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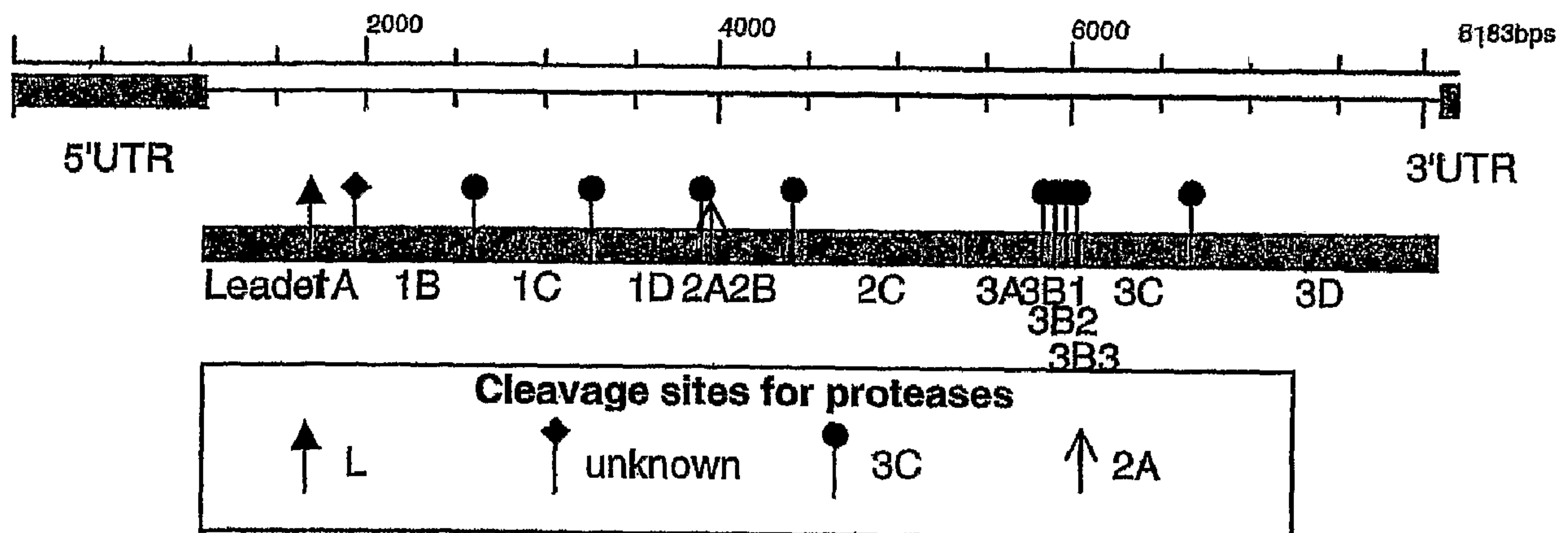
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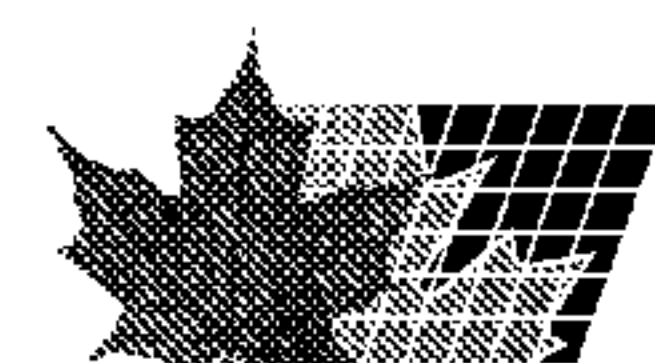
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(54) Title: RECOMBINANT FOOT AND MOUTH DISEASE VACCINE



(57) Abrégé/Abstract:

A foot and mouth disease virus (FMDV) vaccine and method for producing same is described wherein the N terminal portion of the FMDV polypeptide, encoding the four structural proteins, 1A, 1B, 1C, and 1D, are each separated by a non-FMDV protease, preferably a cellular protease, for example, furin. The expression system may be transformed into a cell expressing the non-FMDV protease and the resulting particles recovered for use as a vaccine



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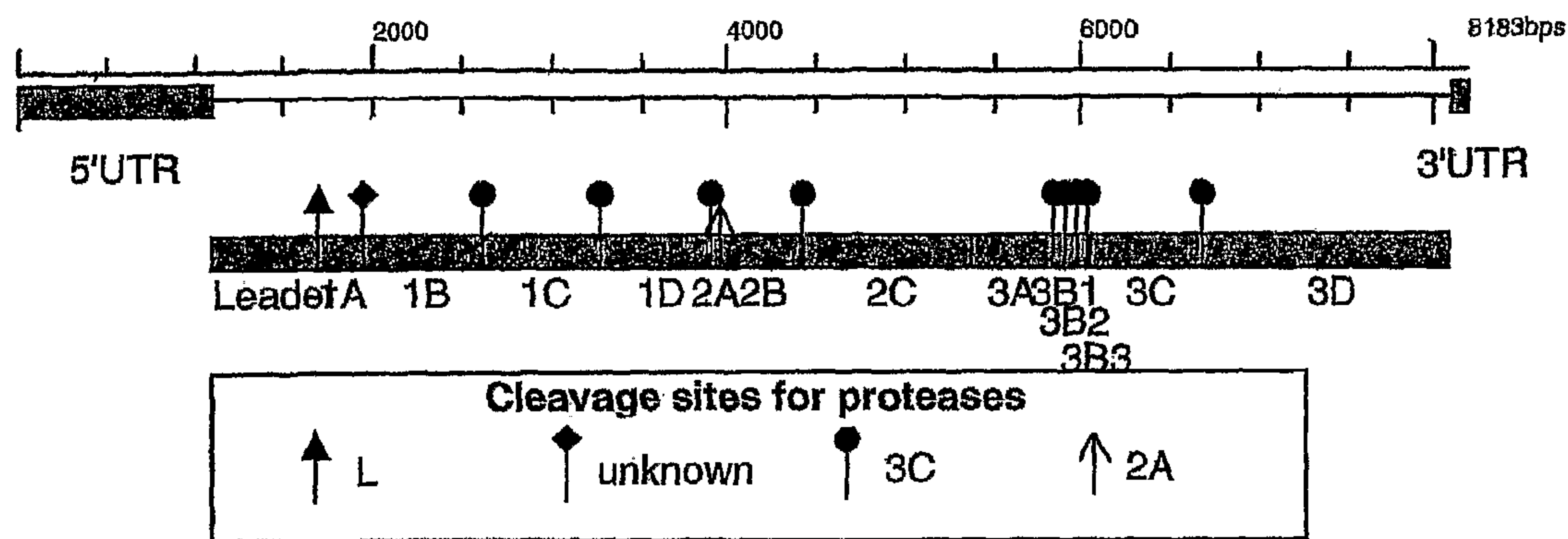
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(54) Title: RECOMBINANT FOOT AND MOUTH DISEASE VACCINE



(57) Abstract: A foot and mouth disease virus (FMDV) vaccine and method for producing same is described wherein the N terminal portion of the FMDV polyprotein, encoding the four structural proteins, 1A, 1B, 1C, and 1D, are each separated by a non-FMDV protease, preferably a cellular protease, for example, furin. The expression system may be transformed into a cell expressing the non-FMDV protease and the resulting particles recovered for use as a vaccine

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RECOMBINANT FOOT AND MOUTH DISEASE VACCINE

5

BACKGROUND OF THE INVENTION

Foot-and-mouth disease (FMD) is a usually acute disease affecting cloven-
10 hoofed domestic and wild animals like cattle, buffalo, sheep, deer, and pigs. The
disease is associated with a high morbidity and low mortality. Subclinical and
persistent infections occur and pose major problems for disease control. The virus
is highly contagious and is transmitted by contact with infected animals and
contaminated materials, humans, and non-susceptible animals. Over the past
15 twenty years, FMD has been endemic in large areas of Asia, Africa, Southern
America, and occasionally Europe, but not in Australia and Northern America.
Disease control measures often included massive culling. This strategy has
received intense criticism. Current vaccines for FMD are readily available and safe;
however, due to the complex production process and other drawbacks they are not
20 employed as a universal and global weapon against FMD.

Outbreaks of FMD result in devastating and drastic consequences for both
animals and humans. Affected countries suffer from substantial loss in livestock
and animal products, and in export markets, both short- and long-term. Additional
costs, distress and suffering arise from eradication measurements, compensation
25 policies, and disruption of normal living.

Vaccination against FMDV is an established and specific tool to help control
both FMD eradication and outbreaks. Definitive strategies, however, do not exist
and depend on a broad range of implications. There are no antiviral treatments for
FMDV.

30 FMDV is an antigenically variable virus consisting of seven serotypes
(European types A, O and C; African types SAT1, SAT2 and SAT3; and an Asiatic
type Asia 1) and dozens of subtypes (see for example Kleid et al., 1981, Science
214: 1125-1129). Immunity to one serotype does not provide protection against the

others and in some cases, immunity to one subtype will not protect against other members of the same subtype. Currently used vaccines consist of tissue culture grown virus, which for some preparations are partially purified and which are typically inactivated by binary ethyleneimine (BEI).

5 Modern FMD vaccines, in combination with other measures, can be used to contain and eradicate FMD outbreaks. Contact transmission of FMDV is rapidly reduced within 3-5 days after vaccination of pigs, cattle, sheep, and other animals.

 However, some concerns exist over the use of FMD vaccines. After exposure to FMDV, vaccination may only prevent disease but not infection, and
10 some animals may become persistently infected carriers of FMDV. Using approved diagnostic tests, it is difficult, if not impossible to differentiate vaccinated from infected or convalescent animals. Based on the current technology, production of vaccines requires handling of live virus in high containment facilities, which excludes countries such as the USA from vaccine production.

15 US Published Patent Application 2004/0001864 teaches a vaccine against foot-and-mouth disease wherein empty capsids are produced by coexpressing P1 and protease 3C.

 US Patent 5,864,008 teaches a Th-cell epitope derived from VP3 capsid protein of FMDV.

20 US Patent 5,612,040 teaches a foot-and-mouth disease vaccine comprising deletion of the G-H loop of VP1 which results in an antigenic but non-infectious virus.

 US Patent 5,824,316 teaches a genetically engineered foot-and-mouth disease virus wherein the leader proteinase has been deleted. The L proteinase-
25 deleted viruses are able to assemble and grow in cells in culture, but are less toxic to infected cells within the cells, thereby producing an attenuated infection.

 US Patent 6,048,538 teaches the use of immunodominant domains from FMDV non-structural proteins 3A, 3B and 3C and the use thereof for detecting anti-FMDV antibodies in animal body fluids.

30 Published US Patent Application 2003/0171314 teaches early protection of susceptible animals against FMDV by inoculating the animals with a vaccine comprising an interferon DNA sequence and optionally a foot-and-mouth disease vaccine.

US Patent 6,107,021 teaches a peptide composition comprising at least one target antigenic site derived from VP1 capsid protein of FMDV covalently linked to a helper T cell epitope.

Published PCT Application WO 03/083095 teaches insertion of a
5 heterologous sequence between two furin cleavage sites within a carrier glycoprotein, such as the furin cleavage sites of an F protein of a Respiratory Syncytial Virus and using the resulting mutant virus as a multivalent vaccine.

Published US Patent Application 2004/0001864 teaches the preparation of empty FMDV capsids by expression of the P1 region and protease 3C. Mason et
10 al. (Vaccines for OIE List A and Emerging Animal Diseases, 2003, Brown and Roth eds, Dev Biol Basel, Karger, vol 114: 79-88) teaches a similar method, involving the expression of a fragment of the P1 region and protease 3C for producing empty capsids.

Structures on the surface of the virus particle present antigenic sites that
15 are important for the immune response to FMDV. In particular, fragments derived from surface peptide 1D elicit neutralizing antibodies that could protect animals from challenge. However, when used alone, 1D-based vaccines failed to induce sufficient immunity in challenge experiments. In general, the entire accessible surface of a virus would be expected to be antigenic and may thus assist in the
20 generation of a strong immunity. Specific formulations of all, recombinantly expressed non-infectious FMDV capsid proteins appear to be as efficacious as a commercial vaccine, with regard to immunogenicity and resistance to challenge with FMDV.

25 SUMMARY OF THE INVENTION

According to a first aspect of the invention, there is provided an expression system comprising

a promoter operably linked to a nucleic acid molecule encoding a poly-protein, said polyprotein comprising:

30 FMDV 1A protein-nonFMDV protease recognition sequence-FMDV 1B protein-nonFMDV protease recognition sequence-FMDV 1C protein-nonFMDV protease recognition sequence-FMDV 1D protein.

According to a second aspect of the invention, there is provided a

method of producing a foot and mouth disease virus-like particle comprising:

providing a host cell including an expression system comprising a promoter operably linked to a nucleic acid molecule encoding a poly-protein, said polyprotein comprising FMDV 1A protein-nonFMDV protease recognition sequence-FMDV 1B protein-nonFMDV protease recognition sequence-FMDV 1C protein-nonFMDV protease recognition sequence-FMDV 1D protein, said host cell expressing a protease recognizing said nonFMDV protease recognition sequence;

growing the host cell under conditions such that the poly-protein is produced, resolved into 1A, 1B, 1C and 1D by the protease and 1A, 1B, 1C and 1D assemble into virus-like particles; and

recovering the virus-like particles.

According to a third aspect of the invention, there is provided the use of the virus-like particles prepared as described above as a vaccine.

According to a further aspect of the invention, there is provided an expression system comprising a promoter operably linked to a nucleic acid molecule encoding a poly-protein, said polyprotein comprising: FMDV 1A protein-furin protease recognition sequence-FMDV 1B protein-furin protease recognition sequence-FMDV 1C protein-furin protease recognition sequence-FMDV 1D protein, wherein the polyprotein lacks pol2A.

According to yet another aspect of the invention, there is provided a method of producing a foot and mouth disease virus-like particle comprising: providing a host cell comprising an expression system having a promoter operably linked to a nucleic acid molecule encoding a poly-protein, said polyprotein comprising FMDV 1A protein-furin protease recognition sequence-FMDV 1B protein-furin protease recognition sequence-FMDV 1C protein-furin protease recognition sequence-FMDV 1D protein, said host cell expressing furin protease; growing the host cell under conditions such that the poly-protein is produced and resolved into 1A, 1B, 1C and 1D by the furin protease and 1A, 1B, 1C and 1D assemble into virus-like particles; and recovering the virus-like particles.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. Schematic diagram of the FMDV genome, strain 0, UKGJ3512001, and the open reading frame for the polyprotein. Protein cleavage sites and the respective proteases are indicated as arrows.

4a

Figure 2. Protein chart for the authentic and modified capsid polyproteins. Amino acid changes of the modified polyprotein are underlined in blue. These sites represent newly introduced furin cleavage sites.

Figure 3. Hydrophilicity of FMDV capsid proteins.

Figure 4. Blot showing cleavage of polypeptide by furin. Cells have been transfected with 3 different plasmids encoding for the original (left lane; "no cut") or modified (center and right lane) FMDV capsid (VP1-4). New cleavage sites (A,B,C) have been introduced as indicated (center and right lane) and utilized. The authentic A cleavage site is recognized by a cellular protease and partially cleaved (left lane). The modified FMDV capsids are cleaved to completion at B (center lane) and at A, B, and C (right lane). Since the blot is probed with a monoclonal antibody directed towards VP1 only proteins containing VP1 are visualised.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications mentioned hereunder are incorporated herein by reference.

As used herein, "cloven-hoofed" animal refers to domestic and wild animals, for example, but by no means limited to cattle, buffalo, sheep, deer, and pigs.

Non-infectious molecular approaches should preferably offer a safe production of vaccines, a platform based technology for all viral strains, and the inclusion of a marker for distinguishing between vaccinated and non-vaccinated animals. That is, one needs to be able to distinguish between vaccinated and infected animals. In one embodiment, as discussed herein, a vaccine or expression system that includes only FMDV capsid and not the FMDV polymerase proteins is used so that vaccinated animals (which will not have anti-polymerase antibodies but will have anti-capsid antibodies) and infected animals (which will have both anti-polymerase antibodies and anti-capsid antibodies) can be distinguished. In an alternative embodiment, the expression system or vaccine includes a marker gene. As will be appreciated by one of skill in the art, when expressed, the marker gene will produce a detectable marker, for example, an immune response to the product of the marker gene. Other suitable markers known in the art may also be used.

FMDV contains a single-stranded positive sense ribonucleic acid (RNA) genome of approximately 8,300 bases surrounded by an icosahedral capsid composed of 60 copies each of four structural proteins, 1A, 1B, 1C, and 1D. The RNA genome is translated as a single, long open-reading frame and codes for the four structural proteins and a number of non-structural proteins, which function in various aspects of the virus cycle. The viral polyprotein is co-translationally processed by at least three viral encoded proteinases (L^{pro} , 2A oligopeptide and $3C^{pro}$). Most of the cleavages are catalysed by $3C^{pro}$ or a $3C^{pro}$ -containing precursor, including the processing of the capsid precursor polypeptide, P1, into

1AB, 1C, and 1D. One exception is the maturation cleavage of the precursor capsid protein 1AB in the provirion to generate the capsid proteins 1A and 1B that occurs by an unknown mechanism. Only 1D, 1B, and 1C have been shown to be surface-exposed and an immunologically important loop found between the G and
5 H beta strands of 1D has been identified as a prominent surface structure on the viral capsid. Cleavage of the polyprotein is essential and sufficient for virus particle formation.

Described herein is an FMDV vaccine and method for producing same wherein the N-terminal portion of the FMDV polyprotein, encoding the four
10 structural proteins, 1A, 1B, 1C, and 1D, are expressed from an mRNA having at least a 5' cap and a 3' poly-A tail, transcribed from a newly manufactured cDNA. As will be appreciated by one of skill in the art, other modifications to the mRNA and/or cDNA may also be made, for example, sequence modifications including but by no means limited to those discussed below and structural modifications
15 known in the art. The protein cleavage recognition sites at either ends of the proteins are modified and are accessible for a non-FMDV protease, preferably a cellular protease, for example, Furin. As will be appreciated by one of skill in the art, the protease cleavage sites are found at the junctions between 1A and 1B, between 1B and 1C and between 1C and 1D. As such, in most embodiments, the
20 5' end of 1A and the 3' end of 1D will not be modified.

As used herein, 1A, 1B, 1C and 1D refer to the amino acid sequences (and nucleotide sequences derived therefrom) of these proteins known in the art as discussed herein. Specifically, as shown in Table 1, sequences for a number of FMDV isolates are known and as discussed below sequences from these isolates
25 can be used in the invention.

The consensus sequence for furin is Arg-X-Lys/Arg-Arg↓-, (Molloy et al., 1999, Trends in Cell Biology 9: 28-35).

As will be appreciated by one of skill in the art, other suitable cellular proteases may be used. Preferably, the protease cleavage site is approximately
30 the same length and has a similar hydrophobicity and/or three dimensional structure and/or charge distribution as the native FMDV protease cleavage site.

Thus, in one embodiment of the invention, there is provided an expression system comprising a nucleic acid molecule encoding a polypeptide comprising 1A,

1B, 1C and 1D of FMDV each separated by a non-native FMDV protease cleavage site. In a preferred embodiment of the invention, the expression system comprises a suitable promoter operably linked to a nucleic acid encoding a polypeptide comprising 1A-non-FMDV PCS-1B-non-FMDV-PCS-1C-non-FMDV-PCS-1D, wherein "PCS" refers to "protease cleavage site". In a yet further embodiment, the nucleic acid encodes a polyprotein comprising 1A-furin PCS-1B-furin PCS-1C-furin PCS-1D.

An example of such a construct is shown in Figure 2 and in SEQ ID No. 1. As shown in Figure 4, this construct was cleaved by furin into 1A, 1B, 1C and 1D proteins and assembled into virus-like particles. As will be apparent to one of skill in the art on examination of the sequence shown in Figure 2 and SEQ ID No. 1, the FMDV strain is O Manisa. A similar construct was constructed using 1A, 1B, 1C and 1D proteins from A24 Cruzeiro also with furin sites engineered between the proteins and similar results were obtained, clearly indicating that the invention can be used to produce virus-like particles from different FMDV strains, as discussed below.

In another embodiment of the invention, there is provided a nucleic acid molecule encoding a polypeptide having a first domain that has at least 80% homology or at least 85% homology or at least 90% homology or at least 95% homology to amino acids 1-80 of SEQ ID No. 1, a second domain adjacent to the first domain that is a non-FMDV protease cleavage site; a third domain that has at least 80% homology or at least 85% homology or at least 90% homology or at least 95% homology to amino acids 86-298 of SEQ ID No. 1; a fourth domain that is a non-FMDV protease cleavage site; a fifth domain that has at least 80% homology or at least 85% homology or at least 90% homology or at least 95% homology to amino acids 304-518 of SEQ ID No. 1; a sixth domain that is a non-FMDV protease cleavage site; and a seventh domain that has at least 80% homology or at least 85% homology or at least 90% homology or at least 95% homology to amino acids 524-733 of SEQ ID No. 1. In a preferred embodiment, the non-FMDV protease cleavage site is a furin cleavage site as described above.

In another embodiment, there is provided a nucleic acid molecule having at least 80% homology or at least 85% homology or at least 90% homology or at least 95% homology to SEQ ID No. 1 and wherein the sequence of the furin

cleavage sites (amino acids 81-85, 299-303 and 519-523 of SEQ ID No. 1) are such that the cleavage sites are recognized by furin, that is, are within the furin consensus sequence described above and are therefore functional for cleavage by furin.

5 In some embodiments, the expression system further includes a signal sequence for translocating the protein into the ER/golgi apparatus of the host cells.

Examples of suitable promoters include but are by no means limited to CMV-driven and baculovirus-driven promoters and vectors. As will be appreciated by one of skill in the art, any suitable promoter active in a cell line expressing the
10 non-FMDV protease of choice may be used, although clearly, the stronger or more efficient the promoter, the higher the yield of particles.

As will be appreciated by one of skill in the art, any suitable cell line or cell type may be transfected or transformed with the expression system described herein. For example, in those embodiments wherein the non-FMDV protease is
15 furin, any cell expressing the furin protease may be used. It is of note that the expression system may be expressed from a transient genetic element such as a plasmid or linear DNA or may be integrated into the genome of the host cell.

As will be appreciated by one of skill in the art, the cell or cell line of choice must also express the non-FMDV protease of choice. It is of note that the cell or
20 cell line may express the protease naturally or as the result of genetic manipulation.

Examples of suitable cell lines include but are by no means limited to BHK and 293T.

Specifically, the expression system is transformed or transfected as
25 discussed above and the cells are grown under conditions suitable for expression from the expression system. A poly-protein is produced which is cleaved by the non-FMDV protease, thereby resolving the poly-protein into 1A, 1B, 1C and 1D which in turn assemble into a particle. In some embodiments, the particles are secreted from the cell and can be recovered using means known in the art. In
30 other embodiments, the particles are recovered using other suitable means known in the art.

As discussed herein, the particles can be used as a vaccine for vaccinating animals at risk of developing or contracting foot and mouth disease. It is of note

that as discussed herein, the particles are non-replicative and can safely be used as a vaccine that accurately mimics the structure of native FMDV.

Thus, the cellular protease replaces the viral proteases L^{pro}, 2A oligopeptide and 3C^{pro} and an unknown protease. As a result of this arrangement,
5 non-infectious eukaryotic and prokaryotic expression systems can be used to produce empty particles for use as a vaccine. Alternatively, the particles can also be used as diagnostic tools and/or to study old or new substances/drugs/mechanisms for potential antiviral activity against FMDV.

Referring to Figure 2 and to SEQ ID No. 1, 1A corresponds to amino acids 1
10 to 80; 1B corresponds to amino acids 86 to 288; 1C corresponds to amino acids 304 to 518; and 1D corresponds to amino acids 524 to 734. As will be appreciated by one of skill in the art, these designations are relative and may vary between different serotypes and sub-types. Furthermore, the specific sequences of 1A, 1B, 1C and 1D are variable amongst serotypes and sub-types, several of which are
15 documented and well known in the art (see for example, GenBank database accession numbers X00429 (A10), X00871 (O1K), AJ251476 (A24) and AJ133357 (C Spain Olot) as well as Table 1).

Thus, in one embodiment of the invention, there is provided an expression system which expresses a fusion comprising 1A, 1B, 1C and 1D, each separated
20 by a protease cleavage site. As will be appreciated by one of skill in the art, the specific amino acid sequence used for 1A, 1B, 1C and/or 1D may all be of any of the serotypes or subtypes of FMDV. In other embodiments, a multivalent vaccine may be generated for example by using 1A from one serotype or subtype fused to 1B and/or 1C and/or 1D from a different serotype or subtype.

25 Any suitable adjuvant known in the art may be used in combination with the vaccine. Examples of suitable adjuvants include but are by no means limited to alum, an acrylic or methacrylic acid polymer, or a water-in-oil or oil-in-water emulsion.

In some embodiments, disulphide bridges are added to increase the stability
30 of the empty capsids using means known in the art.

In one embodiment of the invention, a cDNA molecule is generated by RT-PCR amplification of the 5' end of the FMDV genome, for example, strain 0, although any suitable FMDV could be used, including an unknown serotype or

subtype implicated in an outbreak. Specifically, the primers are designed such that the resulting cDNA sequence will include the ORFs for 1A, 1B, 1C, and 1D. The cDNA is then subcloned into an appropriate expression vector. In some embodiments, the expression vector may be arranged such that the inserted cDNA includes for example an addition of an initial methionine, a stop codon and a poly-A tail.

The cDNA is then mutated to introduce cellular protease recognition sites, for example, furin cleavage sites between 1A-1B, 1B-1C, and 1C-1D. The expression vector is then transformed or transfected into a suitable host which is grown under conditions promoting expression of the cDNA, which in turn results in the production of empty FMDV capsid particles which are then recovered and used in the preparation of a vaccine.

In an alternative embodiment, the FMDV responsible for the outbreak is cloned or amplified by RT-PCR as discussed above and is sequenced. A cDNA template comprising 1A-PCS-1B-PCS-1C-PCS-1D wherein the 1A, 1B, 1C and 1D sequences are either derived from consensus sequences or from a specific FMDV isolate, for example, a common FMDV isolate is then mutated or otherwise modified so as to substantially correspond or correspond verbatim with the 1A, 1B, 1C and/or 1D sequence of the FMDV responsible for the outbreak. It is of note that a bank of template cDNAs as described above could be generated and the one with the greatest sequence homology to the FMDV responsible for the outbreak selected for mutation or modification.

As shown in Figure 3, FMDV proteins were translated from DNA and analyzed for hydrophilicity. The capsid polyprotein for FMDV, strain 0, is shown in black, and the modified capsid in red. Red arrows indicate newly introduced furin cleavage site. Predictions are calculated using methods derived from Kyte & Doolittle (KD) and Hopp & Woods (HW), and for surface exposure (SE). The analysis results are shown in a table format of numerical values and as a set of line graphs. For each amino acid residue, numerical values are given for KD, HW, and SE analyses. All three methods provide an indication of the hydrophilic character of the environment, and the range for each analysis is shown at the top of the column. Three line graphs plot the values calculated for each of the three analyses. For all three graphs, values above the axis line are hydrophilic or

predicted to be exposed at the surface of the protein. KD values fall within a range of +4 to -4, with hydrophilic residues having a negative score. The most hydrophilic residue has a value of -4.5 (arginine). On the graphic display, values above the axis line are hydrophilic; values below the axis line are hydrophobic. KD represents a composite hydrophobicity scale derived from interpretation of free energy changes on a water-vapor phase transition and an analysis of buried side chains. Each value is the average of the values of 5 adjacent residues and is plotted at the middle residue. The range of values is approximately ± 4 relative units. HW values fall within a range of -3 to +3, with hydrophilic residues having a positive score. The most hydrophilic residues have a value of ± 3.0 . On the graphic display, values above the axis line are hydrophilic; values below the axis line are hydrophobic. HW derived hydrophilicity values from a study of antigenicity and adjusted the values to maximize the accuracy of predicting antigenic determinants. Each value is the average of the values of 6 adjacent residues and is plotted at the middle point. The range of values is approximately ± 3 relative units. The SE value is presented as a proportion of the residue, which is exposed on the surface of the protein. These values fall within a range of 0 to 1.000. The most exposed amino acid has a value of 0.97 (lysine). On the graphic display, peak values, which fall above the axis line, are predicted to be exposed on the surface of the protein. SE analysis uses the data of Janin, et al., which provides values representing the fraction of residues of a given amino acid that have a surface area of greater than 20 angstroms squared. High values therefore represent amino acids that are likely to be exposed on the surface of the protein. Plotted values are the average of 6 residues and are plotted at the middle point. Based on these predictions, the three-dimensional structure, the stability, and the immunogenicity of the modified capsid protein are expected to be very similar to the authentic FMDV, strain 0, capsid protein.

As will be appreciated by one of skill in the art, the native FMDV protease is of viral origin and would need to be co-expressed with the expression system expressing the capsid. This approach is inefficient due to the requirement for co-expression of both capsid proteins and protease in a single cell and would result in lower yield.

Table 1 Exemplary FMDV Sequences

Foot-and-mouth disease virus A isolate a12valle 119 iso20, complete genome
gi|46810760|gb| AY593752.1|[46810760]

- 5 Foot-and-mouth disease virus A isolate a13brazil iso75, complete genome
gi|46810762|gb| AY593753.1|[46810762]

Foot-and-mouth disease virus A isolate a14 spain iso39, complete genome
gi|46810764|gb| AY593754.1|[46810764]

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Foot-and-mouth disease virus A isolate a15thailand iso43, complete genome
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- 15 Foot-and-mouth disease virus A isolate a16belem iso80, complete genome
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Foot-and-mouth disease virus A isolate a17 Aguarulbos iso83, complete genome
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- 20 Foot-and-mouth disease virus A isolate a18zulia iso40, complete genome
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Foot-and-mouth disease virus A isolate a1b AYern iso41, complete genome
gi|46810774|gb| AY593759.1|[46810774]

25

Foot-and-mouth disease virus A isolate a20ussr iso10, complete genome
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- 30 Foot-and-mouth disease virus A isolate a21kenya iso77, complete genome
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Foot-and-mouth disease virus A isolate a22iraq-95 iso95, complete genome
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Foot-and-mouth disease virus A isolate a22iraq64 iso86, complete genome
gi|46810782|gb|AY593763.1|[46810782]

- 5 Foot-and-mouth disease virus A isolate a22iraq70 iso92, complete genome
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Foot-and-mouth disease virus A isolate a22turkey iso66, complete genome
gi|46810786|gb|AY593765.1|[46810786]

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Foot-and-mouth disease virus A isolate a23kenya iso8, complete genome
gi|46810788|gb|AY593766.1|[46810788]

- 15 Foot-and-mouth disease virus A isolate a24 argentina iso9, complete genome
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Foot-and-mouth disease virus A isolate a24cruzeiro iso71, complete genome
gi|46810792|gb|AY593768.1|[46810792]

- 20 Foot-and-mouth disease virus A isolate a25 argentina iso38, complete genome
gi|46810794|gb|AY593769.1|[46810794]

Foot-and-mouth disease virus A isolate a26arg iso74, complete genome
gi|46810796|gb|AY593770.1|[46810796]

25

Foot-and-mouth disease virus A isolate a27columbia iso78, complete genome
gi|46810798|gb|AY593771.1|[46810798]

- 30 Foot-and-mouth disease virus O strain Akesu/58, complete genome
gi|21239433|gb|AF511039.1|[21239433]

Foot-and-mouth disease virus O strain China/1/99(Tibet), complete genome
gi|21542501|gb|AF506822.2|[21542501]

Foot-and-mouth disease virus O, strain TAW/2/99 TC, complete genome
gi|30145772|emb|AJ539136.1|FOO539136[30145772]

- 5 Foot-and-mouth disease virus O, strain TAW/2/99 BOV, complete genome
gi|30145774|emb|AJ539137.1|FOO539137[30145774]

Foot-and-mouth disease virus O, strain Tibet/CHA/99, complete genome
gi|30145776|emb|AJ539138.1|FOO539138[30145776]

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Foot-and-mouth disease virus O, strain SKR/2000, complete genome
gi|30145778|emb|AJ539139.1|FOO539139[30145778]

- 15 Foot-and-mouth disease virus O, strain SAR/19/2000, complete genome
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Foot-and-mouth disease virus O, strain UKG/35/2001, complete genome
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- 20 Foot-and-mouth disease virus HKN/2002, complete genome gi|33348772|gb|
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Foot-and-mouth disease virus O strain OMIII, complete genome gi|33943915|gb|
AY359854.1|[33943915]

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Foot-and-mouth disease virus O isolate O/NY00, complete genome
gi|37575129|gb| AY333431.1|[37575129]

- 30 Foot-and-mouth disease virus polyprotein gene, genomic RNA, serotype O, isolate
FRA/1/2001, complete genome gi|45725010|emb|AJ633821.1|[45725010]

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Foot-and-mouth disease virus O isolate o10phil76 iso76, complete genome
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- 5 Foot-and-mouth disease virus O isolate o11indonesia iso52, complete genome
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Foot-and-mouth disease virus O isolate o1argentina iso5, complete genome
gi|46810884|gb| AY593814.1|[46810884]

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Foot-and-mouth disease virus O isolate o1bfs iso18, complete genome
gi|46810886|gb| AY593815.1|[46810886]

- 15 Foot-and-mouth disease virus O isolate o1bfs46 iso46, complete genome
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Foot-and-mouth disease virus O isolate o1brugge iso79, complete genome
gi|46810890|gb| AY593817.1|[46810890]

- 20 Foot-and-mouth disease virus O isolate o1campos iso96, complete genome
gi|46810892|gb| AY593818.1|[46810892]

Foot-and-mouth disease virus (FMDV) strain C, isolate c-s8c1, genomic RNA
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Foot-and-mouth disease virus (FMDV) strain C, isolate rp99, genomic RNA
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- 30 Foot-and-mouth disease virus (FMDV) strain C, isolate rp146, genomic RNA
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Foot-and-mouth disease virus C1 isolate c1noville iso56, complete genome
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- 5 Foot-and-mouth disease virus C3 isolate c3ind iso19, complete genome
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Foot-and-mouth disease virus C3 isolate c3resende iso1, complete genome
gi|46810870|gb| AY593807.1|[46810870]

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Foot-and-mouth disease virus C4 isolate C4 Tierra del Fuego iso2, complete
genome gi|46810872|gb| AY593808.1|[46810872]

- 15 Foot-and-mouth disease virus C5 isolate c5arg iso60, complete genome
gi|46810874|gb| AY593809.1|[46810874]

Foot-and-mouth disease virus C isolate cwald iso32, complete genome
gi|46810876|gb| AY593810.1|[46810876]

- 20 Foot-and-mouth disease virus Asia1 strain YNBS/58, complete genome
gi|37223495|gb| AY390432.1|[37223495]

Foot-and-mouth disease virus Asia 1 isolate asia1-1pak iso3, complete genome
gi|46810846|gb| AY593795.1|[46810846]

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Foot-and-mouth disease virus Asia 1 isolate asia1-2isrl3-63 iso6, complete
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- 30 Foot-and-mouth disease virus Asia 1 isolate asia1-3kimron iso61, complete
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Foot-and-mouth disease virus Asia 1 isolate asia1leb-89 iso89, complete genome
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Foot-and-mouth disease virus Asia 1 isolate asia1leb4 iso4, complete genome
gi|46810854|gb| AY593799.1|[46810854]

- 5 Foot-and-mouth disease virus Asia 1 isolate asia1leb83 iso28, complete genome
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Foot-and-mouth disease virus Asia 1 isolate IND 321/01, complete genome
gi|51340579|gb| AY687333.1|[51340579]

10

Foot-and-mouth disease virus Asia 1 strain IND 491/97, complete genome
gi|51340581|gb| AY687334.1|[51340581]

- 15 Foot-and-mouth disease virus SAT 1 isolate sat1-20 iso11, complete genome
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Foot-and-mouth disease virus SAT 1 isolate sat1-3swa iso14, complete genome
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- 20 Foot-and-mouth disease virus SAT 1 isolate sat1-4srhod iso24, complete genome
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Foot-and-mouth disease virus SAT 1 isolate sat1-6swa iso16, complete genome
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- 30 Foot-and-mouth disease virus SAT 1 isolate sat1-7isrl iso12, complete genome
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Foot-and-mouth disease virus SAT 1 isolate sat1bot iso47, complete genome
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Foot-and-mouth disease virus SAT 1 isolate sat1rhod iso33, complete genome
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- 5 Foot-and-mouth disease virus SAT2 genomic RNA for L, VP4, VP2, VP3, VP1, 2A, 2B, 2C, 3A, VPg1, VPg2, VPg3, pro coding polypolyprotein, strain KEN/3/57
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- 10 Foot-and-mouth disease virus SAT 2 clone ZIM/7/83, complete genome
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Foot-and-mouth disease virus SAT 2 isolate sat2-1rhod iso26, complete genome
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- 15 Foot-and-mouth disease virus SAT 2 isolate sat2-2 iso25, complete genome
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Foot-and-mouth disease virus SAT 1 isolate sat1rhod iso33, complete genome
gi|46810948|gb|AY593846.1|[46810948]

- 5 Foot-and-mouth disease virus SAT2 genomic RNA for L, VP4, VP2, VP3, VP1, 2A, 2B, 2C, 3A, VPg1, VPg2, VPg3, pro coding polypolyprotein, strain KEN/3/57
gi|6572136|emb|AJ251473.1|FDI251473[6572136]

- 10 Foot-and-mouth disease virus SAT 2 clone ZIM/7/83, complete genome
gi|33332022|gb|AF540910.1|[33332022]

Foot-and-mouth disease virus SAT 2 isolate sat2-1rhod iso26, complete genome
gi|46810950|gb|AY593847.1|[46810950]

- 15 Foot-and-mouth disease virus SAT 2 isolate sat2-2 iso25, complete genome
gi|46810952|gb|AY593848.1|[46810952]

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 19

NOTE : Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 19

NOTE: For additional volumes, please contact the Canadian Patent Office

NOM DU FICHER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

CLAIMS

1. An expression system comprising
a promoter operably linked to a nucleic acid molecule encoding a poly-protein,
said polyprotein comprising:

5 FMDV 1A protein-furin protease recognition sequence-FMDV 1B protein-furin
protease recognition sequence-FMDV 1C protein-furin protease recognition sequence-FMDV
1D protein, wherein the polyprotein lacks pol2A.

2. A method of producing a foot and mouth disease virus-like particle
comprising:

10 providing a host cell comprising an expression system having a promoter
operably linked to a nucleic acid molecule encoding a poly-protein, said polyprotein
comprising FMDV 1A protein-furin protease recognition sequence-FMDV 1B protein-furin
protease recognition sequence-FMDV 1C protein-furin protease recognition sequence-FMDV
1D protein, said host cell expressing furin protease;

15 growing the host cell under conditions such that the poly-protein is produced
and resolved into 1A, 1B, 1C and 1D by the furin protease and 1A, 1B, 1C and 1D assemble
into virus-like particles; and

recovering the virus-like particles.

3. The expression system according to claim 1 wherein the poly-protein
20 has at least 85% identity to the polypeptide as set forth in SEQ ID NO:1.

4. The expression system according to claim 1 wherein the poly-protein
has at least 90% identity to the polypeptide as set forth in SEQ ID NO:1.

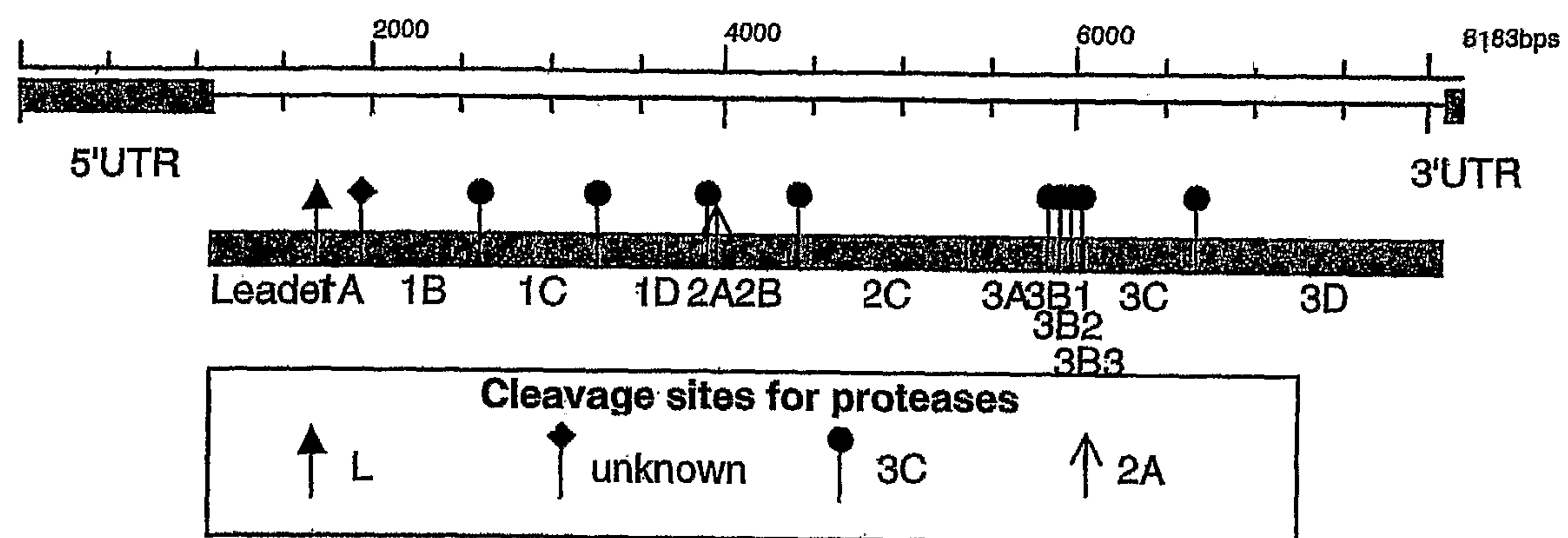
5. The expression system according to claim 1 wherein the poly-protein
has at least 95% identity to the polypeptide as set forth in SEQ ID NO:1

25 6. The method according to claim 2 wherein the poly-protein has at least
85% identity to the polypeptide as set forth in SEQ ID NO:1.

7. The method according to claim 2 wherein the poly-protein has at least
90% identity to the polypeptide as set forth in SEQ ID NO:1.

8. The method according to claim 2 wherein the poly-protein has at least
30 95% identity to the polypeptide as set forth in SEQ ID NO:1.

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Modified	101	ttrnghtttsttqssvgvtygyataedfvsgpntsgletrvvqaerffkth
Capsid	151	lfdwvtsdpfgrcylllptdhkgvygsltdsyaymrngwdvevtavgnq
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FIGURE 2

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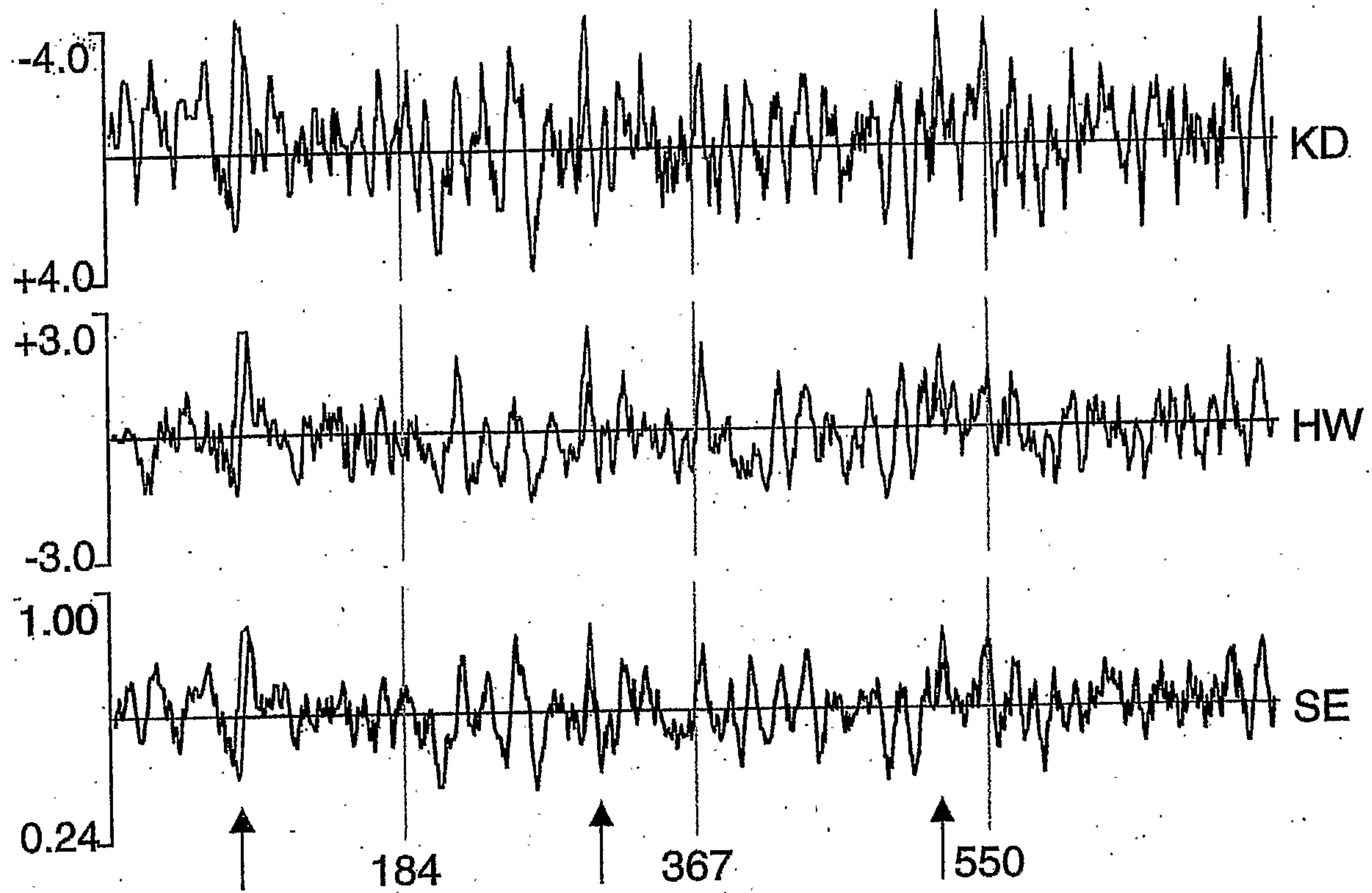


FIGURE 3

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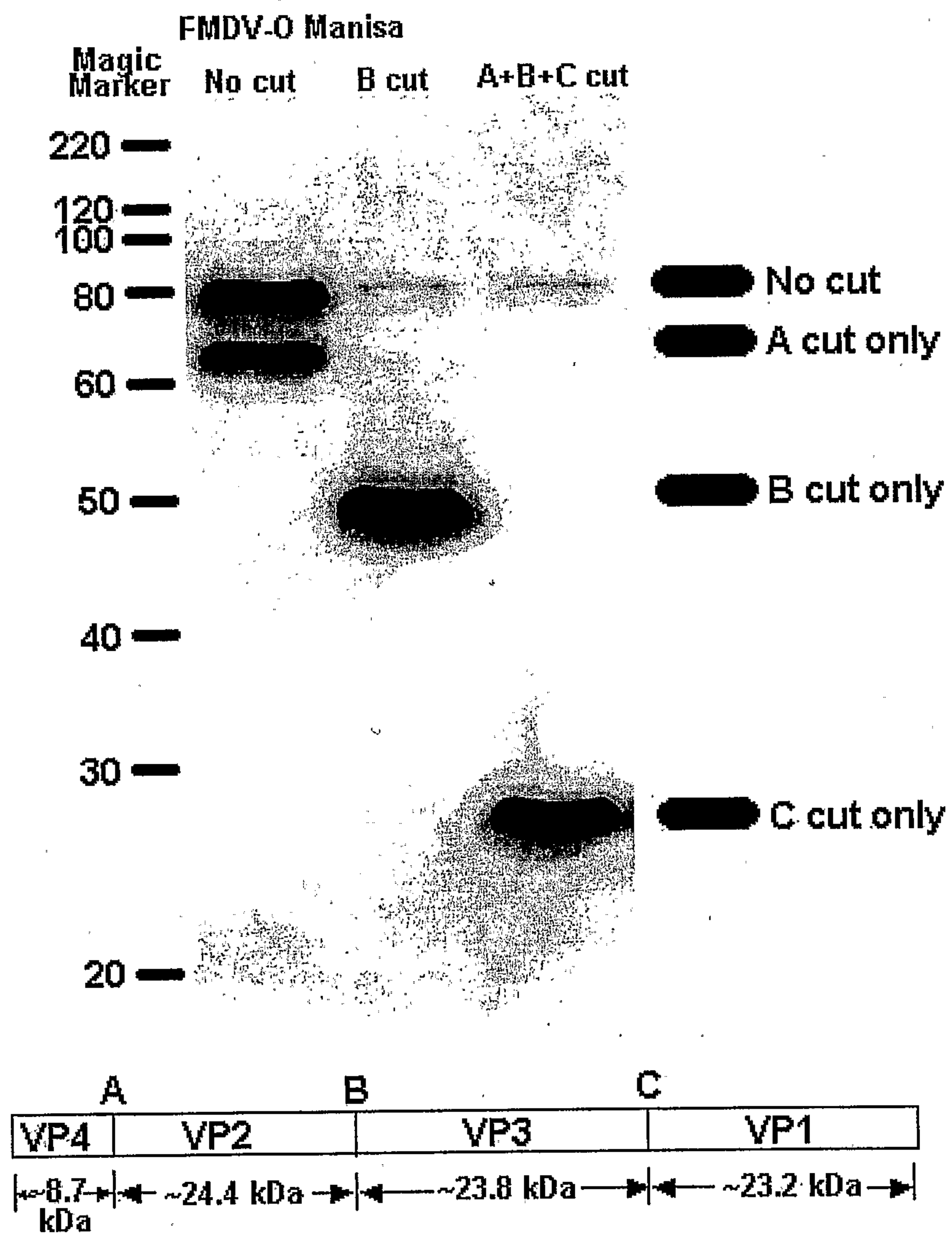
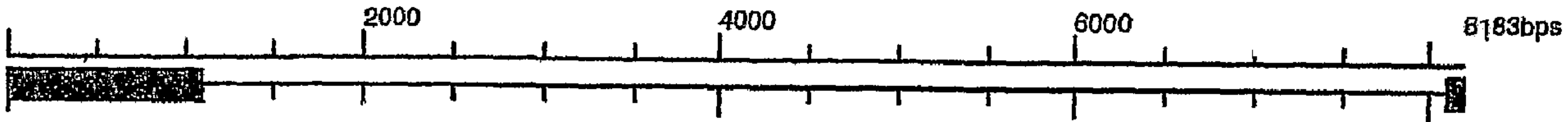


FIGURE 4



5'UTR

3'UTR

