PRRSV SUBUNIT VACCINES

RELATED APPLICATIONS

This application claims the benefit of Provisional Application Serial No. 60/581,350, filed on June 17, 2004, the teachings and content of which are expressly incorporated by reference herein.

SEQUENCE LISTING

A printed Sequence Listing accompanies this application, and has also been submitted with identical contents in the form of a computer readable ASCII file on a CD-ROM.

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention is broadly concerned with vaccines for porcine reproductive and respiratory syndrome (PRRS). More particularly, the invention is concerned with the prevention of PRRS in swine by the administration of a vaccine comprising DNA subunits of PRRS virus (PRRSV). Still more particularly, the invention pertains to the use of open reading frame 1 (ORF1) in a DNA subunit vaccine which provides protective immunity against PRRSV to swine. Even more particularly, the invention pertains to the use of selected portions of ORF1 both alone and in combination with other portions of the PRRSV genome or in combination with other vaccines against PRRSV.

Description of the Prior Art

PRRS is a major disease in the swine industry worldwide. PRRS is caused by PRRSV infection. Currently, there are modified-live vaccines (MLV) available that, when used correctly, provide swine with protection against the clinical disease resulting from PRRSV infection. PRRS MLV vaccines require replication in the vaccinated animal in order to insure that an efficacious immune response is induced (for example, *see* Meng, X.J., Heterogeneity of Porcine Reproductive and Respiratory Syndrome Virus: Implications for Current Vaccine Efficacy and Future Vaccine Development; 74 Vet. Micro., 309-329 (2000)). However, such replication presents problems in that the PRRS MLV can persist in the animal for several weeks after vaccination and can also be shed to other PRRSV-negative swine. The shedding of PRRS MLV

from vaccinated animals can be a problem in some swine herds that do not have good biosecurity measures in place to prevent shedding of PRRSV MLV from vaccinated animals to a PRRSV-naive population. Although millions of PRRS MLV doses have been used without issue, there are also sporadic reports in the literature as to the ability of the PRRS MLV to revert to a more virulent, wild-type strain of PRRSV. Attempts to solve the problems of PRRS MLV shed and possible reversion to virulence have also been tried by utilization of a vaccine comprised of inactivated PRRS virus (i.e. PRRS KV). However, research has shown that despite the fact that PRRS KV can induce a strong humoral response in vaccinated swine, it is not effective in preventing PRRS-associated disease.

Accordingly, what is needed in the art is a method of vaccination and vaccine that could induce the protective immune response, without the problems associated with PRRS MLV. Preferably, administration of the vaccine would not actively replicate in the vaccinated animal and would induce a strong humoral and cell-mediated immune response.

SUMMARY OF THE INVENTION

The present invention solves the problems inherent and the prior art provides a distinct advance in the state of the art by providing PRRSV DNA vaccines. Theoretically, the DNA vaccine plasmid expressing the PRRS antigen serves as a template to synthesize PRRSV antigens (i.e. like a PRRS MLV), but also has the characteristic of not actively replicating in the animal (i.e. like a PRRS KV). The protective immunogens needed to induce a protective host response to PRRSV are not known. Since the PRRS MLV can induce a protective response in vaccinated swine, it is thought that the replication of the PRRS MLV in the vaccinated animal must induce both a strong humoral and cell-mediated immune response in the vaccinated animal.

ORF1 of PRRSV encodes for the replication machinery necessary for PRRSV replication and generation of new progeny. ORF1 has two regions, designated as ORF1a and ORF1b, that comprise the ORF1 replicase complex (Dea, et al., Current Knowledge on the Structural Proteins of Porcine Reproductive and Respiratory Syndrome (Prrs) Virus: Comparison of the North American and European Isolates; 145 (4) Archives of Virology, 659-688 (2000)). The replicase-encoded proteins are thought to be key immunogens in other virus families (Leitner et al., DAN and RNA-Based Vaccines: Principles, Progress and Prospects; 18 Vaccine 765-777 (2000)). When a cell is infected with PRRSV, the activity of the viral replicase may provide a powerful

adjuvant-effect as the replicase-associated antigens are expressed during infection of the cell. The replicase-associated antigens may serve as "danger signals" generated in transfected cells and induce strong host immune responses (i.e. IFN, HSP, apoptosis). Thus, replicase-associated "danger signals" could be a key factor in why PRRS MLV can induce protection whereas a non-replicating PRRS (i.e. inactivated antigen in PRRS KV) does not confer protection from challenge.

ORF1 is nearly 12,000 nucleotides in length which makes transfection and adequate expression in a eukaryotic cell difficult. Thus, ORF1 was sequentially and arbitrarily divided up into smaller sections using Expression Library Immunization (ELI) as a tool to determine the protective immunogens of various pathogens. ELI shears the genome of a particular pathogen into small fragments that are cloned into a DNA vaccine vector and thereafter administered to a host to determine if any fragment is capable of inducing an immune response (Johnston and Barry; Genetic to Genomic Vaccination; 15(8) Vaccine, 808-809 (1997)). Preferably, the immune response is protective. The invention is predicated on the hypothesis that host immune responses to ORF1-generated proteins are essential for protection from PRRSV challenge. It is relatively easy to place the regions encoding for PRRSV ORFs 2-7 in a DNA vaccine vector since these ORFs range from 317 -720 nucleotides in length. As noted above, the size of the ORF1 region of PRRSV is nearly 12,000 nucleotides in length. Placing a region of this size into a DNA vaccine vector would not be amenable to transfection and subsequent expression in a eukaryotic cell. Accordingly, it was essential to break the ORF1 region into smaller sections to better ensure adequate expression of all areas of ORF1. Expression Library Immunization (ELI) has been employed as a tool to determine the protective immunogens of various pathogens. ELI employs that shearing of the genome of a particular pathogen into small fragments. These small fragments are then cloned into a DNA vaccine vector and then administered to the host to determine if any fragment is capable of inducing a protective immune response. Herein, the ELI technique has been modified for development of a PRRSV DNA vaccine that is sequentially comprised of the ORF 1 encoding region of the PRRSV genome. This method has been designated as SELI (sequential expression library immunization). This is in contrast to Barfoed et al., (DNA Vaccination of Pigs with Open Reading Frame 1-7 of PRRS Virus; 22 Vaccine, 3628-3641 (2004)) that used the entire ORF1 region as a DNA vaccine.

Vaccines of the present invention comprise portions of PRRSV ORF1 alone, in combination with other portions of PRRSV ORF1, and together with other compositions effective at generating an immune response to PRRSV infection including other PRRSV vaccines. ORF1 portions useful for purposes of the present invention are of sufficient size to invoke an immune response in an animal receiving the vaccine. Preferably, the portion will include up to about 9,000 base pairs, More preferably, the ORF-1 portion will include between about 21-9,000 contiguous nucleotide base pairs, still more preferably between about 21-6,000 contiguous nucleotide base pairs, even more preferably between about 21-3,000 contiguous nucleotide base pairs, still more preferably between about 21-2,000 contiguous nucleotide base pairs, even more preferably between about 21-1,000 contiguous nucleotide base pairs, still more preferably between about 21-500 contiguous nucleotide base pairs, even more preferably between about 21-300 contiguous nucleotide base pairs, still more preferably between about 21-150 contiguous nucleotide base pairs, even more preferably between about 21-75 contiguous nucleotide base pairs, still more preferably between about 21-50 contiguous nucleotide base pairs, even more preferably between about 21-25 contiguous nucleotide base pairs, still more preferably between about 21-23, and most preferably at least about 21 contiguous nucleotide base pairs. The protein resulting from any one of these preferred portions is also a part of the present invention. Any ORF1 or portion thereof from any strain of PRRSV could be used for purposes of the present invention, however, it is preferred to use a strain that is virulent.

The selected portion(s) can be cloned into a suitable expression vector. Examples of suitable vectors include adenovirus vectors, *Shigella* vectors, pVC1650 (Valentis, Inc., Burlingame, California), WRG720 (W.R. Grace, New York, New York) and pcDNA3 (Invitrogen, Carlsbad, California). Some preferred vectors contain the immediate early cytomegalovirus promoter, intron A, and a poly-a adenylation portion (e.g. Bovine growth hormone (BGH) or human growth hormone (HGH)). Additionally, purified PRRSV proteins could be expressed in insect cell culture using, for example, the baculovirus expression system. Such proteins could then be combined with an adjuvant and administered. Of course, those of skill in the art would be able to select suitable expression systems and vectors that can direct the expression of various PRRSV ORFs in eukaryotic cells. Preferably, after cloning the respective portions of ORF1 into a suitable expression vector, the orientation of the clone is verified.

In one example of the present invention, the PRRSV virus VR-2332 was selected for use

in accordance with the present invention. Genbank U87392 was used to generate 13 overlapping clones of ORF1. This ORF1 includes 12,071 nucleotide base pairs. The portions ranged in size from 773 bp to 975 bp. The clones were designated with the letters A-M with clone A (SEQ ID No. 2) being 939 bp, clone B (SEQ ID No. 3) being 957 bp, clone C (SEQ ID No. 4) being 976, clone D (SEQ ID No. 5) being 954 bp, clone E (SEQ ID No. 6) being 939 bp, clone F (SEQ ID No. 7) being 957 bp, clone G (SEQ ID No. 8) being 957 bp, clone H (SEQ ID No. 9) being 852 bp, clone I (SEQ ID No. 10) being 917 bp, clone J (SEQ ID No. 11) being 972 bp, clone K (SEQ ID No. 12) being 966 bp, clone L (SEQ ID No. 13) being 783 bp, and clone M (SEQ ID No. 14) being 774 bp. Clones A-H are from region 1a and clones I-M are from region 1b of ORF1. Clone A utilizes the authentic ORF1A ATG start codon. The remaining ORF1 clones had an inframe ATG start codon added to their five prime ends. Each of these clones were respectively cloned into the DNA expression vector pVC1650. This vector contains the immediate early cytomegalovirus promoter and intron A and directs the expression of the various PRRSV ORFs in eukaryotic cells. Table 1 provides information regarding each clone and which region of the nucleotide sequence each clone is derived from.

Table 1

BIV PRRSV ORF1a/1b Sequential Expression Library Immunization (SELI) Clones

SEQ ID	ORF1 SELI Clone	Size (base pairs)	Region of clone	Nucleotide span of clone (using Genbank U87392 as reference)	Status Cloned into expression vector pVC1650 and orientation verified	IFA reaction following transfection using procine anti-PRRSV convalescent sera
2	A	939	ORF 1a	190-1128	✓	⊕
3	B	957	ORF 1a	1126-2082	✓	⊕
4	C	976	ORF 1a	2082-3057	✓	⊕
5	D	954	ORF 1a	3037-3990	✓	⊕
6	E	939	ORF 1a	3985-4923	✓	⊕
7	F	957	ORF 1a	4924-5880	✓	-
8	G	957	ORF 1a	5863-6819	✓	-
9	H*	852	ORF 1a	6808-7659	✓	⊕

10	I*	917	ORF 1b	7735-8651	✓	-
11	J	972	ORF 1b	8634-9605	✓	weak ⊕
12	K	966	ORF 1b	9588-10553	✓	-
13	L	783	ORF 1b	10536-11318	✓	-
14	M	774	ORF 1b	11298-12071	✓	-

* Note: Original H and I clones flank the ORF1a/1b minus 1 frameshift region and new primers were designed to give slightly smaller RT-PCR products.

Each portion was then utilized in various combinations as well as alone in vaccine preparations comprising other PRRSV ORFs.

In another example, clones A-M and clones of ORFs 2-6 were cloned into the pVC1650 expression vector and a clone for ORF7 was cloned into the WRG720 expression vector. Of course, those of skill in the art will be able to select suitable vectors. Additionally, the nucleic acid sequences of the present invention can be produced by standard techniques, including, without limitation, common molecular cloning, mutagenesis, and chemical nucleic acid synthesis techniques. For purposes of the present invention, DNA sequences having at least 75% sequence identity, more preferably at least 75%, even more preferably at least 80%, still more preferably at least 85%, even more preferably at least 90%, still more preferably at least 95%, even more preferably at least 98%, more preferably at least 99% and most preferably 100% sequence identity with any one of clones A-M would be covered by the present invention.

In one aspect of the present invention, each of the clones A-M are used individually as a vaccine component. Animals are immunized with the vaccine by administration by any conventional means. Examples of administration methods include oral, transdermal, intravenous, subcutaneous, intramuscular, intraocular, intraperitoneal, intrarectal, intravaginal, intranasal, intragastrical, intratracheal, intrapulmonarial, or any combination thereof. Preferred modes of administration are intramuscular, subcutaneous and intranasal. If desired or necessary, booster immunizations may be given once or several times at various intervals. After administration of such a vaccine, an immune response is elicited in the animal and clinical signs of PRRSV infection are reduced in incidence and/or severity after challenge with a virulent form of PRRSV.

In another aspect of the present invention, combinations of clones A-M are administered to animals as described above. Such combinations include two or more of the above-referenced clones. Because some of these clones (A, B, C, D, E, H, and J) elicited an IFA reaction following

transfection using porcine anti-PRRSV convalescent sera, combinations of these clones are preferred for purposes of the present invention.

In another aspect of the present invention, clones A-M, either individually or in combinations as described above, are used in combinations with other ORF(s) of PRRSV in vaccine preparations. Suitable ORFs include ORFs 2-7.

In another aspect of the present invention, PRRSV ORF DNA is combined with another PRRSV vaccine. Preferably the vaccine is effective at inducing an immune response prior to the addition of the PRRSV ORF1 DNA.

In yet another aspect of the present invention, a vector is provided. Vectors in accordance with the present invention have inserted therein foreign DNA (not derived from the vector) that comprises at least a portion of PRRSV ORF1 DNA. In preferred forms, the vector is a plasmid. Preferably, the portion of PRRSV ORF1 DNA will have at least 21 contiguous nucleotides from PRRSV ORF1 DNA. In some preferred forms, the portion will have at least 150 contiguous nucleotides from a sequence selected from the group consisting of sequences having at least 85% sequence identity with any one of SEQ ID Nos. 1-14, and combinations thereof. As with the composition itself, the percentage of sequence identity and length of sequence can vary as described above. In other preferred forms, the vector further comprises a second portion of PRRSV DNA. This second portion is selected from the group consisting of least 21 contiguous nucleotides from a PRRSV ORF other than ORF1, at least 21 contiguous nucleotides from ORF1, and combinations thereof. In embodiments having an additional 21 contiguous nucleotides from ORF1, these 21 nucleotides are distinct from the at least 21 nucleotides contained in the first portion of PRRSV ORF1 DNA. It is also preferred that the PRRSV DNA used to construct the vector is derived from a virulent strain of PRRSV.

Another aspect of the present invention encompasses host cells containing the plasmids of the invention. This would include the plasmids created by the introduction of the various ORF1 fragments noted above. Preferably, such a cell would contain a plasmid comprising at least 21 contiguous nucleotides from PRRSV ORF1 DNA. In other preferred forms, the cell will include a plasmid comprising at least 150 contiguous nucleotides from a sequence selected from the group consisting of sequences having at least 85% sequence identity with any one of SEQ ID Nos. 1-14, and combinations thereof. In still other preferred forms, the plasmid in the cell will comprise a second portion of PRRSV DNA selected from the group consisting of least 21

contiguous nucleotides from a PRRSV ORF other than ORF1, at least 21 contiguous nucleotides from ORF1, and combinations thereof. Preferably, the PRRSV DNA used to generate the plasmid contained in the cell is derived from a virulent strain of PRRSV.

In another aspect of the present invention, compositions of the present invention are useful in methods for the inducement of immune responses in animals as well as for the complete prevention or a reduction in the severity of conditions and symptoms caused by PRRSV infection.

The compositions of the present invention may include pharmaceutically acceptable adjuvants, carriers, and/or excipients.

As used herein, the following definitions will apply: "Sequence Identity" as it is known in the art refers to a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, namely a reference sequence and a given sequence to be compared with the reference sequence. Sequence identity is determined by comparing the given sequence to the reference sequence after the sequences have been optimally aligned to produce the highest degree of sequence similarity, as determined by the match between strings of such sequences. Upon such alignment, sequence identity is ascertained on a position-by-position basis, e.g., the sequences are "identical" at a particular position if at that position, the nucleotides or amino acid residues are identical. The total number of such position identities is then divided by the total number of nucleotides or residues in the reference sequence to give % sequence identity. Sequence identity can be readily calculated by known methods, including but not limited to, those described in Computational Molecular Biology, Lesk, A. N., ed., Oxford University Press, New York (1988), Biocomputing: Informatics and Genome Projects, Smith, D.W., ed., Academic Press, New York (1993); Computer Analysis of Sequence Data, Part I, Griffin, A.M., and Griffin, H. G., eds., Humana Press, New Jersey (1994); Sequence Analysis in Molecular Biology, von Heinge, G., Academic Press (1987); Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M. Stockton Press, New York (1991); and Carillo, H., and Lipman, D., SIAM J. Applied Math., 48: 1073 (1988), the teachings of which are incorporated herein by reference. Preferred methods to determine the sequence identity are designed to give the largest match between the sequences tested. Methods to determine sequence identity are codified in publicly available computer programs which determine sequence identity between given sequences. Examples of such programs include, but are not limited to, the GCG program package (Devereux, J., et al.,

Nucleic Acids Research, 12(1):387 (1984)), BLASTP, BLASTN and FASTA (Altschul, S. F. et al., J. Molec. Biol., 215:403-410 (1990). The BLASTX program is publicly available from NCBI and other sources (BLAST Manual, Altschul, S. et al., NCVI NLM NIH Bethesda, MD 20894, Altschul, S. F. et al., J. Molec. Biol., 215:403-410 (1990), the teachings of which are incorporated herein by reference). These programs optimally align sequences using default gap weights in order to produce the highest level of sequence identity between the given and reference sequences. As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "sequence identity" to a reference nucleotide sequence, it is intended that the nucleotide sequence of the given polynucleotide is identical to the reference sequence except that the given polynucleotide sequence may include up to 5 point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, in a polynucleotide having a nucleotide sequence having at least 95% identity relative to the reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. Analogously, by a polypeptide having a given amino acid sequence having at least, for example, 95% sequence identity to a reference amino acid sequence, it is intended that the given amino acid sequence of the polypeptide is identical to the reference sequence except that the given polypeptide sequence may include up to 5 amino acid alterations per each 100 amino acids of the reference amino acid sequence. In other words, to obtain a given polypeptide sequence having at least 95% sequence identity with a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total number of amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or the carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in the one or more contiguous groups within the reference sequence. Preferably, residue positions which are not identical differ by conservative amino acid substitutions.

However, conservative substitutions are not included as a match when determining sequence identity.

Similarly, "sequence homology", as used herein, also refers to a method of determining the relatedness of two sequences. To determine sequence homology, two or more sequences are optimally aligned as described above, and gaps are introduced if necessary. However, in contrast to "sequence identity", conservative amino acid substitutions are counted as a match when determining sequence homology. In other words, to obtain a polypeptide or polynucleotide having 95% sequence homology with a reference sequence, 95% of the amino acid residues or nucleotides in the reference sequence must match or comprise a conservative substitution with another amino acid or nucleotide, or a number of amino acids or nucleotides up to 5% of the total amino acid residues or nucleotides, not including conservative substitutions, in the reference sequence may be inserted into the reference sequence.

A "conservative substitution" refers to the substitution of an amino acid residue or nucleotide with another amino acid residue or nucleotide having similar characteristics or properties including size, hydrophobicity, etc., such that the overall functionality does not change significantly.

"Isolated" means altered "by the hand of man" from its natural state., i.e., if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or polypeptide naturally present in a living organism is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein.

"Nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides.

"Promoter" means a DNA sequence that regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in cells. The term encompasses "tissue specific" promoters, i.e. promoters, which effect expression of the selected DNA sequence only in specific cells (e.g. cells of a specific tissue). The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in

one tissue, but cause expression in other tissues as well. The term also encompasses non-tissue specific promoters and promoters that constitutively express or that are inducible (i.e. expression levels can be controlled).

"Transfection" means the introduction of a nucleic acid, e.g., via an expression vector, into a recipient cell by nucleic acid-mediated gene transfer. "Transformation", as used herein, refers to a process in which a cell's genotype is changed as a result of the cellular uptake of exogenous DNA or RNA, and, for example, the transformed cell expresses a recombinant form of a polypeptide or, in the case of anti-sense expression from the transferred gene, the expression of a naturally-occurring form of theprotein is disrupted. Transfection may also use a chemical reagent (i.e. a lipid).

The term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of preferred vector is an episome, i.e., a nucleic acid capable of extra-chromosomal replication. Preferred vectors are those capable of autonomous replication and/expression of nucleic acids to which they are linked. Vectors capable of directing the expression of genes to which they are operatively linked are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of "plasmids" which refer generally to circular double stranded DNA loops which, in their vector form are not bound to the chromosome. In the present specification, "plasmid" and "vector" are used interchangeably as the plasmid is the most commonly used form of vector. Vectors also include other replicons such as phages or comsmids, into which another DNA segment may be inserted so as to bring about the replication of the inserted segment. The invention is intended to include such other forms of expression vectors which serve equivalent functions and which become known in the art subsequently hereto.

"Amplification" of nucleic acids or polynucleotides is any method that results in the formation of one or more copies of a nucleic acid or polynucleotide molecule (exponential amplification) or in the formation of one or more copies of only the complement of a nucleic acid or polynucleotide molecule (linear amplification). Methods of amplification include the polymerase chain reaction (PCR) based on repeated cycles of denaturation, oligonucleotide primer annealing, and primer extension by thermophilic template dependent polynucleotide polymerase, resulting in the exponential increase in copies of the desired sequence of the polynucleotide analyte flanked by the primers. The two different PCR primers, which anneal to

opposite strands of the DNA, are positioned so that the polymerase catalyzed extension product of one primer can serve as a template strand for the other, leading to the accumulation of a discrete double stranded fragment whose length is defined by the distance between the 5' ends of the oligonucleotide primers. The reagents for conducting such an amplification include oligonucleotide primers, a nucleotide polymerase and nucleoside triphosphates such as, e.g., deoxyadenosine triphosphate (dATP), deoxyguanosine triphosphate (dGTP), deoxycytidine triphosphate (dCTP) and deoxythymidine triphosphate (dTTP). Other methods for amplification include amplification of a single stranded polynucleotide using a single oligonucleotide primer, the ligase chain reaction (LCR), the nucleic acid sequence based amplification (NASBA), the Q-beta-replicase method, and 3SR.

The teachings and content of all references cited herein are expressly incorporated by reference.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

The following example sets forth a preferred embodiment of the present invention. It is to be understood, however, that this example is provided by way of illustration and nothing therein should be taken as a limitation upon the overall scope of the invention.

EXAMPLE 1

This example provides data as to the efficacy of DNA vaccines comprising various regions of the PRRSV genome. The example began with 40 PRRSV-negative mixed sex pigs from Spring Prairie Colony, Hawley, MN 56549. The pigs were 3-4 weeks of age at the initiation of the study. Throughout the study, the pigs were provided food sufficient for the size, age and condition of the animals. Water was provided ad libitum.

To generate PRRSV DNA vaccines, nineteen cDNA clones were generated from the PRRS virus. Thirteen cDNA clones were generated that sequentially represent the open reading

frame (ORF) 1a/1b region of the pRRSV genome. Clone A utilizes the authentic ORF1a ATG start codon. The remaining ORF1a/1b clones B through M had an ATG start codon added to their respective 5' ends. All of the above clones were respectively cloned into the DNA expression vector pVC1650. The pVC1650 vector contains the immediate early cytomegalovirus promoter and intron A to direct the expression of the various PRRSV ORFs in eukaryotic cells. The six additional cDNA clones represented the PRRSV structural protein ORFs 2, 3, 4, 5, 6 and 7. The ORF 2, 3, 4, 5, and 6 clones were also respectively cloned into the DNA expression vector pVC1650 described above. The ORF 7 gene was cloned into a similar expression vector designated WRG7020. The WRG7020 vector also contains the immediate early cytomegalovirus promoter and intron A to direct the expression of PRRSV ORF 7 in eukaryotic cells.

Two sets of vaccines were created, designated "A1-19" and "T1-19". For the A1-19 vaccines, the aforementioned clones were cloned into the Valentis, Inc. pVC1650 expression plasmid. Each plasmid construct was separately formulated with aluminum phosphate (Adju-Phos®) (Ulmer et al., Enhancement of DNA Vaccine Potency Using Conventional Aluminum Adjuvants; 18 Vaccine, 18-28 (1999) to yield 250μg of respective ORF clone with 1000 μg calculated aluminum in a 1 ml dose. The final vaccine consisted of a separate 1ml IM dose of each formulated ORF clone. For the T1-19 vaccines, the aforementioned clones were cloned into the Valentis, Inc. pVC1650 expression plasmid. Each plasmid construct was separately formulated with TGV200 PINC-polymer to yield 250 μg of respective ORF clone in a 1 ml dose. The final vaccine consisted of a separate 1 ml IM dose of each formulated ORF clone.

To generate a control, DNA vaccines consisting of cDNA clones of ORF PCV2 and the HA gene of SIV were created. Both ORFs were separately cloned into the Valentis, Inc. pVC1650 expression plasmid. Both the PCV2 ORF2 and the SIV HA gene plasmid constructs were separately formulated with aluminum phosphate (Adju-Phos®) to yield 250 μg of the

respective ORF clone with 1000 μg calculated aluminum in a 1 ml dose (called A20 and A21). Additionally, both the PCV2 ORF2 and the SIV HA gene plasmid constructs were separately formulated with TGV200 PINC-polymer to yield 250 μg of each respective clone in a 1 ml dose (called T20 and T21). The final vaccine consisted of a four separate 1 ml IM doses of each formulated clone. Table 2 shows all of the created vaccines, including the control vaccines.

Table 2

Plasmid	Region of clone	Nucleotide span of clone (using Genbank U87392 as reference)
1	ORF 1a	190-1128
2	ORF 1a	1126-2082
3	ORF 1a	2082-3057
4	ORF 1a	3037-3990
5	ORF 1a	3985-4923
6	ORF 1a	4924-5880
7	ORF 1a	5863-6819
8	ORF 1a	6808-7659
9	ORF 1b	7735-8651
10	ORF 1b	8634-9605
11	ORF 1b	9588-10553
12	ORF 1b	10536-11318
13	ORF 1b	11298-12071
14	ORF2	NA
15	ORF3	NA
16	ORF4	NA
17	ORF5	NA
18	ORF6	NA
19	ORF7	NA
20	ORF2	NA
21	SIV HA	NA

The forty pigs were divided into four groups: Group 1 was administered 19 x 1 ml doses of A1-A19 Adju-Phos on Days 0, 21, and 42. Group 2 was administered 19 x 1 ml doses of T1-T19 TGV200 on Days 0, 21, and 42. Group 3 was administered 4 x 1 ml respective doses of A20, A21, T20, and T21 on Days 0, 21, and 42. Group 4, the negative control, had no treatment

administered at all.

On day 56 of the study, pigs in groups 1, 2, and 3 were all administered the virulent SDSU#73 strain of PRRSV. The virulent SDSU#73 strain of PRRSV was diluted 1:10 in EMEM with 4% fetal bovine serum prior to administration to the pigs. A total of 2 ml of the diluted challenge virus was delivered intranasally to the appropriate pigs with 1 ml of the diluted virus administered to each nostril. The prechallenge and postchallenge titer of the PRRSV challenge virus was $10^{4.59}$ $TCID_{50}$/ml and $10^{4.65}$ $TCID_{50}$/ml, respectively.

The pigs were bled on days 0, 21, 42 and 56 of the trial to monitor seroconversion to vaccination. The pigs were also bled on days 57, 59, 61, 63, 66 and 70 of the trial to monitor seroconversion and viremia postchallenge. Clinical observations were recorded daily from day 54-70. On day 70, pigs were necropsied and gross lung lesions were recorded as percent lung involvement due to PRRSV. Pigs were weighed prior to the study start and on Days 56 and Days 70. A summary of the protocol in this example can be seen in Table 3.

Table 3

Group	Pigs/ group	First vaccination (Day = 0)	Second vaccination (Day = 21)	Third vaccination (Day = 42)	Challenge (Day = 56)	Sample collection and study termination (Day = 70)
1	10	A1-A19 Adju-Phos	A1-A19 Adju-Phos	A1-A19 Adju-Phos	2 ml of virulent SDSU#73 PRRSV administered intranasally.	Evaluate clinical health, rectal temperature. Evaluate animals for lung lesions at necropsy and collect designated lung tissue.
2	10	T1-T19 TGV200	T1-T19 TGV200	T1-T19 TGV200	Same as above	Same as above
3	10	A20-A21 T20-T21	A20-A21 T20-T21	A20-A21 T20-T21	Same as above	Same as above
4	10	None	None	None	None	Same as above

In order to evaluate the results of the example, the main criteria used to determine the efficacy of the test treatments was the development of lung lesions characteristic of PRRSV. Serological response, postchallenge ADG, and rectal temperatures were evaluated as supporting criteria. The results of the example are summarized in Table 4.

Table 4

Group	Group average lung scores	Percent of pigs in each group with lung consolidation scores of ≥ 20%	Highest group avg. temp. post-challenge (°F)	Highest percentage of peak viremia postchallenge	Group average postchallenge ADG
1 (A1-A19 Adju-Phos)	19.84	37.5	105.9	100%	0.16
2 (T1-T19 TGV200)	28.42	70.0	106.0	100%	0.43
3 (Chall. Ctrl)	37.68	70.0	106.1	100%	0.68
(Neg. control)	0.0A	0.0	103.9	0%	1.48

There was no seroconversion to PRRSV as determined by the IDEXX PRRS ELISA in the any of the pigs receiving three doses of the respective A1-A19 Adju-Phos or T1-T19 TGV200 DNA vaccine prototypes. After virulent PRRSV challenge, there appeared to be a more rapid increase in the ELISA S/P ratios in the Group 2 than in the Group 1 pigs. Pigs in Group 3 (unvaccinated/challenged controls) had negative S/P ratios until exposed to virulent PRRSV challenge. The strict negative control pigs in Group 4 had negative S/P ratios throughout the study. The serology results are reported in Table 5.

Table 5

			Day 0	Day 21	Day 42	Day 56	(0 dpc)	Day 59	(3 dpc)	Day 61	(5 dpc)	Day 63	(7 dpc)	Day 66	(10 dpc)	Day 70	(14 dpc)
	Group	Pig	ELISA	ELISA	ELISA	ELISA	VI	ELISA	VI	ELISA	VI	ELISA	VI	ELISA	VI	ELISA	VI
	1	802	0.14	-0.09	0.01	0.22	N	0.21	POS	0.97	POS	2.29	POS	2.66	N	2.69	N
	1	808	0.00	-0.01	-0.01	0.02	N	0.02	POS	0.08	POS	0.66	POS	1.01	N	1.22	N
	1	812	-0.02	0.01	-0.02	0.00	N	0.02	N	0.10	POS	0.60	POS	0.92	N	1.21	N
	1	814	-0.03	0.01	-0.03	0.02	N	0.02	N	0.13	POS	0.54	POS	1.15	N	1.80	N
	1	818	0.01	-0.01	0.36	0.23	N	0.18	POS	0.83	POS	2.74	POS	2.97	N	3.24	N
	1	826	0.00	0.00	-0.02	0.01	N	0.01	N	0.10	POS	0.37	POS	0.45	POS	ND	ND
	1	830	-0.01	0.00	0.04	0.02	N	-0.01	POS	0.06	POS	0.39	POS	0.97	POS	1.68	N
	1	832	-0.02	0.00	-0.02	0.03	N	0.04	N	0.18	POS	0.93	POS	1.39	POS	1.71	N
	1	839	0.01	-0.05	0.01	0.08	N	0.06	POS	0.13	POS	0.36	POS	0.72	N	1.13	POS
	1	842	0.02	-0.01	-0.01	0.17	N	0.19	N	0.92	POS	2.30	POS	2.48	N	ND	ND
		Mean	0.01	-0.02	0.03	0.08		0.07		0.35		1.12		1.47		1.84	
	2	806	0.01	0.05	0.11	0.31	N	0.26	POS	0.58	POS	2.51	POS	3.22	N	3.34	N
	2	813	-0.02	0.00	-0.03	0.05	N	0.07	POS	0.22	POS	0.83	POS	1.47	POS	1.73	N
	2	821	0.00	0.05	0.04	0.07	N	0.10	POS	0.15	POS	1.12	POS	2.28	N	2.52	N
	2	822	-0.01	0.00	-0.01	0.03	N	0.05	POS	0.41	POS	1.78	POS	2.37	N	2.01	POS
	2	836	-0.02	0.05	0.12	0.22	N	0.23	POS	0.79	POS	2.93	POS	3.52	POS	3.62	N
	2	844	0.00	-0.02	0.00	0.05	N	0.03	POS	0.31	POS	1.72	POS	2.33	POS	2.17	N
	2	845	0.04	0.01	0.06	0.32	N	0.19	POS	1.00	POS	2.80	POS	3.44	N	3.26	N
	2	846	-0.01	-0.02	-0.03	0.09	N	0.09	N	0.75	POS	2.57	POS	3.17	POS	3.06	N
	2	847	-0.01	0.01	0.02	0.04	N	0.02	POS	0.43	POS	2.05	POS	2.94	POS	2.96	N
	2	849	0.03	-0.02	-0.01	0.11	N	0.08	POS	0.45	POS	1.97	POS	2.48	N	2.56	N

		Mean	0.00	0.01	0.03	0.13		0.11		0.51		2.03		2.72		2.72	
	3	811	-0.03	-0.02	0.02	0.00	N	0.01	POS	0.05	POS	0.55	POS	1.44	POS	1.77	N
	3	815	0.00	-0.01	0.06	0.06	N	0.03	POS	0.07	POS	0.57	POS	1.32	POS	1.33	N
5	3	819	-0.01	0.00	0.04	0.01	N	0.02	POS	0.08	POS	0.25	POS	0.87	POS	1.13	N
	3	823	0.00	-0.01	0.03	0.02	N	0.01	POS	0.04	N	0.44	POS	1.13	POS	1.61	N
	3	831	0.00	-0.02	0.00	0.01	N	0.01	POS	0.07	POS	0.78	POS	1.48	N	1.75	POS
	3	833	-0.02	-0.02	0.00	0.01	N	0.01	POS	0.03	POS	0.15	POS	0.43	POS	0.90	N
	3	840	0.00	-0.02	0.01	0.05	N	0.12	POS	0.18	POS	0.41	POS	1.30	POS	2.15	POS
10	3	841	-0.02	-0.01	-0.02	0.06	N	0.06	POS	0.14	POS	0.71	POS	1.33	POS	1.50	N
	3	843	0.00	-0.02	-0.01	0.02	N	0.02	N	0.11	POS	0.41	POS	0.84	N	0.80	N
	3	848	0.03	-0.02	0.00	0.05	N	0.05	POS	0.10	POS	0.30	POS	0.74	N	1.35	N
		Mean	0.00	-0.02	0.01	0.03		0.03		0.09		0.46		1.09		1.43	
15	4	803	-0.03	0.00	0.04	0.04	N	0.04	N	0.04	N	0.02	N	0.01	N	-0.02	N
	4	804	0.01	-0.03	0.02	0.12	N	0.11	N	0.12	N	0.08	N	0.13	N	0.10	N
	4	805	0.03	-0.01	-0.03	0.00	N	-0.01	N	0.00	N	0.01	N	-0.01	N	-0.03	N
	4	810	0.01	-0.06	-0.03	0.08	N	0.08	N	0.06	N	0.02	N	0.02	N	0.02	N
	4	817	0.03	-0.02	-0.15	-0.02	N	-0.01	N	-0.01	N	-0.04	N	-0.04	N	-0.10	N
20	4	828	-0.02	-0.03	0.04	0.00	N	-0.01	N	0.01	N	-0.02	N	0.00	N	-0.01	N
	4	834	-0.01	-0.02	0.03	0.00	N	0.00	N	0.00	N	-0.17	N	-0.02	N	-0.01	N
	4	837	0.00	-0.03	0.01	0.03	N	0.03	N	0.05	N	0.02	N	0.03	N	-0.02	N
	4	838	0.00	-0.01	0.00	0.08	N	0.11	N	0.11	N	0.09	N	0.07	N	0.01	N
	4	850	0.04	-0.01	0.03	0.09	N	0.06	N	0.07	N	0.08	N	0.07	N	0.06	N
25		Mean	0.01	-0.02	0.00	0.04		0.04		0.05		0.01		0.03		0.00	

The pig temperatures were monitored from two days prechallenge throughout fourteen days postchallenge. The baseline group average temperature throughout the challenge period for the Group 4 unvaccinated/unchallenged controls was 103.4 °F.

The group average temperatures among all PRRSV-challenged groups were elevated at some point following challenge, however there was a temporal difference in days post challenge in which the group average temperature peaked. The group average peak temperatures in all groups challenged with PRRSV ranged from 105.9 to 106.1 °F, whereas the negative controls group average peak temperature was 103.9. Group 3 showed a gradual increase in temperature postchallenge with a peak of 106.1°F at nine days postchallenge. Groups 1 and 2 displayed a sharp increase in temperatures at two days postchallenge with peak temperatures of 105.9°F and 105.6°F, respectively. Of note, the manner in which the postchallenge temperatures of the DNA vaccinated pigs in Group 1 and 2 rapidly increased, is similar to the manner in which PRRS KV vaccinated animals respond postchallenge. It has been observed that pigs vaccinated with experimental PRRS KV prototypes are usually "humorally-primed" (i.e. seropositive to PRRSV following vaccination). The animals vaccinated with these experimental PRRS KV prototypes also display a rapid increase in temperature soon after challenge, as was seen in this study with the DNA vaccinated pigs in Groups 1 and 2. This similarity in rapid temperature elevation following PRRSV challenge is an additional indication that the immune systems of the DNA vaccinated pigs were indeed primed to PRRSV antigen.

The Group 3 pigs displayed lung lesions characteristically found in a successful PRRSV challenge. The Group 4 pigs had no lung lesions at necropsy. The Group 1 and 2 pigs had group average lung lesions of 19.84 and 28.42, respectively. The lung scores for the individual pigs are reported in Table 6.

Table 6

Group	Animal	Lung Scores
1	802	2.00
1	808	0.90
1	812	55.00
1	814	0.20
1	818	1.00
1	826	ND
1	830	70.00
1	832	2.90
1	839	26.75
1	842	ND
	Mean	19.84
2	806	23.00
2	813	32.50
2	821	4.00
2	822	28.95
2	836	37.50
2	844	67.00
2	845	16.70
2	846	52.50
2	847	14.00
2	849	8.00
	Mean	28.42
3	811	2.75
3	815	33.50
3	819	51.00
3	823	72.00
3	831	75.00
3	833	15.50
3	840	39.00
3	841	37.50
3	843	9.50
3	848	41.00
	Mean	37.68
4	803	0.00
4	804	0.00
4	805	0.00
4	810	0.00
4	817	0.00

4	828	0.00
4	834	0.00
4	837	0.00
4	838	0.00
4	850	0.00
	Mean	0.00

From these results, it is clear that DNA vaccines comprising various regions of the PRRSV genome can induce protection from virulent challenge in the respiratory model

I/We Claim:

1. A vaccine capable of inducing an immune response against PRRSV comprising:

a first portion of PRRSV ORF1 DNA, said portion having at least 21 contiguous nucleotides from said PRRSV ORF1 DNA; and

a suitable pharmacological carrier.

2. The vaccine of claim 1, said portion having at least 150 contiguous nucleotides from a sequence selected from the group consisting of sequences having at least 85% sequence sequence identity with any one of SEQ ID Nos. 1-14, and combinations thereof.

3. The vaccine of claim 2, said portion being selected from the group consisting of sequences having at least 85% sequence identity with any of SEQ ID Nos. 1-6, 9, 10, and combinations thereof.

4. The vaccine of claim 1, further comprising a portion of DNA from PRRSV selected from the group consisting of at least 21 contiguous nucleotides from a PRRSV ORF other than ORF1, at least 21 contiguous nucleotides from PRRSV ORF1, and combinations thereof.

5. The vaccine of claim 1, further comprising another composition effective at inducing an immune response against PRRSV infection.

6. The vaccine of claim 1, said PRRSV ORF1 being derived from a virulent strain of PRRSV.

7. The vaccine of claim 1, further comprising an ingredient selected from the group consisting of adjuvants, excipients, and combinations thereof.

8. A method of inducing an immune response against PRRSV in an animal susceptible to PRRSV infection, said method comprising the steps of:

administering a composition to the animal, said composition comprising at least 21 contiguous nucleotides from a portion of PRRSV ORF1 DNA; and

causing said inducement of said immune response.

9. The method of claim 8, further comprising the step of providing a second administration of said composition.

10. The method of claim 8, said portion comprising at least 150 contiguous nucleotides from a sequence selected from the group consisting of sequences having at least 85% sequence identity with any one of SEQ ID Nos. 1-14, and combinations thereof.

11. The method of claim 10, said portion being selected from the group consisting of sequences having at least 85% sequence identity with any of SEQ ID Nos. 1-6, 9, 10, and combinations thereof.

11. The method of claim 9, said composition further comprising a second DNA portion selected from the group consisting of at least 21 contiguous nucleotides from a

PRRSV ORF other than ORF1, at least 21 contiguous nucleotides from ORF1, and combinations thereof.

13. The method of claim 9, said composition further comprising a second composition effective at inducing an immune response against PRRSV infection.

14. The method of claim 9, said composition further comprising an ingredient selected from the group consisting of adjuvants, excipients, and combinations thereof.

15. A vector comprising at least a portion of PRRSV ORF1 DNA.

16. The vector of claim 15, said vector being a plasmid.

17. The vector of claim 15, said portion of PRRSV ORF1 DNA comprising at least 21 contiguous nucleotides from PRRSV ORF1 DNA.

18. The vector of claim 17, said portion of PRRSV ORF1 DNA having at least 150 contiguous nucleotides from a sequence selected from the group consisting of sequences having at least 85% sequence identity with any one of SEQ ID Nos. 1-14, and combinations thereof.

19. The vector of claim 1, said vector further comprising a second portion of PRRSV DNA selected from the group consisting of least 21 contiguous nucleotides from a PRRSV ORF other than ORF1, at least 21 contiguous nucleotides from ORF1, and combinations

thereof.

20. The vector of claim 15, said PRRSV DNA being derived from a virulent strain of PRRSV.

21. A cell containing a plasmid comprising at least 21 contiguous nucleotides from PRRSV ORF1 DNA.

22. The cell of claim 21, said plasmid further comprising at least 150 contiguous nucleotides from a sequence selected from the group consisting of sequences having at least 85% sequence identity with any one of SEQ ID Nos. 1-14, and combinations thereof.

23. The cell of claim 21, said plasmid further comprising a second portion of PRRSV DNA selected from the group consisting of least 21 contiguous nucleotides from a PRRSV ORF other than ORF1, at least 21 contiguous nucleotides from ORF1, and combinations thereof.

24. The cell of claim 21, said PRRSV DNA being derived from a virulent strain of PRRSV.