Title: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES THEREOF

Abstract: The present invention provides the complete genomic sequence of a novel human coronavirus, coined as human coronavirus-HKU1 ("HCoV\(^{-}\)HKU1"), isolated in Hong Kong. The virus belongs to the order Nidovirales of the family Coronaviridae, being a single-stranded RN virus of positive polarity. Further study on nasopharyngeal aspirates from patients with community-acquired pneumonia has revealed that there are two genotypes, genotype A and genotype B, for this virus. In addition to the genomic sequences of these two genotypes, the invention provides the deduced amino acid sequences of the complete genome of the CoV-HKU1. The nucleotide sequences and deduced amino acid sequences of the HCoV\(^{-}\)HKU1 are useful in preventing, diagnosing and/or treating the infection by HCoV\(^{-}\)HKU1. Furthermore, the invention provides immunogenic and vaccine preparations using recombinant and chimeric forms as well as subunits of the HCoV\(^{-}\)HKU1 based on the nucleotide sequences and deduced amino acid sequences of the HCoV\(^{-}\)HKU1.
A NOVEL HUMAN VIRUS CAUSING
RESPIRATORY TRACT INFECTION AND USES THEREOF

This is a continuation-in-part application of U.S. patent application serial no. 10/895,064 filed July 21, 2004, which is incorporated by reference in its entirety.

SEQUENCE LISTING

The instant application contains a “lengthy” Sequence Listing which has been submitted via CD-R in lieu of a printed paper copy, and is hereby incorporated by reference in its entirety. Said CD-R, recorded on March 21, 2005, are labeled “CRF”, “Copy 1” and “Copy 2”, respectively, and each contains only one identical 2.84 MB file (V0690044.APP).

1. INTRODUCTION

The present invention relates to a novel virus causing respiratory tract infection in humans ["coronavirus-HKU1 (CoV-HKU1)"]]. Phylogenetic analysis has revealed that the CoV-HKU1 is a new group 2 coronavirus, which has, at least, two (2) genotypes, A and B. The present invention relates to nucleotide sequences comprising the complete genomic sequences of the CoV-HKU1. The invention further relates to nucleotide sequences comprising a portion of the genomic sequences of the CoV-HKU1. The invention also relates to the deduced amino acid sequences of the complete genomes 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

Since no microbiological cause has been identified in a significant proportion of patients with respiratory tract infections (Macfarlane, J. T. et al., 1993, Prospective study of


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 cicatrization of right upper lobe and bronchiectasis 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 37.6°C. Physical examination showed tracheal deviation to the right and inspiratory crackles over the anterior left lower zone. His haemoglobin level was 14.7 g/dL, total white cell count 12.1×10⁹/L, with neutrophil 9.7×10⁹/L, lymphocyte 1.6×10⁹/L and monocyte 0.5×10⁹/L, and plate count 20 303×10⁹/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. His fever subsided two days after admission. His 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 as disclosed herein. Further studies disclosed herein have revealed that CoV-HKU1 is a human coronavirus and there are, at least, two (2) genotypes, A and B, within CoV-HKU1. The invention is useful in both clinical and scientific research applications.

3. SUMMARY OF INVENTION

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 first 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, *Coronaviridae*. Further studies based on prospectively collected nasopharyngeal aspirates (NPAs) from patients with community-acquired pneumonia during a 12-month period, have revealed that there are, at least, two (2) genotypes for CoV-HKU1. Accordingly, the invention relates to CoV-HKU1 that phylogenetically relates to known members of *Coronaviridae* and specifically belongs to group 2 coronavirus. In a specific embodiment, the invention provides complete genomic sequences of two (2) genotypes of CoV-HKU1. In a preferred embodiment, the virus comprises a nucleotide sequence of SEQ ID NO:1, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966. 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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, 2920, 2922, 2924, 2926, 2928, 2930, 2932, or 2934, a complement thereof or a portion thereof, preferably at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, 1,350, 1,400, 1,450, 1,500, 1,550, 1,600, 1,650, 1,700, 1,750, 1,800, 1,850, 1,900, 1,950, 2,000, 2,100, 2,200, 2,300, 2,400, 2,500, 2,600, 2,700, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:1, 2920, 2922, 2924, 2926, 2928, 2930, 2932, or 2934, 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 or 2919, a complement thereof or a portion thereof, preferably at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 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 2919, or a complement thereof. In yet another specific embodiment, the present invention provides isolated nucleic acid molecules comprising or, alternatively, consisting of the nucleotide sequence of SEQ ID NO: 2936, 2938, 2940, 2942, 2944, 2946, 2948, or 2950, a complement thereof, or a portion thereof, preferably at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, 1,350, 1,400, 1,450, 1,500, 1,550, 1,600, 1,650, 1,700, 1,750, 1,800, 1,850, 1,900, 1,950, 2,000, 2,100, 2,200, 2,300, 2,400, 2,500, 2,600, 2,700, 2,800, 2,900, 3,000, 3,100, 3,200, 3,300, 3,400, 3,500, 3,600, 3,700, 3,800, 3,900, 4,000, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 2936, 2938, 2940, 2942, 2944, 2946, 2948, or 2950, or a complement thereof. In yet another specific embodiment, the present invention provides isolated nucleic acid molecules comprising or, alternatively, consisting of the nucleotide sequence of SEQ ID NO: 2952, 2954, 2956, 2958, 2960, 2962, 2964, or 2966, a complement thereof, or a portion thereof, preferably at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 2952, 2954, 2956, 2958, 2960, 2962, 2964, or 2966, 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932,
In another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, 1,350, 1,400, 1,450, 1,500, 1,550, 1,600, 1,650, 1,700, 1,750, 1,800, 1,850, 1,900, 1,950, 2,000, 2,100, 2,200, 2,300, 2,400, 2,500, 2,600, 2,700, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:1, 2920, 2922, 2924, 2926, 2928, 2930, 2932, or 2934, or a complement thereof. In yet another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, 1,350, 1,400, 1,450, 1,500, 1,550, 1,600, 1,650, 1,700, 1,750, 1,800, 1,850, 1,900, 1,950, 2,000, 2,100, 2,200, 2,300, 2,400, 2,500, 2,600, 2,700, 2,800, 2,900, 3,000, 3,100, 3,200, 3,300, 3,400, 3,500, 3,600, 3,700, 3,800, 3,900, 4,000, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:2936, 2938, 2940, 2942, 2944, 2946, 2948, or 2950, or a complement thereof. In yet another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, 1,350, 1,400, 1,450, 1,500, 1,550, 1,600, 1,650, 1,700, 1,750, 1,800, 1,850, 1,900, 1,950, 2,000, 2,100, 2,200, 2,300, 2,400, 2,500, 2,600, 2,700, 2,800, 2,900, 3,000, 3,100, 3,200, 3,300, 3,400, 3,500, 3,600, 3,700, 3,800, 3,900, 4,000, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 2952, 2954, 2956, 2958, 2960, 2962, 2964, or 2966, a complement thereof. In yet another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 2952, 2954, 2956, 2958, 2960, 2962, 2964, or 2966, a complement thereof. In yet another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 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 2919, or a complement thereof. The polypeptides or proteins include those having the amino acid
sequences of SEQ IDNO:2, 34-2918 shown in Figures 2 and 3, and SEQ ID NOS:2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and 2970-4236 shown in Figures 9. 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, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, 1,350, 1,400, 1,450, 1,500, 1,550, 1,600, 1,650, 1,700, 1,750, 1,800, 1,850, 1,900, 1,950, 2,000, 2,100, 2,200, 2,300, 2,400, 2,500, 2,600, 2,700, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:1, 2920, 2922, 2924, 2926, 2928, 2930, 2932, or 2934. In another embodiment, 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, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, 1,350, 1,400, 1,450, 1,500, 1,550, 1,600, 1,650, 1,700, 1,750, 1,800, 1,850, 1,900, 1,950, 2,000, 2,100, 2,200, 2,300, 2,400, 2,500, 2,600, 2,700, 2,800, 2,900, 3,000, 3,100, 3,200, 3,300, 3,400, 3,500, 3,600, 3,700, 3,800, 3,900, 4,000, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:2936, 2938, 2940, 2942, 2944, 2946, 2948, or 2950, or a complement thereof. Furthermore, in another embodiment, 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, 1,250, 1,300, 1,350, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:2952, 2954, 2956, 2958, 2960, 2962, 2964, or 2966, or a complement thereof. 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, 1,250, 1,300, 1,350, 1,400, 1,450, 1,500, 1,550, 1,600, 1,650, 1,700, 1,750, 1,800, 1,850, 1,900, 1,950, 2,000, 2,100, 2,200, 2,300, 2,400, 2,500, 2,600, 2,700, 2,800, 2,900, 3,000, 3,100, 3,200, 3,300, 3,400, 3,500, 3,600, 3,700, 3,800, 3,900, 4,000, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:2936, 2938, 2940, 2942, 2944, 2946, 2948, or 2950, 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, or a fragment thereof, including the polypeptide having the amino acid sequence of SEQ ID NO:2 or any one of SEQ ID NOS:34-2918.
shown in Figures 2 and 3, 2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and 2970-4236 shown in Figures 9, or encoded by a nucleic acid comprising a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO: 1, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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 Fvs, 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 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 invention, 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, or a fragment thereof, including the polypeptides having the amino acid sequences of SEQ ID NO:2 or any one of SEQ ID NOS:34-2918, 2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and 2970-4236. 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, or a complement thereof, by administering to the host cell the anti-viral agents of the present invention, alone or in combination with other antiviral 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
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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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.

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.

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.

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, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, 1,350, 1,500, 2,000, 2,500, 3,000, 3,500, 4,000, 4,500, 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 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, 1,000, 1,500, 2,000, 2,500, 3,000, 3,500, 4,000, 4,100, 4,200, 4,300, 4,350, 4,360, 4,370, 4,380 amino acid residues in length of the relevant protein or polypeptide and having at least one functional feature of the protein or polypeptide.

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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, or the polypeptide having any one of the amino acid sequences of SEQ ID NOS:2, 34-2918, 2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and 2970-4236, or a
complement thereof. Such common biological activities of the polypeptides of the invention include antigenicity and immunogenicity.

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 2X SSC, 0.5% SDS at room temperature. Another preferred, non-limiting example of stringent hybridization conditions is hybridization in 6X SSC at about 45°C followed by one or more washes (e.g., about 5 to 30 min each) in 0.2X SSC, 0.1% SDS at about 45-65°C.

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. BRIEF DESCRIPTION OF FIGURES

Figure 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.

Figure 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.

Figure 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 NOS: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.

Figure 4 shows genome organization of CoV-HKU1. Overall organization of the 29926-nucleotide CoV-HKU1 genomic RNA. Predicted ORFs 1a and 1b, encoding the nonstructural polyproteins (p28, p65 and nsp1-13) and those encoding the hemagglutinin-esterase, spike, envelope, membrane and nucleocapsid structural proteins are indicated. Arrows indicate putative cleavage sites (with the corresponding nucleotide positions) of the replicase polyprotein encoded by ORF 1a and ORF 1b. ATR, PL1pro and PL2pro represent the acidic tandem repeat and the two papain-like proteases, respectively, in nsp1.

Figure 5A shows the phylogenetic analysis of the chymotrypsin like protease (3CL\textsuperscript{pro}), RNA-dependent RNA polymerase (Pol), helicase, and hemagglutinin-esterase (HE); and Figure 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, 595, 418, 1356, 75, 225 and 406 amino acid positions in 3CL\textsuperscript{pro}, Pol, helicase, HE, S, B, M, and N, respectively, were included in the analysis. The scale bar indicates the estimated number of substitutions per 10 amino acids. HCoV-229E; human coronavirus 229E; PEDV: porcine epidemic diarrhea virus; PTGV: porcine transmissible gastroenteritis virus; CCoV, canine enteric coronavirus; HCoV-NL63: human coronavirus NL63; HCoV-OC43: human coronavirus OC43; MHV: murine hepatitis virus; BCoV: bovine coronavirus; SDAV: rat sialodacryoadenitis coronavirus; ECoV: equine coronavirus NC99; PHEV: porcine hemagglutinating encephalomyelitis virus; IBV: infectious bronchitis virus; SARS-CoV: SARS coronavirus.

Figure 6 shows the spike protein of CoV-HKU1 (residues 7-336 of SEQ ID NO: 420) and those of other group 2 coronaviruses (SEQ ID NOS 21-26, respectively, in order of
The spike protein (1356 amino acids) of CoV-HKU1 is depicted by the horizontal bar [SS = N terminal signal sequence (amino acid residues 1 to 13), HR1 = heptad repeat 1 (amino acid residues 982 to 1083), HR2 = heptad repeat 2 (amino acid residues 1250 to 1297), TM = transmembrane domain (amino acid residues 1301 to 1323)], (the seven sequences below the horizontal bar disclose residues 752-766 of SEQ ID NO: 420 and SEQ ID NOS 28-33, respectively, in order of appearance). Alignment of the N-terminal region important for receptor binding (amino acid residues 1 to 330) and the region upstream to the cleavage site between S1 and S2 of CoV-HKU1 and other group 2 coronaviruses was generated with ClustalX 1.83. Residues that match the CoV-HKU1 exactly are boxed. The three conserved regions (sites I, II, and III) for receptor binding in MHV are shaded. The positions of the four conserved amino acids important for receptor binding in MHV are indicated with arrows. (GenBank accession nos. MHV: P11224; BCoV: NP 150077; HCoV-OC43: NP 937950; SDAV: AAF97738; PHEV: AAL80031; BCoV: AAQ67205).

Figure 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).

Figure 8 shows the Western blot analysis of purified recombinant CoV-HKU1 N protein antigen. Prominent immunoreactive protein bands of about 53 kDa (i.e., purified recombinant CoV-HKU1 N protein) 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 (lane 4 and 5), respectively.

Figure 9 shows the entire genomic DNA sequence (SEQ ID NO:2919) 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: 2970-3474; the second-frame translation and amino acid sequences: SEQ ID NOS: 3475-3721; and the third-frame translation and amino acid sequences: SEQ ID NOS: 3722-4236.

Figure 10 shows arrangements of proteins in replicase polyprotein in CoV-HKU1 compared with those in HCoV-OC43, BCoV, and MHV. Alignment of the AC domains of HCoV-OC43 (SEQ ID NO: 4239), BCoV (SEQ ID NO: 4238), and MHV (SEQ ID NO:
and the AC domains and ATR (underlined) of CoV-HKU1 in the two patients (SEQ ID NO: 4240 and 4241) was generated with ClustalX 1.83. AC domain = acidic domain, ATR = acidic tandem repeat. (GenBank accession no. MHV: NC_001846; BCoV: NC_003045; HCoV-OC43: AY585229).

Fig. 11 shows the multiple alignments of the replicase genes of CoV-HKU1 from patients 1 (SEQ ID NO: 2920 which encodes SEQ ID NO: 2921), 2 (SEQ ID NO: 2922 which encodes SEQ ID NO: 2923), 4 (SEQ ID NO: 2924 which encodes SEQ ID NO: 2925), 5 (SEQ ID NO: 4242 which encodes SEQ ID NO: 4243), 6 (SEQ ID NO: 2926 which encodes SEQ ID NO: 2927), 7 (SEQ ID NO: 2928 which encodes SEQ ID NO: 2929), 8 (SEQ ID NO: 2930 which encodes SEQ ID NO: 2931), 9 (SEQ ID NO: 2932 which encodes SEQ ID NO: 2933) and 10 (SEQ ID NO: 2934 which encodes SEQ ID NO: 2935).

Fig. 12 shows the chest radiographs of the two patients who died of community acquired pneumonia associated with CoV-HKU1. The chest radiograph of the first patient (Fig. 12A; patient no. 2 in Table 5) showed patchy airspace shadows in both lungs with predominant involvement of the lower zones. The chest radiograph of the second patient (Fig. 12B; patient no. 10 in Table 5), with Luque instrumentation in situ, showed extensive airspace shadows in both lungs with the middle zones more severely involved.

Fig. 13 shows the multiple alignments of the spike genes of CoV-HKU1 from patients 1 (SEQ ID NO: 2936 which encodes SEQ ID NO: 2937), 2 (SEQ ID NO: 2938 which encodes SEQ ID NO: 2939), 4 (SEQ ID NO: 2940 which encodes SEQ ID NO: 2941), 5 (SEQ ID NO: 4244 which encodes SEQ ID NO: 4245), 6 (SEQ ID NO: 2942 which encodes SEQ ID NO: 2943), 7 (SEQ ID NO: 2944 which encodes SEQ ID NO: 2945), 8 (SEQ ID NO: 2946 which encodes SEQ ID NO: 2947), 9 (SEQ ID NO: 2948 which encodes SEQ ID NO: 2949) and 10 (SEQ ID NO: 2950 which encodes SEQ ID NO: 2951).

Fig. 14 shows the multiple alignments of the nucleocapsid genes of CoV-HKU1 from patients 1 (SEQ ID NO: 2952 which encodes SEQ ID NO: 2953), 2 (SEQ ID NO: 2954 which encodes SEQ ID NO: 2955), 4 (SEQ ID NO: 2956 which encodes SEQ ID NO: 2957), 5 (SEQ ID NO: 4246 which encodes SEQ ID NO: 4247), 6 (SEQ ID NO: 2958 which encodes SEQ ID NO: 2959), 7 (SEQ ID NO: 2960 which encodes SEQ ID NO: 2961), 8 (SEQ ID NO: 2962 which encodes SEQ ID NO: 2963), 9 (SEQ ID NO: 2964
which encodes SEQ ID NO: 2965) and 10 (SEQ ID NO: 2966 which encodes SEQ ID NO: 2967).

Fig. 15 shows phylogenetic trees and non-synonymous mutations and corresponding amino acid changes of complete pol, S and N gene sequences of HCoV-HKU1 from nine patients with community acquired pneumonia. The trees were inferred from pol (Fig. 15A), S (Fig. 15B) and N (Fig. 15C) gene data by the neighbor-joining method and bootstrap values calculated from 1000 trees. The trees were rooted using pol, S and N gene sequences of HCoV-OC43, respectively. 2784 nucleotide positions in each pol gene, 4071 nucleotide positions in each S gene, and 1326 nucleotide positions in each N gene, were included in the analysis. The scale bar indicates the estimated number of substitutions per 100 (Fig. 15A) and 50 (Figs. 15B and 15C) bases, respectively, using Jukes-Cantor correction. The shaded nucleotides are those that differ from the majority at the corresponding locations. Due to the large number of non-synonymous mutations in the S gene, only the NH2 terminal 45, out of the total of 306, non-synonymous mutations are shown.

Fig. 16 shows the multiple alignments of nucleotides 1806-1835 and 2229-2258 of the pol genes in the nine HCoV-HKU1 and those of HCoV-OC43, HCoV-229E, HCoV-NL63 and SARS-CoV. Marked differences between the 3' ends of the two primers for RT-PCR (LPW1926; SEQ ID NO: 4248 and LPW1927; SEQ ID NO: 4249) and the corresponding bases in HCoV-OC43 (SEQ ID NOS 4250 and 4251), HCoV-229E (SEQ ID NOS 4254 and 4255), HCoV-NL63 (SEQ ID NOS 4256 and 4257) and SARS-CoV (SEQ ID NOS 4252 and 4253) are observed, indicating the high specificity of the two primers for HCoV-HKU1. The positions of LPW1926 (SEQ ID NO: 4248) and LPW1927 (SEQ ID NO: 4249) are boxed. The bases in HCoV-OC43, HCoV-229E, HCoV-NL63 and SARS-CoV that were different from those in the sequence of the primers, were shaded.

Fig. 17 show a phylogenetic tree of pol gene sequences of the 10 HCoV-HKU1 from patients with community acquired pneumonia. The tree was inferred from pol gene data by the neighbor-joining method and bootstrap values calculated from 1000 trees. The tree was rooted using pol gene sequence of HCoV-229E and 393 nucleotide positions (primer sequences excluded) in each pol gene were included in the analysis. The scale bar indicates the estimated number of substitutions per 50 bases using Jukes-Cantor correction. HCoV-HKU1: human coronavirus HKU1; HCoV-229E: human coronavirus 229E; HCoV-OC43:
human coronavirus OC43; MHV: murine hepatitis virus; BCoV: bovine coronavirus; PHEV: porcine hemagglutinating encephalomyelitis virus.

5. DETAILED DESCRIPTION OF THE INVENTION

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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966. 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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, 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, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000, 2,100, 2,200, 2,300, 2,400, 2,500, 2,600, 2,700, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:1, 2920, 2922, 2924, 2926, 2928, 2930, 2932, or 2934, or a complement thereof. In yet another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, 1,350, 1,400, 1,450, 1,500, 1,550, 1,600, 1,650, 1,700, 1,750, 1,800, 1,850, 1,900, 1,950, 2,000, 2,100, 2,200, 2,300, 2,400, 2,500, 2,600, 2,700, 2,800, 2,900,
3,000, 3,100, 3,200, 3,300, 3,400, 3,500, 3,600, 3,700, 3,800, 3,900, 4,000, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 2936, 2938, 2940, 2942, 2944, 2946, 2948, or 2950, or a complement thereof. In yet another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 2952, 2954, 2956, 2958, 2960, 2962, 2964, or 2966, a complement thereof. In yet another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, 1,350, 1,400, 1,500, 1,600, 1,700, 1,800, 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 2919, or a complement thereof. The polypeptides or the proteins of the present invention preferably have one or more biological activities of the proteins encoded by the sequence of SEQ ID NO:1, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, or the native viral proteins containing the amino acid sequences encoded by the sequence of SEQ ID NO:1, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, or a portion thereof.

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 2919), or fragments, or complement thereof. Furthermore, the present invention relates to a nucleic acid molecule that hybridizes any portion of the genome of the CoV-HKU1 (SEQ ID NO: 3 or 2919) 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932,
2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, or a portion thereof. The invention further encompasses chimeric or recombinant viruses or viral proteins encoded by said nucleotide sequences.

The invention further provides antibodies that specifically bind a polypeptide of the invention encoded by the nucleotide sequence of SEQ ID NO:1, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, or a fragment thereof, or any CoV-HKU1 epitope as well as the polypeptides having the amino acid sequences of any one of SEQ ID NO:2, SEQ ID NOS:34-2918 shown in Figures 2 and 3, SEQ ID NOS:2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and 2970-4236 shown in Figures 9. 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 Fvs, 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, 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.

In another embodiment, the invention provides vaccine preparations comprising the CoV-HKU1 recombinant and chimeric forms of said virus, or subunits of the virus.
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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, or a fragment thereof, including the polypeptides having the amino acid sequences of SEQ ID NO:2, SEQ ID NOS:34-2918, 2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and/or 2970-4236. 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 (ddl), lamivudine (3TC), zalcitabine (dDC), stavudine (d4T), nevirapine, delavirdine, indinavir, ritonavir, vidarabine, nelfinavir, saquinavir, relenza, tamiflu, pleconaril, interferons, etc.], steroids and corticosteroids such as prednisone, cortisone, fluticasone, and glucocorticoid, antibiotics, analgesics, bronchodilators, or other treatments for respiratory and/or viral infections. In one aspect, the anti-viral agent of the present invention prevents or inhibit the binding of the virus or viral proteins to a host cell under a physiological condition, thereby preventing or inhibiting the infection of the host cell by the virus. In another aspect, the anti-viral agent of the invention prevents or inhibits replication of the viral nucleic acid molecules in the host cell under a physiological condition by interacting with the viral nucleic acid molecules or its transcription mechanisms. In a specific embodiment, the anti-viral agent of the invention includes the vaccine or immunogenic preparations of the invention or an antibody that immunospecifically binds CoV-HKU1 or any CoV-HKU1 epitope and may neutralizes CoV-HKU1. In another specific embodiment, the anti-viral agent is a polypeptide or protein of the invention or a nucleic acid molecule of the invention.
In addition, the present invention provides a method of preventing or inhibiting replication in a host cell of a nucleic acid molecule having the nucleotide sequence of SEQ ID NO: 1, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, or inhibiting the activities of the polypeptides encoded by the nucleotide sequence of SEQ ID NO: 1, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, a complement thereof, or a portion thereof, including the polypeptides having the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 34–2918, 2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and/or 2970–4236, by administering to said host cell the anti-viral agent of the invention. In a specific embodiment the host cell is a mammalian cell, such as a cell of humans, primates, horses, cows, sheep, pigs, goats, dogs, cats, arivan species and rodents. Preferably, the 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 present invention also provides kits comprising pharmaceutical compositions of the present invention.

5.1 Recombinant and Chimeric CoV-HKU1

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 or 2919. 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 or 2919) of CoV-HKU1, due to one or more naturally occurred 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-HKU, 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, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, or a fragment thereof. In a specific embodiment, there are more than one ORF within the nucleotide sequence of SEQ ID NO:3 or 2919, or a fragment thereof. In another embodiment, the polypeptides encoded by the ORF comprises or consists of amino acid sequences of SEQ ID NO:34-2918 shown in Fig. 2 and 8, or SEQ ID NO:2, SEQ ID NO:2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and/or 2970-4236, 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.

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 endogenous or native nucleotide sequences have been replaced with heterologous nucleotide sequences.

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.

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; Skiadopoulos 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.

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.

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 ORF 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.

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.

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.

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 and bacterial antigens, tumor antigens, allergen antigens, and auto antigens 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.

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
heterologous sequences are epitopes or antigens of pathogens, these chimeric viruses may be used to induce a protective immune response against the disease agent from which these determinants are derived.

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.

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.

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.

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

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 envelop protein (E protein), integral membrane protein (M protein), spike protein (S protein), nucleocapsid protein (N protein), hemagglutinin esterase (HE protein), and RNA-dependent RNA polymerase. Such molecules, or antigenic 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, including the polypeptides having the amino acid sequences of SEQ ID NOS:34-2918 in Fig. 2 and 3, or SEQ ID NO:2, 2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and/or 2970-4236 in Fig. 9, 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 bounds and metes of ORFs, 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).

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.

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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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
molecule 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 nucleic acid molecule of the present invention.

Many methods may be used to introduce the vaccine formulations described above. These 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; Raz, E., 1994, Intradermal gene immunization: The possible role of DNA uptake in the induction of cellular immunity to viruses, Proc. Natl. Acad. Sci. USA 91:9519-9523). Another way to administer DNA vaccines is called "gene gun" method, whereby microscopic gold beads coated with the DNA molecules of interest are 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 Immunology 9(5):269-270; and Robinson, H.L. et al., 1997, DNA vaccines, Seminars in Immunology 9(5):271-283.

5.3 Adjuvants and Carrier Molecules

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 adjuvant or mineral salt gel adjuvant. Such mineral salt and mineral salt gel adjuvants include, but are not limited to, aluminum hydroxide (ALHYDROGEL, REHYDRAGEL), aluminum phosphate gel, aluminum hydroxyphosphate (ADJU-PHOS), and calcium phosphate.

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 interleukin-1β (IL-1β), and IL-1β peptide or Sclavo Peptide), cytokine-containing liposomes, triterpenoid glycosides or saponins (e.g., QuilA and QS-21, also sold under the trademark STIMULON, ISCOPREP), Muramyl Dipeptide (MDP) derivatives, such as N-acetyl-muramyl-L-threonyl-D-isoglutamine.
(Threonyl-MDP, sold under the trademark TERMURTIDE), GMMP, N-acetyl-nor-
muramyl-L-alanyl-D-isoglutamine, N-acetylmuramyl-L-alanyl-D-isoglutaminy-
L-alanine-2-(1'-2'-dipalmitoyl-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 polyphosphazenes.

In another embodiment, the adjuvant used is a particular 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 SAF and MF59, e.g.,
prepared with block-copolymers, such as L-121 (polyoxypropylene/polyoxyethylene) sold
under the trademark PLURONIC L-121, Liposomes, Virosomes, cochleates, and immune
stimulating complex, which is sold under the trademark ISCOM.

In another embodiment, a microparticulate adjuvant is used. Microparticulate
adjuvants include, but are not limited to biodegradable and biocompatible polyelecters, homo-
copolymers of lactic acid (PLA) and glycolic acid (PGA), poly(lactide-co-glycolides)
(PLGA) microparticles, polymers that self-associate into particulates (poloxamer particles),
soluble polymers (polyphosphazenes), and virus-like particles (VLPs) such as recombinant
protein particulates, e.g., hepatitis B surface antigen (HbsAg).

Yet another class of adjuvants that may be used include mucosal adjuvants,
including but not limited to heat-labile enterotoxin from Escherichia coli (LT), cholera
holotoxin (CT) and cholera Toxin B Subunit (CTB) from Vibrio cholerae, mutant toxins
(e.g., LTK63 and LTR72), microparticles, and polymerized liposomes.

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 combination adjuvant preparations that can be used to administer 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. Other adjuvants known in the art are also
included within the scope of the invention (see Vaccine Design: The Subunit and Adjuvant
York, 1995, which is incorporated herein in its entirety).
The effectiveness of an adjuvant may be determined by measuring the induction of antibodies directed against an immunogenic polypeptide containing a CoV-HKU1 polypeptide epitope, the antibodies resulting from administration of this polypeptide in vaccines which are also comprised of the various adjuvants.

The polypeptides may be formulated into the vaccine as neutral or salt forms. Pharmaceutically acceptable salts include the acid additional salts (formed with free amino groups of the peptid) 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, procaine and the like.

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.

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

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

Antibodies which specifically recognize a polypeptide 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, 2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and/or 2970-4236, 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 specific 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, Western blot, etc., for the detection of a polypeptide of the invention 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, naseopharyngeal aspirates, etc.

Antibodies specific for a polypeptide of the invention 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, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, including the polypeptides shown in Fig. 2 (SEQ ID NOS:34-1318), Fig. 3 (SEQ ID NOS:1319-2918), as well as SEQ ID NO:2, 2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and/or 2970-4236, can be produced by various procedures well known in the art. For example, an antigen can be administered 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, mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, 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).

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 antibodies 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 antibody” as used herein is not limited to antibodies produced through hybridoma technology. The term “monoclonal antibody” 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.

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.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, Fab and F(ab’)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’)2 fragments). F(ab’)2 fragments contain the complete light chain, and the variable region, the CH1 region and the hinge region of the heavy chain.

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.

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.

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.

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.
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.

In another embodiment, antibodies can also be generated using various phage display methods known in the art. In phage 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 phage display methods that can be used to make the immunoglobulins, 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; Persic 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 95/20401; and U.S. Patent 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.

As described in the above references, after phage selection, the antibody coding regions from the phage 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 92/22324; 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 Fv's and antibodies include those described in U.S. Patent Nos.

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.

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,
Methods, 125:191-202, 1989; U.S. Patent Nos. 5,807,715; 4,816,567; and 4,816,397,
which are incorporated herein by reference in their entireties. Humanized antibodies are
antibody molecules from non-human species that bind the desired antigen having one or
more complementarity determining regions (CDRs) 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. Patent No. 5,585,089; Riechmann et al.,
Nature, 332:323, 1988, which are incorporated herein by reference in their entireties.
Antibodies can be humanized using a variety of techniques known in the art including,
for example, CDR-grafting (EP 239,400; PCT publication WO 91/09967; U.S. Patent Nos.
5,225,539; 5,530,101 and 5,585,089), veneering or resurfacing (EP 592,106; EP 519,596;
Padlan, Molecular Immunology, 28(4/5):489-498, 1991; Studnicka 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. Patent No. 5,565,332), all of which are hereby
incorporated by reference in their entireties.

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 phage display methods described above using antibody libraries derived from
human immunoglobulin sequences. See U.S. Patent Nos. 4,444,887 and 4,716,111; and
PCT publications WO 98/46645; WO 98/50433; 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.

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
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 No. 0 598 877;
U.S. Patent 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 entireties. In addition, companies such as Abgenix, Inc. (Fremont, CA), Medarex
(NJ) and Genpharm (San Jose, CA) can be engaged to provide human antibodies directed
against a selected antigen using technology similar to that described above.
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, 12:899-903, 1988).

Antibodies fused or conjugated to heterologous polypeptides may be used in in vitro immunoassays 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; Naramura et al., Immunol. Lett., 39:91-99, 1994; U.S. Patent 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 entireties.

Antibodies may also be attached to solid supports, which are particularly useful for immunoassays 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, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

5.5 Pharmaceutical Compositions and Kits

The present invention encompasses pharmaceutical compositions comprising antiviral agents of the present invention. In a specific embodiment, the anti-viral agent is an antibody which immunospecifically 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, intranasal, epidural, 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 fibers. 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., in 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, silica gel, sodium stearate, glycerol monostearate, 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 routine 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, triethylamine, 2 ethylamino ethanol, histidine, procaine, etc.

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 intravenous 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.

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

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 anti-viral agent of the invention, e.g., an antibody specific for the polypeptides
encoded by a nucleotide sequence of SEQ ID NO:1, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966 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. 3 (SEQ ID NOS:1319-2918), Fig. 9 (SEQ ID NOS: 2970-4236) and SEQ ID NO:2, or a nucleic acid molecule of the invention, alone or in combination with adjuvants, antivirals, antibiotics, analgesic, bronchodilataters, or other pharmaceutically acceptable excipients.

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

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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, 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. 3, or SEQ ID NO:2, 2921, 2923, 2925, 2927, 2929, 2931, 2933, 2935, 2937, 2939, 2941, 2943, 2945, 2947, 2949, 2951, 2953, 2955, 2957, 2959, 2961, 2963, 2965, 2967, and/or 2970-4236 shown in Figs. 9, directly immobilized on a substrate and detecting the virus-bound antibody directly or indirectly by a labeled heterologous anti-isotype 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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964 and/or 2966, and expressing the polypeptides encoded thereby, and the bound antibody can be detected by immunofluorescent assay.

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, 3, 2919, 2920, 2922, 2924, 2926, 2928, 2930,
2932, 2934, 2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960,
2962, 2964 and/or 2966, 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-HKU1 mRNA or genomic RNA.

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 2919, or based on a
nucleotide sequence of SEQ ID NO:1, 2920, 2922, 2924, 2926, 2928, 2930, 2932, 2934,
2936, 2938, 2940, 2942, 2944, 2946, 2948, 2950, 2952, 2954, 2956, 2958, 2960, 2962, 2964
and/or 2966. In a non-limiting specific embodiment, preferred primers to be used in a RT-
PCR method are: 5'-GGTTGGGACTATCTAAGTGTA-3' (SEQ ID NO:4) and 5'-
CCATCATCAGATAGAATCATA-3' (SEQ ID NO:5), or 5'-AAAGGATGTTGAC-
AACCCTGT-3' (LPW1926; SEQ ID NO: 2968) and 5'-ATCATCATACTAAAATGCT-
TACA-3' (LPW1927; SEQ ID NO: 2969), 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, 5, 2968 and 2969,
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.

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(\text{ab}')_2) can be used.

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.

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.
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 DNA or mRNA encoding the polypeptide). Kits can also include instructions for use.

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.

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

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

METHODS AND RESULTS

6.1 Example 1

6.1.1 Clinical subject

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.

6.1.2 Antibody detection

To produce a fusion plasmid for protein purification, primers, 5'-TTTTCTTTTT
GCGGCCGCTTAAGCAACAGAGTCTTCTA-3' (SEQ ID NO:6) and 5'-CGGAATT
GATGTCTTATACTCCCGGT-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-28b(+) (Novagen, Madison, WI, USA) in frame and downstream of
the series of six histidine residues. The (His)_6-tagged (SEQ ID NO:27) recombinant N
protein was expressed in E. coli and purified using the Ni^{2+}-loaded HiTrap Chelating
System (Amersham Pharmacia, USA) according to the manufacturer’s instructions.

Western blot analysis was performed as follows: Two-hundred ng of purified (His)_6-
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 electroblotted
onto a nitrocellulose membrane (Bio-Rad, Hercules, CA, 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).

Several prominent immunoreactive bands were visible for serum samples collected
during the second and fourth weeks of the patient’s illness (Fig. 8, 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)_6-tagged (SEQ ID NO:27) N protein, whereas the other bands were
consistent with the degradation products of the (His)_6-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. 8, lane 1) and two healthy blood donors (Fig. 8, lanes 4 and 5).

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 ng of purified (His)$_6$-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)$_6$-tagged (SEQ ID NO:27) recombinant N protein-coated plates in a total volume of 100 µl per well and incubated at 37°C for 2 h. 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, CA, 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 H$_2$SO$_4$ 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.

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.

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 100 sera from healthy blood donors, the mean ELISA OD$_{450}$ 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, 1:2000, and 1:8000, respectively (Fig. 7), and those for IgM were 1:20, 1:40, and 1:80, respectively (data not shown).
6.1.3 RT-PCR and real time quantitative PCR

**RT-PCR Assay**

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’-GGTTGGGACTATCCTAAGTGTA-3’ (SEQ ID NO:4) and 5’-CCATCATCAGATAGAATCATA-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).

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

1. RNA extraction

RNA from 140 µl of NPA samples was extracted by QIAquick® viral RNA extraction kit and was eluted in 50 µl of elution buffer.

2. Reverse transcription

<table>
<thead>
<tr>
<th>RNA</th>
<th>11.5 µl</th>
</tr>
</thead>
<tbody>
<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>
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<tr>
<td>Random hexamers, 0.3 µg/µl</td>
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<td>Reaction condition</td>
<td>42°C, 50 min</td>
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<td></td>
<td>94°C, 3 min</td>
</tr>
<tr>
<td></td>
<td>4°C</td>
</tr>
</tbody>
</table>

3. PCR

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

| cDNA | 2 µl |
10 mM dNTP 0.5 µl
10x buffer 5 µl
25 mM MgCl₂ 5 µl
25 µM Forward primer 0.5 µl
25 µM Reverse primer 0.5 µl
AmpliTaq Gold® polymerase, 5U/µl (Applied Biosystems) 0.25 µl
Water 36.25 µl

Thermal-cycle condition: 95°C, 10 min, followed by 40 cycles of 95°C, 1 min;
50°C 1 min; 72°C, 1 min.

4. Primer sequences
Primer sequences were designed based on the RNA-dependent RNA polymerase encoding
sequence (SEQ ID NO:1) of the CoV-HKU1.

Forward primer: 5'-GGTTGGGACTATCCTAAAGTGTGA-3' (SEQ ID NO:4)
Reverse primer: and 5'-CCATCATCAGATAGAATCATCATA-3' (SEQ ID NO:5)
Product size: 440 bps

**Real-Time Quantitative PCR Assay**

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, IN) mixtures. Briefly, 20 µl reaction
mixtures containing 2µl of cDNA, 3.5 mmol/L MgCl₂, 0.25 µmol/L of forward primer [5'-
GGTTGGGACTATCCTAAAGTGTGA-3' (SEQ ID NO:4)] and 0.25 µmol/L reverse primer
[5'-CCATCATCAGATAGAATCATCATA-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).

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 $8.5 \times 10^5$ and $9.6 \times 10^6$ copies per ml in two nasopharyngeal aspirates collected in the first week of the illness, $1.5 \times 10^5$ 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. 7). 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**

The genome of CoV-HKU1 is a 29,926-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 comparison of genomic features of CoV-HKU1 and other coronaviruses and amino acid identities between the predicted chymotrypsin-like protease (3CL^pro^), RNA dependent RNA polymerase (Pol), helicase (Hel), hemagglutinin-esterase (HE), spike (S), envelope (E), membrane (M), and nucleocapsid (N) proteins of CoV-HKU1 and the corresponding proteins of other coronaviruses.
<table>
<thead>
<tr>
<th>Coronavirusesa</th>
<th>Genome features</th>
<th>Pairwise amino acid identity (%)</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>Size (bases)</td>
<td>G + C content</td>
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<tr>
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</tr>
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<tr>
<td>PTGV</td>
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<tr>
<td>CCoV</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>HCoV-NL63</td>
<td>27553</td>
<td>0.34</td>
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<tr>
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<tr>
<td>PHEV</td>
<td>-</td>
<td>-</td>
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<tr>
<td>SARS-CoV</td>
<td>29751</td>
<td>0.41</td>
</tr>
</tbody>
</table>

\(^a\)HCoV-229E, human coronavirus 229E; PEDV, porcine epidemic diarrhea virus; PTGV, porcine transmissible gastroenteritis virus; CCoV, canine enteric coronavirus; HCoV-NL63, human coronavirus NL63; HCoV-OC43, human coronavirus OC43; MHV, murine hepatitis virus; BCoV, bovine coronavirus; SDAV, rat sialodacryoadenitis coronavirus; ECoV, equine coronavirus NC99; PHEV, porcine hemagglutinating encephalomyelitis virus; IBV, infectious bronchitis virus; SARS-CoV, SARS coronavirus
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 2

<table>
<thead>
<tr>
<th>Number of base upstream of AUG</th>
<th>ORF</th>
<th>TRS sequence</th>
<th>SEQ ID NO.</th>
</tr>
</thead>
<tbody>
<tr>
<td>-140</td>
<td>Leader</td>
<td>UUAAAUCUAAACUUUAAA (127) AUG</td>
<td>8</td>
</tr>
<tr>
<td>-7</td>
<td>Hemagglutinin esterase</td>
<td>UUAAAUCUAAACUAUG</td>
<td>9</td>
</tr>
<tr>
<td>-6</td>
<td>Spike</td>
<td>UUAAAUCUAAACUAUG</td>
<td>10</td>
</tr>
<tr>
<td>-13</td>
<td>ORF 5</td>
<td>UUAAAUCUAAACUUUuUAUG</td>
<td>11</td>
</tr>
<tr>
<td>-9</td>
<td>Membrane</td>
<td>CUAAACUAAACUAUUG</td>
<td>12</td>
</tr>
<tr>
<td>-13</td>
<td>Nucleocapsid</td>
<td>UUAAAUCUAAACUAUUGGAUG</td>
<td>13</td>
</tr>
<tr>
<td>-35</td>
<td>ORF 9</td>
<td>UUAAAUCUAAACUUAGGAUGUCUUAU ACUCGCGGCUAAUG</td>
<td>14</td>
</tr>
</tbody>
</table>

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.

The coding potential of the CoV-HKU1 genome is shown in Fig. 4 and Table 3 and the phylogenetic analyses of the chymotrypsin-like protease (3CL(pro)), replicase, helicase, haemagglutinin-esterase (HE), S, E, M and N, are shown in Figures 5A and 5B.
Table 3

<table>
<thead>
<tr>
<th>ORFs</th>
<th>Start-end (base)</th>
<th>No. of bases</th>
<th>No. of amino acids</th>
<th>Frame</th>
<th>Candidate TRS</th>
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<tr>
<td>ORF 1a</td>
<td>206-13600</td>
<td>13395</td>
<td>4465</td>
<td>+2</td>
<td>-</td>
</tr>
<tr>
<td>ORF 1b</td>
<td>13600-21753</td>
<td>8154</td>
<td>2717</td>
<td>+1</td>
<td>-</td>
</tr>
<tr>
<td>HE (ORF 2)</td>
<td>21773-22933</td>
<td>1161</td>
<td>386</td>
<td>+2</td>
<td>Strong</td>
</tr>
<tr>
<td>S (ORF 3)</td>
<td>22942-27012</td>
<td>4071</td>
<td>1356</td>
<td>+1</td>
<td>Strong</td>
</tr>
<tr>
<td>ORF 4</td>
<td>26960-27070</td>
<td>111</td>
<td>36</td>
<td>+2</td>
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</tr>
<tr>
<td>ORF 5</td>
<td>27051-27380</td>
<td>330</td>
<td>109</td>
<td>+3</td>
<td>Strong</td>
</tr>
<tr>
<td>E (ORF 6)</td>
<td>27373-27621</td>
<td>249</td>
<td>82</td>
<td>+1</td>
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<tr>
<td>M (ORF 7)</td>
<td>27633-28304</td>
<td>672</td>
<td>223</td>
<td>+3</td>
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</tr>
<tr>
<td>N (ORF 8)</td>
<td>28320-29645</td>
<td>1326</td>
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<tr>
<td>ORF 9</td>
<td>28342-28959</td>
<td>618</td>
<td>205</td>
<td>+1</td>
<td>Strong</td>
</tr>
</tbody>
</table>

The replicase 1a ORF (bases 206-13600) and replicase 1b ORF (bases 13600-21753) 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. 4). 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 (UUUAATC) upstream of a pseudoknot structure at the junction of ORF 1a and ORF 1b. This ribosomal frameshift would result in a polyprotein of 7182 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. 5A). Table 4 shows amino acid identities between the predicted chymotrypsin-like protease (3CL^pro), replicase (Rep), helicase (Hel), hemagglutinin-esterase (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>3CL\textsuperscript{pro}</th>
<th>Rep</th>
<th>Hel</th>
<th>HE</th>
<th>S</th>
<th>E</th>
<th>M</th>
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<td>31</td>
<td>26</td>
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<tr>
<td></td>
<td>PEDV</td>
<td>44</td>
<td>56</td>
<td>55</td>
<td>-</td>
<td>30</td>
<td>34</td>
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<tr>
<td></td>
<td>PTGV</td>
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<td>57</td>
<td>57</td>
<td>-</td>
<td>32</td>
<td>34</td>
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</tr>
<tr>
<td></td>
<td>CCoV</td>
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<td>-</td>
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<td>-</td>
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<td>HCoV-NL63</td>
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<td>2</td>
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<tr>
<td></td>
<td>SARS-CoV</td>
<td>48</td>
<td>65</td>
<td>63</td>
<td>-</td>
<td>33</td>
<td>27</td>
<td>34</td>
<td>31</td>
</tr>
</tbody>
</table>

HCoV-229E=human coronavirus 229E; PEDV=porcine epidemic diarrhea virus; PTGV=porcine transmissible gastroenteritis virus; CCoV=canine enteric coronavirus; HCoV-NL63=human coronavirus NL63; HCoV-OC43=human coronavirus OC43; MHV=murine hepatitis virus; BCoV=bovine coronavirus; SDAV=rat sialodacryoadenitis coronavirus; ECoV=equine coronavirus NC99; PHEV=porcine hemagglutinating encephalomyelitis virus; IBV=infectious bronchitis virus; SARS-CoV=SARS coronavirus

The catalytic histidine and cysteine amino acid residues, conserved among the 3CL\textsuperscript{pro} in all coronaviruses, are present in the predicted 3CL\textsuperscript{pro} of CoV-HKU1 (amino acids His\textsuperscript{3375} and Cys\textsuperscript{3479} of ORF 1a). In the N-terminal of the putative PLP (amino acid residues 945 to 1104 of ORF 1a), there are 14 tandem copies of a 30-base repeat, which encode NDDEDVVTGD (SEQ ID NO:15), followed by two 30-base regions that encode NNDEBEIVTG (SEQ ID NO:16) and NDDQIVVTGD (SEQ ID NO:17), located upstream to the first copy of PLP domain, PLP1\textsuperscript{pro}. This repeat is not observed in other coronaviruses.

ORF 2 (bases 21773-22933) encodes the predicted HE glycoprotein with 386 amino acids. The HB protein of CoV-HKU1 has 50-57% amino acid identities with the HB proteins of other Group 2 coronaviruses (Table 4 and Fig. 5A). PFAM and InterProScan analyses of the ORF show that amino acid residues 1 to 349 of the predicted protein is a member of the haemagglutinin esterase family (PFAM accession no.: PF03996 and
INTERPRO accession no. IPR007142). This family contains membrane glycoproteins that are present on viral surface and are involved with the cell infection process. It contains haemagglutinin chain 1 (HE1) and haemagglutinin chain 2 (HE2), and forms a homotrimer with each monomer being formed by two chains linked by a disulphide bond. Furthermore, PFAM and InterProScan analyses of the ORF show that amino acid residues 122 to 236 of the predicted protein are the haemagglutinin domain of HB-fusion glycoprotein family (PFAM accession no.: PF02710 and INTERPRO accession no. IPR003860). HE is also present in other Group 2 coronaviruses and influenza C virus. SignalP analysis reveals a signal peptide probability of 0.738, with a cleavage site between residues 13 and 14.

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 puffedosis virus.

PrositeScan analysis of the HB protein of CoV-HKU1 reveals eight potential N-linked glycosylation (six NXS and two NXT) 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 neuraminidase O-acetyl-esterase activity, FGDS (SEQ ID NO:18), is located at positions 31-34.

ORF 3 (bases 22942-27012) encodes the predicted S glycoprotein (PFAM accession no. PF01601) with 1356 amino acids. The S protein of CoV-HKU1 has 58-61% amino acid identities with 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. 5B). InterProScan analysis predicts it as a type I membrane glycoprotein. Important features of the S protein of CoV-HKU1 are depicted in Fig. 6. 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 RRKRR (SEQ ID NO:19), between residues 760 and 761, where S will be cleaved into S1 and S2, is identified. Immediately upstream to RRKRR (SEQ ID NO:19), there is a series of five serine residues that are not present in any other known coronaviruses (Fig. 6). 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 carcinoembryonic antigen (CEA) family of glycoproteins in the immunoglobulin superfamily. Furthermore, it has been shown, by site-directed mutagenesis, that three conserved regions (sites I, II, and III) and some amino acid residues (Thr^{63}, Thr^{212}, Tyr^{214}, and Tyr^{216} 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. 6). 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-OC43, 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-OC43 that are important for receptor binding are not well defined.

ORF 4 (bases 26960-27070) 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.

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.

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. 5B). 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.

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. 5B). 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 68, 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.

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. 5B).

ORF 9 (bases 28342-28959) 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 I protein (Corona_I) 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.

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.

Genomic analysis has reveals 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 (Figures 4A and 4B).

In addition to phylogenetic analysis of the putative proteins, 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 1b
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 1b 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 30-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 structures. 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.

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.

6.2 Example 2

We prospectively collected nasopharyngeal aspirates (NPAs) from patients with community-acquired pneumonia during a 12-month period. A 453-bp fragment of the *pol* gene of CoV-HKU1 was amplified from the extracted RNA by RT-PCR using CoV-HKU1 specific primers. The epidemiological, clinical, laboratory and radiological features of patients with pneumonia associated with CoV-HKU1 were analyzed. Specific antibodies were detected using a recombinant CoV-HKU1 N protein based ELISA. The complete *pol*, *S* and *N* genes of the CoV-HKU1 were amplified and sequenced. RNA extracted from 208 nasopharyngeal swabs and fecal samples from 56 wild and domestic animals in Hong Kong and southern China were subject to RT-PCR of *pol* gene of CoV-HKU1 using CoV-HKU1 specific primers.

6.2.1 Patients and microbiological methods

All prospectively collected NPAs from patients with community-acquired pneumonia sent to the clinical microbiology laboratories of four regional hospitals in Hong Kong during a 12-month period [March 22 2003 (beginning of SARS epidemic in Hong Kong) -- March 21 2004] for detection of SARS-CoV but negative for SARS-CoV RNA by RT-PCR were included in the study. Community-acquired pneumonia is defined as symptoms and signs consistent with an acute lower respiratory tract infection associated with new radiographic shadowing for which there is no other explanation that develop prior to or within 48 h after presentation to hospital. Once CoV-HKU1 was detected from NPAs, the hospital records, laboratory results and chest radiographs of the corresponding patients were retrieved and examined by two infectious disease physicians. The RNA extracted from the NPAs was subject to RT-PCR for influenza A virus and human metapneumovirus (Peiris JSM *et al.*, *Lancet* 2003; 361: 1319-25). Available stored serum samples were
subject to serological assays for detection of antibodies against *Mycoplasma*, *Chlamydia*, *Legionella* and SARS-CoV by SERODIA-MYCO II (Fujirebio Inc., Tokyo, Japan), *Chlamydia pneumoniae* MIF IgG (Focus technologies, Cypress, CA, USA), indirect immunofluorescence (MRL, San Diego, CA, USA) and our recently developed enzyme-linked immunosorbent assay (ELISA), respectively (Woo PCY *et al.*, *Lancet* 2004; 363:841-5).

To determine the possible risk factors associated with CoV-HKU1 pneumonia, two age- and sex-matched controls per patient with CoV-HKU1 pneumonia were randomly selected from those with community-acquired pneumonia but their NPAs negative for CoV-HKU1. Controls were within five years older or younger than the corresponding patients with CoV-HKU1 pneumonia, and were admitted within 15 days before or after admission of the corresponding patients with CoV-HKU1 pneumonia. The hospital records, laboratory results and chest radiographs of the controls were retrieved and examined by the two infectious disease physicians.

### 6.2.2 RNA extraction

Viral RNA was extracted from NPAs using QIAamp Viral RNA Mini Kit (QIAGen, Hilden, Germany) according to the manufacturer's instructions within 10 h upon receipt of specimens. The eluted RNA was used as the template for RT-PCR. All extracted RNA was stored immediately at -70°C until use.

### 6.2.3 RT-PCR of RNA-dependent RNA polymerase gene of coronavirus-HKU1 using coronavirus-HKU1 specific primers and DNA sequencing

A 453-bp fragment of the RNA dependent RNA polymerase (*pol*) gene of CoV-HKU1 was amplified by RT-PCR using CoV-HKU1 specific primers, 5'-AAAGGATGTTTGACAAACCTGGT-3' (LPW1926; SEQ ID NO:2968) and 5'-ATCATCATACTAAAATGC-TTACA-3' (LPW1927; SEQ ID NO:2969) designed by multiple alignment of the nucleotide sequences of the *pol* genes of the two CoV-HKU1 (Woo, PC. *et al.*, *J. of Virol.*, 2005, p.884-895) and those of the available *pol* genes of other known human coronaviruses. RT was performed using the SuperScript II kit (Invitrogen, San Diego, CA, USA) according to manufacturer's instructions. The PCR mixture (50 μl)
contained cDNA, PCR buffer (10 mM Tris-HCl pH 8.3, 50 mM KCl, 3 mM MgCl₂ and 0.01% gelatin), 200 μM of each dNTPs and 1.0 U Taq polymerase (Boehringer Mannheim, Germany). The mixtures were amplified in 40 cycles of 94°C for 1 min, 48°C for 1 min and 72°C for 1 min, and a final extension at 72°C for 10 min in an automated thermal cycler (Perkin-Elmer Cetus, Gouda, The Netherlands). Distilled water was used as the negative control. To ensure the high specificity of the CoV-HKU1 specific primers, RNA extracted from 200 NPAs positive for influenza A and B viruses, parainfluenza viruses 1-3, respiratory syncytial virus (RSV), or adenovirus antigens and RNA of HCoV-229E, HCoV-OC43, HCoV-NL63 and SARS-CoV were also subject to RT-PCR using the two CoV-HKU1 specific primers.

Ten microlitres of each amplified product was electrophoresed in 1.5% (w/v) agarose gel, with a molecular size marker (ΦX-174 DNA HaeIII digest, Boehringer Mannheim, Germany) in parallel. Electrophoresis in Tris-borate-EDTA buffer was performed at 100 V for 1.5 h. The gel was stained with ethidium bromide (0.5 μg/ml) for 15 minutes, rinsed and photographed under ultraviolet light illumination.

The PCR products were gel-purified using the QIAquick gel extraction kit (QIAgen, Hilden, Germany). Both strands of the PCR products were sequenced twice with an ABI Prism 3700 DNA Analyzer according to manufacturers' instructions (Applied Biosystems, Foster City, CA, USA), using the two PCR primers. The sequences of the PCR products were compared with the sequences of the pol genes of the two CoV-HKU1 (Woo, PC. et al., *J. of Virol.*, 2005, p.884-895) and those of the pol genes of coronaviruses in the GenBank database.

### 6.2.4 ELISA using recombinant nucleocapsid protein of CoV-HKU1

The ELISA-based IgG and IgM antibody tests were performed according to our published protocol (Woo, PC. et al., *J. of Virol.*, 2005, p.884-895). Briefly, each well of a Nunc immunoplate (Roskilde, Denmark) was coated with purified (His)₅-tagged recombinant N protein (20 ng for IgG and 80 ng for IgM) for 1 h and then blocked in phosphate-buffered saline with 5% skim milk. The serum samples obtained from the patients during the acute and convalescent phase of the illness were serially diluted and were added to the wells of the (His)₅-tagged (SEQ ID NO: 27) recombinant N protein-coated plates in a total volume of 100 μl and incubated at 37°C for 2 h. After washing with
washing buffer five times, 100 µl of diluted horse radish peroxidase-conjugated goat anti-
human IgG (1:4000) and mouse anti-human IgM (1:1000) antibodies (Zymed Laboratories
Inc., South San Francisco, CA, USA) were added to the wells and incubated at 37°C for 1 h.
After washing with washing buffer five times, 100 µl diluted 3,3',5,5'-tetramethylbenzidine
(Zymed Laboratories Inc.) were added to each well and incubated at room temperature for
15 min. One hundred microlitres 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.

6.2.5 RT-PCR and sequencing of the complete RNA-dependent RNA polymerase,
spike and nucleocapsid genes of coronavirus-HKU1 and phylogenetic analysis

The complete pol, spike (S) and N genes of CoV-HKU1 from NPAs of nine of the
10 patients, with adequate amount of RNA available, were amplified and sequenced using
the RNA extracted from the NPAs as template. The RNA was converted to cDNA by a
combined random-priming and oligo(dT) priming strategy. The cDNA was amplified by
degenerate primers designed by multiple alignment of the regions encoding the pol, S and N
genes in the genomes of the two CoV-HKU1 (Woo, PC. et al., J. of Virol., 2005, p.884-895)
and those of other group 2 coronaviruses and additional primers designed from the results of
the first and subsequent rounds of sequencing. Sequences were assembled and manually
edited to produce the complete sequences of the pol, S and N genes of CoV-HKU1 from
different patients. The nucleotide and the deduced amino acid sequences of the pol, S and
N genes were compared to those of the two CoV-HKU1 (Woo, PC. et al., J. of Virol., 2005,
p.884-895) and other group 2 coronaviruses. Phylogenetic tree construction was performed
using PileUp method with GrowTree (Genetics Computer Group, Inc.).

6.2.6 Animal surveillance

Two hundred and eight nasopharyngeal swabs and faecal samples from 56 wild and
domestic animals [including Chinese ferret-badger (Melogale moschata), domestic cat
(Felis catus), hog-badger (Arctonyx collaris), masked palm civet (Paguma larvata), raccoon
dog (Nyctereutes procyonoides), Chinese pygmy dormouse (Typhlomys cinereus), common
pangolin (Manis pentadactyla), nutria (Myocastor coypus), dog (Canis familiaris), rabbit
(Leporidae family), snake (Serpentes suborder) and bat (Microchiroptera suborder)] in Hong Kong and southern China (Guan Y, et al., Science 2003; 302: 276-8) were subjected to RNA extraction and RT-PCR of pol gene of CoV-HKU1 using the CoV-HKU1 specific primers (LPW1926; SEQ ID NO:2968 and LPW1927; SEQ ID NO:2969) and protocol described above.

6.2.7 Results

Clinical and laboratory characteristics

During the 12-month period, NPAs from 418 patients [male:female = 198:220, age (mean ± SD) = 49 ± 26] with community-acquired pneumonia, for detection of SARS-CoV but were negative for SARS-CoV RNA by RT-PCR, were identified in the four hospitals. A 453-bp fragment of the pol gene of CoV-HKU1 was amplified and sequenced in 10 (2.5%) patients. Sequence analysis revealed 0-2% nucleotide differences between the sequences of the fragments and the sequence of the pol gene of the CoV-HKU1 from the reported index patient (patient no. 5) described in Example 1 above (Fig. 11) (Woo, PC. et al., J. of Virol., 2005, p.884-895). In contrast, using our CoV-HKU1 specific primers, none of the 200 NPAs that were positive for influenza A and B viruses, parainfluenza viruses 1-3, RSV, or adenovirus antigens and RNA of HCoV-229E, HCoV-OC43, HCoV-NL63 and SARS-CoV, was RT-PCR positive.

The epidemiological, clinical and radiological characteristics of the 10 patients, including patient no. 5 (Woo, PC. et al., J. of Virol., 2005, p.884-895), with community-acquired pneumonia associated with CoV-HKU1 are summarized in Table 5. No epidemiological linkage was identified among the 10 cases. All cases occurred in either winter or spring (January – May). The median age was 71.5 (range: 13-96). Seven were males and three were females. Nine were Chinese and one was an Arabian. Eight had underlying diseases, and four had underlying diseases of the respiratory tract. Four had recent travel histories to southern China. Five were smokers. Clinically, the illness was not distinguishable from other community-acquired pneumonia. Fever, productive cough and dyspnoea were common presenting symptoms. Upper respiratory tract symptoms were present in only two patients (patient nos. 1 and 5). One patient (patient no. 7) had loose stool diarrhea. Oxygen saturation on room air upon admission was <95% in two. Airspace shadows were observed in the right lungs of six patients and the left lungs of six patients.
The upper, middle and lower zones were affected in two, four and nine patients respectively. All patients, except patient no. 10, had normal platelet counts and normal liver and renal function tests. Bacterial or mycobacterial pathogens were not detected in any of the sputum samples from the patients. Direct antigen detection for influenza A and B viruses, parainfluenza viruses 1-3, RSV, adenovirus (Woo PCY et al., J Clin Microbiol 1997; 35: 1579-81) and RT-PCR for influenza A virus and metapneumovirus, was negative in all NPAs. Antibodies against M. pneumoniae, C. pneumoniae, C. psittaci, L. pneumophila and SARS-CoV were negative in all the six patients (patient nos. 1, 4, 5, 6, 8 and 9) whose serum samples were available. All these six patients showed a four-fold change in IgG titer (patient nos. 4, 5 and 6) and/or the presence of IgM (patient nos. 1, 5, 8 and 9) against CoV-HKU1.
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<td>Survived</td>
<td>Survived</td>
<td>Survived</td>
<td>Survived</td>
<td>Survived</td>
<td>Survived</td>
<td>Died</td>
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<td>5</td>
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</table>

*present; --absent; RLZ=right upper zone; LUZ=left upper zone; RMZ=right middle zone; LMZ=left middle zone; RLZ=right lower zone; LLZ=left lower zone
In comparison with age- and sex-matched controls with non-CoV-HKU1 pneumonia, no epidemiological, clinical, haematological, serum biochemical and radiological risk factors were identified in patients with CoV-HKU1 pneumonia (Table 6).

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<td>Cough</td>
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<tr>
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<td>1</td>
</tr>
<tr>
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</table>

*Continuous variables are expressed as median and categorical variables as no. of patients with the presence of the characteristics.
Two of the 10 patients died of CoV-HKU1 pneumonia. The first patient (patient no. 2) was a 66-year-old man who presented with dyspnoea for one day. He had type 2 diabetes mellitus, old myocardial infarction and gastric lymphoma with total gastrectomy in 2002 and was put on chemotherapy. He had severe lymphopenia (0.2×10^9/L) and an oxygen saturation of only 83% on admission. Chest radiograph revealed patchy airspace shadows in both lungs with predominant involvement of the lower zones (Fig. 12A). He died 11 days after admission. The other patient (patient no. 10) was a 72-year-old man who presented with fever and productive cough for one week. He had type 2 diabetes mellitus, cerebrovascular accident and prostatic carcinoma with bone metastasis complicated by spinal cord compression with laminectomy and Luque instrumentation performed. He had lymphopenia (0.9×10^9/L), thrombocytopenia (33×10^9/L), deranged liver and renal function tests and an oxygen saturation of only 88% on admission. Chest radiograph revealed extensive airspace shadows in both lungs, with the middle zones more severely involved (Fig. 12B). He died 5 days after admission.

The clinical, laboratory and radiological characteristics of patients who survived and those who died with community acquired pneumonia associated with CoV-HKU1 were compared (Table 7). Patients who died had lower hemoglobin concentration (P=0.04), monocyte count (P=0.04), serum albumin (P=0.04) and oxygen saturation on admission (P=0.03) and bilateral involvement (P=0.003) and more number of zones involved (P=0.01) on chest radiograph.
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*Continuous variables are expressed as median and categorical variables as no. of patients with the presence of the characteristics.
RT-PCR and sequencing of the complete RNA-dependent RNA polymerase, spike and nucleocapsid genes of coronavirus-HKU1 and phylogenetic analysis

The complete pol (Fig. 11), S (Fig. 13) and N (Fig. 14) genes of CoV-HKU1 from NPAs of nine of the 10 patients, with adequate amount of RNA available, were amplified and sequenced. The phylogenetic trees and non-synonymous mutations and the corresponding amino acid changes are shown in Fig. 15. In all three genes, the phylogenetic trees using nucleotides or amino acids for construction showed the same topologies. For the S gene, there were 317 and 306 nucleotide positions with synonymous and non-synonymous mutations respectively (Fig. 15B). For the N gene, there were 42 and 53 nucleotide positions with synonymous and non-synonymous mutations respectively (Fig. 15C). The nucleotide sequences of seven of the nine S or N genes showed similar sequences (genotype A, Figs. 16B and 16C) and those of the other two also showed similar sequences (genotype B, Figs. 16B and 16C). For the CoV-HKU1 from patient 1, two peaks (T and C) were consistently observed at nucleotide position 1300 of the N gene, suggesting the presence of quasi-species (Fig. 15C). For the pol gene, there were 95 and 13 nucleotide positions with synonymous and non-synonymous mutations respectively (Fig. 15A). The nucleotide sequences of the pol genes in the seven CoV-HKU1 of genotype A were also clustered together (Fig. 15A). Interestingly, the seven CoV-HKU1 of genotype A were from seven patients with underlying diseases and the two of genotype B were from the two patients without underlying diseases (Table 5). Furthermore, multiple alignments of the nucleotides sequences of the pol genes of the nine CoV-HKU1 and those of HCoV-OC43, HCoV-229E, HCoV-NL63 and SARS-CoV revealed that the primers we used in the present study should be specific for CoV-HKU1 (Fig. 16).

Animal surveillance

None of the 208 nasopharyngeal swabs and faecal samples from 56 wild and domestic animals in Hong Kong and southern China was positive for CoV-HKU1 RNA.

6.2.8 Discussion

CoV-HKU1, a novel group 2 coronavirus, is associated with community-acquired pneumonia. Since the SARS epidemic in 2003, we have started to prospectively collect NPAs and store the extracted RNA from patients with community-acquired pneumonia so
that when a novel virus is discovered, the epidemiology and hence the clinical, laboratory and radiological features of the disease can be studied timely. In January 2004, we discovered a novel coronavirus, CoV-HKU1, from a patient with community-acquired pneumonia (Woo, PC. et al., J. of Virol., 2005, p.884-895). The RNA extracted from prospectively collected NPAs were immediately retrieved and the presence of CoV-HKU1 RNA looked for. Ten of the 418 NPAs were positive for RNA of CoV-HKU1, giving an incidence of 2.5%. The presence of CoV-HKU1 RNA in these specimens was genuine, instead of due to contamination, as amplification and sequencing of multiple genes (pol, S and N) of CoV-HKU1 indicated the presence of CoV-HKU1 with different nucleotide sequences in the NPAs from the different patients. Moreover, the clinical significance of CoV-HKU1 was further confirmed by the presence of specific antibody responses in all six patients whose serum samples were available.

Similar to HCoV-229E, HCoV-OC43 and HCoV-NL63, CoV-HKU1 is probably a human coronavirus that is endemic in human. Similar to other human coronavirus infections, cases of CoV-HKU1 pneumonia also occurred in winter and spring. Most patients with CoV-HKU1 pneumonia were old (80% older than 65) with major underlying diseases, especially those of the respiratory and cardiovascular systems. In order to study the phylogeny and relationships among the 10 CoV-HKU1, we sequenced the pol, S and N genes of the nine CoV-HKU1 cases which provided adequate amount of RNA. Combined with the data of partial sequencing of the pol genes of the 10 CoV-HKU1 (Fig. 17), results showed that unlike the epidemiology of SARS-CoV, the 10 CoV-HKU1 were not clonal and the topology of the phylogenetic trees did not follow the pattern of a clonal outbreak (Fig. 15). Interestingly, the phylogenetic tress constructed using the sequences of both the S and N genes showed that CoV-HKU1 of genotype B was associated with the two patients without underlying diseases, but CoV-HKU1 of genotype A was associated with patients with underlying diseases (Table 5; and Figs. 16B and 16C). Sequencing of more CoV-HKU1 may reveal the presence of genotypes or clades of CoV-HKU1 with differential virulence. To investigate for the possibility of an animal reservoir of CoV-HKU1, we tried to look for the presence of CoV-HKU1 RNA from wild and domestic animals in Hong Kong and southern China by RT-PCR. Our results revealed that none of the specimens showed the presence of CoV-HKU1 RNA. With the results of these clinical epidemiology, molecular epidemiology and eco-epidemiology studies, we conclude that CoV-HKU1 is
probably a human coronavirus, and propose to rename CoV-HKU1 as human coronavirus HKU1 (HCoV-HKU1).

Compared with SARS-CoV pneumonia, HCoV-HKU1 pneumonia is a monophasic disease and most patients had relatively mild symptoms that were localized to the respiratory tract and were only briefly hospitalized. SARS-CoV pneumonia is often described as a biphasic disease, with the first phase due to cell lysis as a result of active viral replication, and the second phase may be due to immunopathological damage (Peiris JSM et al., *Lancet* 2003; 361: 1319-25; Peiris JSM et al., *Lancet* 2003; 361: 1767-72). On the other hand, all 10 patients with HCoV-HKU1 pneumonia showed the pattern of a monophasic disease. Although dyspnoea was present in half of the patients with HCoV-HKU1 pneumonia at initial presentation, as compared to only about 20% of patients with SARS-CoV pneumonia at initial presentation (Peiris JSM et al., *Lancet* 2003; 361: 1319-25), patients with HCoV-HKU1 pneumonia often recovered quickly, but patients with SARS-CoV pneumonia deteriorated after 7-10 days (Peiris JSM et al., *Lancet* 2003; 361: 1319-25; Peiris JSM et al., *Lancet* 2003; 361: 1767-72). For the eight patients who recovered, the median duration of hospitalization was only 5.5 days. This rapid recovery of patients with HCoV-HKU1 pneumonia could be related to the rapid control of the virus by the immune system. This is in line with our previous study showing the index patient (patient 5) with HCoV-HKU1 pneumonia had his peak viral load at around day 3 after onset of illness (Woo, PC. et al., *J. of Virol.*, 2005, p.884-895). Moreover, only one of the patients had extrapulmonary symptoms and all available extrapulmonary specimens (stool, urine and serum) were RT-PCR negative for CoV-HKU1 (unpublished data). On the other hand, for SARS-CoV pneumonia, patients usually had their peak viral loads 7-10 days after the onset of illness (Peiris JSM et al., *Lancet* 2003; 361: 1767-72). Furthermore, the virus can be readily detected in extrapulmonary specimens, in which the viral loads correlated with the manifestations in the corresponding systems (Hung, IFN et al., *Emerg Infect Dis* 2004; 10: 1550-1557). These imply that the virus was not well controlled by the immune system in the initial phase of the illness.

Despite the relatively mild disease in most patients, HCoV-HKU1 pneumonia is associated with mortality in a minority of patients who had lower haemoglobin concentration, monocyte count, serum albumin and oxygen saturation on admission and more extensive involvement on chest radiograph. As in most cases of pneumonia, more
extensive involvement in the lungs will result in poor gaseous exchange and hence hypoxia and eventually fatality. The lower haemoglobin concentration, monocyte count and serum albumin could represent poorer premorbid states and narrower margins to fight against infections. Both patients who died had underlying diabetes mellitus, malignancy (gastric lymphoma in one and carcinoma of the prostate in the other) and cardiovascular disease (old myocardial infarct in one and cerebrovascular accident in the other).
7. MARKET POTENTIAL

The two genomic types of CoV-HKU1 are completely sequenced. These sequences allow the development of various diagnostic tests and therapeutic methods as described hereinabove. In addition, the genetic information of CoV-HKU1 is extremely important and valuable for clinical and scientific research applications.

8. EQUIVALENTS

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.

All publications, patents and patent applications mentioned in this specification are herein incorporated by reference into the specification.

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

WHAT IS CLAIMED:

1. An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1 or a complement thereof.

2. An isolated nucleic acid molecule comprising a nucleotide sequence having at least 5, 10, 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.

3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO:2 or a complement of said nucleotide sequence.

4. An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:3 or a complement thereof.

5. An isolated nucleic acid molecule comprising the nucleotide sequence having 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, or 29,000 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:3, or a complement thereof.

6. An isolated nucleic acid molecule which hybridizes under stringent conditions to a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:1, 3, or a complement thereof, wherein the nucleic acid molecule encodes an amino acid sequence which has a biological activity exhibited by a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1 or 3.

7. The nucleic acid molecule of any one of claims 1-6, wherein the molecule is RNA.

8. The nucleic acid molecule of any one of claims 1-6, wherein the molecule is DNA.

9. A vector comprising the nucleic acid molecule of claim 8.
10. A host cell comprising the vector of claim 9

11. A host cell comprising the nucleic acid molecule of claim 8 operably linked to a heterologous promoter.

12. The host cell of claim 11 being a prokaryotic cell.

13. The host cell of claim 11 is an eukaryotic cell.

14. The host cell of claim 13 is a mammalian cell.

15. A method for producing a polypeptide comprising expressing the polypeptide encoded by the DNA from the host cell of claim 10, and recovering the polypeptide.

16. A method for producing a polypeptide comprising expressing the polypeptide encoded by the DNA from the host cell of claim 11, and recovering the polypeptide.

17. A method for preparing a cell or progeny thereof capable of expressing a polypeptide comprising transflecting the cell with the vector of claim 9.

18. An isolated polypeptide encoded by the nucleic acid molecule of any one of claims 1-6.

19. An isolated polypeptide comprising the amino acid sequence having at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110 and 120 contiguous amino acid residues of the amino acid sequence of SEQ ID NO:2.

20. An isolated polypeptide comprising the amino acid sequence having any one of the amino acid sequence of SEQ ID NOS:34-2918.

21. An isolated antibody or an antigen-binding fragment thereof which immunospecifically binds to the polypeptide of claim 18.

22. An isolated antibody or an antigen-binding fragment thereof which immunospecifically binds to the polypeptide of claim 19 or 20.

23. A method for detecting the presence of the polypeptide of claim 18 in a biological sample, said method comprising:
(a) contacting the biological sample with a compound that selectively binds to said polypeptide; and

(b) detecting whether the compound binds to said polypeptide in the sample.

24. The method of claim 23, wherein the biological sample is selected from the group consisting of cells, blood, serum, plasma, saliva, urine, stool, sputum, and nasopharyngeal aspirates.

25. The method of claim 23, wherein the compound that binds to said polypeptide is an antibody or an antigen-binding fragment thereof.

26. A method for detecting the presence of the polypeptide of claim 19 or 20 in a biological sample, said method comprising:

(a) contacting the biological sample with a compound that selectively binds to said polypeptide; and

(b) detecting whether the compound binds to said polypeptide in the sample.

27. The method of claim 26, wherein the biological sample is selected from the group consisting of cells, blood, serum, plasma, saliva, urine, stool, sputum, and nasopharyngeal aspirates.

28. The method of claim 26, wherein the compound that binds to said polypeptide is an antibody or an antigen-binding fragment thereof.

29. 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.
30. The method of claim 29, 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.

31. The method of claim 29, wherein the compound that binds to said first nucleic acid molecule is a second nucleic acid molecule comprising at least 5, 10, 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.

32. 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.

33. The method of claim 32, 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.

34. The method of claim 32, wherein the compound that binds to said first nucleic acid molecule is a second nucleic acid molecule comprising at least 5, 10, 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.

35. The method of claim 32, wherein the compound that binds to said first nucleic acid molecule is a second nucleic acid molecule comprising 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 or 29,000 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:3, or a complement thereof.
36. A method of preventing or inhibiting a replication in a host cell of a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1 and/or 3, or a portion thereof, or a complement thereof, comprising administering to the host cell an effective amount of a compound that selectively binds to said first nucleic acid molecule under a physiological condition.

37. The method of claim 36, 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.

38. The method of claim 36, wherein the compound that binds to said first nucleic acid molecule is a second nucleic acid molecule comprising at least 5, 10, 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.

39. The method of claim 36, wherein the compound that binds to said first nucleic acid molecule is a second nucleic acid molecule comprising 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 or 29,000 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:3, or a complement thereof.

40. A method of preventing or inhibiting a binding to a host cell of the polypeptide encoded by a nucleotide sequence of SEQ ID NO:1 or 3, or a fragment thereof, or a complement thereof, comprising administering to the host cell an effective amount of a compound that specifically binds to the polypeptide under a physiological condition.

41. The method of claim 40, wherein the compound that specifically binds to the polypeptide is an antibody or an antigen-binding fragment thereof which immunospecifically binds to the polypeptide.

42. A method for detecting the presence of an antibody in a biological sample that immunospecifically binds the polypeptides of claim 18, said method comprising:

(a) contacting the biological sample with the polypeptide of claim 18; and
(b) detecting the antibody bound to the polypeptide.

43. A method for detecting the presence of an antibody in a biological sample that immunospecifically binds the polypeptides of claim 19 or 20, said method comprising:

(a) contacting the biological sample with the polypeptide of claim 19; and

(b) detecting the antibody bound to the polypeptide.

44. 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.

45. The method of claim 44, wherein the set of primers have the nucleotide sequence of SEQ ID NOS:4 and 5, respectively.

46. The method of claim 44, wherein the set of primers have the nucleotide sequence of SEQ ID NOS:6 and 7, respectively.

47. An immunogenic formulation comprising an immunogenically effective amount of the polypeptide of claim 18, and a pharmaceutically acceptable carrier.

48. An immunogenic formulation comprising an immunogenically effective amount of the polypeptide of claim 19 or 20, and a pharmaceutically acceptable carrier.

49. An immunogenic formulation comprising an immunogenically effective amount of a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, a complement thereof or a fragment thereof, and a pharmaceutically acceptable carrier.

50. An immunogenic formulation comprising an immunogenically effective amount of a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:3, a complement thereof or a fragment thereof, and a pharmaceutically acceptable carrier.
51. An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2919, a complement thereof, or a fragment thereof.

52. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes a replicase gene of CoV-HKU1.

53. The nucleic acid molecule of claim 2 comprising the nucleotide sequence of SEQ ID NO:2920, 2922, 2924, 2926, 2928, 2930, 2932 or 2934.

54. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes a spike gene of CoV-HKU1.

55. The nucleic acid molecule of claim 4 comprising the nucleotide sequence of SEQ ID NO:2936, 2938, 2940, 2942, 2944, 2946, 2948 or 2950.

56. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes a nucleocapsid gene of CoV-HKU1.

57. The nucleic acid molecule of claim 6 comprising the nucleotide sequence of SEQ ID NO:2952, 2954, 2956, 2958, 2960, 2962, 2964 or 2966.

58. An isolated nucleic acid molecule which hybridizes under stringent conditions to the nucleic acid molecule of claim 1, wherein the nucleic acid molecule encodes an amino acid sequence which has a biological activity exhibited by a polypeptide encoded by the nucleic acid molecule of claim 51.

59. A vector comprising the nucleic acid molecule of claim 51.

60. A vector comprising the nucleic acid molecule of claim 52.

61. A vector comprising the nucleic acid molecule of claim 54.

62. A vector comprising the nucleic acid molecule of claim 56.

63. A host cell comprising the vector of claim 59.

64. A host cell comprising the vector of claim 60.
65. A host cell comprising the vector of claim 61.

66. A host cell comprising the vector of claim 62.

67. An isolated polypeptide encoded by the nucleic acid molecule of claim 51.

68. An isolated polypeptide encoded by the nucleic acid molecule of claim 52.

69. An isolated polypeptide encoded by the nucleic acid molecule of claim 54.

70. An isolated polypeptide encoded by the nucleic acid molecule of claim 56.

71. A nucleic acid molecule encoding the polypeptide of claim 67.

72. A nucleic acid molecule encoding the polypeptide of claim 68.

73. A nucleic acid molecule encoding the polypeptide of claim 69.

74. A nucleic acid molecule encoding the polypeptide of claim 70.
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ATGGAAACAAAAATACATTTTTGAAAAATCGACAAAAATTCGCCAGAAAATCTCGAACAGAT
YRTKHLNNLQKYPLN*LN*K
TGQCIYII*NHNILFTKSTSK
VKN*TF*KTT*LSEPQLFKV*

ACAGACCCAGAGTAAAAACAGAGGAGCACTTTAAAATGATAACAAAATCTCATAAAAT
HRARMQEQQQSN*KHKHLIK
IDPE*IKNRSHIKSINIYFK
TQSEYKTGTAFKV*T*STN*

ACCAAGAAATAAAAAACACAAAAACAGATAAAAATATGATACGTATTCATTTATAGTAT
HNYKIKHKS*K*L*AYY*DHC
ITTN*TNKSNKYSHMNTNIM
FQIKHTKAIKIVICLIL*SM

AAAAAGAATACACAAAAACGCATTTATATATATAATAGATAACACCTAAACCC
KKKSTPKQYFL*KLK*TTNQ
WKQHMKQNTSYNS*NHRHPK
KEKINKTFLITYKIEIHYKF

CACTTAATCTCTCTCTCAACAAAAAAATAAATATGTGACAAAAATCGTCGATGATATAC
TSNLLFPHKTIA*LRKLYKYM
PRI*FLINO*KNCGK*TSIC
DFKSSSTTKNIVAKKPV*VH

CTGTTGAAAACGACATATGTTGTATGTTTAAAACAGAAATATTACACACAAAGAATATA
SS*KTMHL*LLLQQ*NNTQQY
PGSNO*SYCFNNNSIFQRNIV
VVIKDNAILAITALQNDTL

AAAAATAAAAAGATCATGAAATATATATTTAATGAGACTATGAGACTGAGAAATATATAC
IKNLHVKY*ISERSNSI*L
YKIKCICYRINQHQT*KY
N*KYSTG*ILNIRKL*KNIP

CAATAAAAAGAGAGACTACCCCTAAAAGAGAGAGGCTTGTGAAAATCTTTGGS
TYKIKNNPFIKREKLCHK*FA
PIN*RTIPSKRK*VTNKS
YIKDQ*QNKRKFILTGL

ATCCCAACAAATATATTATTTAAAGAGAGATCTCTTTACGAAATATATCTTAC
*PHKNYFYFRQELIANYSKH
RHTNIIFIFNRLFQ*TIHIST
IFT*L*LIE*T*SNR*IPALF

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1081 TTGTTGTAATTAAATATGTTGCGAACCCTACAAGAGATGATGAGTATGAGCTGATAGTTAT 1140
   L W Y * I C T T Y R R C S R W S C S Y
   C G I K Y V VA Q P T E D V D G A V I
   V V L N M L H N L Q K M * * M E L * L Y

1141 AGCTGAACCTGTAACATATTTATTTATCTGTCAGTGCATAGTTTTTTAAAGCTGCTACATTTGAT 1200
   T * T C T F I I C * C N S F K A S * F D
   R E P V H L L S A D D A I V L K L P L S L M
   V N L Y I Y Y Y L L M Q * F * S F L V * *

1201 GAAAGTTATATGACTCAATAGGAGATATTTTTATTAAATAGTATTACTATACATAGTTGTATGTTG 1260
   E S Y D S Y G * F F Y * I Y I Q C * F V
   K V M T H M D D F S I K S I Y N V D L C
   K L * L I W M I F L L N L Y T M L I C V

1261 TGATGTGTGTTTTGTATATGCAGATGTATGATGATTGTTTTTTAATGTATATTGTTGTATT 1320
   * L W F C Y A V W L C R L F * * * L F
   D C G F V M Q Y G Y V D C F N D N C D F
   I V V L L C S M V M * I V L M I I V I F

1321 TTATGATTGCTTCAGTTAATATGATGAGTATGTTTTTTATCTGCTTTACGT 1380
   L W L G F R * Y D G W F F F L S I V L Y S
   Y G W V S G N M M D G F S C P L C C T V
   M V G F Q V I * W M V F L V H C V V Q F

1381 TTATGACCTAGTTGAAGTTAAGCCCAATCATTCTGTGTATTATTCTGTATCCGATAACTGTTGT 1440
   L * L * * S * S P I W C Y S * E S C V
   Y D S S E V K A Q S S G V I P E N P V L
   M T L V K L K P N H L V L F L R I L C Y

1441 ATTATCTAATATCATCTGTATACCTGTTAATTTTTATGATTTGTTATTCTGT 1500
   I Y * * Y * Y C * F * F F * F V W L F C
   F T N S T D T V N P D S F N L Y G Y S V
   L L I V L I L L I L L I C M V I L L

1501 TACACCATTGGTTCTGTATATATATTGTCACCGGGTCTCTGGATTTGGATATCTATCAT 1560
   Y T I W F L Y I L V T A S W I V D S Y H
   T P F G S C I Y W S P R P G L W I P I I
   H H L V L V L Y I G H R V L D C G F L S L

1561 TAAACTTCTACATGTAAGTTATATGATTTTGTATATCTGTAATGGATTAGTTGTTAAAATC 1620
   * I F S Q V L * * F G L F R C S R L * I
   K S S V K S Y D D L V Y S G V V G C K S
   N L Q S S L M I W F I Q V * * V V N L

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13501 TTTTTRRAACGGGTTTGGGTTACTGCTGGTAATGGCCCTCTAGATCCCTCGTGGCTG 13560
F EK R Y R G T S V N A R L V F P C A S G
F L N G F G V L V * M P V * Y P V L V V
F * T G S G Y * C E C P S S T L C * W F

13561 TTAATCTACTGATGTTCAATTTAGGGCATTTTGGTATATTTGTAATCTAATAGAGCTCGTTATA 13620
L S T D V Q L R A F D I C N T N R A G I
Y L L M F N * G H L I F V I L E I L V *
I Y * C S I K G I * Y L * Y * S W Y R

13621 GGTATTATATTTATATATAGGATTTTTGCCGTTTTTCAGCCTATAGATGAGCAGGGTATAAATAAA 13680
G L Y Y K V N C C R F Q R I D D D G N K
V Y I I K * I V A V F S V * M T T V I N
F I L * S E L L P F S A Y R * R R * * I

13681 TTGGATATAGTTCTTTTGTTATTTAAGAACTATATCTCTGAGATTATTTATATTTATAAAGAGAAACT 13740
L D K F F V V K R T N L E V Y N K E K T
W I S S L L L K E L I * K F I I K R K L
G * V L C C * K N * S R S L * * R E N L

13741 TATATTAGGTGTGGACTTTTTTTGAATTTTGCTGGTGCTGGCTGTGTGTGGCTGAACATGATTTCTATTTATGAT 13800
Y Y E L T K S C G V V A E H D F F T F D
I M S * L K V V V L W L N M I S L H L I L
L * V D * K L W C C G * T * F L Y I * Y

13801 ATTTGATGGTGTGACTGTTTTTTTGAATTTTGCTGGTGCTGGCTGTGTGTGGCTGAACATGATTTCTATTTATGAT 13860
I D G S R V P H I V R K N L S K Y T M L
L M V V V C H I * F V R T S Q S I L C *
* W * S C A T Y S S * E P L K V V Y Y V R

13861 GATCTTTGCTATGCAATGCGCCATTATTGTTATATTGTATGTGCTATGATTTGTGTGAATT 13920
D L C Y A L R H F D C N D C S V L C E I
I F A M H C A I L I V M I V Q Y C V K F
S L L C I A P F * L * * L F S I V * N S

13921 CTTTGAGATATGCTGATTTTGGTAAAGAAATCTCTTTTCTATGAAAGGATTTGGTAATGTT 13980
L C E Y A D C K E S Y F S K K D W Y D F
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13981 GTGGAAAAATCTCGATATATTATATTATATTTATAAAAATATTAGGCCTTTTTTTATAGAGCCT 14040
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FIG. 9 CONT.
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FIG. 9 CONT.
FIG. 9 CONT.
FIG. 9 CONT.
154/201

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18841 AACATGATATATAATTGTGATATGCATAAAGGTGGATGCGTGCATACTGTGTCAGATT
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**FIG. 9 CONT.**
FIG. 9 CONT.
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FIG. 9 CONT.
FIG. 9 CONT.
175/201

29701 TTAGAGTGTTATATTAGTTTACCTAGTTATTAAAAGACCCCTCCGCCGGAAGCTACCAATTAT 29760
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 * S S Y K V * L * Y K R L R E E L A I I  
 R V V I R F S C S I N A S G K S * Q L *  

29761 AGTATTTTTATATATATATTATTATATGATGAAATAATATATAGCCTTTGGAGGAATTA 29820
 S I * Y I Y * Y M I E I N Y S L L E E L  
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 Y L I Y I L V Y D * N * L * P F G G I T  

29821 CAAAAAAA AAAAA 29836
 Q K K K K X
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FIG. 9 CONT.
**FIG. 11 CONT.**
FIG. 11 CONT.
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** FIG. 11 CONT. **
**FIG. 13 CONT.**
FIG. 13 CONT.
FIG. 13 CONT.
FIG. 13 CONT.
FIG. 13 CONT.
FIG. 13 CONT.
FIG. 13 CONT.
FIG. 13 CONT.
FIG. 14 CONT.
198/201

Patient 5  CCAAGACAGTGTGACTCTCTTATTTTTGACCACTCAACGATTTCAGATTTTTT  1260
Patient 1  CCTGATCGGCTTGACTCTCTTATTTTTGACCACTCAACGATTTCAGATTTTTT  1260
Patient 8  CCTGATCGGCTTGACTCTCTTATTTTTGACCACTCAACGATTTCAGATTTTTT  1260

** ***  *****************************************  *****************************************  *******************************************

Patient 4  ACCTCTGAGGATCATAGTTTAACCTGTACATCGCAGATCTCTTTATTTTTGACCACTCAACGATTTCAGATTTTTT  1320
Patient 6  ACTCTGAGGATCATAGTTTAACCTGTACATCGCAGATCTCTTTATTTTTGACCACTCAACGATTTCAGATTTTTT  1320
Patient 7  ACCTCTGAGGATCATAGTTTAACCTGTACATCGCAGATCTCTTTATTTTTGACCACTCAACGATTTCAGATTTTTT  1320
Patient 9  ACCTCTGAGGATCATAGTTTAACCTGTACATCGCAGATCTCTTTATTTTTGACCACTCAACGATTTCAGATTTTTT  1320
Patient 10 ACCTCTGAGGATCATAGTTTAACCTGTACATCGCAGATCTCTTTATTTTTGACCACTCAACGATTTCAGATTTTTT  1320
Patient 2  ACCTCTGAGGATCATAGTTTAACCTGTACATCGCAGATCTCTTTATTTTTGACCACTCAACGATTTCAGATTTTTT  1320
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Patient 1  ACCTCTGAGGATCATAGTTTAACCTGTACATCGCAGATCTCTTTATTTTTGACCACTCAACGATTTCAGATTTTTT  1320
Patient 8  ACCTCTGAGGATCATAGTTTAACCTGTACATCGCAGATCTCTTTATTTTTGACCACTCAACGATTTCAGATTTTTT  1320

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Patient 4  GCTTAA  1326
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FIG. 14 CONT.
FIG. 15
FIG. 16
INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER

IPC  C12N 15/50  C12N 15/63  C12N 7/00  C07K14/165  A61K3/215  A61P11/00  G01N33/53  C12Q1/68
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC  C12N , C07K , A61K, A61P, G01N, C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic database consulted during the international search (name of database and, where practical, search terms used)

Database: EPDOC, WPI, CNPAT,CNKL,CA,BA; Search Terms: human, coronavirus, hcoV, genomic sequence

C. DOCUMENTS CONSIDERED TO BE RELEVANT

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☐ Further documents are listed in the continuation of Box C. ☒ See patent family annex.

* Special categories of cited documents:
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  "&" document member of the same patent family

Date of the actual completion of the international search

Date of mailing of the international search report
27.OCT 2005 (27.10.2005)

Name and mailing address of the ISA/CN
The State Intellectual Property Office, the P.R. China
6 Xitucheng Rd., Jinsen Bridge, Haidian District, Beijing, China 100088
Facsimile No. 86-10-62019451

Authorized officer
Wang Qi Yang

Telephone No. (86-10)62055988

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CN1450173A                             | 22.OCT 2003(22.10.2003) | NONE

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