NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES THEREOF

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ABSTRACT

The present invention provides the complete genomic sequence of a novel human coronavirus, coined as coronavirus-HKU1 ("CoV-HKU1"), isolated in Hong Kong from a patient who had a recent history of visit to Shenzhen, China. The virus belongs to the order Nidovirales of the family Coronaviridae, being a single-stranded RNA virus of positive polarity. The invention also provides the deduced amino acid sequences of the complete genome of the CoV-HKU1. The nucleotide sequences and deduced amino acid sequences of the CoV-HKU1 are useful in preventing, diagnosing and/or treating the infection by CoV-HKU1. Furthermore, the invention provides immunogenic and vaccine preparations using recombinant and chimeric forms as well as subunits of the CoV-HKU1 based on the nucleotide sequences and deduced amino acid sequences of the CoV-HKU1.
SEQ: 1
1  TCGTCTATGCGAAATTTTTGCTATGTAGTTAGTTAGTTTGCTGGCCGCAACAT  58
SEQ: 2
1  RAMPNILRIVSSLVLARKH  19

59  GAATTGTGTGTACATGGTGTTAGATTTTATCGCCTTGGCAATGATGCTCAAGTT
20  EPCSSHGDRFYRLANECACQV  39

119  TTTAAGTGAAAATATGTATTGTGCTGCTAATATTAGTTAAGCCTGTTGCTACTAGT
40  LSEIVMCGGYVKPGGTS  59

179  GGTGATGAACATCTCTTTGCTAAATCTGTATTTTTATATATATGCAAGCCTGTTACTGCT
60  GDATTAFANSVPNGICQAVTA  79

239  AATGTTTGGTTCTTATGCGCTGTTATGCGCATAGATTAGTTAAAGATTAAATATAOGCAAT
80  NVCSSLMACNGHKIEDSIRN  99

299  TTACAAAAACGCTTTACTCTATGTTATGACAGATTGATTATACATTACATTTGCT
100  LQKRLYSNVVRTDYVTDFV  119

359  AATGAGTATTGTAAATTATTTATATTACGCTATTAG
120  NSYTFEFLCKHF  130

FIG. 1
SEQ:3

1  GAATAAGAGCGAATTCCGCTCAGCTATCAGTATTACGATCTTGTGGTCAGATCTCAT
E*ERIASVPSISLRSLLVRSSHNKSELPYRLSAYDLLLLDIL
IRANCURTQVQLTISCISS

61  TAAATCTAAACCTTTTAAAAACAGAYCCTCTCCGCTATCCCATGGCTGAGTTGAGTTGGTTATC
*I*TFTFRFPVIHACECGLIKSKLFKQDSLSSLMLSVSVS
LNLNLNPLNKNKIPCPCLVWFFN

121  ATAAATCTTGATTTTTACCTTCCACACTTTTCCTCTCCTGCAGTGACCTTGGTGTTGGTGC
IILYFTFTHSALASDVLV
*SCILLSTFLISLPVTCCWLS
HNLVLYFPFPFSSLQC'VRGEC

181  TCTAGCCCTTCCGATAGTCCGAAATATACCTACACTGGCTCATCCCTCAA
LSVPPIGRNNDNQQIRSRQL
SASLPVAMIKTSKYGLGFK
PQRPSPHRSPQ'LPKANTVSA

241  GTGGCAGCCAAGTTTCCCTTTCCGCGATCCGAGCGGGTGGCTGCTACG
VGARISLAAAGCCSGGTVG'SY
WAPERFRWLLLPPDAASELSMPM
SGRQNPVGVCFRMQRSSWLV

301  GAAGTCAGATGAGCGGCGGTATGCAAAACCTACTCTTCGGCCCTGGTTAGAT
EVRS*GWVKMPLYWSDDSKCWIKSDSDEGGCLPSTGQAMESVGF
'SQMRYGVYAPLLVVKRVKVL

361  CGTTTATGATATTGATAGAGGCGGATGCTGTCCGCAATCCCTTGACAGAT
RL'SCEDRSLSLHISWTROMACVYDNHVKIDCRICILGQEBWHV
SFMIIM'RIVAAFLDKNMG

421  GCAATCCCAACTTTTACCTCAGATGAAATACCTCAGTATGATAGAGGCTGAGT
AVKSYP'YFCS'RSTCRSSQSNLIRDIYVHEDLHVVEVLC
CSQILSVIPLFMKIIYML'KFK

481  AACTAAAAACGCGCTAAGGATCCCTTACGGCAGTATAGAATTTTAAATACCTACCTTTTACGATGTT
N*NRSRKVRYGHNFN'SITPA'ALTKTAVKSGBTALIKSKPLHSL
*LKQP'SPVRQF'LNHLICIA

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SEQ: 1
CTTATTTCTGCCTTAACGGCACAGGTGGACATGTGGAATGTGACTAGAGAGACMGCTGATAGTA
YSRIADTGDILKRDRTLD
ILAFQTRVT*SVIESIETFLSNRGRYRRDASKRDSDRM

61
ATTTAGATTTGAAAAATTTTTTTTCTAATGAGCAATAGTGATCAGGACACTACCACACCAAGTAG
*IVK*VLNGTINAQSHPKINFPRFKKFLIGQ*GKHHTHNL
LDLSCSERNMSTLTTLT

121
TATTAGACATATATAGAAGGTTGAGAAATGGAGAGAIAGAGACGTCATCGCATGACACCCAAAAG
MIKYKVKVKK*KREALSTNTT
*LRNT*KGCKEDRQWHRTPOYDQIKSEVSMERGTVVHQN

181
GATTCGCAAGGAGGTATACCGTATCTAATTTTTTGCTGATGTTATGCGAAGGCGGAAAGTT
RLGGMMPRLSFWCIRDRS*G*RGEWLDCHNFGAIVTEAS
EADRGYTAIILVLLLLYRPKL

241
CACCCCGGCGTCTAAAGCAACACAGGAAGGCGCTACGGCTCTCTCAACCGATCGAGATA
TPALIENAEAPHLPPTP*D
LRWFKTPQKRICRLQLQSTRHAGSNRSRSGSAASSNALG

301
CTTGACTCTCTCCACCCCAATATCAGGAGATGACACGCTCTACCTTTGCAACACTAA
STLHPHTIGR*QDSLSPFHQI
HL*ILTP*AGRSTLRHFTNSFDSSPPNHEVPAISLTPN

361
GCAAATACTATTTAGTAATTCTCTAATAGGACGCTAACGGAGAAACGCTCTCTCCACCAG
RKHYDHSLSNLSDCEQVLIAHENIIIIMHLYITAAKNKSLPFMM
T*SL*TFISQQRMRPCSHCT

421
GTCGATTGAAATAGGGCTATATAAACAAGTGAGTTCTACATGTCATGCACATCTTCAAG
ATLD*GHYKQHEHLDVHQILEHL*IKDITNKHMFI*MNYYFN
CFRIRSIKTSRSCTTSTR

481
TTGATTGTTTCGCTGCAAATTTTCTAGGGCAGTGGCTTTAATAATTAATTTTAGAAGACGTATCGAA
LFRLRLTRYPLKL*IKVAYS
SFCGYLGTRCN*NFRQRMA
VLVATFDPVAIXILDGDGCILK

FIG. 3
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FIG. 5B
NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application is a continuation of U.S. application Ser. No. 10/895,064, filed Jul. 21, 2004, which is hereby incorporated by reference in its entirety.

SEQUENCE LISTING

[0002] The Sequence listing for this application is labeled “seq-list.txt”, which was created on Jul. 21, 2004, and is 1,548 KB. The entire contents is hereinby referenced in its entirety.

1. INTRODUCTION

[0003] The present invention relates to a novel virus causing respiratory tract infection in 10 humans ["coronavirus-HKU1 (CoV-HKU1)"]. The CoV-HKU1 is identified to be phylogenetically similar to known members of Coronavirusae. The present invention relates to a nucleotide sequence comprising the complete genomic sequence of the CoV-HKU1. The invention further relates to nucleotide sequences comprising a portion of the genomic sequence of the CoV-HKU1. The invention also relates to the deduced amino acid sequences of the complete genome of the CoV-HKU1. The invention further relates to the nucleic acids and peptides encoded by and/or derived from these sequences and their use in diagnostic methods and therapeutic methods, such as for immunogens. The invention further encompasses chimeric or recombinant viruses encoded by said nucleotide sequences and antibodies directed against polypeptides encoded by the nucleotide sequence. Furthermore, the invention relates to vaccine preparations comprising the CoV-HKU1 recombinant and chimeric forms of said virus as well as protein extracts and subunits of said virus.

2. BACKGROUND OF THE INVENTION

[0004] In January, 2004, a 71-year-old Chinese man was admitted to hospital because of fever and chills for two days associated with sore throat, rhinorrhea, productive cough with purulent sputum, headache and nausea. He had history of pulmonary tuberculosis more than 40 years ago complicated by eihelialization of right upper lobe and bronchectasis with chronic Pseudomonas aeruginosa colonization of airways. He was a chronic smoker and also had chronic obstructive airway disease, hyperlipidemia, and asymptomatic abdominal aortic aneurysm. He had just returned from Shenzhen of China three days before admission. During his three-day trip to Shenzhen, he had no history of contact with or consumption of wild animals. On admission, his oral temperature was 37.8°C. Physical examination showed tracheal deviation to the right and inspiratory crackles over the anterior left lower zone. H is haemoglobin level was 14.7 g/dL, total white cell count 12.1 x 10^9/L, with neutrophils 9.7 x 10^9/L, lymphocyte 1.6 x 10^9/L and monocyte 0.5 x 10^9/L, and plate count 305 x 10^9/L. His liver and renal function tests were within normal limits. Chest radiograph showed right upper lobe collapse and new patchy infiltrates over the left lower zone. Blood culture was performed. Empirical oral amoxicillin/clavulanate and azithromycin were commenced. Nasopharyngeal aspirates for direct antigen detection for respiratory viruses, RT-PCR for influenza A virus, human metapneumovirus and SARS-CoV, and viral cultures were negative. Sputum for bacterial culture only recovered P. aeruginosa. Sputum for mycobacterial culture was negative. Blood culture was negative. Paired sera for antibodies against Mycoplasma, Chlamydia, Legionella, and SARS-CoV did not show any rise in antibody titres. H is fever subsided two days after admission. H is cough improved and he was discharged after five days of hospitalization. Amoxicillin/clavulanate and azithromycin were continued for a total of seven days. The present inventors were the group involved in the investigation of this patient. All tests for identifying commonly recognized viruses and bacteria were negative in these patients. The etiologic agent responsible for this disease was not known until the complete genome of CoV-HKU1 from this patient by the present inventors disclosed herein. Namely, the present invention discloses a novel human virus that has been identified from a patient suffering from pneumonia. The invention is useful in both clinical and scientific research applications.

3. SUMMARY OF INVENTION

[0005] The present invention is based upon the inventor’s complete genome sequencing of a novel virus ("CoV-HKU1") causing pneumonia in humans. The virus was discovered from a patient suffering from pneumonia in Hong Kong. The virus is a single-stranded RNA virus of positive polarity which belongs to the order, Nidovirales, of the family, Coronavirusae. Accordingly, the invention relates to CoV-HKU1 that phylogenetically relates to known members of Coronavirusae. In a specific embodiment, the invention provides complete genomic sequence of CoV-HKU1. In a preferred embodiment, the virus comprises a nucleotide sequence of SEQ ID NO:1 and/or 3. In another specific embodiment, the invention provides nucleic acids isolated from the virus. The virus preferably comprises a nucleotide sequence of SEQ ID NO:1 and/or 3 in its genome. In a specific embodiment, the present invention provides isolated nucleic acid molecules comprising or, alternatively, consisting of the nucleotide sequence of SEQ ID NO:1, a complement thereof or a portion thereof, preferably at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 1, or a complement thereof. In another specific embodiment, the present invention provides isolated nucleic acid molecules comprising or, alternatively, consisting of the nucleotide sequence of SEQ ID NO:3, a complement thereof or a portion thereof, preferably at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:3, or a complement thereof. Furthermore, in another specific embodiment, the invention provides isolated nucleic acid molecules which hybridize under stringent conditions, as defined herein, to a nucleic acid molecule having the sequence of SEQ ID NO:1 or 3, or a complement thereof. In preferred embodiments, such nucleic acid molecules encode amino acid sequences that have biological activities exhibited by the polypeptides encoded by the nucleotide sequence of SEQ ID NO:1 or 3. In another specific embodiment, the
invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternately consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000 or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:3, or a complement thereof. The polypeptides or proteins include those having the amino acid sequences of SEQ ID NO:2 and SEQ ID NO:S:34-2918 shown in FIGS. 2 and 3, respectively. The invention further provides proteins or polypeptides that are isolated from the CoV-HKU1, including viral proteins isolated from cells infected with the virus but not present in comparable uninfected cells. The polypeptides or the proteins of the present invention preferably have a biological activity of the protein (including antigenicity and/or immunogenicity) encoded by the nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, or more contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:1. In other embodiments, the polypeptides or the proteins of the present invention have a biological activity of the protein (including antigenicity and/or immunogenicity) encoded by a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000 or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:3, or a complement thereof.

In one aspect, the invention relates to the use of CoV-HKU1 for diagnostic methods. In a specific embodiment, the invention provides a method of detecting in a biological sample an antibody that immunospecifically binds to the CoV-HKU1, or any proteins or polypeptides thereof. In another specific embodiment, the invention provides a method of detecting in a biological sample an antibody that immunospecifically binds to the CoV-HKU1-infected cells. In yet another specific embodiment, the invention provides a method of screening for an antibody that immunospecifically binds and neutralizes CoV-HKU1. Such an antibody is useful for a passive immunization or immunotherapy of a subject infected with CoV-HKU1.

The invention further relates to the use of the sequence information of the isolated virus for diagnostic methods. In a specific embodiment, the invention provides nucleic acid molecules which are suitable for use as primers consisting of or comprising the nucleotide sequence of SEQ ID NO:1 or 3, a complement thereof, or at least a portion of the nucleotide sequence thereof. In another specific embodiment, the invention provides nucleic acid molecules which are suitable for hybridization to CoV-HKU1 nucleic acid, including, but not limited to, as PCR primers, Reverse Transcriptase primers, probes for Southern or Northern analysis or other nucleic acid hybridization analysis for the detection of CoV-HKU1 nucleic acids, e.g., consisting of or comprising the nucleotide sequence of SEQ ID NO:1 or 3, a complement thereof, or a portion thereof.

The invention further provides antibodies that specifically bind a polypeptide of the invention encoded by the nucleotide sequence of SEQ ID NO:1 or 3 or a fragment thereof, including the polypeptide having the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:S:34-2918 shown in FIGS. 2 and 3, or encoded by a nucleic acid comprising a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO:1 or 3 and/or any CoV-HKU1 epitope, having one or more biological activities of a polypeptide of the invention. The invention further provides antibodies that specifically bind cells or tissues that are infected by CoV-HKU1. Such antibodies include, but are not limited to polyclonal, monoclonal, bi-specific, multi-specific, human, humanized, chimeric antibodies, single chain antibodies, Fab fragments, F(ab)2 fragments, disulfide-linked Fv's, intrabodies and fragments containing either a VL or VH domain or even a complementary determining region (CDR) that specifically binds to a polypeptide of the invention.

In one embodiment, the invention provides methods for detecting the presence, activity or expression of the CoV-HKU1 of the invention in a biological material, such as cells, blood, saliva, urine, and so forth. The increased or decreased activity or expression of the CoV-HKU1 in a biological sample relative to a control sample can be determined by contacting the biological material with an agent which can detect directly or indirectly the presence, activity or expression of the CoV-HKU1. In a specific embodiment, the detecting agents are the antibodies or nucleic acid molecules of the present invention. Antibodies of the invention may also be used to detect and/or treat other coronaviruses, such as Severe Acute Respiratory Syndrome ("SARS") viruses.

In another embodiment, the invention provides vaccine preparations, comprising the CoV-HKU1 recombinant and chimeric forms of said virus, or protein subunits of the virus. In a specific embodiment, the present invention provides methods of preparing recombinant or chimeric forms of CoV-HKU1. In another specific embodiment, the vaccine preparations of the present invention comprise a nucleic acid or fragment of the CoV-HKU1, or nucleic acid molecules having the sequence of SEQ ID NO:1 or 3, or a fragment thereof. In another embodiment, the invention provides vaccine preparations comprising one or more polypeptides isolated from or produced from nucleic acid of CoV-HKU1. In a specific embodiment, the vaccine preparations comprise a polypeptide of the invention encoded by the nucleotide sequence of SEQ ID NO:1 or 3, or a fragment thereof, including the polypeptides having the amino acid sequences of SEQ ID NO:2 or SEQ ID NO:S:34-2918 shown in FIGS. 2 and 3, respectively. Furthermore, the present invention provides methods for treating, ameliorating, managing or preventing respiratory tract infections caused by CoV-HKU1 by administering to a subject in need thereof the anti-viral agents of the present invention, alone or in combination with various anti-viral agents as well as adjuvants, and/or other pharmaceutically acceptable excipients.

In another aspect, the present invention provides methods for preventing or inhibiting, under a physiological condition, binding to a host cell, or infection of a host cell, or
replication in a host cell of CoV-HKU1 or a virus comprising a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1 or 3 or a complement thereof, by administering to the host cell the anti-viral agents of the present invention, alone or in combination with other anti-viral agents. In a specific embodiment, the anti-viral agent of the invention includes the immunogenic preparations of the invention or an antibody that immunospecifically binds CoV-HKU1 or any CoV-HKU1 epitope and/or neutralizes CoV-HKU1. In another specific embodiment, the anti-viral agent is a polypeptide or protein of the present invention or a nucleic acid molecule of the invention. In a specific embodiment, the host cell is a mammalian cell, including a cell of human, primates, cows, horses, sheep, pigs, fowl (e.g., chickens), goats, cats, dogs, hamsters, mice and rats. Preferably a host cell is a primate cell, and most preferably a human cell. Furthermore, the present invention provides pharmaceutical compositions comprising anti-viral agents of the present invention and a pharmaceutically acceptable carrier. The invention also provides kits containing a pharmaceutical composition of the present invention.

3.1 Definitions

[0012] The term “an antibody or an antibody fragment that immunospecifically binds a polypeptide of the invention” as used herein refers to an antibody or a fragment thereof that immunospecifically binds to the polypeptide encoded by the nucleotide sequence of SEQ ID NO:1 or 3, or a fragment thereof, and does not non-specifically bind to other polypeptides. An antibody or a fragment thereof that immunospecifically binds to the polypeptide of the invention may cross-react with other antigens. Preferably, an antibody or a fragment thereof that immunospecifically binds to a polypeptide of the invention does not cross-react with other antigens. An antibody or a fragment thereof that immunospecifically binds to the polypeptide of the invention, can be identified by, for example, immunoassays or other techniques known to those skilled in the art.

[0013] An “isolated” or “purified” peptide or protein is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language “substantially free of cellular material” includes preparations of a polypeptide/protein in which the polypeptide/protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, a polypeptide/protein that is substantially free of cellular material includes preparations of the polypeptide/protein having less than about 30%, 20%, 10%, 5%, 2.5%, or 1%, (by dry weight) of contaminating protein. When the polypeptide/protein is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When polypeptide/protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, i.e., it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly, such preparations of the polypeptide/protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than polypeptide/protein fragment of interest. In a preferred embodiment of the present invention, polypeptides/proteins are isolated or purified.

[0014] An “isolated” nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. Moreover, an “isolated” nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In a preferred embodiment of the invention, nucleic acid molecules encoding polypeptides/proteins of the invention are isolated or purified. The term “isolated” nucleic acid molecule does not include a nucleic acid that is a member of a library that has not been purified away from other library clones containing other nucleic acid molecules.

[0015] The term “portion” or “fragment” as used herein refers to a fragment of a nucleic acid molecule containing at least about 10, 15, 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 11000, 12000, 13000, 14000, 15000, 16000, 17000, 18000, 19000, 20000, 21000, 22000, 23000, 24000, 25000, 26000, 27000, 28000, 29000, or more contiguous nucleic acids in length of the relevant nucleic acid molecule and having at least one functional feature of the nucleic acid molecule (or the encoded protein has one functional feature of the protein encoded by the nucleic acid molecule); or a fragment of a protein or a polypeptide containing at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320, 340, 360, 380, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, 10000, 11000, 12000, 13000, 14000, 15000, 16000, 17000, 18000, 19000, 20000, 21000, 22000, 23000, 24000, 25000, 26000, 27000, 28000, 29000, or more contiguous amino acids in length of the relevant protein or polypeptide and having at least one functional feature of the protein or polypeptide.

[0016] The term “having a biological activity of the protein” or “having biological activities of the polypeptides of the invention” refers to the characteristics of the polypeptides or proteins having a common biological activity similar or identical structural domain and/or having sufficient amino acid identity to the polypeptide encoded by the nucleotide sequence of SEQ ID NO:1 or 3, or the polypeptide having the amino acid sequence of SEQ ID NO:2, or a complement thereof. Such common biological activities of the polypeptides of the invention include antigenicity and immunogenicity.

[0017] The term “under stringent condition” refers to hybridization and washing conditions under which nucleotide sequences having at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% identity to each other remain hybridized to each other. Such hybridization conditions are described in, for example but not limited to, Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.; Basic Methods in Molecular Biology, Elsevier Science Publishing Co., Inc., N.Y. (1986), pp. 75-78, and 84-87; and Molecular Cloning, Cold Spring Harbor Laboratory, N.Y. (1982), pp. 387-389, and are well known to those skilled in the art. A preferred, non-limiting example of stringent hybridization conditions is hybridization in 6x sodium chloride/sodium citrate (SSC), 0.5% SDS at about 68°C followed by one or more washes (e.g., about 5 to 30 min each) in 2xSSC, 0.5% SDS at room temperature. Another preferred, non-limiting example of stringent hybridization conditions is hybridization in 6xSSC at about 45°C.
followed by one or more washes (e.g., about 5 to 30 min each) in 0.1x SSC, 0.1% SDS at about 45-65° C.

[0018] The term “variant” as used herein refers either to a naturally occurring genetic mutant of CoV-HKU1 or a recombinantly prepared variation of CoV-HKU1 each of which contain one or more mutations in its genome compared to CoV-HKU1. The term “variant” may also refers either to a naturally occurring variation of a given peptide or a recombinantly prepared variation of a given peptide or protein in which one or more amino acid residues have been modified by amino acid substitution, addition, or deletion.

4. DESCRIPTION OF FIGURES

[0019] FIG. 1 shows a partial DNA sequence (SEQ ID NO:1) and its deduced amino acid sequence (SEQ ID NO:2) obtained from CoV-HKU1 that has 91% amino acid identity to the RNA-dependent RNA polymerase protein of known Coronaviruses.

[0020] FIG. 2 shows the entire genomic DNA sequence (SEQ ID NO:3) of CoV-HKU1 and its deduced amino acid sequences therefrom in three frames. An asterisk (*) indicates a stop codon which marks the end of a peptide. The first-frame translation and amino acid sequences: SEQ ID NOS:34-456; the second-frame translation and amino acid sequences: SEQ ID NOS:457-723; and the third-frame translation and amino acid sequences: SEQ ID NOS:724-1318.

[0021] FIG. 3 shows the complement (SEQ ID NO: 1319) of the entire genomic DNA sequence (SEQ ID NO:3) of CoV-HKU1 in 3'→5' orientation and its deduced amino acid sequences therefrom in three frames. An asterisk (*) indicates a stop codon which marks the end of a peptide. The first-frame translation and amino acid sequences: SEQ ID NO:1319-1907; the second-frame translation and amino acid sequences: SEQ ID NO:1908-2453; and the third-frame translation and amino acid sequences: SEQ ID NOS:2454-2918.

[0022] FIG. 4 shows the genome organization of CoV-HKU1. Arrows indicate the putative cleavage sites of the polyprotein encoded by ORF 1a and ORF 1b. The peptides are shown in SEQ ID NOS:15-17, respectively, in order of appearance.

[0023] FIG. 5A shows the phylogenetic analysis of the chymotrypsin like protease (3CLpr), replicase (Rep), helicase (Hel), and hemagglutinin esterase (HE); and FIG. 5B shows that of the spike (S), envelope (E), membrane (M), and nucleocapsid (N) proteins of CoV-HKU1. The trees were constructed by the neighbor joining method using the Jukes-Cantor correction and bootstrap values were calculated from 1000 trees. A total of 303, 928, 603, 386, 1356, 82, 223 and 441 amino acid positions in 3CLpr, Rep, Hel, HE, S, E, M, and N respectively were included in the analysis. The scale bar indicates the estimated number of substitutions per 10 amino acids.

[0024] FIG. 6 shows the important features of the S protein of CoV-HKU1 (residues 7-336 of SEQ ID NO:420) in comparison with those of other viruses, i.e., HCoV-OC43 (human coronavirus OC43; SEQ ID NO:21), MHV (murine hepatitis virus; SEQ ID NO:22), SDAV (rat salivary adenitis encephalomyelitis virus; SEQ ID NO:23), BCoV (bovine coronavirus; SEQ ID NO:24), PHEV (porcine hemagglutinating encephalomyelitis virus; SEQ ID NO:25), and ECoV (equine coronavirus; SEQ ID NO:26). The cleavage site peptides are shown in residues 752-766 of SEQ ID NO:420 and SEQ ID NOS:28-33, respectively, in order of appearance.

[0025] FIG. 7 shows the sequential quantitative RT-PCR (closed squares: copies/ml) for CoV-HKU1 in nasopharyngeal aspirates; and serum IgG antibody titers against N protein of CoV-HKU1 (closed triangles).

[0026] FIG. 8 shows the Western blot analysis of purified recombinant CoV-HKU1 N protein antigen. Prominent immunoreactive protein bands of about 53 kDa were detected by the Western blot using the patient’s sera obtained during the second and fourth weeks of the illness (lanes 2 and 3). Only very faint bands were observed with the serum samples obtained from the patient during the first week of the illness (lane 1) and two healthy blood donors (lanes 4 and 5), respectively.

5. DETAILED DESCRIPTION OF THE INVENTION

[0027] The present invention relates to the CoV-HKU1 that phylogenetically relates to known Coronaviruses. In a specific embodiment, CoV-HKU1 comprises a nucleotide sequence of SEQ ID NO:1 and/or 3. In a specific embodiment, the present invention provides isolated nucleic acid molecules of the CoV-HKU1, comprising or, alternatively, consisting of the nucleotide sequence of SEQ ID NO:1 and/or 3, a complement thereof or a portion thereof. In another specific embodiment, the invention provides isolated nucleic acid molecules which hybridize under stringent conditions, as defined herein, to a nucleic acid molecule having the sequence of SEQ ID NO:1 or 3, or specific genes of known member of Coronaviridae, or a complement thereof. In another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising a nucleotide sequence that is at least about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 150, 200, 300, 400, 500, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000 or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:3, or a complement thereof. The polypeptides or the proteins of the present invention preferably have one or more activities of the proteins encoded by the sequence of SEQ ID NO:1, 3, or the native viral proteins containing the amino acid sequences encoded by the sequence of SEQ ID NO:1 or 3.

[0028] The invention further relates to the use of the sequence information of the isolated virus for diagnostic and therapeutic methods. In a specific embodiment, the invention provides the entire nucleotide sequence of CoV-HKU1 (SEQ ID NO:3), or fragments, or complement thereof. Further, the present invention relates to a nucleic acid molecule that hybridizes any portion of the genome of the CoV-HKU1 (SEQ ID NO:3) under the stringent conditions. In a specific embodiment, the invention provides nucleic acid molecules which are suitable for use as primers consisting of or comprising the nucleotide sequence of SEQ ID NO:1 or 3, or a complement thereof, or a portion thereof. In another specific embodiment, the invention provides nucleic acid molecules
which are suitable for use as hybridization probes for the detection of nucleic acids encoding a polypeptide of the invention, consisting of or comprising the nucleotide sequence of SEQ ID NO:1 or 3, a complement thereof, or a portion thereof. The invention further encompasses chimeric or recombinant viruses or viral proteins encoded by said nucleotide sequences.

[0029] The invention further provides antibodies that specifically bind a polypeptide of the invention encoded by the nucleotide sequence of SEQ ID NO:1 or 3, or a fragment thereof, or any CoV-HKU1 epitope as well as the polypeptides having the amino acid sequences of SEQ ID NO:2 and SEQ ID NO:3-34-2918, respectively, shown in FIGS. 2 and 3. Such antibodies include, but are not limited to polyclonal, monoclonal, bi-specific, multi-specific, humanized, chimeric antibodies, single chain antibodies, Fab fragments, F(ab')2 fragments, disulfide-linked Fvs, intrabodies and fragments containing either a V.L or V.H domain or even a complementary determining region (CDR) that specifically binds to a polypeptide of the invention.

[0030] In one embodiment, the invention provides methods for detecting the presence, activity or expression of the CoV-HKU1 of the invention in a biological material, such as cells, blood, saliva, urine, sputum, nasopharyngeal aspirates, and so forth. The presence of the CoV-HKU1 in a sample can be determined by contacting the biological material with an agent which can detect directly or indirectly the presence, activity or expression of the CoV-HKU1. In a specific embodiment, the detection agents are the antibodies of the present invention. In another embodiment, the detection agent is a nucleic acid of the present invention.

[0031] In another embodiment, the invention provides vaccine preparations comprising the CoV-HKU1 recombinant and chimeric forms of said virus, or subunits of the virus.

[0032] The present invention further provides methods of preparing recombinant or chimeric forms of CoV-HKU1. In another specific embodiment, the vaccine preparations of the present invention comprise one or more nucleic acid molecules comprising or consisting of the sequence of SEQ ID NO:1 and/or 3, or a fragment thereof. In another embodiment, the invention provides vaccine preparations comprising one or more polypeptides of the invention encoded by a nucleotide sequence comprising or consisting of the nucleotide sequence of SEQ ID NO:1 and/or 3, or a fragment thereof, including the polypeptides having the amino acid sequences of SEQ ID NO:2 or SEQ ID NO:3-34-2918 shown in FIGS. 2 and 8. Furthermore, the present invention provides methods for treating, ameliorating, managing, or preventing respiratory tract infections by administering to a subject in need thereof the anti-viral agents of the present invention, alone or in combination with other antivirals [e.g., amantadine, rimantadine, gancyclovir, acyclovir, ribavirin, penciclovir, oseltamivir, foscarnet zidovudine (AZT), didanosine (ddI), lamivudine (3TC), zalcitabine (d4c), stavudine (d4T), nevirapine, delavirdine, indinavir, ritonavir, vidarabine, nelfinavir, saquinavir, remdesivir, lamivudine, zalcitabine, abacavir, nevirapine, delavirdine, indinavir, ritonavir], nucleosides, nucleotides, and analogues thereof, for example, 3′-azido-2′,3′-dideoxythymidine, 2′,3′-dideoxyinosine, 2′,3′-dideoxycytidine, 2′,3′-dideoxyadenosine, 2′,3′-dideoxyadenosine, 2′,3′-dideoxyguanosine, and 2′,3′-dideoxythymidine, and their prodrugs, such as acyclovir, penciclovir, famciclovir, aciclovir, penciclovir, famciclovir, and valaciclovir, and the like.

[0033] Furthermore, the present invention provides pharmaceutical compositions comprising anti-viral agents of the present invention and a pharmaceutically acceptable carrier. The present invention also provides kits comprising pharmaceutical compositions of the present invention.

5.1 Recombinant and Chimeric CoV-HKU1

[0034] The present invention encompasses recombinant or chimeric viruses encoded by viral vectors derived from the genome of CoV-HKU1 or natural variants thereof. In a specific embodiment, a recombinant virus is one derived from the CoV-HKU1. In a specific embodiment, the virus has a nucleotide sequence of SEQ ID NO:3. In another specific embodiment, a recombinant virus is one derived from a natural variant of CoV-HKU1. A natural variant of CoV-HKU1 has a sequence that is different from the genomic sequence (SEQ ID NO:3) of CoV-HKU1, due to one or more naturally occurring mutations, including, but not limited to, point mutations, rearrangements, insertions, deletions etc., to the genomic sequence that may or may not result in a phenotypic change. In accordance with the present invention, a viral vector which is derived from the genome of the CoV-HKU1, is one that contains a nucleic acid sequence that encodes at least a part of one ORF of the CoV-HKU1. In a specific embodiment, the ORF comprises or consists of a nucleotide sequence of SEQ ID NO:1 or a fragment thereof. In an additional embodiment, there are more than one ORF within the nucleotide sequence of SEQ ID NO:3 or a fragment thereof. In another embodiment, the polypeptides encoded by the ORFs comprises or consists of amino acid sequences of SEQ ID NO:3-2918 shown in FIGS. 2 and 8, or SEQ ID NO:2, or a fragment thereof. In accordance with the present invention, these viral vectors may or may not include nucleic acids that are non-native to the viral genome.

[0035] In another specific embodiment, a chimeric virus of the invention is a recombinant CoV-HKU1 which further comprises a heterologous nucleotide sequence. In accordance with the invention, a chimeric virus may be encoded by a nucleotide sequence in which heterologous nucleotide sequences have been added to the genome or in which endog-
enous or native nucleotide sequences have been replaced with heterologous nucleotide sequences.

[0036] According to the present invention, the chimeric viruses are encoded by the viral vectors of the invention which further comprise a heterologous nucleotide sequence. In accordance with the present invention a chimeric virus is encoded by a viral vector that may or may not include nucleic acids that are non-native to the viral genome. In accordance with the invention a chimeric virus is encoded by a viral vector to which heterologous nucleotide sequences have been added, inserted or substituted for native or non-native sequences. In accordance with the present invention, the chimeric virus may be encoded by nucleotide sequences derived from different strains or variants of CoV-HKU1. In particular, the chimeric virus is encoded by nucleotide sequences that encode antigenic polypeptides derived from different strains or variants of CoV-HKU1.

[0037] A chimeric virus may be of particular use for the generation of recombinant vaccines protecting against two or more viruses (Tao et al., J. Virol. 72, 2955-2961; Durbin et al., 2000, J. Virol. 74, 6821-6831; Skaidropoulos et al., 1998, J. Virol. 72, 1762-1768 (1998); Teng et al., 2000, J. Virol. 74, 9317-9321). For example, it can be envisaged that a virus vector derived from the CoV-HKU1 expressing one or more proteins of variants of CoV-HKU1, or vice versa, will protect a subject vaccinated with such vector against infections by both the native CoV-HKU1 and the variant. Attenuated and replication-defective viruses may be of use for vaccination purposes with live vaccines as has been suggested for other viruses.

[0038] In accordance with the present invention the heterologous sequence to be incorporated into the viral vectors encoding the recombinant or chimeric viruses of the invention include sequences obtained or derived from different strains or variants of CoV-HKU1.

[0039] In certain embodiments, the chimeric or recombinant viruses of the invention are encoded by viral vectors derived from viral genomes wherein one or more sequences, intergenic regions, termini sequences, or portions or entire ORFs have been substituted with a heterologous or non-native sequence. In certain embodiments of the invention, the chimeric viruses of the invention are encoded by viral vectors derived from viral genomes wherein one or more heterologous sequences have been inserted or added to the vector.

[0040] The selection of the viral vector may depend on the species of the subject that is to be treated or protected from a viral infection.

[0041] In accordance with the present invention, the viral vectors can be engineered to provide antigenic sequences which confer protection against infection by the CoV-HKU1 and natural variants thereof. The viral vectors may be engineered to provide one, two, three or more antigenic sequences. In accordance with the present invention the antigenic sequences may be derived from the same virus, from different strains or variants of the same type of virus, or from different viruses.

[0042] The expression products and/or recombinant or chimeric virions obtained in accordance with the invention may advantageously be utilized in vaccine formulations. The expression products and chimeric virions of the present invention may be engineered to create vaccines against a broad range of pathogens, including viral antigens, tumor antigens, and autoantigens involved in autoimmune disorders. In particular, the chimeric virions of the present invention may be engineered to create vaccines for the protection of a subject from infections with CoV-HKU1 and variants thereof.

[0043] In certain embodiments, the expression products and recombinant or chimeric virions of the present invention may be engineered to create vaccines against a broad range of pathogens, including viral antigens, tumor antigens and autoantigens involved in autoimmune disorders. One way to achieve this goal involves modifying existing CoV-HKU1 genes to contain foreign sequences in their respective external domains. Where the heterogeneous sequences are epitopes or antigens of pathogens, these chimeric virions may be used to induce a protective immune response against the disease agent from which these determinants are derived.

[0044] Thus, the present invention relates to the use of viral vectors and recombinant or chimeric viruses to formulate vaccines against a broad range of viruses and/or antigens. The present invention also encompasses recombinant viruses comprising a viral vector derived from the CoV-HKU1 or variants thereof which contains sequences which result in a virus having a phenotype more suitable for use in vaccine formulations. The mutations and modifications can be in coding regions, in intergenic regions and in the leader and trailer sequences of the virus.

[0045] The invention provides a host cell comprising a nucleic acid or a vector according to the invention. Plasmid or viral vectors containing the polymerase components of CoV-HKU1 are generated in prokaryotic cells for the expression of the components in relevant cell types (bacteria, insect cells, eukaryotic cells). Plasmid or viral vectors containing full-length or partial copies of the CoV-HKU1 genome will be generated in prokaryotic cells for the expression of viral nucleic acids in-vitro or in-vivo. The latter vectors may contain other viral sequences for the generation of chimeric viruses or chimeric virus proteins, may lack parts of the viral genome for the generation of replication defective virus, and may contain mutations, deletions or insertions for the generation of attenuated viruses.

[0046] In addition, eukaryotic cells, transiently or stably expressing one or more full-length or partial CoV-HKU1 proteins can be used. Such cells can be made by transfection (proteins or nucleic acid vectors), infection (viral vectors) or transduction (viral vectors) and may be useful for complementation of mentioned wild type, attenuated, replication-defective or chimeric viruses.

[0047] The viral vectors and chimeric viruses of the present invention may be used to modulate a subject's immune system by stimulating a humoral immune response, a cellular immune response or by stimulating tolerance to an antigen. As used herein, a subject means: humans, primates, horses, cows, sheep, pigs, goats, dogs, cats, avian species and rodents.

5.2 Formulation of Vaccines and Antivirals

[0048] In a preferred embodiment, the invention provides a proteinaceous molecule or CoV-HKU1-specific viral protein or functional fragment thereof encoded by a nucleic acid according to the invention. Useful proteinaceous molecules are for example derived from any of the genes or genomic fragments derivable from the virus according to the invention, including envelope protein (E protein), integrase protein (M protein), spike protein (S protein), nucleocapsid protein (N protein), hemagglutinin esterase (HE protein), and RNA-dependent RNA polymerase. Such molecules, or anti-
genic fragments thereof, as provided herein, are for example useful in diagnostic methods or kits and in pharmaceutical compositions such as subunit vaccines. Particularly useful are polypeptides encoded by the nucleotide sequence of SEQ ID NO:1 or 3, including the polypeptides having the amino acid sequences of SEQ ID NOS:34-2918 in FIGS. 2 and 8, or SEQ ID NO:2, or antigenic fragments thereof for inclusion as antigen or subunit immunogen, but inactivated whole virus can also be used. Particularly useful are also those proteinaceous substances that are encoded by recombinant nucleic acid fragments of the CoV-HKU1 genome; of course preferred are those that are within the preferred bands and moles of ORF's, in particular, for eliciting CoV-HKU1 specific antibody or T cell responses, whether in vivo (e.g. for protective or therapeutic purposes or for providing diagnostic antibodies) or in vitro (e.g. by phage display technology or another technique useful for generating synthetic antibodies).

[0049] The invention provides vaccine formulations for the prevention and treatment of infections with CoV-HKU1. In certain embodiments, the vaccine of the invention comprises recombinant and chimeric viruses of the CoV-HKU1.

[0050] In another aspect, the present invention also provides DNA vaccine formulations comprising a nucleic acid or fragment of the CoV-HKU1, or nucleic acid molecules having the sequence of SEQ ID NO:1 or 3, or a fragment thereof. In another specific embodiment, the DNA vaccine formulations of the present invention comprises a nucleic acid or fragment thereof encoding the antibodies which immunospecifically binds CoV-HKU1. In DNA vaccine formulations, a vaccine DNA comprises a viral vector, such as that derived from the CoV-HKU1, bacterial plasmid, or other expression vector, bearing an insert comprising a nucleic acid molecules of the present invention operably linked to one or more control elements, thereby allowing expression of the vaccinating proteins encoded by said nucleic acid molecule in a vaccinated subject. Such vectors can be prepared by recombinant DNA technology as recombinant or chimeric viral vectors carrying a核酸 acid molecule of the present invention.


[0052] Many methods may be used to introduce the vaccine formulations described above. Those include, but are not limited to, oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes. Alternatively, it may be preferable to introduce the chimeric virus vaccine formulation via the natural route of infection of the pathogen for which the vaccine is designed. The DNA vaccines of the present invention may be administered in saline solutions by injections into muscle or skin using a syringe and needle (Wolff J. A. et al., 1990, Direct gene transfer into mouse muscle in vivo, Science 247:1465-1468; Razu, E., 1994, Intradermal gene immunization: The possible role of DNA uptake in the induction of cellular immunity to viruses, Proc. Natl. Acad. Sci. USA 91:5951-5953). Another way to administer DNA vaccines is called "gene gun" method, whereby microscopic gold beads coated with the DNA molecules of interest is fired into the cells (Tang, D. et al., 1992, Genetic immunization is a simple method for eliciting an immune response, Nature 356:152-154). For general reviews of the methods for DNA vaccines, see Robinson, H. L., 1999, DNA vaccines: basic mechanism and immune responses (Review), Int. J. Mol. Med. 4(5):549-555; Barber, B., 1997, Introduction: Emerging vaccine strategies, Seminars in Immunoloy 9(5):269-270, and Robinson, H. L. et al., 1997, DNA vaccines, Seminars in Immunoloy 9(5):271-283.

5.3 Adjuvants and Carrier Molecules

[0053] CoV-HKU1-associated antigens are administered with one or more adjuvants. In one embodiment, the CoV-HKU1-associated antigen is administered together with a mineral salt adjuvants or mineral salt gel adjuvant. Such mineral salt and mineral salt gel adjuvants include, but are not limited to, aluminum hydroxide (ALUM), REHYD-DIRAGEL), aluminum phosphate gel, aluminum hydroxy-phosphate (ADU-PHOS), and calcium phosphate.

[0054] In another embodiment, CoV-HKU1-associated antigen is administered with an immunostimulatory adjuvant. Such class of adjuvants, include, but are not limited to, cytokines (e.g., interleukin-2, interleukin-7, interleukin-12, granulocyte-macrophage colony stimulating factor (GM-CSF), interferon-γ, interferon-1β (IFN-β), and IFN-1β (IFN-β) or Schlto Peptide, cytokine-containing liposomes, interpenen glycodies or saponins (e.g., QuilA and QS-21, also sold under the trademark STIMULON, ISCOPED), Muramyl Dipetide (MDP) derivatives, such as N-acetylmuramyl-L-threonyl-D-isoglutamine (Threonyl-MDP, sold under the trademark TERMURIDE), GMPD, N-acetly-nor-muramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1,2'-dipentanoyl-sn-glycero-3-hydroxy-phosphoryloxy)-ethylamine, muramyl tripeptide phosphatidylethanolamine (MTP-PE), unmethylated CpG dinucleotides and oligonucleotides, such as bacterial DNA
and fragments thereof, LPS, monophosphoryl Lipid A (3D-MLA sold under the trademark MPL), and polystyrene-

[0055] In another embodiment, the adjuvant used is a particu-
tular adjuvant, including, but not limited to, emulsions, e.g.,
Freund’s Complete Adjuvant, Freund’s Incomplete Adjuvant,
squalene or squalane oil-in-water adjuvant formulations,
such as SAIF and MF59, e.g., prepared with block-copoly-
mers, such as L-121 (polyoxypropylene/polyoxyethylene)
sold under the trademark PLURONIC L-121, Liposomes,
Virosomes, coacelates, and immune stimulating complex,
which is sold under the trademark ISCOM.

[0056] In another embodiment, a microparticulate adjuvant is
used. Microparticulate adjuvants include, but are not limited
to biodegradable and biocompatible polymers, homo-
copolymers of lactolic acid (PLA) and glycolic acid (PGA),
poly(lactide-co-glycolide) (PLGA) microparticles, poly-
mer-coated inorganic hydroxide (polyoxamer parti-
cles), soluble polymers (polysiloxazenes), and virus-like
particles (VLPs) such as recombinant protein particulates,
e.g., hepatitis B surface antigen (HBsAg).

[0057] Yet another class of adjuvants may be used include
cutaneous adjuvants, including but not limited to heat-
labile enterotoxin from Escherichia coli (LT), choleratoxin (CT)
and choleratoxin B Subunit (CTB) from Vibrio cholerae,
mutant toxins (e.g., LTK63 and LTR72), micropar-
ticles, and polymerized liposomes.

[0058] In other embodiments, any of the above classes of
adjuvants may be used in combination with each other or
with other adjuvants. For example, non-limiting examples of com-
bination adjuvant preparations that can be used to adminis-
ter the CoV-HKU1-associated antigens of the invention include
liposomes containing immunostimulatory protein, cytokines,
or T-cell and or B-cell peptides, or microbes with or without
entrapped IL-2 or microparticles containing enterotoxin.
Adjuvants other known in the art are also included within the
scope of the invention (see Vaccine Design: The Subunit and
Adjuvant Approach, Chap. 7, Michael F. Powell and Mark J.
Newman (eds.), Plenum Press, New York, 1995, which is
incorporated herein in its entirety).

[0059] The effectiveness of an adjuvant may be determined
by measuring the induction of antibodies directed against
an immunogenic polypeptide containing a CoV-HKU1 poly-
peptide epitope, the antibodies resulting from administration
of this polypeptide in vaccines which are also comprised of
the various adjuvants.

[0060] The polypeptides may be formulated into the vac-
cine as neutral or salt forms. Pharmaceutically acceptable
salts include the acid additional salts (formed with free amino
groups of the peptide) and which are formed with inorganic
acids, such as, for example, hydrochloric or phosphoric acids,
or organic acids such as acetic, oxalic, tartaric, maleic, and
the like. Salts formed with free carboxyl groups may also be
derived from inorganic bases, such as, for example, sodium
potassium, ammonium, calcium, or ferric hydroxides, and
such organic bases as isopropylamine, trimethylamine,
2-ethylamino ethanol, histidine, proline and the like.

[0061] The vaccines of the invention may be multivalent or
univalent. Multivalent vaccines are made from recombinant
viruses that direct the expression of more than one antigen.

[0062] Many methods may be used to introduce the vaccine
formulations of the invention; these include but are not limited
to oral, intradermal, intramuscular, intraperitoneal, intra-
venous, subcutaneous, intranasal routes, and via scarification
(scratching through the top layers of skin, e.g., using a bifur-
cated needle).

[0063] The patient to which the vaccine is administered is
preferably a mammal, most preferably a human, but can also
be a non-human animal including but not limited to cows,
horses, sheep, pigs, fowl (e.g., chickens), goats, cats, dogs,
hamsters, mice and rats.

5.4 Preparation of Antibodies

[0064] Antibodies which specifically recognize a polypep-
tide of the invention, such as, but not limited to, polypeptides
comprising the sequence of SEQ ID NO:2 or any of SEQ ID
NOS: 34-2918 or CoV-HKU1 epitope, or antigen-binding
fragments thereof, can be used for detecting, screening,
and isolating the polypeptide of the invention or fragments
thereof, or similar sequences that might encode similar
enzymes from the other organisms. For example, in one spe-
cific embodiment, an antibody which immunospecifically
binds CoV-HKU1 epitope, or a fragment thereof, can be used
for various in vitro detection assays, including enzyme-linked
immunosorbent assays (ELISA), radioimmunoassays, West-
ern blot, etc., for the detection of a polypeptide of the inven-
tion or, preferably, CoV-HKU1, in samples, for example, a
biological material, including cells, cell culture media (e.g.,
bacterial cell culture media, mammalian cell culture media,
insect cell culture media, yeast cell culture media, etc.),
blood, plasma, serum, tissues, sputum, nasopharyngeal aspi-
rates, etc.

[0065] Antibodies specific for a polypeptide of the inven-
tion or any epitope of CoV-HKU1 may be generated by any
suitable method known in the art. Polyclonal antibodies to an
antigen-of-interest, for example, the CoV-HKU1 epitopes or
polypeptides encoded by a nucleotide sequence of SEQ ID
NO:1 or 3, including the polypeptides shown in FIG. 2 (SEQ
ID NOS:34-1318), FIG. 8 (SEQ ID NOS:1319-2918), as well
as SEQ ID NO:2, can be produced by various procedures well
known in the art. For example, an antigen can be adminis-
tered to various host animals including, but not limited to,
rabbits, mice, rats, etc., to induce the production of antisera
containing polyclonal antibodies specific for the antigen.
Various adjuvants may be used to increase the immunological
response, depending on the host species, and include but are
not limited to, Freund's (complete and incomplete) adjuvant,
mamalian gel such as aluminium hydroxide, surface active
substances such as lysolecithin, pluronic polyols, polyby-
olases, peptides, oil emulsions, keyhole limpet hemocyanins,
dinotrophaleum, and potentially useful adjuvants for humans such as
BCG (Bacille Calmette-Guerin) and Corynebacterium
parvum. Such adjuvants are also well known in the art (see
Section 5.4, supra).

[0066] Monoclonal antibodies can be prepared using a
wide variety of techniques known in the art including the use
of hybridoma, recombinant, and phage display technologies,
or a combination thereof. For example, monoclonal antibo-
dies can be produced using hybridoma techniques including
those known in the art and taught, for example, in Harlow et
al., Antibodies: A Laboratory Manual, (Cold Spring Harbor
Laboratory Press, 2nd ed. 1988); Hammerling, et al., in:
Monoclonal Antibodies and T-Cell Hybridomas, pp. 563-681
(Elsevier, N.Y., 1981) (both of which are incorporated by
reference in their entireties). The term “monoclonal anti-
body” as used herein is not limited to antibodies produced
through hybridoma technology. The term “monoclonal anti-
body” refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

0067 Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art. In a non-limiting example, mice can be immunized with an antigen of interest or a cell expressing such an antigen. Once an immune response is detected, e.g., antibodies specific for the antigen are detected in the mouse serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells. Hybridomas are selected and cloned by limiting dilution. The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding the antigen. Ascites fluid, which generally contains high levels of antibodies, can be generated by inoculating mice intraperitoneally with positive hybridoma clones.

0068 Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, Fab and F(\(ab\)\(^{\prime}\))\(_2\) fragments may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(\(ab\)\(^{\prime}\))\(_2\) fragments). F(\(ab\)\(^{\prime}\))\(_2\) fragments contain the complete light chain, and the variable region, the CH1 region and the hinge region of the heavy chain.

0069 The antibodies of the invention or fragments thereof can be also produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or preferably, by recombinant expression techniques.

0070 The nucleotide sequence encoding an antibody may be obtained from any information available to those skilled in the art (i.e., from Genbank, the literature, or by routine cloning and sequence analysis). If a clone containing a nucleic acid encoding a particular antibody or an epitope-binding fragment thereof is not available, but the sequence of the antibody molecule or epitope-binding fragment thereof is known, a nucleic acid encoding the immunoglobulin may be chemically synthesized or obtained from a suitable source (e.g., an antibody cDNA library, or a cDNA library generated from, or nucleic acid, preferably poly A+ RNA, isolated from any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by PCR may then be cloned into replicable cloning vectors using any method well known in the art.

0071 Once the nucleotide sequence of the antibody is determined, the nucleotide sequence of the antibody may be manipulated using methods well known in the art for the manipulation of nucleotide sequences, e.g., recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., supra; and Ausubel et al., eds., 1998, Current Protocols in Molecular Biology, John Wiley & Sons, NY, which are both incorporated by reference herein in their entireties), to generate antibodies having a different amino acid sequence by, for example, introducing amino acid substitutions, deletions, and/or insertions into the epitope-binding domain regions of the antibodies or any portion of antibodies which may enhance or reduce biological activities of the antibodies.

0072 Recombinant expression of an antibody requires construction of an expression vector containing a nucleotide sequence that encodes the antibody. Once a nucleotide sequence encoding an antibody molecule or a heavy or light chain of an antibody, or portion thereof has been obtained, the vector for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well known in the art as discussed in the previous sections. Methods which are well known to those skilled in the art can be used to construct expression vectors containing antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. The nucleotide sequence encoding the heavy-chain variable region, light-chain variable region, both the heavy-chain and light-chain variable regions, an epitope-binding fragment of the heavy- and/or light-chain variable region, or one or more complementarity determining regions (CDRs) of an antibody may be cloned into such a vector for expression. Thus-prepared expression vector can be then introduced into appropriate host cells for the expression of the antibody. Accordingly, the invention includes host cells containing a polynucleotide encoding an antibody specific for the polypeptides of the invention or fragments thereof.

0073 The host cell may be co-transfected with two expression vectors of the invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides or different selectable markers to ensure maintenance of both plasmids. Alternatively, a single vector may be used which encodes, and is capable of expressing, both heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, Nature, 322:52, 1986; and Kohler, Proc. Natl. Acad. Sci. USA, 77:2 197, 1980). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

0074 In another embodiment, antibodies can also be generated using various plauge display methods known in the art. In plaque display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In a particular embodiment, such phage can be utilized to display antigen binding domains, such as Fab and Fv or disulfide-bond stabilized Fv, expressed from a repertoire or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage, including fd and M13. The antigen binding domains are expressed as a recombinantly fused protein to either the phage gene III or gene VIII protein. Examples of plaque display methods that can be used include the immunoglobulin display, or fragments thereof, of the present invention include those disclosed in Brinkman et al., J. Immunol. Methods, 182:41-50, 1995; Ames et al., J. Immunol. Methods, 184:177-186, 1995; Kettleborough et al., Eur. J. Immunol., 24:952-958, 1994; Persie et al., Gene, 187:9-18, 1997; Burton et al., Advances in Immunology, 57:191-280, 1994; PCT application No. PCT/GB91/01134; PCT publications WO 90/02809;
WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20041; and U.S. Pat. Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

[0075] As described in the above references, after plaque selection, the antibody coding regions from the plaque can be isolated and used to generate whole antibodies, including human antibodies, or any other desired fragments, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab)2 fragments can also be employed using methods known in the art such as those disclosed in PCT publication WO 92/2324; Mullinax et al., BioTechniques, 12(6):864-869, 1992; and Sawai et al., AJRI, 34:26-34, 1995; and Better et al., Science, 240:1041-1043, 1988 (each of which is incorporated by reference in its entirety). Examples of techniques which can be used to produce single-chain Fvs and antibodies include those described in U.S. Pat. Nos. 4,946,778 and 5,258,498; Huston et al., Methods in Enzymology, 203:46-88, 1991; Shu et al., PNAS, 90:7995-7999, 1993; and Skerra et al., Science, 240:1038-1040, 1988.

[0076] Once an antibody molecule of the invention has been produced by any methods described above, it may then be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen after Protein A or Protein G purification, and sizing column chromatography), centrifugation, differential solubility, or by any other standard techniques for the purification of proteins. Further, the antibodies of the present invention or fragments thereof may be fused to heterologous polypeptide sequences described herein or otherwise known in the art to facilitate purification.

[0077] For some uses, including in vivo use of antibodies in humans and in vitro detection assays, it may be preferable to use chimeric, humanized, or human antibodies. A chimeric antibody is a molecule in which different portions of the antibody are derived from different animal species, such as antibodies having a variable region derived from a murine monoclonal antibody and a constant region derived from a human immunoglobulin. Methods for producing chimeric antibodies are known in the art. See e.g., Morrison, Science, 229:1202, 1985; Oi et al., BioTechniques, 4:214 1986; Gillies et al., J. Immunol., Methods, 125:191-202, 1989; U.S. Pat. Nos. 5,807,715; 4,816,567; and 4,816,397, which are incorporated herein by reference in their entirety. Humanized antibodies are antibody molecules from non-human species that bind the desired antigen having one or more complementarity determining regions (CDR) from the non-human species and framework regions from a human immunoglobulin molecule. Often, framework residues in the human framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, preferably improve, antigen binding. These framework substitutions are identified by methods well known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual framework residues at particular positions. See, e.g., Queen et al., U.S. Pat. No. 5,585,809; Riechmann et al., Nature, 332:323, 1988, which are incorporated herein by reference in their entirety.

Antibodies can be humanized using a variety of techniques known in the art including, for example, CDR-grafting (EP 230,406; PCT publication WO 91/00967; U.S. Pat. Nos. 5,225,539; 5,530,101 and 5,585,089), veneering or resurfacing (EP 592,106; EP 519,596; Podlán, Molecular Immunology, 28(4/5):489-498, 1991; Studniczka et al., Protein Engineering, 7(6):805-814, 1994; Roguska et al., Proc Natl Acad. Sci. USA, 91:969-973, 1994), and chain shuffling (U.S. Pat. No. 5,565,632), all of which are hereby incorporated by reference in their entirety.

[0078] Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Human antibodies can be made by a variety of methods known in the art including plaque display methods described above using antibody libraries derived from human immunoglobulin sequences. See U.S. Pat. Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645; WO 96/50435; WO 98/24893; WO 98/16654; WO 96/34096; WO 96/33735; and WO 91/10741, each of which is incorporated herein by reference in its entirety.

[0079] Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, Int. Rev. Immunol., 13:65-93, 1995. For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; European Patent Number 0 598 877; U.S. Pat. Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825; 5,661,016; 5,545,806; 5,814,318; 5,885,793; 5,916,771; and 5,939,598, which are incorporated by reference herein in their entirety. In addition, companies such as Abgenix, Inc. (Fremont, Calif.), Medarex (NJ) and Genpharm (San Jose, Calif.) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

[0080] Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as “guided selection.” In this approach a selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., Bio/technology, 12:809-903, 1998).

[0081] Antibodies filched or conjugated to heterologous polypeptides may be used in vitro immunosays and in purification methods (e.g., affinity chromatography) well known in the art. See e.g., PCT publication Number WO 93/21232; EP 439,095; Numamura et al., Immuno. Lett., 39:91-99, 1994; U.S. Pat. No. 5,474,981; Gillies et al., PNAS, 89:1428-1432, 1992; and Fell et al., J. Immunol., 146:2446-2452, 1991, which are incorporated herein by reference in their entirety.

[0082] Antibodies may also be attached to solid supports, which are particularly useful for immunosays or purification of the polypeptides of the invention or fragments, derivatives, analogs, or variants thereof, or similar molecules having the similar enzymatic activities as the polypeptide of the invention. Such solid supports include, but are not limited to, glass, cellulose, polycrylamide, nylon, polystyrene, polyvinyl chloride or polypolyrene.

5.5 Pharmaceutical Compositions and Kits

[0083] The present invention encompasses pharmaceutical compositions comprising anti-viral agents of the present
invention. In a specific embodiment, the anti-viral agent is an antibody which immunspecifically binds CoV-HKU1 or variants thereof, or any proteins derived therefrom. In another specific embodiment, the anti-viral agent is a polypeptide or nucleic acid molecule of the invention. The pharmaceutical compositions have utility as an anti-viral prophylactic agent and may be administered to a subject where the subject has been exposed or is expected to be exposed to a virus.

Various delivery systems are known and can be used to administer the pharmaceutical composition of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the mutant viruses, receptor mediated endocytosis (see, e.g., Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432). Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intramuscular, epidermal, and oral routes. The compounds may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. In a preferred embodiment, it may be desirable to introduce the pharmaceutical compositions of the invention into the lungs by any suitable route. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, by means of nasal spray, or by means of an implant, said implant being of a porous, non porous, or gelatinous material, including membranes, such as sialastic membranes, or filters. In one embodiment, administration can be by direct injection at the site (or former site) infected tissues.

In another embodiment, the pharmaceutical composition can be delivered in a vesicle, in particular a liposome (see Langer, 1990, Science 249:1527-1533; Treat et al., Liposomes in the Therapy of Infectious Disease and Cancer, Lopez Berestein and Fidler (eds.), Liss, New York, pp. 353-365 (1989); Lopez-Berestein, ibid., pp. 317-327; see generally ibid.).


Other controlled release systems are discussed in the review by Langer (Science 249:1527-1533 (1990)).

The pharmaceutical compositions of the present invention comprise a therapeutically effective amount of recombinant or chimeric CoV-HKU1, and a pharmaceutically acceptable carrier. In a specific embodiment, the term “pharmaceutically acceptable” means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term “carrier” refers to a diluent, adjuvant, excipient, or vehicle with which the pharmaceutical composition is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silicone, rubber, glycerol monooleate, talc, sodium chloride, dried skim milk, glycerol, propylene glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in “Remington’s Pharmaceutical Sciences” by E. W. Martin. The formulation should suit the mode of administration.

In a preferred embodiment, the composition is formulated in accordance with referenced procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The pharmaceutical compositions of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those derived from sodium, potassium,
ammonium, calcium, ferric hydroxides, isopropylamine, triethylenamine, 2-ethylamino ethanol, histidine, procaine, etc.

[0092] The amount of the pharmaceutical composition of the invention which will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient’s circumstances. However, suitable dosage ranges for intranasal administration are generally about 20-500 micrograms of active compound per kilogram body weight. Suitable dosage ranges for intranasal administration are generally about 0.01 pg/kg body weight to 1 mg/kg body weight. Effective doses may be extrapolated from dose response curves derived from in vitro or animal model test systems.

[0093] Suppositories generally contain active ingredient in the range of 0.5% to 10% by weight; oral formulations preferably contain 10% to 95% active ingredient.

[0094] The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In a preferred embodiment, the kit contains an antiviral agent of the invention, e.g., an antibody specific for the polypeptides encoded by a nucleotide sequence of SEQ ID NO:1 or 3, or any CoV-HKU1 epitope, or a polypeptide or protein of the present invention, including those shown in FIG. 2 (SEQ ID NOS:34-1318), FIG. 8 (SEQ ID NOS:1319-2918), and SEQ ID NO:2, or a nucleic acid molecule of the invention, alone or in combination with adjuvants, antivirals, antibiotics, analgesics, bronchodilators, or other pharmaceutically acceptable excipients.

[0095] The present invention further encompasses kits comprising a container containing a pharmaceutical composition of the present invention and instructions for use.

5.6 Detection Assays

[0096] The present invention provides a method for detecting an antibody, which immunospecifically binds to the CoV-HKU1, in a biological sample, for example blood, serum, plasma, saliva, urine, etc., from a patient suffering from respiratory tract infection. In a specific embodiment, the method comprising contacting the sample with the polypeptides or protein encoded by the nucleotide sequence of SEQ ID NO:1 and/or 3, including the polypeptides having the amino acid sequences of SEQ ID NOS:34-1318 shown in FIG. 2, SEQ ID NOS:1319-2918 shown in FIG. 8, or SEQ ID NO:2, directly immobilized on a substrate and detecting the virus-bound antibody directly or indirectly by a labeled heterologous antiserum antibody. In another specific embodiment, the sample is contacted with a host cell comprising a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:1 or 3 and expressing the polypeptides encoded therein, and the bound antibody can be detected by immunofluorescent assay.

[0097] An exemplary method for detecting the presence or absence of a polypeptide or nucleic acid of the invention in a biological sample involves obtaining a biological sample from various sources and contacting the sample with a compound or an agent capable of detecting an epitope or nucleic acid (e.g., mRNA, genomic RNA) of CoV-HKU1 such that the presence of CoV-HKU1 is detected in the sample. A preferred agent for detecting CoV-HKU1 mRNA or genomic RNA of the invention is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic RNA encoding a polypeptide of the invention. The nucleic acid probe can be, for example, a nucleic acid molecule comprising or consisting of the nucleotide sequence of SEQ ID NO:1 or 3, or a portion thereof, or a complement thereof, such as an oligonucleotide of at least 15, 20, 25, 30, 50, 100, 250, 500, 750, 1,000 or more contiguous nucleotides in length and sufficient to specifically hybridize under stringent conditions to a CoV-

[0098] In another preferred specific embodiment, the presence of CoV-HKU1 is detected in the sample by an reverse transcription polymerase chain reaction (RT-PCR) using the primers that are constructed based on a partial nucleotide sequence of the genome of CoV-HKU1 or a genomic nucleic acid sequence of SEQ ID NO:3, or on a nucleotide sequence of SEQ ID NO: 1. In a non-limiting specific embodiment, preferred primers to be used in a RT-PCR method are: 5'-GTTGGGACTATTCAAGTGTTGAA-3' (SEQ ID NO:4) and 5'-CCATGATAGAATAGTCAATGTT-3' (SEQ ID NO:5), in the presence of 3 mM MgCl2, and the thermal cycles are, for example, but not limited to, 94°C for 8 min followed by 40 cycles of 94°C for 1 min, 50°C for 1 min, 72°C for 1 min. In more preferred specific embodiment, the present invention provides a real-time quantitative PCR assay to detect the presence of CoV-HKU1 in a biological sample by subjecting the cDNA obtained by reverse transcription of the extracted total RNA from the sample to PCR reactions using the specific primers, such as those having nucleotide sequences of SEQ ID NOS:4 and 5, and a fluorescence dye, such as SYBR® Green I, which fluoresces when bound non-specifically to double-stranded DNA. The fluorescence signals from these reactions are captured at the end of extension steps as PCR product is generated over a range of the thermal cycles, thereby allowing the quantitative determination of the viral load in the sample based on an amplification plot.

[0099] A preferred agent for detecting CoV-HKU1 is an antibody that specifically binds a polypeptide of the invention or any CoV-HKU1 epitope, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')2) can be used.

[0100] The term “labeled”, with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The detection method of the invention can be used to detect mRNA, protein (or any epitope), or genomic RNA in a sample in vitro as well as in vivo. For example, in vitro techniques for detection of mRNA include northern hybridizations, in situ hybridizations, RT-PCR, and RNase protection. In vitro techniques for detection
of an epitope of CoV-HKU1 include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. In vitro techniques for detection of genomic RNA include northern hybridizations, RT-PCR, and RNase protection. Furthermore, in vivo techniques for detection of CoV-HKU1 include introducing into a subject organism a labeled antibody directed against the polypeptide. For example, the antibody can be labeled with a radioactive marker whose presence and location in the subject organism can be detected by standard imaging techniques, including autoradiography.

[0101] In a specific embodiment, the methods further involve obtaining a control sample from a control subject, contacting the control sample with a compound or agent capable of detecting CoV-HKU1, e.g., a polypeptide of the invention or mRNA or genomic RNA encoding a polypeptide of the invention, such that the presence of CoV-HKU1 or the polypeptide or mRNA or genomic RNA encoding the polypeptide is detected in the sample, and comparing the absence of CoV-HKU1 or the polypeptide or mRNA or genomic RNA encoding the polypeptide in the control sample with the presence of CoV-HKU1, or the polypeptide or mRNA or genomic DNA encoding the polypeptide in the test sample.

[0102] The invention also encompasses kits for detecting the presence of CoV-HKU1 or a polypeptide or nucleic acid of the invention in a test sample. The kit, for example, can comprise a labeled compound or agent capable of detecting CoV-HKU1 or the polypeptide or a nucleic acid molecule encoding the polypeptide in a test sample and, in certain embodiments, a means for determining the amount of the polypeptide or mRNA in the sample (e.g., an antibody which binds the polypeptide or an oligonucleotide probe which binds to mRNA or mRNA encoding the polypeptide). Kits can also include instructions for use.

[0103] For antibody-based kits, the kit can comprise, for example: (1) a first antibody (e.g., attached to a solid support) which binds to a polypeptide of the invention or CoV-HKU1 epitope; and, optionally, (2) a second, different antibody which binds to either the polypeptide or the first antibody and is conjugated to a detectable agent.

[0104] For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide, e.g., a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a polypeptide of the invention or to a sequence within the CoV-HKU1 genome or (2) a pair of primers useful for amplifying a nucleic acid molecule containing an CoV-HKU1 sequence. The kit can also comprise, e.g., a buffering agent, a preservative, or a protein stabilizing agent. The kit can also comprise components necessary for detecting the detectable agent (e.g., an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample contained. Each component of the kit is usually enclosed within an individual container and all of the various containers are within a single package along with instructions for use.

6. EXAMPLES

[0105] The following examples illustrate the identification of the novel CoV-HKU1. These examples should not be construed as limiting.

Methods and Results


6.1 Clinical Subject

[0107] The patient is an in-patient of the United Christian Hospital in Hong Kong. Nasopharyngeal aspirates were collected from the patient weekly from the first till the fifth week of the illness, stool and urine in the first and second week of the illness, and sera in the first, second, and fourth weeks of the illness.

6.2 Antibody Detection

[0108] To produce a fusion plasmid for protein purification, primers, 5’-TTTTCCTTTT 6CGCGCGCTTAAGCAACA-GATCTTTCA-3’ (SEQ ID NO:6) and 5’-CAGGTCTTATCCGCTGAC-3’ (SEQ ID NO:7) were used to amplify the gene encoding the N protein of the CoV-HKU1 by RT-PCR. The sequence coding for amino acid residues 1 to 441 of the N protein was amplified and cloned into the EcoRI and NotI sites of expression vector pET-28a(+) (Novagen, Madison, Wis., USA) in frame and downstream of the series of six histidine residues. The (His)s-tagged (SEQ ID NO:27) recombinant N protein was expressed in E. coli and purified using the Ni2+-loaded HiTrap Chelating System (Amersham Pharmacia, USA) according to the manufacturer’s instructions.

[0109] Western blot analysis was performed as follows: Two hundred µg of purified (His)s-tagged (SEQ ID NO:27) recombinant N protein of CoV-HKU1 were loaded into each well of a sodium dodecyl sulfate (SDS)-10% polyacrylamide gel and subsequently electrophoresed onto a nitrocellulose membrane (Bio-Rad, Hercules, Calif., USA). The blot was cut into strips and the strips were incubated separately with 1:2000 dilution of serum samples obtained during the first, second, and fourth weeks of the patient’s illness. Serum samples of two healthy blood donors were used as controls. Antigen-antibody interaction was detected with an ECL fluorescence system (Amersham Life Science, Buckinghamshire, UK).

[0110] Several prominent immunoreactive bands were visible for serum samples collected during the second and fourth weeks of the patient’s illness (FIG. 7, lanes 2 and 3). The sizes of the largest bands were about 53 kDa, consistent with the expected size of 52.8 kDa for the full-length (His)s-tagged (SEQ ID NO:27) N protein, whereas the other bands were consistent with the degradation products of the (His)s-tagged (SEQ ID NO:27) N protein. Only very faint bands were observed for serum samples obtained from the patient during the first week of the illness (FIG. 7, lane 1) and two healthy blood donors (FIG. 7, lanes 4 and 5).

[0111] ELISA was performed using the recombinant N protein of CoV-HKU1 prepared as described above. Each well of a Nunc immunoplate (Roskilde, Denmark) was coated with 20 µg of purified (His)s-tagged (SEQ ID NO:27) recombinant N protein for 12 h and then blocked in phosphate-buffered saline with 2% bovine serum albumin. The serum samples obtained from the patient during the first, second, and fourth weeks of the illness were serially diluted and were added to the wells of the (His)s-tagged (SEQ ID NO:27) recombinant N protein-coated plates in a total volume of 100 µl per well and incubated at 37°C. After washing with
washing buffer five times, 100 μl per well of 1:4000 diluted horse radish peroxidase-conjugated goat anti-human IgG antibody (Zymed Laboratories Inc., South San Francisco, Calif., USA) were added to the wells and incubated at 37°C for 1 h. After washing with washing buffer five times, 100 μl of diluted 3,3',5,5'-tetramethylbenzidine (Zymed Laboratories Inc.) were added to each well and incubated at room temperature for 15 min. One hundred microliters of 0.3 M H2SO4 were added and the absorbance at 450 nm of each well was measured. Each sample was tested in duplicate and the mean absorbance for each serum was calculated.

[0112] Box titration was carried out with different dilutions of (His)6-tagged (SEQ ID NO:27) recombinant N protein coating antigen and serum obtained from the fourth week of the patient's illness. The results identified 20 ng and 80 ng of purified (His)6-tagged recombinant N protein per ELISA well as the ideal amount for plate coating and 1:1000 and 1:20 as the most optimal serum dilution for IgG and IgM detection, respectively.

[0113] To establish the baseline for the tests, serum samples (diluted at 1:1000 and 1:20 for IgG and IgM, respectively) from 100 healthy blood donors were tested in the CoV-HKU1 antibody ELISA. For the sera from healthy blood donors, the mean ELISA OD540 values for IgG and IgM detection were 0.178 and 0.224, with standard deviations of 0.070 and 0.117. Absorbance values of 0.387 and 0.576 were selected as the cutoff values (that equal the sum of the mean value from the healthy control and three times the standard deviation) for IgG and IgM, respectively. Using these cutoff values, the titers for IgG of the patient's serum samples obtained during the first, second, and fourth weeks of the illness were <1:1000, 1:1000, and 1:9000, respectively (FIG. 6), and those for IgM were 1:20, 1:40, and 1:80, respectively (data not shown).

6.3 RT-PCR and Real Time Quantitative PCR

[0114] RT-PCR Assay

[0115] An RT-PCR was developed to detect the CoV-HKU1 sequence from NPA samples. Total RNA from clinical samples was reverse transcribed using random hexamers and cDNA was amplified using primers 5'-GGTTGGGACTACTC-TAAAGTGTGA-3' (SEQ ID NO:4) and 5'-CACATCATCAGATGATAT-CATA-3' (SEQ ID NO:5), which were constructed based on the RNA-dependent RNA polymerase-encoding sequence (SEQ ID NO: 1) of the CoV-HKU1 in the presence of 2.5 mM MgCl2, 94°C for 8 min followed by 40 cycles of 94°C for 1 min, 50°C for 1 min, 72°C for 1 min).

[0116] The summary of a typical RT-PCR protocol is as follows:

1. RNA Extraction
2. Reverse Transcription

<table>
<thead>
<tr>
<th>Component</th>
<th>Volume</th>
</tr>
</thead>
<tbody>
<tr>
<td>RNA</td>
<td>11.5 μl</td>
</tr>
<tr>
<td>0.1 M DTT</td>
<td>2 μl</td>
</tr>
<tr>
<td>5x buffer</td>
<td>4 μl</td>
</tr>
<tr>
<td>10 mM dNTP</td>
<td>1 μl</td>
</tr>
<tr>
<td>Superscript II, 200 U/μl (Invitrogen)</td>
<td>1 μl</td>
</tr>
<tr>
<td>Random hexamers, 0.3 μg/μl</td>
<td>0.5 μl</td>
</tr>
<tr>
<td>Reaction condition</td>
<td>42°C, 50 min</td>
</tr>
<tr>
<td>94°C, 3 min</td>
<td>4°C</td>
</tr>
</tbody>
</table>

3. PCR

cDNA generated by random primers was amplified in a 50 μl reaction as follows:

<table>
<thead>
<tr>
<th>Component</th>
<th>Volume</th>
</tr>
</thead>
<tbody>
<tr>
<td>cDNA</td>
<td>2 μl</td>
</tr>
<tr>
<td>10 mM dNTP</td>
<td>0.5 μl</td>
</tr>
<tr>
<td>10x buffer</td>
<td>5 μl</td>
</tr>
<tr>
<td>25 mM MgCl2</td>
<td>5 μl</td>
</tr>
<tr>
<td>25 μM Forward primer</td>
<td>0.5 μl</td>
</tr>
<tr>
<td>25 μM Reverse primer</td>
<td>0.5 μl</td>
</tr>
<tr>
<td>Amplicor Gold &amp; polymerase</td>
<td>0.25 μl</td>
</tr>
<tr>
<td>5 U/μl (Applied Biosystems)</td>
<td>Water</td>
</tr>
<tr>
<td></td>
<td>36.25 μl</td>
</tr>
</tbody>
</table>

4. Primer Sequences

[0124] Primers were designed based on the RNA-dependent RNA polymerase encoding sequence (SEQ ID NO:1) of the CoV-HKU1:

Forward primer: (SEQ ID NO: 4)
5'-GGTTGGGACTACTC-TAAAGTGTGA-3'

Reverse primer: (SEQ ID NO: 5)
5'-CACATCATCAGATGATAT-CATA-3'

Product size: 440 bps

[0125] Real-Time Quantitative PCR Assay

[0126] Total RNA from 140 μl of nasopharyngeal aspirate (NPA) was extracted by QIAamp® virus RNA mini kit (Qiagen) as instructed by the manufacturer. Ten μl of eluted RNA samples were reverse transcribed by 200 U of SuperScript® II reverse transcriptase (Invitrogen) in a 20 μl reaction mixture containing 0.15 μg of random hexamers, 10 mMol/L DTT, and 0.5 mMol/L dNTP, as instructed. Complementary DNA was then amplified in a SYBR® Green I fluorescence reaction (Roche, Ind.) mixtures. Brieﬂy, 20 μl reaction mixtures containing 2 μl of cDNA, 3.5 mMol/L MgCl2, 0.25 μMol/L of forward primer 5'-GGTTGGGACTACTC-TAAAGTGTGA-3' (SEQ ID NO:4) and 0.25 μMol/L reverse primer 5'-CACATCATCAGATGATAT-CATA-3' (SEQ ID NO:5) were thermal-cycled by a LightCycler® (Roche) with the PCR program, 95°C, 10 min followed by 50 cycles of 95°C, 10 min, 57°C, 5 sec; 72°C, 9 sec). Plasmids containing the target sequence were used as positive controls. Fluorescence signals from these reactions were captured at the end of extension step in each cycle. To determine the specificity of the assay, PCR products (440 base pairs) were subjected to a melting curve analysis at the end of the assay (65°C to 95°C, 0.1°C per second) (data not shown).

[0127] The amount of CoV-HKU1 RNA in the nasopharyngeal aspirates was followed weekly. Quantitative RT-PCR showed that the amounts of CoV-HKU1 RNA were 8.5×10^6 and 9.6×10^6 copies per ml in two nasopharyngeal aspirates collected in the first week of the illness, 1.5×10^6 copies per ml of NPA, respectively, at two time points collected in the second week of the illness, but CoV-HKU1 RNA was undetectable in the NPA collected in the third, fourth and fifth weeks of the illness (FIG. 6). CoV-HKU1 RNA was also
undetectable in the urine and stool of the patient collected in the first and second weeks of the illness.

**Discussion**

[0128] The genome of CoV-HKU1 is a 29,942-nucleotide long, polyadenylated RNA. The G+C content is 32%, which is the lowest among all known coronaviruses with genome sequences available, with a GC skew of 0.19. Table 1 shows the comparison of genomic features of CoV-HKU1 and other coronavirus.

<table>
<thead>
<tr>
<th>TABLE 1</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Coronaviruses</strong></td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td><strong>Group 1</strong></td>
</tr>
<tr>
<td>HCoV-229E</td>
</tr>
<tr>
<td>PEDV</td>
</tr>
<tr>
<td>HCoV-NL63</td>
</tr>
<tr>
<td><strong>Group 2</strong></td>
</tr>
<tr>
<td>CoV-HKU1</td>
</tr>
<tr>
<td>HCoV-OC43</td>
</tr>
<tr>
<td>BCoV</td>
</tr>
<tr>
<td>MHV</td>
</tr>
<tr>
<td><strong>Group 3</strong></td>
</tr>
<tr>
<td>IBV</td>
</tr>
<tr>
<td>SARS-CoV</td>
</tr>
</tbody>
</table>

HCoV-229E = human coronavirus 229E; PEDV = porcine epidemic diarrhea virus; HCoV-NL63 = human coronavirus NL63; HCoV-OC43 = human coronavirus OC43; MHV = murine hepatitis virus; BCoV = bovine coronavirus; IBV = infectious bronchitis virus; SARS-CoV = SARS coronavirus; GC skew = (G - C)/(G + C) |

[0129] The genome organization is the same as other coronaviruses, with the characteristic gene order 5'-replicase, S, E, M, N-3'. Both 5' and 3' ends contain short untranslated regions. The 5' end of the genome consists of a putative 5' leader sequence. A putative transcription regulatory sequences (TRS) motif, 5'-CUAAC-3', was found at the 3' end of the leader sequence and precedes each translated ORF except ORF4 and ORF6 which encodes the putative E protein. Table 2 shows the putative transcription regulatory sequences in the genome of CoV-HKU1.

<table>
<thead>
<tr>
<th>TABLE 2-continued</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Number of base upstream</strong></td>
</tr>
<tr>
<td>of AUG</td>
</tr>
<tr>
<td>-13 Nucleocapsid</td>
</tr>
<tr>
<td>-35 ORF 9</td>
</tr>
</tbody>
</table>

[0130] As in SDAV (Sialodacryoadenitis virus) and MHV (mouse hepatitis virus), ORF6 may share the same TRS with ORF 5, suggesting that the translation of the E protein is cap-independent, possibly via an internal ribosomal entry site. The 3' untranslated region contains a predicted pseudoknot structure 59-119 bp downstream of N gene. This pseudoknot structure is highly conserved among coronaviruses and plays a role in coronavirus RNA replication.

[0131] The coding potential of the CoV-HKU1 genome is shown in Figs. 3 and Table 3 and the phylogenetic analyses of the chymotrypsin-like protease (3CL_pro), replicase, helicase, hemagglutinin-esterase (HE), S, E, M and N, are shown in FIGS. 4A and 4B.

<table>
<thead>
<tr>
<th>TABLE 3</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>ORFs</strong></td>
</tr>
<tr>
<td>(base)</td>
</tr>
<tr>
<td>ORF 1a</td>
</tr>
<tr>
<td>ORF 1b</td>
</tr>
<tr>
<td>HE (ORF 2)</td>
</tr>
<tr>
<td>S (ORF 3)</td>
</tr>
<tr>
<td>ORF 4</td>
</tr>
<tr>
<td>ORF 5</td>
</tr>
<tr>
<td>E (ORF 6)</td>
</tr>
<tr>
<td>M (ORF 7)</td>
</tr>
<tr>
<td>N (ORF 8)</td>
</tr>
<tr>
<td>ORF 9</td>
</tr>
</tbody>
</table>

[0132] The replicase 1a ORF (bases 206-13660) and replicase 1b ORF (bases 13600-21735) occupy 21.5 kb of the CoV-HKU1 genome. Similar to other coronaviruses, a frame shift interrupts the protein-coding regions and separates the 1a and 1b ORFs. This ORF encodes a number of putative proteins, including papain-like protease (PLP) with two copies of the PLP domain, PLP1_pro and PLP2_pro, 3CL_pro, replicase, helicase, and other proteins of unknown functions. These proteins are produced by proteolytic cleavages of a large polyprotein (Fig. 3). The sequence of the resulting putative proteins is the same as that in the MHV genome. This polyprotein is synthesized by a -1 ribosomal frameshift at a conserved site (UUUAAC) upstream of a pseudoknot structure at the junction of ORF 1a and ORF 1b. This ribosomal frameshift would result in a polyprotein of 7192 amino acids, which has 75-77% amino acid identities with the polyprotein in other Group 2 coronaviruses and 43-47% amino acid identities with the polyprotein in other non-Group 2 coronaviruses. The replicase gene of CoV-HKU1, which encodes 928 amino acids, has 87-89% amino acid identities with the replicase of other Group 2 coronaviruses and 54-65% amino acid identities with the replicase of other non-Group 2 coronaviruses (Table 4 and FIG. 4A). Table 4 shows amino acid identities between the predicted chymotrypsin-like protease (3CL_pro), replicase (Rep), helicase (Hel), hemagglutinin-es-
terase (HE), spike (S), envelope (E), membrane (M), and nucleocapsid (N) proteins of CoV-HKU1 and the corresponding proteins of other coronaviruses.

Table 4

<table>
<thead>
<tr>
<th>Group</th>
<th>Virus</th>
<th>3CLpro</th>
<th>Rep</th>
<th>Hel</th>
<th>HE</th>
<th>S</th>
<th>E</th>
<th>M</th>
<th>N</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>HCoV-229E</td>
<td>45</td>
<td>54</td>
<td>55</td>
<td>31</td>
<td>26</td>
<td>35</td>
<td>28</td>
<td></td>
</tr>
<tr>
<td></td>
<td>PDCV</td>
<td>44</td>
<td>56</td>
<td>55</td>
<td>30</td>
<td>34</td>
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<td></td>
<td>PDDV</td>
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<td>57</td>
<td>57</td>
<td>32</td>
<td>34</td>
<td>37</td>
<td>27</td>
<td></td>
</tr>
<tr>
<td></td>
<td>PDCV</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>31</td>
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<td>HCoV-NL63</td>
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<td>54</td>
<td>30</td>
<td>28</td>
<td>32</td>
<td>28</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>HCoV-OCA4</td>
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<td>87</td>
<td>88</td>
<td>57</td>
<td>60</td>
<td>54</td>
<td>76</td>
<td>58</td>
</tr>
<tr>
<td></td>
<td>MHV</td>
<td>85</td>
<td>89</td>
<td>87</td>
<td>50</td>
<td>58</td>
<td>55</td>
<td>78</td>
<td>60</td>
</tr>
<tr>
<td></td>
<td>BCoV</td>
<td>84</td>
<td>88</td>
<td>88</td>
<td>56</td>
<td>61</td>
<td>55</td>
<td>76</td>
<td>57</td>
</tr>
<tr>
<td></td>
<td>SADB</td>
<td>91</td>
<td>88</td>
<td>88</td>
<td>56</td>
<td>61</td>
<td>55</td>
<td>76</td>
<td>57</td>
</tr>
<tr>
<td></td>
<td>EGCoV</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>50</td>
<td>61</td>
<td>80</td>
<td>77</td>
</tr>
<tr>
<td></td>
<td>PHEV</td>
<td>—</td>
<td>91</td>
<td>87</td>
<td>54</td>
<td>61</td>
<td>54</td>
<td>77</td>
<td>57</td>
</tr>
<tr>
<td>3</td>
<td>IBV</td>
<td>41</td>
<td>60</td>
<td>57</td>
<td>32</td>
<td>28</td>
<td>38</td>
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<td></td>
</tr>
<tr>
<td></td>
<td>SARS-CoV</td>
<td>48</td>
<td>65</td>
<td>63</td>
<td>33</td>
<td>27</td>
<td>34</td>
<td>31</td>
<td></td>
</tr>
</tbody>
</table>

HCoV-229E = human coronavirus 229E; PDCV = porcine epidemic diarrhea virus; PDDV = porcine transmissible gastroenteritis virus; CCov = canine enteric coronavirus; HCoV-NL63 = human coronavirus NL63; HCoV-OCA4 = human coronavirus OCA4; MHV = mouse hepatitis virus; BCoV = bovine coronavirus; SADB = rat skeletal myositis coronavirus; EGCoV = equine coronavirus EGCoV; PHEV = porcine hemagglutinating encephalomyelitis virus; IBV = infectious bronchitis virus; SARS-CoV = SARS coronavirus.

Although TMPred and TMHMM analyses of the ORF show four and three transmembrane domains, respectively, PHDhtm analysis of the ORF shows only one transmembrane domain at positions 354 to 376. This concurs with only one transmembrane region reported in the C-terminal of the HE of BCoV (bovine coronavirus) and puffsinos virus. PrositeScan analysis of the HE protein of CoV-HKU1 reveals eight potential N-linked glycosylation sites. These are located at positions 83 (NYT), 110, (NGS), 145 (NVS), 168 (NYS), 193 (NFS), 286 (NSS), 314 (NVS), and 328 (NFT). The putative active site for neuraminic O-acetyl-esterase activity, FGIDS (SEQ ID NO: 18), is located at positions 31-34.

[0135] ORF 3 (bases 22942-27012) encodes the predicted S glycoprotein (PFAM accession no. PF01601) with 1356 amino acids. The protein of CoV-HKU1 has 55-61% identity with the amino acid identities of the S proteins of other Group 2 coronaviruses, but has fewer than 35% amino acid identities with the S proteins of Group 1, Group 3, and SARS-CoV (Table 4 and FIG. 4B). InterProScan analysis predicts it as a type 1 membrane glycoprotein. Important features of the S protein of CoV-HKU1 are depicted in FIG. 5. PrositeScan of the S protein of CoV-HKU1 reveals 28 potential N-linked glycosylation (12 NXS and 16 NXT) sites. SignalP analysis reveals a signal peptide probability of 0.909, with a cleavage site between residues 13 and 14. By multiple alignments with the S proteins of other Group 2 coronaviruses, a potential cleavage site located after RRKR (SEQ ID NO: 19), between residues 760 and 761, where S will be cleaved into S1 and S2, is identified. Immediately upstream of RRKR (SEQ ID NO: 19), there is a series of five serine residues that are not present in any other known coronaviruses (FIG. 5). Most of the S protein (residues 15 to 1300) is exposed on the outside of the virus, with a transmembrane domain at the C terminus (TMHMM analysis of the ORF shows one transmembrane domain at positions 1301 to 1356), followed by a cytoplasmic tail rich in cysteine residues. Two heptad repeats (HR), located at residues 982 to 1083 (HR1) and 1250 to 1297 (HR2), identified by multiple alignments with other coronaviruses, are present. In MHV, it has been confirmed that the receptor for its S protein binding is CEACAM1, a member of the carciernoembryonic antigen (CEA) family of glycoproteins in the immunoglobulin superfamily. Furthermore, it has been shown by site-directed mutagenesis, that three conserved regions (sites T, II, and III) and some amino acid residues (Thr372, Thr372, Tyr281, and Tyr219) in MHV in the N-terminal of the S protein are particularly important for its receptor-binding activity. By multiple alignments with the N-terminal 330 amino acids of the S protein of MHV and other group 2 coronaviruses, it is observed that these conserved regions and amino acids are present in CoV-HKU1 (FIG. 5). This infers that the receptor for CoV-HKU1 could be a member of the CEA family on the surface of the cells in the respiratory tract. On the other hand, for HCoV-OCA4, it has been shown in vitro that the receptor for the S protein is a sialic acid. However, the amino acid residues on the S protein of HCoV-OCA4 that are important for receptor binding are not well defined.

[0136] ORF 4 (bases 26960-27270) encodes a predicted protein with 36 amino acids. This ORF overlaps with the ORF that encodes the S protein. This ORF is not present in other coronaviruses and BlastP analysis of the ORF does not show any hits.

[0137] ORF 5 (bases 27051-27380) encodes a predicted protein with 109 amino acids. This ORF overlaps with the...
ORF that encodes the E protein. PFAM analysis of the ORF shows that the predicted protein is a member of the coronavirus non-structural protein NS2 family (PFAM accession no.: PF04753). TMpred and TMHMM analysis do not reveal any transmembrane helix. This predicted protein of CoV-HKU1 has 44-51% amino acid identities with the corresponding proteins of other Group 2 coronaviruses.

[0138] ORF 6 (bases 27373-27621) encodes the predicted E protein with 82 amino acids. The E protein of CoV-HKU1 has 54-60% amino acid identities with the E proteins of other Group 2 coronaviruses, but has fewer than 35% amino acid identities with the E proteins of Group 1, Group 3, and SARS-CoV (Table 4 and Fig. 4B). PFAM and InterProScan analyses of the ORF show that the predicted E protein is a member of the non-structural protein NS3/Small envelope protein E (NS3_envE) family (PFAM accession no.: PF02723). SignalP analysis predicts the presence of a transmembrane anchor (probability 0.995). TMpred analysis of the ORF shows two transmembrane domains at positions 16 to 34 and 39 to 59, and TMHMM analysis of the ORF shows two transmembrane domains at positions 10 to 32 and 39 to 58, consistent with the anticipated association of the E protein with the viral envelope. Both programs predict that both the N and C termini are located on the surface of the virus.

[0139] ORF 7 (bases 27633-28304) encodes the predicted M protein with 223 amino acids. The M protein of CoV-HKU1 has 76-78% amino acid identities with the M proteins of other Group 2 coronavirus, but has fewer than 40% amino acid identities with the M proteins of Group 1, Group 3, and SARS-CoV (Table 4 and Fig. 4B). PFAM analysis of the ORF shows that the predicted M protein is a member of the coronavirus matrix glycoprotein (Corona_M) family (PFAM accession no.: PF01635). SignalP analysis predicts the presence of a transmembrane anchor (probability 0.926). TMpred analysis of the ORF shows three transmembrane domains at positions 21 to 42, 53 to 74, and 77 to 98. TMHMM analysis of the ORF shows three transmembrane domains at positions 20 to 39, 46 to 69, and 78 to 100. The N-terminal 19-20 amino acids are located on the outside and the C-terminal 123-125 amino acid hydrophilic domain on the inside of the virus.

[0140] ORF 8 (bases 28320-29645) encodes the predicted N protein (PFAM accession no.: PF00937) with 441 amino acids. The N protein of CoV-HKU1 has 57-62% amino acid identities with the N proteins of other Group 2 coronaviruses, but has fewer than 40% amino acid identities with the N proteins of Group 1, Group 3, and SARS-CoV (Table 4 and Fig. 4B).

[0141] ORF 9 (bases 28342-28859) encodes a hypothetical protein (N2) of 205 amino acids within the ORF that encodes the predicted N protein. PFAM analysis of the ORF shows that the predicted protein is a member of the coronavirus nucleocapsid 1 protein (Corona-1) family (PFAM accession no.: PF03187). This hypothetical N2 protein of CoV-HKU1 has 32-39% amino acid identities with the N2 proteins of other Group 2 coronaviruses.

[0142] We report the characterization and complete genome sequence of a novel coronavirus detected in the nasopharyngeal aspirates of patients with pneumonia. The clinical significance of the virus in the first patient was evident by the high viral loads in the patient's nasopharyngeal aspirates during the first week of his illness, which coincided with the acute symptoms developed in the patient. The viral load decreased during the second week of the illness and was undetectable in the third week of the illness. In addition, the fall in viral load was accompanied by the recovery from the illness and development of specific antibody response to the recombinant N protein of the virus. Similar to other recently discovered viruses, such as hepatitis C virus, GB virus C, transfusion transmitted virus, and SEN virus, the present virus could not be recovered from cell cultures using the standard cell lines. This could be related to the inherently low recovery rate of coronaviruses. Human coronaviruses are particularly difficult to culture in vitro. Many decades after the recognition of HCoV-229E and HCoV-OC43, there are still only a handful of primary virus isolates available and organ culture is required for primary isolation of HCoV-OC43. In our experience, SARS-CoV can only be recovered from less than 20% of patients with serologically and RT-PCR documented SARS-CoV pneumonia. Therefore, it is not surprising that the new coronavirus CoV-HKU1 has been so far proven difficult to culture in vitro. After the discovery of CoV-HKU1 in the first patient, we conducted a preliminary study on 400 nasopharyngeal aspirates that were collected last year during the SARS epidemic period. Among these 400 nasopharyngeal aspirates, CoV-HKU1 was detected in one specimen, with a viral load comparable to that of the first patient. These results have suggested that CoV-HKU1 is not only incidentally found in one patient, but a previously unrecognized coronavirus associated with pneumonia.

[0143] Genomic analysis has revealed that CoV-HKU1 is a Group 2 coronavirus. The genome organization of CoV-HKU1 concurs with those of other coronaviruses, with the characteristic gene order, i.e., 5'-replicase, S, E, M, N-3', short untranslated regions in both 5' and 3' ends, 5' conserved coronavirus core leader sequence, putative TRS upstream to multiple ORFs, and conserved pseudoknot in the 3' untranslated region. In contrast to coronaviruses of other groups, CoV-HKU1 contains certain features that are characteristics of Group 2 coronaviruses, including the presence of HE, ORF 5, and N2. Phylogenetic analysis of the 3CLpro' replicase, helicase, S, E, M, and N proteins showed that these genes of CoV-HKU1 were clustered with the corresponding genes in other Group 2 coronaviruses. However, the proteins of CoV-HKU1 formed distinct branches in the phylogenetic trees, indicating that CoV-HKU1 is a distinct member of the group, and is not very closely related to any other known members of Group 2 coronaviruses (Figs. 4A and 4B).

[0144] In addition to phylogenetic analysis of the putative replicase, CoV-HKU1 exhibits certain features that are distinct from other Group 2 coronaviruses. Compared to other Group 2 coronaviruses, there is a deletion of about 800 bps between the replicase ORF 1 b and the HE ORF 2 in CoV-HKU1. In other Group 2 coronaviruses, including MHV, SDAV, HCoV-OC43 and BCoV, an ORF of 798-837 bp (273-278 amino acids) is present between the replicase 1 b ORF and the HE ORF 2. This ORF encodes a protein of the coronavirus non-structural protein NS2a family (PFAM accession no.: PF05213). The absence of this ORF in CoV-HKU1 indicates that this is probably a non-essential gene of coronavirus. In addition to the deletion, the N-terminal of the putative PLP in ORF 1a contains 14 tandem copies of a 34-bp repeat that codes for a highly acidic domain. Similar repeats, with different amino acid compositions, have been found in the genomes of human, rat and parasites, but have not been found in other coronaviruses. The function of these repeats is not well understood, although some authors have suggested that the repeats could be important antigens, and their biological role may be related to their special three-dimensional struc-
tures. The vitellaria antigenic protein of *Clonorchis sinensis* contains 23 tandem copies of a 30-bp repeat that codes for DGGAQPPKSG (SEQ ID NO:20). In the case of *Plasmodium falciparum*, it has been shown that the antigenicity of the circumsporozoite protein is due to its repeating epitope structure. It has also been suggested that the tandemly repeated peptide may induce strong humoral immune response in the infected host and thus may also be useful in serological diagnosis. Further experiments should be performed to delineate the antigenic properties, biological role, and possible clinical usefulness of the repeat in the PLP of CoV-HKU1.

[0145] The geographical, political, and economic location of Hong Kong makes it a unique place for the study of emerging infectious disease. Hong Kong, as the gateway of southern China, with thousands of people crossing the border on surface and by air every day, has a high potential of importing and exporting infectious diseases to and from China, countries in Southeast Asia and from the rest of the world. In 1997, the first 18 human cases of avian influenza A H5N1 virus infection were reported in Hong Kong. In early 2003, two cases of human infection caused by avian influenza A (H5N1) that was acquired in Fujian, were diagnosed in Hong Kong, which provided an early warning of the impending disease threat for humans and poultry in Southeast Asia that followed in 2004. For the SARS epidemic, although both epidemiological and genomic evidence revealed that the disease had first occurred in southern China in November 2002, it did not receive as much international attention until the disease was spread to Hong Kong and through Hong Kong to Singapore, Toronto, Vietnam, and the United States of America. As for emerging bacterial infections, 50% of the patients with gastroenteritis associated with the recovery of *Laribacter hongkongensis* had recent history of travel to southern China. In this report, one of the patients also had recent history of travel to Shenzhen of China prior to the development of the respiratory illness. We speculate that he might have contacted the virus in Shenzhen. More intensive surveillance of emerging infectious pathogens in this locality is warranted.

7. MARKET POTENTIAL

[0146] The genome of CoV-HKU1 is completely sequenced. This allows the development of various diagnostic tests as described hereinabove. In addition, this virus contains genetic information which is extremely important and valuable for clinical and scientific research applications.

8. EQUIVALENTS

[0147] Those skilled in the art will recognize, or be able to ascertain many equivalents to the specific embodiments of the invention described herein using no more than routine experimentation. Such equivalents are intended to be encompassed by the following claims.

[0148] All publications, patents and patent applications mentioned in this specification are herein incorporated by reference into the specification to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference.

[0149] Citation or discussion of a reference herein shall not be construed as an admission that such is prior art to the present invention.

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SEQUENCE LISTING

The patent application contains a lengthy “Sequence Listing” section. A copy of the “Sequence Listing” is available in electronic form from the USPTO Web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20090305282A1). An electronic copy of the “Sequence Listing” will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed:

1. A method for detecting the presence of a first nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1 or a fragment thereof, or a complement thereof in a biological sample, said method comprising:

(a) contacting the biological sample with a compound that selectively binds to said first nucleic acid molecule; and

(b) detecting whether the compound binds to said nucleic acid molecule in the sample.

2. The method of claim 1, wherein the compound that binds to said first nucleic acid molecule is a second nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1 or a complement thereof.

3. The method of claim 1, wherein the compound that binds to said first nucleic acid molecule is a second nucleic acid molecule comprising at least 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, or 350 contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 1, or a complement thereof.

4. A method for detecting the presence of a first nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 3 or a fragment thereof or a complement thereof in a biological sample, said method comprising:

(a) contacting the biological sample with a compound that selectively binds to said first nucleic acid molecule; and

(b) detecting whether the compound binds to said nucleic acid molecule in the sample.

5. The method of claim 4, wherein the compound that binds to said first nucleic acid molecule is a second nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1 or 3, or a complement thereof.

6. The method of claim 4, wherein the compound that binds to said first nucleic acid molecule is a second nucleic acid molecule comprising at least 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, or 350 contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 1, or a complement thereof.

7. The method of claim 4, wherein the compound that binds to said first nucleic acid molecule is a second nucleic acid molecule comprising at least 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, or 350 contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 1, or a complement thereof.
molecule comprising at least 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 11000, 12000, 13000, 14000, 15000, 16000, 17000, 18000, 19000, 20000, 21000, 22000, 23000, 24000, 25000, 26000, 27000, 28000, or 29000 contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 3, or a complement thereof.

8. A method for identifying a subject infected with CoV-HKU1, comprising:
(a) obtaining total RNA from a biological sample obtained from the subject
(b) reverse transcribing the total RNA to obtain cDNA; and
(c) amplifying the cDNA using a set of primers derived from the nucleotide sequence of SEQ ID NO: 1 or 3, or a complement thereof.

9. The method of claim 8, wherein the set of primers have the nucleotide sequence of SEQ ID NOS: 4 and 5, respectively.

10. The method of claim 8, wherein the set of primers have the nucleotide sequence of SEQ ID NOS: 6 and 7, respectively.