90 96
Thr Thr Thr Gly Tyr Lys Thr Pro Pro Arg Tyr Lys Thr Gln Ser Ser
100 105 110
Thr Leu Gly Thr Met Thr Val Thr Gly Leu Leu Glu Gln Ile Leu Ser
115 120 125
Lys Asp Phe Ser Asn Ser Pro Gln Arg Arg Arg Arg Arg Arg Arg
130 135 140
Thr His Ser Leu Asp Lys Gln Gln Ser His Tyr Gln Thr Pro
145 150 155 160
Thr Lys Arg Ala Leu Ser Gln Ala Arg Ala Val Asp Pro Leu Lys Lys
165 170 175
Lys Arg Arg Arg Glu Glu Asp Ser Thr Ser Glu Ala Ser Asp Asp Ser
180 185 190
Ser Ser Thr Ser Ser Gly Trp
195

<210> SEQ ID NO 29
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 29
tccgatggc tgagtttatg c 21

<210> SEQ ID NO 30
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 30
tccgotacgc tgtcct 17

<210> SEQ ID NO 31
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 31
ggtggttaag agatgaa 18

<210> SEQ ID NO 32
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 32
aatagattgg acacaggag 19

<210> SEQ ID NO 33
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 33
tatcgggcag gagcaget 18

<210> SEQ ID NO 34
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 34
tagggcgcgc cttcagct

<210> SEQ ID NO 35
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 35
cctacatgaa ggagaagac t

<210> SEQ ID NO 36
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 36
ccaggtctc caggttc

<210> SEQ ID NO 37
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 37
agcteccaa gggctgg

<210> SEQ ID NO 38
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 38
gcgctctggt agcggtagt

<210> SEQ ID NO 39
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 39
cgaatggctg agtttatge g

<210> SEQ ID NO 40
<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 40
agtcctcatt t

<210> SEQ ID NO 41
<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 41
aaccaatcag a
<210> SEQ ID NO 42
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 42
cggggcggt gocggag

<210> SEQ ID NO 43
<211> LENGTH: 14
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 43
cggagtcagggc

<210> SEQ ID NO 44
<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 44
tacgggccag g

<210> SEQ ID NO 45
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 45
tacacttcgg ggttcagggc
gct

<210> SEQ ID NO 46
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 46
actcagccat togaaacttc ac

<210> SEQ ID NO 47
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 47
casatttgcg cggttcgctgc

c
<210> SEQ ID NO 48
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 48
tacttatatt cggttcgctgc ggaac

<210> SEQ ID NO 49
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 49
agttacacatat accaccaas cc
<210> SEQ ID NO 50
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 50
attaccgct goccogatagg c 21

<210> SEQ ID NO 51
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 51
ccaaaccaca ggaaactgtg c 21

<210> SEQ ID NO 52
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 52
cttgacttccg ctctcaaggag 20

<210> SEQ ID NO 53
<211> LENGTH: 2878
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 53
tacacttccg ggttcaaggag gtcgacatttg gttcgatttcg ctggaacacac gtttggtgct 60
agccggagctc gattgaacac gcgaaanctgta taaattcaca tttgaaatag gcgcggcagaac 120
tggcgcag cggcgccggt ttgcggcaat caggcttga ccgtgctgca ggccggggagc 180
ttmaatttaga caaagtggaa gacggatatttag ctggtctgta ggcgtctgtgcgtgctgct 240
gcatagttgg taccatacatc gattgacggt ctgctctgctgctgctgctgctgctgctgctgct 300
gttcaaatcatg ggtttttttt gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 360
tggtacgagacg agctttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt 420
tggtgacgatgctt gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 480
tacaagaactac acacagttca accgttca cagcttttt cagcttttt cagcttttt cagcttttt 540
tttgggcttc gtttcatcag ggttcggcttt gcgtgtcatt tctttttttttt ttttttttttt ttttttttttt 600
gggggttacg ggtttttttt gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 660
tgacacacacac cttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt 720
ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt 780
ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt 840
ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt 900
ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt 960
ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt 1020
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ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt 1140
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ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt 1260
ttcattatt taactgggcc tgtatctgta tagacatgga caacgcgttc gactacaaag
1320
ggcgtatggc aaatgtcttg tgcgcttaa gaaagcaacc atggggttca
1380
tagagagctg ccagacagc acagacagc atggggttca
1440
tcaaggccag gggtgtcgg aacactatca gaaaggcagc tattcgaga tataaccct
1500
tagtagctg ctagctgtag gaggaggttg cagtcggttag ccactgttga
1560
tggccagtta agacgcttaa ccacatgtaa ttatctggta gcacatgtaa
1620
tatatttcat ccagacagc acagacagc atggggttca
1680
tgggtgcttg ccttattccaa tcagactttg ggttattgta tgggtgcttg
1740
tagggcattc cactgttta tcagacggtg ctagcatttg tattattttg
1800
cactgttta ccacatgtaa ccacatgtaa ccacatgtaa ccacatgtaa
1860
tgggtgcttg ccttattccaa tcagactttg ggttattgta tgggtgcttg
1920
ttaggtggttgt gcgtattgcg ccactgttga ttcctgttga tgggtgcttg
1980
tgggtgcttg ccttattccaa tcagactttg ggttattgta tgggtgcttg
2040
ttaggtggttgt gcgtattgcg ccactgttga ttcctgttga tgggtgcttg
2100
tgggtgcttg ccttattccaa tcagactttg ggttattgta tgggtgcttg
2160
ttaggtggttgt gcgtattgcg ccactgttga ttcctgttga tgggtgcttg
2220
tgggtgcttg ccttattccaa tcagactttg ggttattgta tgggtgcttg
2280
ttaggtggttgt gcgtattgcg ccactgttga ttcctgttga tgggtgcttg
2340
tgggtgcttg ccttattccaa tcagactttg ggttattgta tgggtgcttg
2400
ttaggtggttgt gcgtattgcg ccactgttga ttcctgttga tgggtgcttg
2460
tgggtgcttg ccttattccaa tcagactttg ggttattgta tgggtgcttg
2520
ttaggtggttgt gcgtattgcg ccactgttga ttcctgttga tgggtgcttg
2580
tgggtgcttg ccttattccaa tcagactttg ggttattgta tgggtgcttg
2640
ttaggtggttgt gcgtattgcg ccactgttga ttcctgttga tgggtgcttg
2700
tgggtgcttg ccttattccaa tcagactttg ggttattgta tgggtgcttg
2760
ttaggtggttgt gcgtattgcg ccactgttga ttcctgttga tgggtgcttg
2820
tgggtgcttg ccttattccaa tcagactttg ggttattgta tgggtgcttg
2878

<210> SEQ ID NO 54
<211> LENGTH: 635
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 54

Met Arg Phe Arg Arg Arg Arg Arg Phe Gly Arg Arg Arg Arg Tyr Tyr Arg
1 5 10 15
Lys Arg Arg Gly Gly Trp Arg Arg Arg Phe Arg Ile Arg Arg Arg Arg
20 25 30
Pro Trp Arg Arg Arg Arg Val Arg Arg Trp Arg Arg Ser Val Phe Arg
35 40 45
Arg Arg Gly Arg Arg Ala Arg Pro Tyr Arg Ile Ser Ala Trp Atn Pro
50 55 60
Lys Val Leu Arg Atn Cys Arg Ile Thr Gly Trp Trp Pro Val Ile Gln
65 70 75 80
Cys Met Asp Gly Met Glu Trp Ile Lys Tyr Lys Pro Met Asp Leu Arg
Val Glu Ala Asn Arg Ile Phe Asp Lys Gln Gly Ser Lys Ile Glu Thr
Glu Gln Met Gly Tyr Leu Met Gln Tyr Gly Gly Gly Trp Ser Ser Gly
Val Ile Ser Leu Glu Leu Phe Asn Glu Asn Arg Leu Trp Arg Asn
Ile Trp Ser Ser Asn Asp Gly Met Asp Leu Val Arg Tyr Phe Gly
Cys Arg Ile Arg Leu Tyr Pro Thr Gln Asn Glu Gly Tyr Leu Phe Trp
Tyr Asp Thr Glu Phe Asp Glu Gin Gin Arg Arg Met Leu Asp Glu Tyr
Thr Gln Pro Ser Val Met Leu Gin Ala Lys Asn Ser Arg Leu Ile Val
Cys Lys Gin Lys Met Pro Ile Arg Arg Arg Val Lys Ser Ile Phe Ile
Pro Pro Pro Ala Gin Leu Thr Thr Gin Trp Lys Phe Gin Gin Glu Leu
Cys Gin Phe Pro Leu Phe Asn Trp Ala Cys Ile Cys Ile Asp Met Asp
Thr Pro Phe Asp Tyr Asn Gln Gin Ala Trp Arg Asn Ala Trp Trp Leu Met
Arg Arg Leu Gin Asn Gin Met Gin Tyr Ile Gin Gly Arg Tyr Gin Met
Ile Pro Met Thr Gly Asp Thr Glu Leu Pro Pro Ala Asp Asp Phe Lys
Ala Gly Gin Asn Gin Met Arg Lys Arg Gin Arg Gin Lys 310 315 320
Tyr Pro Ile Val Ala Val Cys Leu Val Glu Gly Asn Gin Arg Val Val
Lys Trp Ala Thr Val His Gin Gin Pro Ile Asp Arg Trp Arg Lys Lys
Gln Thr Gly Thr Leu Lys Leu Ser Ala Leu Arg Arg Leu Val Leu Arg
Val Cys Ser Glu Ser Glu Thr Tyr Tyr Lys Trp Thr Ala Ser Glu Phe
Thr Gly Ala Phe Gin Gin Asp Trp Trp Pro Val Ser Gly Thr Glu Tyr
Pro Leu Cys Thr Ile Lys Met Gin Pro Glu Phe Gin Gin Asn Pro Thr Val
Glu Val Trp Ser Trp Lys Ala Thr Ile Pro Thr Ala Gly Thr Leu Lys
Asp Tyr Phe Gin Gly Ser Ser Gly Gin Gin Trp Lys Gin Asp Thr Gin Met
Gly Arg Leu Gin Leu Pro Arg Ser Ser His Gin Val Gin Phe Gin Gin
Lys Ala Arg Phe Gin Pro Phe Cys Val Lys Gin Pro Pro Val Gin Phe
Arg Asp Ser Ala Pro Gin Pro Leu Gin Gin Ile Gin Lys Gin Gin Gin
Tyr Phe Gin Gin Phe Gin Gin Met Tyr Gin Gin Pro Pro Thr Gin Ile Gin Asp

85 90 95
100 105 110
115 120 125
130 135 140
145 150 155 160
165 170 175
180 185 190
195 200 205
210 215 220
225 230 235 240
245 250 255
260 265 270
275 280 285
290 295 300
305 310 315 320
325 330 335
340 345 350
355 360 365
370 375 380
385 390 395 400
405 410 415
420 425 430
435 440 445
450 455 460
465 470 475 480
485 490 495
500 505 510
Pro Cys Thr Ser Asn Pro Thr Tyr Pro Val Arg Met Val Gly Ala Val
515 520 525
Thr His Pro Lys Tyr Ala Gly Gin Gly Gly Ile Ala Thr Gin Ile Gly
530 535 540
Asp Gin Gly Ile Thr Ala Ala Ser Leu Arg Ala Ile Ser Ala Ala Pro
546 550 555 560
Pro Asn Thr Tyr Thr Gin Ser Ala Phe Leu Lys Ala Pro Glu Thr Glu
565 570 575
Lys Glu Glu Glu Arg Glu Ser Glu Thr Ser Phe Thr Ser Ala Glu Ser
580 585 590
Ser Ser Glu Gly Asp Gly Ser Ser Asp Asp Gin Ala Glu Arg Arg Ala
595 600 605
Ala Arg Lys Arg Val Ile Lys Leu Leu Leu Arg Leu Ala Asp Arg
610 615 620
Pro Val Asp Asn Lys Arg Arg Arg Phe Ser Glu
625 630 635

<210> SEQ ID NO 55
<211> LENGTH: 73
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 55

Met Lys Glu Lys Asp Tyr Trp Glu Glu Ala Trp Leu Thr Ser Cys Thr
1 5 10 15
Ser Ile His Asp His His Cys Gly Ser Trp Arg Asp His Leu
20 25 30
Trp Thr Leu Cys Ala Leu Asp Ala Asp Leu Ala Ala Ala Ala Asp
35 40 45
Ile Ile Glu Arg Glu Ala Asp Gly Gly Gly Gly Asp Phe Gly Phe Val
50 55 60
Asp Gly Asp Pro Gly Asp Ala Gly Gly
65 70

<210> SEQ ID NO 56
<211> LENGTH: 2872
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2719)...(2732)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 56
tacaccttgg gttcaggag gctcaatttg gctcggttcg ctgcacacg gttggctgcc 60
agggccacct gattgaagaac tgaaaaccgt taattcataa attgaaattgg cgggcaaaaa 120
tgcccggaggg ggggaggttt ttatgcaaat taattttagc aaaagttttag gacgttgtat 180
ttatatttt ccaattttaga ggattcaaat ctgattggct ggagacctcaag tgcctcatttt 240
gcataagggtg taacattaaca gaattaagcc gtcccacag aagccgtaat aagtaggtga 300
gttccgagat gcgtgcgttt atgccgcccc ggcggagcag aacgctgtctg ccgctgggccg 360
gtgccggag gatcctgtag cgggatgctg aagggcgctc ggggagcgc acgggtgagg 420
agggctactg cgccaaactc gggaggagcc ctgctgtaa cgcaccagc gcgtagccgg 480
tctgactgc gcgtgctgga actggcgga ccacatttgg ctctreacetc gcgtatgggg 540
cggcgctttgc ggcccgcccg tagacgtcat agaagagac gcctagtgcgtg gacgagccgc 600
tacctacgt acctacgtcct cctcacactgc gacgtatggtc tggtaagggc aagcgagggcgt  
650  
tcggctccacc ggagcttagag ccggggccctg cctccctcgg acctgttttcta cccaaagagta 
660  
atgcggagtag taagtaattg gggggtggtgc ctattttcata aatgatttaaa aagacagagag 
670  
gcactaagtag tataccctag atcaggggagc cgacagagagc agtggagagg gtagattaac 
680  
tccgcgggacc aggctcagaa cctcgtgcac ctcctgacgg gccgagatgg ggcagatctg 
690  
acacagttag gcacgacagg cggccacagca acgcgccgtc gctgatagctc gctgagcttg 
700  
ggtgtaaggtc aagaggtggtc aggacggagc cgcctagcgtcacc tgggaggtgc 
710  
gtcagagcc gcaaatagcta cggggcagct ccgggccgcc gcgggggcttc 
720  
<210> SEQ ID NO 57
LENGTH: 637
TYPE: PRT
ORGANISM: Torque teno sus virus
SEQUENCE: 57

Met Ala Pro Thr Arg Arg Trp Arg Arg Phe Gly Arg Arg Arg Arg
Arg Tyr Arg Lys Arg Arg Tyr Gly Trp Arg Arg Arg Tyr Arg Tyr Arg Arg
Arg Pro Arg Asp Tyr Arg Arg Trp Leu Val Arg Arg Arg Arg Arg
Ser Val Tyr Arg Arg Gly Gly Arg Arg Ala Arg Pro Tyr Arg Leu Phe
Asn Pro Lys Val Met Arg Val Val Val Arg Gly Gly Gly Trp Trp Pro Ile
Leu Gln Cys Leu Lys Gly Gln Ala Leu Arg Tyr Arg Pro Leu Gln
Trp Asp Thr Glu Arg Glu Trp Val Arg Arg Ser Asp Phe Glu Asp Glu
Tyr Gly Tyr Leu Val Glu Tyr Gly Gly Gly Trp Gly Ser Gly Asp Val
Thr Leu Glu Gly Leu Tyr Glu His Leu Leu Arg Trp Arg Asn Ser Trp
Ser Lys Gly Asn Asp Gly Met Asp Leu Val Arg Tyr Phe Gly Cys Val
Val Tyr Leu Tyr Pro Leu Lys Asp Glu Tyr Trp Phe Trp Trp Asp
Thr Asp Phe Lys Glu Leu Tyr Ala Glu Asn Ile Lys Gly Gly Ser Glu
Pro Ser Val Met Met Ala Lys Arg Thr Arg Ile Val Ile Ala Arg
Glu Arg Ala Pro His Arg Arg Lys Val Arg Lys Ile Phe Ile Pro Pro
Pro Ser Arg Asp Thr Glu Trp Gln Phe Cys Asn
Arg Lys Leu Phe Thr Trp Ala Ala Gly Leu Ile Asp Met Glu Lys Pro
Phe Asp Ala Asn Gly Ala Phe Arg Asn Ala Trp Trp Leu Glu Glu Arg
Asn Asp Gln Gly Glu Met Tyr Ile Glu Leu Trp Gly Arg Val Pro
Pro Glu Gly Asp Ser Glu Leu Pro Lys Lys Gly Phe Ser Tyr Gly
Thr Asp Asn Pro Asn Tyr Asn Val Glu Asp Asn Glu Lys Asn Ile
Arg Lys Leu Tyr Val Asp Glu Lys Asp Glu Lys Pro Arg Lys
Lys Tyr Cys Val Cys Tyr Asn Lys Thr Leu Asn Arg Trp Arg Leu Gly
Gln Ala Ser Thr Leu Lys Ile Gly Asn Leu Lys Gly Leu Val Leu Arg
Gln Leu Met Asn Glu Glu Met Thr Tyr Ile Trp Lys Glu Gly Glu Tyr
Ser Ala Pro Phe Val Glu Arg Trp Lys Gly Ser Arg Phe Ala Val Ile
Asp Ala Arg Lys Ala Asp Gln Glu Asn Pro Lys Val Ser Thr Trp Pro
Ile Glu Gly Thr Trp Asn Thr Gln Asp Thr Val Leu Lys Asp Val Phe
Gly Ile Asn Leu Gln Asn Gln Phe Arg Ala Ala Asp Phe Gly Lys
Leu Thr Leu Pro Lys Ser Pro His Asp Leu Asp Phe Gly His His Ser
Arg Phe Gly Pro Phe Cys Val Lys Asn Glu Pro Leu Glu Phe Gln Val
Tyr Pro Pro Glu Pro Thr Asn Leu Trp Phe Gln Tyr Arg Phe Phe
Gln Phe Gly Glu Tyr Gln Pro Pro Thr Gly Ile Arg Asp Pro Cys
Val Asp Thr Pro Ala Tyr Pro Val Pro Gln Ser Gly Ser Ile Thr His
Pro Lys Phe Ala Gly Lys Gly Gly Met Leu Thr Glu Thr Asp Arg Trp
Gly Ile Thr Ala Ala Ser Ser Ala Leu Ser Ala Asp Thr Pro Thr
Glu Ala Ala Gln Ser Ala Leu Arg Gly Asp Ser Glu Ala Lys Gly
Glu Glu Thr Glu Thr Ala Ser Ser Ser Ser Ile Thr Ser Ala Glu
Ser Ser Thr Glu Gly Asp Gly Ser Ser Asp Gln Glu Thr Ile Arg
Arg Arg Arg Thr Trp Lys Arg Leu Arg Met Val Arg Glu Gln
Leu Asp Arg Arg Met Asp His Lys Arg Gln Arg Leu His

<210> SEQ ID NO 58
<211> LENGTH: 72
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus

<400> SEQUENCE: 59
Met Pro Glu His Trp Glu Glu Ala Trp Leu Glu Ala Thr Lys Gly Trp
1 5 10 15
His Asp Leu Asp Cys Arg Cys Gly Asn Trp Glu Asp His Leu Trp Leu
20 25 30
Leu Leu Ala Asp Gly Asp Ala Leu Ala Ala Val Asp Ala Ile
35 40 45
Glu Arg Asp Ala Met Ala Gly Asp Ala Thr Thr Ala Thr Gly Arg
50 55 60
Val Thr Ile Gly Asp Asp Gly Trp
65 70

<210> SEQ ID NO 59
<211> LENGTH: 2735
<212> TYPE: DNA
<213> ORGANISM: Torque teno sus virus

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2596) .. (2622)
<223> OTHER INFORMATION: n is a, c, g, or t
<400> SEQUENCE: 59

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ccaaaacccaa ggaactctgg caaaaaaagag gaaataaggct aattttggggt ggacgtaaagc 180
cctcttataa ataataaaag aaccccaact cggccaaacc ttccttaaat tagtaaagaa 240
agtgactcga ggaatttacc ccatactgct agttgttgag gctgtgggta gacgcaacaa gagctgagtg 300
tcttaaccgcc tgggcggtgc cccagacgcc ttgagcggga gttcaaggggc ctatgggaca 360
gcggttaaatc cagcggaacct gggcccccct cgtgtagaaga aagattgctg acgtaagctg 420
actgcgcaca cggattatttc ggcaagctgt aataaagggg cggccgcgtc acaagggagct 480
ttcagagcgc tatcgcagac gcgcagaaag accgcagagc agagagagag aagagagagc 540
gagactcata cttccgcattt ggtcgcgcat ggcacggtgc ccggcggcct cagagatagtg 600
gacagagggg aaaaaatctt ccctgccattc ggggctcagtc cccttcaattc ggggacgactc 660
catagcgagct tttggggggc ggtcgcggtg ggggctcagtc cctccttttt cagcggagtc 720
ggcgttaaatc cagcggaacct gggcccccct cgtgtagaaga aagattgctg acgtaagctg 780

aaaaccttttc aatgaaaaac ttaactggag aaatatatgg acagctagta atgttggaat 840
ggattctgct gattgtattc atggatctct atccttaaaa gaagttctat ttttcttctgc ggaagagttc 900
tataaatct tgggtaagc atataccagt cagcgaacta cttatatcag gactgatcctc 960
actctatagt ctactaaaaa aacgacacaa aatattcatt tctacgaaa aactgtaacc 1020
aaacgaaaaa caaacctctg tcaacatat attccaaacc cggccaaacc tatacattc 1080
agtgactcga agtagaagag tagaagagag tagaagagag tagaagagag 1140
agactcaca gaacacaggt tagaagagag tagaagagag tagaagagag 1200
tgctgcctag aagattttta aaggaaagtt ttactttttc ggcgctcata gcatcggaga 1260
ctgtagaaga aagattttta aaggaaagtt ttactttttc ggcgctcata gcatcggaga 1320
ctcttataa ataataaaag aaccccaact cggccaaacc ttccttaaat tagtaaagaa 1380
agtgactcga ggaatttacc ccatactgct agttgttgag gctgtgggta gacgcaacaa gagctgagtg 1440
ttcagagcgc tatcgcagac gcgcagaaag accgcagagc agagagagag aagagagagc 1500
gagactcata cttccgcattt ggtcgcgcat ggcacggtgc ccggcggcct cagagatagtg 1560
gacagagggg aaaaaatctt ccctgccattc ggggctcagtc cccttcaattc ggggacgactc 1620
catagcgagct tttggggggc ggtcgcggtg ggggctcagtc cctccttttt cagcggagtc 1680
ggcgttaaatc cagcggaacct gggcccccct cgtgtagaaga aagattgctg acgtaagctg 1740

aaaaccttttc aatgaaaaac ttaactggag aaatatatgg acagctagta atgttggaat 1800
ggattctgct gattgtattc atggatctct atccttaaaa gaagttctat ttttcttctgc ggaagagttc 1860
ctcttataa ataataaaag aaccccaact cggccaaacc ttccttaaat tagtaaagaa 1920
agtgactcga ggaatttacc ccatactgct agttgttgag gctgtgggta gacgcaacaa gagctgagtg 1980
ttcagagcgc tatcgcagac gcgcagaaag accgcagagc agagagagag aagagagagc 2040
gagactcata cttccgcattt ggtcgcgcat ggcacggtgc ccggcggcct cagagatagtg 2100
gacagagggg aaaaaatctt ccctgccattc ggggctcagtc cccttcaattc ggggacgactc 2160
gagactcata cttccgcattt ggtcgcgcat ggcacggtgc ccggcggcct cagagatagtg 2220
gacagagggg aaaaaatctt ccctgccattc ggggctcagtc cccttcaattc ggggacgactc 2280
ccacacgcag agcaagcac gactcctcaag gcacctcag cgggtgtaa agaggatgaa 2340
aacactgtga tagataaata tagaaaccta gcagacccct cactcaatgt cacaggacac 2400
atggaaaaat tcatgcagtt acatattcaa aacgtacaag aaataagage taaaaatgct 2460
aaaaaatcce tcaataaact ttacttttct gattaatage ggectcctgt gtccaaccta 2520
ttttctctaa accccttcaag aatggagaaa gggagctggc tcagagtcag 2580
ggctgacgcc cccctnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 2640
accccccect gegggggcte cgcecccctge acceceggga gggggggaaa cccccectca 2700
acccccegeg gggggcaage cccccctgcac 2735

<210> SEQ ID NO 60
<211> LENGTH: 624
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE:
Ile Glu Leu Ile Asn Gln Gly Trp Pro Tyr Trp Leu Tyr Phe Tyr Gly
Lys Ser Glu Gln Asp Ile Lys Lys Glu Ala His Ser Ala Glu Ile Ser
Arg Glu Tyr Thr Arg Asp Pro Lys Ser Lys Lys Leu Lys Ile Gly Ile
Val Gly Trp Ala Ser Ser Asn Tyr Thr Thr Gly Ser Asp Glu Asn
Ser Gly Gly Ser Thr Thr Ala Ile Gln Gly Gly Tyr Val Ala Tyr Ala
Gly Ser Gly Val Ile Gly Ala Gly Ser Ile Gly Asn Leu Tyr Glu Gln
Gly Trp Pro Ser Asn Glu Asn Trp Pro Asn Thr Asn Arg Asp Lys Thr
Asn Phe Asp Trp Gly Ile Arg Gly Leu Cys Ile Leu Arg Asp Asn Met
His Leu Gly Ser Gln Glu Leu Asp Asp Glu Cys Thr Met Leu Thr Leu
Phe Gly Pro Phe Val Glu Lys Ala Asn Pro Ile Phe Ala Thr Thr
Pro Lys Phe Phe Lys Pro Glu Leu Lys Asp Tyr Asn Ile Met Lys
Thr Ala Phe Lys Phe Gin Trp Gly Gly His Gly Thr Glu Arg Phe Lys
Thr Asn Ile Gly Asp Pro Ser Thr Ile Pro Cys Pro Phe Glu Pro Gly
Asp Arg Phe His Ser Gly Ile Gln Asp Pro Ser Lys Val Gin Asn Thr
Val Leu Asn Pro Trp Asp Tyr Asp Gly Ile Val Arg Lys Asp
Thr Leu Lys Arg Leu Leu Glu Leu Pro Thr Glu Thr Glu Glu Glu
Lys Ala Tyr Pro Leu Leu Gly Gin Lys Thr Glu Lys Glu Pro Leu Ser
Asp Ser Asp Glu Glu Ser Val Ile Ser Ser Thr Ser Ser Gly Ser Ser
Gln Glu Glu Thr Gin Arg Arg Arg His His Lys Pro Ser Lys Arg
Arg Leu Leu Lys His Leu Gin Arg Val Val Lys Arg Met Lys Thr Leu

<210> SEQ ID NO 61
<211> LENGTH: 69
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 61
Met Glu Glu Arg Trp Leu Thr Val Ala Tyr Cys Ala His Gly Leu Phe
1 5 10 15
Cys Ser Cys Lys Asp Pro Lys His Leu Glu Lys Cys Leu Thr Asp
20 25 30
Ala Ile Ala Asp Ala Glu Glu Asp Arg His Gly Asp Gly Gly Thr Gly
35 40 45
Gly Gly Asp Ala Thr Phe Asp Ile Gly Ile Asp Ala Leu Leu Ala Ala
50 55 60
Ala Ala Glu Arg 65

<210> SEQ ID NO 62
<211> LENGTH: 625
<212> TYPE: PRT
<213> ORGANISM: Torque teno sus virus
<400> SEQUENCE: 62
Met Pro Tyr Arg Tyr Arg Arg Arg Arg Arg Pro Thr Arg Arg 1 5 10 15
Trp Arg His Arg Arg Trp Arg Tyr Phe Arg Tyr Arg Tyr Arg Arg 20 25 30
Ala Pro Arg Arg Arg Ala Lys Val Arg Arg Arg Arg Arg Lys Ala 35 40 45
Pro Val Ile Gln Trp Asn Pro Pro Ser Arg Arg Thr Cys Leu Ile Glu 50 55 60
Gly Phe Trp Pro Leu Ser Tyr Gly His Trp Phe Arg Thr Cys Leu Pro 65 70 75 80
Met Arg Arg Leu Asn Gly Leu Ile Phe Thr Gly Gly Gly Cys Asp Trp 85 90 95
Thr Gln Trp Ser Leu Gln Asn Leu Phe His Glu Lys Leu Asn Trp Arg 100 105 110
Asn Ile Trp Thr Ala Ser Asn Val Gly Met Glu Phe Ala Arg Phe Leu 115 120 125
Arg Gly Lys Phe Tyr Phe Phe Arg His Pro Trp Arg Ser Tyr Ile Val 130 135 140
Thr Trp Asp Gln Asp Ile Pro Cys Lys Pro Leu Pro Tyr Gln Asn Leu 145 150 155 160
Gln Pro Leu Leu Met Leu Leu Lys Gln His Lys Leu Val Leu Ser 165 170 175
Gln Lys Asp Cys Asn Pro Ser Arg Lys Gln Lys Pro Val Thr Leu Lys 180 185 190
Phe Arg Pro Pro Pro Lys Leu Thr Ser Gln Trp Arg Leu Ser Arg Glu 195 200 205
Leu Ser Lys Ile Pro Leu Ile Arg Leu Gly Ile Ser Leu Ile Asp Leu 210 215 220
Ser Glu Pro Trp Leu Gly Trp Gln Ala Phe Tyr Ser Val Leu 225 230 235 240
Gly Tyr Glu Ala Ser Lys His Ser Gly Arg Trp Ser Asn Trp Thr Gln 245 250 255
Met Lys Tyr Phe Thr Ile Tyr Asp Thr Gly Val Gly Asn Ala Val Tyr 260 265 270
Val Ile Leu Leu Lys Asp Val Asp Asn Pro Gly Asp Met Ala 275 280 285
Thr Lys Phe Val Thr Gly Gln Gly Gln His Pro Asp Ala Ile Asp His 290 295 300
Ile Glu Met Val Asn Glu Gly Trp Pro Tyr Trp Leu Phe Phe Tyr Gly 305 310 315 320
Gln Ser Glu Gln Asp Ile Lys Leu Ala His Asp Gln Asp Ile Ala 325 330 335
Arg Glu Tyr Ala Arg Asp Pro Lys Ser Lys Lys Leu Lys Ile Gly Val 340 345 350
Ile Gly Trp Ala Ser Ser Asn Tyr Thr Thr Ala Gly Ser Asn Gln Asn
  355 360 365
Thr Thr Ala Gln Thr Pro Glu Ala Ile Gln Gly Gly Tyr Val Ala Tyr
  370 375 380
Ala Gly Ser Arg Ile Pro Gly Ala Gly Ser Ile Thr Asn Leu Phe Gln
  385 390 395 400
Met Gly Trp Pro Gly Asp Gln Asn Trp Pro Pro Thr Asn Gln Glu Glu
  405 410 415
Thr Asn Phe Asn Trp Gly Leu Arg Gly Leu Cys Val Leu Arg Arg Asn
  420 425 430
Met Lys Leu Gly Ala Gln Leu Asp Asp Glu Asp Thr Met Leu Ser
  435 440 445
Leu Phe Gly Pro Phe Val Glu Lys Ala Asn Thr Ala Phe Ala Thr Asn
  450 455 460
Asp Pro Lys Tyr Phe Arg Pro Glu Leu Lys Asp Tyr Asn Val Val Met
  465 470 475 480
Lys Tyr Ala Phe Lys Phe Gln Trp Gly Gly His Gly Thr Glu Arg Phe
  485 490 495
Lys Thr Thr Ile Gly Asp Pro Ser Thr Ile Pro Cys Pro Phe Glu Pro
  500 505 510
Gly Glu Arg Tyr His His Gly Val Glu Asp Pro Ala Lys Val Glu Asn
  515 520 525
Thr Val Leu Asn Pro Trp Asp Tyr Asp Cys Asp Gly Ile Val Arg Thr
  530 535 540
Asp Thr Leu Lys Arg Leu Leu Glu Leu Pro Thr Glu Thr Glu Glu Thr
  545 550 555 560
Glu Lys Ala Tyr Pro Leu Leu Gly Lys Thr Glu Lys Glu Pro Leu
  565 570 575
Ser Asp Ser Asp Glu Glu Ser Val Ile Ser Ser Thr Ser Ser Gly Ser
  580 585 590
Ser Glu Glu Glu Thr Glu Arg Arg Arg Glu His Lys Pro Ser Lys
  595 600 605
Arg Arg Leu Leu Lys His Leu Glu Arg Val Lys Arg Met Lys Thr
  610 615 620
Leu
  625

<n>SEQ ID NO 63
<n>LENGTH: 10
<n>TYPE: DNA
<n>OVERRIDE: Artificial Sequence
<n>ORIGIN: Synthetically synthesized sequence
<n>FEATURE:
<n>NAME/KEY: misc_feature
<n>LOCATION: (1) (2)
<n>OTHER INFORMATION: n is a, c, g, or t
<n>FEATURE:
<n>NAME/KEY: misc_feature
<n>LOCATION: (9) (10)
<n>OTHER INFORMATION: n is a, c, g, or t
<n>SEQUENCE: 63
<n>nggttaacnn

<n>SEQ ID NO 64
<n>LENGTH: 10
<n>TYPE: DNA
What is claimed is:

1. A method for diagnosing a Torque Teno Sus Virus (TTSuV) infection in a pig, or determining whether a pig has been exposed to one or more TTSuV genotypes or subtypes, comprising:

   immobilizing an immunogenic fragment or a complete protein of a recombinantly expressed and purified poly-peptide sequence of an ORF1 protein of one or more TTSuV genotypes or subtypes wherein the immunogenic fragment or complete polypeptide sequence comprises one or more of:

   - amino acids 363 to 375 of a TTSuV2 ORF1 represented by SEQ ID NO: 16,
   - amino acids 388 to 423 of a TTSuV2 ORF1 represented by SEQ ID NO: 16.
contacting a serum sample from a pig suspected of TTsuV infection with the immobilized immunogenic fragment or complete protein; and
detecting captured antibody specific to the immunogenic fragment.

2. The method of claim 1, wherein the TTsuV genotypes or subtypes include one or more of TTsuV1a and TTsuV1b in addition to the TTsuV2 ORF1 immunogenic fragment or complete polypeptide sequence.

3. The method of claim 1, wherein the polypeptide comprises N-terminal truncated ORF1 proteins of one or more of TTsuV genotypes or subtypes TTsuV1a and TTsuV1b in addition to the TTsuV2 ORF1 immunogenic fragment or complete polypeptide sequence.

4. The method of claim 2, wherein the polypeptide sequence comprises amino acids 317-635 of the ORF1 protein of TTsuV1a as referenced by SEQ ID NO: 12.

5. The method of claim 2, wherein the polypeptide sequence comprises amino acids 322-639 of the ORF1 protein of TTsuV1b as referenced by SEQ ID NO: 13.

6. The method of claim 1, wherein the detecting captured antibody is by Western blot.

7. The method of claim 1, wherein the detecting captured antibody is by enzyme-linked immunosorbent assay (ELISA).

9. A diagnostic reagent for use in the detection of Torque Teno Sus Virus (TTsuV) infection in a mammal, comprising ORF1 proteins or immunogenic fragments thereof of one or more TTsuV genotypes or subtypes wherein the immunogenic fragments or complete polypeptide sequences are recombinantly expressed and purified and comprise one or more of: amino acids 363 to 375 of a TTsuV2 ORF1 represented by SEQ ID NO: 16, and amino acids 388 to 423 of a TTsuV2 ORF1 represented by SEQ ID NO: 16.

10. The diagnostic reagent of claim 9, wherein the one or more TTsuV genotypes or subtypes include one or more of TTsuV1a and TTsuV1b in addition to the TTsuV2 immunogenic fragments or complete polypeptide sequences.

11. A method for simultaneously detecting TTsuV1 and TTsuV2 infection comprising:

- extracting DNA from a sample suspected of TTsuV infection;
- performing real-time polymerase chain reaction (RT-PCR) using a TTsuV1-specific primer pair according to SEQ ID NO:29 and SEQ ID NO:30 and a TTsuV2-specific primer pair according to SEQ ID NO:31 and SEQ ID NO:32 in the same real-time PCR reaction; and
- determining a presence of TTsuV1 and/or TTsuV2 DNA based on amplified primer specific sequences.

12. A method for simultaneously detecting TTsuV1 and TTsuV2 infection by duplex nested polymerase chain reaction (PCR) comprising:

- isolating viral DNA from samples of pigs suspected of TTsuV infection;
- performing a first round of PCR using one pair of primers Plab-mF according to SEQ ID NO:33 and Plab-mR according to SEQ ID NO:34;
- performing a second round of PCR using a mixture of two pairs of primers, Pla-nF according to SEQ ID NO:35 and Pla-nR according to SEQ ID NO:36 for detection of TTsuV1a, and Plb-nF according to SEQ ID NO:37 and Plb-nR according to SEQ ID NO:38 for detection of TTsuV1b, and visualizing the PCR products.

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