

The evolution of Genetic Molecular Map and phylogenetic tree of Coronavirus (COVID-19): Review Article

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ABSTRACT

Coronavirus (COVID-19) is suspected to originate from an animal host (zoonotic) followed by a human to human transmission. The purpose of the present study is to determine the genetic affinity of a phylogenetic tree and conformation of protein between human and bat. Through study of genetic sequencing, as shown in the tree design of strains and genetic variants, the main cause of COVID-19 is the Bat Coronavirus RaTG13 (SARS) virus in ID: MN996532.1 and ID: MG772933.1 (24-Jul-2013 and Feb-2017) shows that the evolution of the Corona virus from 2003, 2013 to 2020 which has become the most deadly peak in humans, the virus evolved from the bat effect on Humans. Protein analysis show 98 change of amino acid form RaTG13 (SARS) virus to COVID-19 Homo sapiens. Consequently, this study increased our understanding of the genetic variety of the COVID-19 carried by bats. So we conclude that a protein conformation drawing shows high identity compatibility between a bat and a human.

Keywords: SARS; COVID-19; molecular evolution; *Rhinolophus affinis*.

Introduction

The first cases of SARS were identified in 2002 in China (Guangdong Province). While in 2003 an epidemic has spread across the world that affected more than three thousand people ensuing in more than a hundred deaths (1). SARS-CoV is an element of the Corona viridae family of enveloped positive-Stranded RNA viruses which have a great host range. Some corona virus infect the humans, Domestic birds and ruminant might cause respiratory illness, whereas the other corona virus infected in rodents, feline, sow, and bovine lead to enteric disease. The 27–32 kb genomes of corona viruses are the largest of RNA viruses encode 23 putative proteins, including four major structural proteins with N:nucleocapsid, S:spike, M: membrane and small E:envelope.

The spike protein of the glycoprotein projection on the viral surface is critical for viral attachment and entry into the host cells. In addition, variations of S protein among strains of corona virus are responsible for host range sensitivity and tissue tropism activity (2). An ongoing outbreak of pneumonia related with a novel corona virus that called a severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) in the persons was report in china-Wuhan, Hubei province, China in December-2019 (3). In the following weeks, the infections spread all countries around the world (4-5).

On February 2020, world health organization named the disease caused by the new corona virus as COVID-19 (6). Corona virus is an envelope and single-stranded ribonucleic acid named for its solar corona like appearance due to 9-12 nm-long surface spikes (7). There are four structural proteins encoded important to envelop the corona viruses genome, one of which is the S protein that binds to angiotensin-converting enzyme2 receptor and mediates later merger between the envelope and host plasma membranes to help viral in gress into the host cell (8). The aim of the present study was to determine the genetic affinity of a phylogenetic tree and conformation of protein between human and bat.

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Materials and Methods

In this study data were collected from a date March\2003 to Feb\2020 were genome sequences have been submitted to GenBank. For all sequences, the accession numbers are listed in Supplementary Table (1;2;3). The sequence data have been deposited into the NCBI sequence reads archive below the accession number. Using BLAST-NCBI, Routine sequence alignments were performed (9). MEGA6.0 (Phoenix, AZ, USA) was used to align the nucleotide (nt) and amino acid (aa) sequences using phylogenetic analyses.

Results and Discussion

Phylogenetic tree structuring

The phylogenetic tree diagrammatic was done by molecular evolutionary genetics analysis (MEGA) software version 6.0. Sequences (10).

Construction of the Neighbor-joining tree showed that the identity (80% - 100%), through comparison between isolated *Rhinolophus sinicus* and *Homo sapiens*. hierarchical cluster analysis determine the following clusters: large Clusters divided into several root: first root the SARS coronavirus *Rhinolophus sinicus* in *Homo sapiens* from 2003-2016 in China, Hong Kong, Singapore, USA, Canada, Italy and Taiwan showed compatibility and the highest identity at >99%. Second root COVID-19 in *Homo sapiens* from 2019-2020 in China, Taiwan, USA, Australia, Japan, South Korea, Finland and Nepal showed compatibility and the highest identity at >99%. Third root SARS coronavirus in *Rhinolophus affinis* (2013; 2017 in China ID: MN996532.1, MG772933.1) showed compatibility with COVID-19 in humans and the highest identity at >97% (Figure 1)

In this study, the investigation of the patterns of molecular divergence between SARS-CoV-2 and other related COVID-19. Although the genomic analyses recommended that SARS-CoV-2 was closest to RaTG13, the virus was evolved from the bat might have an effect on the humans (11). It may be that the virus is transmitted to humans from mice through an experiment that conducted the cultivation of SARS virus in mice which led to the development of the virus due to the relationship between mice and humans (12). structural, protein (M: membrane, N:nucleocapsid, S:spike and E:envelop and several non-structural)

Because of interacting and eating rats in China, this leads to transmission to humans and development (13).

The sequencing of amplified product of Amino acid polymorphism of Coronavirus

The result of the sequence analysis was analyzed by blast in the National Center Biotechnology Information (NCBI) online and BioEdit program (14) to detect polymorphism after alignment of product amplification in Corona virus, showed that 98 change of amino acid form RaTG13 (SARS) virus *Rhinolophus affinis* to COVID-19 *Homo sapiens* (Table 4 and Figure 2). The analysis of molecular development and population genetics show some protein changes that might be favored by natural selection during the evolution of SARS-CoV-2 and other related viruses. or f1ab, which encodes replicate/ transcriptase is required for viral genome replication and might also be significant for viral pathogenesis (15). COVID-19 is spherical or polymorphous laminated particles that contain the associated mono-stranded RNA (positive sensation) with a nuclear protein inside a capsule consisting of a matrix protein. The envelope contains club-shaped glycoprotein expectations. Some corona viruses also have hem Agglutinin-esterase protein (HE) (16, 17) (Figure 3).

The result showed the similarity of the conformation of protein for COVID-19 shown in figure 4, between the Bat Coronavirus and human corona virus. Identification of other COV in bat species (*R. sinicus*, *R. ferrumequinum*) (18,19).

Human and animal relations may pose an exacting public health threat in rural communities where frequent contact with animals occurs and where infection prevention measures are less developed (20). Bats (order Chiroptera) are reservoir of a great number of zoonotic viruses, including COVID-19 that have caused disease outbreak in human and livestock populations (21–22), Severe Acute Respiratory Syndrome COVID-19, are the causative agent of the SARS outbreak affecting world countries (23, 24).

Mechanism of action for COVID-19

The genome of coronavirus is comprised of three thousands nucleotides. It encodes four proteins of (Figure 3) (25, 26). **Conformation of protein for COVID-19** The COVID-19 replicate gene-

encoded two poly proteins, poly protein 1a with MW 450 KD and poly protein 1ab with MW 750 KD, these poly proteins are required for viral replication and transcription (27, 28). Several

crystal structure of COVID-19 (Figure 4) in complex with different inhibitor are deposited in the protein by using X-ray diffraction technique at a resolution between a human and a bat (29, 30).

Table 1. Neighbor-joining tree of Coronavirus from animals

Accession	host	isolation source	collection date	Country	Compatibility
ID: AY304488.1 ID: AY304486.1	Animals\ Himalayan palm civets	nasal turbinate	MAY-2003	Hong Kong	14871/18249(81%)
ID: JQ316196.1	Animals\rat	Vero cells	Apr-2003	United Kingdom	14866/18249(81%)
ID: JX163928.1 ID: JX163924.1	Animals\ ferrets	nasal turbinate	Feb-2010	USA	14866/18249(81%)

Table 2. Neighbor-joining tree of Coronavirus from bats

Accession	host	isolation source	collection date	Country	Compatibility
ID: KY417146.1	<i>Rhinolophus sinicus</i>	fecal swab	Apr-2013	China	14879/18255(82%)
ID: MN996532.1	<i>Rhinolophus affinis</i>	fecal swab	Jul-2013	China	20546/21290(97%)
ID: KJ473816.1	<i>Rhinolophus sinicus</i>	fecal swab	2013	China	14872/18254(81%)
ID: MG772934.1	<i>Rhinolophus sinicus</i>	fecal swab	Jul-2015	China	16148/18231(89%)
ID: MK211376.1	<i>Rhinolophus affinis</i>	fecal swab	Sep-2016	China	14875/18254(81%)
ID: MG772933.1	<i>Rhinolophus sinicus</i>	fecal swab	Feb-2017	China	18972/21300(89%)

Table 3. Neighbor-joining tree of Coronavirus from human

Accession	host	isolation source	collection date	Country	Compatibility
ID: AY427439.1	Homo sapiens	sputum	March 2003	Italy	14867/18249(81%)
ID: AY278554.2	Homo sapiens	sputum	APR-2003	China: Hong Kong	14869/18249(81%)
ID: AY283796.1	Homo sapiens	sputum	APR-2003	Singapore	14867/18249(81%)
ID: AY274119.3	Homo sapiens	sputum	APR-2003	Canada: Toronto	14867/18249(81%)
ID: AY291451.1	Homo sapiens	sputum	MAY-2003	Taiwan	14867/18249(81%)
ID: AY502928.1					
ID: AY502923.1					
ID: AY323977.2	Homo sapiens	sputum	JUL-2003	Italy	14867/18249(81%)
ID: AY390556.1	Homo sapiens	sputum	SEP-2003	China: Guangzhou	14870/18249(81%)
ID: AY395003.1	Homo sapiens	sputum	SEP-2003	China	14873/18249(82%)
ID: AY394996.1					
ID: AY559083.1	Homo sapiens	sputum	2003	Singapore	14868/18249(81%)
ID: AY559096.1	Homo sapiens	sputum	FEB-2004	Singapore	14867/18249(81%)
ID: AY559095.1					
ID: AY559086.1					
ID: AY559085.1					
ID: AY714217.1	Homo sapiens	sputum	AUG-2004	USA	14867/18249(81%)
ID: FJ882963.1	Homo sapiens	sputum	Aug-2004	USA	14867/18249(81%)
ID: DQ898174.1	Homo sapiens	sputum	AUG-2006	Canada	14867/18249(81%)

ID: <u>JX163927.1</u>	Homo sapiens	nasal turbinate	Feb-2010	USA	14867/18249(81%)
ID: <u>JX163926.1</u>					
ID: <u>JX163923.1</u>					
ID: <u>JX163925.1</u>	Homo sapiens	lung	Feb-2010	USA	14866/18249(81%)
ID: <u>JX163928.1</u>	Homo sapiens	lung	Feb-2010	USA	14866/18249(81%)
ID: <u>JX163924.1</u>					
ID: <u>MT019529.1</u>	Homo sapiens	bronchoalveolar lavage fluid	Dec-2019	China: Hubei, Wuhan	21287/21290(99%)
ID: <u>MT019532.1</u>	Homo sapiens	bronchoalveolar lavage fluid	Dec-2019	China: Hubei, Wuhan	21290/21290(100%)
ID: <u>MT019530.1</u>	Homo sapiens	bronchoalveolar lavage fluid	Dec-2019	China: Hubei, Wuhan	21290/21290(100%)
ID: <u>MN996530.1</u>	Homo sapiens	bronchoalveolar lavage fluid	Dec-2019	China: Wuhan	21290/21290(100%)
ID: <u>MN996528.1</u>	Homo sapiens	bronchoalveolar lavage fluid	Dec-2019	China: Wuhan	21290/21290(100%)
ID: <u>NC_045512.2</u>	Homo sapiens	bronchoalveolar lavage fluid	Dec-2019	China	21290/21290(100%)
ID: <u>MT019531.1</u>	Homo sapiens	bronchoalveolar lavage fluid	Dec-2019	China: Hubei, Wuhan	21289/21290(99%)
ID: <u>MN996527.1</u>	Homo sapiens	sputum	Dec-2019	China: Wuhan	21289/21290(99%)
ID: <u>MN996531.1</u>	Homo sapiens	sputum	Dec-2019	China: Wuhan	21289/21290(99%)
ID: <u>MN996529.1</u>					
ID: <u>LR757996.1</u>	Homo sapiens	sputum	2019/2020	Wuhan	21290/21290(100%)
ID: <u>LR757995.1</u>	Homo sapiens	sputum	2019/2020	Wuhan	21288/21290(99%)
ID: <u>LC522975.1</u>	Homo sapiens	sputum	2020-01	Japan	21288/21290(99%)
ID: <u>LC522974.1</u>	Homo sapiens	sputum	2020-01	Japan	21288/21290(99%)
ID: <u>LC522972.1</u>	Homo sapiens	sputum	2020-01	Japan	21288/21290(99%)
ID: <u>LC522973.1</u>					
ID: <u>MT039873.1</u>	Homo sapiens	sputum	Jan-2020	China: Hangzhou	21290/21290(100%)
ID: <u>MT019533.1</u>	Homo sapiens	sputum	Jan-2020	China: Hubei, Wuhan	21289/21290(99%)
ID: <u>MN988668.1</u>	Homo sapiens	sputum	Jan-2020	China	21290/21290(100%)
ID: <u>MT027064.1</u>	Homo sapiens	sputum	Jan-2020	USA: CA	21289/21290(99%)
ID: <u>MT066175.1</u>	Homo sapiens	sputum	Jan-2020	Taiwan	21289/21290(99%)
ID: <u>MT007544.1</u>	Homo sapiens	sputum	Jan-2020	Australia: Victoria	21289/21290(99%)
ID: <u>MN994468.1</u>	Homo sapiens	nasopharyngeal swab	Jan-2020	USA: CA	21289/21290(99%)
ID: <u>MN938384.1</u>	Homo sapiens	nasopharyngeal swab	Jan-2020	China: Shenzhen	21289/21290(99%)
ID: <u>MN988713.1</u>	Homo sapiens	sputum	Jan-2020	USA: Illinois	21287/21290(99%)
ID: <u>MT027062.1</u>	Homo sapiens	nasopharyngeal swab	Jan-2020	USA: CA	21288/21290(99%)
ID: <u>MN997409.1</u>	Homo sapiens	buccal swab	Jan-2020	USA: AZ	21288/21290(99%)
ID: <u>MN994467.1</u>	Homo sapiens	nasopharyngeal swab	Jan-2020	USA: CA	21288/21290(99%)
ID: <u>MN985325.1</u>	Homo sapiens	oropharyngeal swab	Jan-2020	USA	21288/21290(99%)
ID: <u>MT039888.1</u>					
ID: <u>MT039887.1</u>					
ID: <u>MT044257.1</u>	Homo sapiens	sputum	Jan-2020	USA: IL	21287/21290(99%)
ID: <u>MN975262.1</u>	Homo sapiens	sputum	Jan-2020	China	21287/21290(99%)

ID: MT039890.1	Homo sapiens	oropharyngeal swab	Jan-2020	South Korea	21285/21290(99%)
ID: MT044258.1	Homo sapiens	oropharyngeal swab	Jan-2020	USA: CA	21266/21290(99%)
ID: LC521925.1	Homo sapiens	oropharyngeal swab	Jan-2020	Japan	21264/21290(99%)
ID: MT020781.1	Homo sapiens	oropharyngeal swab	Jan-2020	Finland	21257/21290(99%)
ID: MT049951.1	Homo sapiens	sputum	Jan-2020	China: Yunnan	21288/21290(99%)
ID: MT093631.1	Homo sapiens	throat swab	Jan-2020	China	21290/21290(100%)
ID: MT072688.1	Homo sapiens	oropharyngeal swab	Jan-2020	Nepal	21290/21290(100%)
ID: MT066176.1	Homo sapiens	oropharyngeal swab	Feb-2020	Taiwan	21288/21290(99%)
ID: MT106053.1	Homo sapiens	nasopharyngeal swab	Feb-2020	USA: CA	21290/21290(100%)

Table 3. Represent type of Amino acid polymorphism of Coronavirus isolate between Rhinolophus affinis and Homo sapiens (the Predicted effect is Missense).

NO.	Amino acid change between <i>Rhinolophus affinis</i> \ <i>Homo sapiens</i> ID: MN996532.1 with COVID-19	Location	NO.	Amino acid change <i>Rhinolophus affinis</i> \ <i>Homo sapiens</i> ID: MN996532.1 with COVID-19	Location
1.	Alanine\ Valine	38	50.	Threonine\ Alanine	1313
2.	Aspartic acid+Asparagine\ Glutamic acid	93	51.	Arginine\ Lysine	1342
3.	Tyrosine \ Histidine	110	52.	Methionine\ Valine	1392
4.	Threonine\ Isoleucine	114	53.	Isoleucine\ Threonine	1541
5.	Valine\ Alanine	117	54.	Isoleucine\ Threonine	1557
6.	Aspartic acid \ Glutamic acid	172	55.	Lysine\ Arginine	1562
7.	Threonine\ Isoleucine	280	56.	Alanine\ Valine	1628
8.	Proline\ Serine	376	57.	Asparagine\ Serine	1732
9.	Proline\ Threonine	395	58.	Glutamine\ Lysine	1794
10.	Tyrosine \Histidine	417	59.	Isoleucine\ Valine	1865
11.	Isoleucine\ Valine	424	60.	Isoleucine\ Threonine	1873
12.	Threonine\ Alanine	498	61.	Isoleucine\ Threonine	1880
13.	Alanine\ Valine	561	62.	Leucine\ Phenylalanine	1936
14.	Valine\ Alanine	591	63.	Phenylalanine \ Leucine	1954
15.	Glutamine\ Lysine	623	64.	Asparagine\ Serine	2014
16.	Proline\ Serine	723	65.	Threonine\ Alanine	2032
17.	Lysine\ Arginine	724	66.	Isoleucine\ Valine	2060
18.	Threonine\ Alanine	859	67.	Aspartic acid \ Asparagine	2081
19.	Isoleucine\ Threonine	891	68.	Glycine \ Serine	2082
20.	Glycine \ Serine	901	69.	Valine\ Alanine	2122
21.	Aspartic acid \ Glutamic acid	940	70.	Phenylalanine \ Serine	2223
22.	Proline\ Serine	944	71.	Threonine\ Lysine	2224
23.	Serine\ Proline	959	72.	Threonine\ Isoleucine	2258
24.	Valine\ Alanine	967	73.	Isoleucine \Threonine	2260

25.	Threonine \ Alanine	968	74.	Glycine \ Serine	2288
26.	Proline\ Leucine	969	75.	Threonine\ Asparagine	2404
27.	Leucine\ Glutamine	975	76.	Serine\ Asparagine	2529
28.	Valine\ Glycine	989	77.	Threonine\ Isoleucine	2583
29.	Glutamic acid\ Glutamine	991	78.	Valine\ Alanine	3142
30.	Aspartic acid \ Glycine	993	79.	Valine\ Isoleucine	3144
31.	Valine\ Aspartic acid	996	80.	Threonine\ Asparagine	3442
32.	Isoleucine\ Threonine	1001	81.	Valine\ Leucine	3605
33.	Threonine\ Isoleucine	1002	82.	Arginine\ Lysine	4534
34.	Serine\ Threonine	1004	83.	Aspartic acid \ Asparagine	4589
35.	Alanine\ Valine	1006	84.	Isoleucine\ Valine	4624
36.	Proline\ Leucine	1016	85.	Histidine\ Tyrosine	5110
37.	Isoleucine\ Valine	1055	86.	Threonine\ Alanine	5828
38.	Histidine\ Aspartic acid	1088	87.	Valine\ Alanine	6004
39.	Glycine \ Serine	1101	88.	Alanine\ Valine	6025
40.	Asparagine\ Histidine	1112	89.	Lysine\ Arginine	6137
41.	Arginine\ Lysine	1123	90.	Arginine\ Leucine	6183
42.	Aspartic acid \ Glutamic acid	1141	91.	Asparagine\ Threonine	6565
43.	Threonine\ Isoleucine	1202	92.	Asparagine\ Aspartic acid	6580
44.	Serine\ Proline	1212	93.	Leucine\ Valine	6623
45.	Serine\ Phenylalanine	1213	94.	Asparagine\ Aspartic acid	6634
46.	Leucine\ Proline	1219	95.	Lysine\ Glutamine	6652
47.	Glutamine\ Lysine	1225	96.	Arginine\ Serine	6694
48.	Valine\ Aspartic acid	1227	97.	Serine\ Phenylalanine	6709
49.	Asparagine\ Serine	1271	98.	Leucine \ Phenylalanine	6714

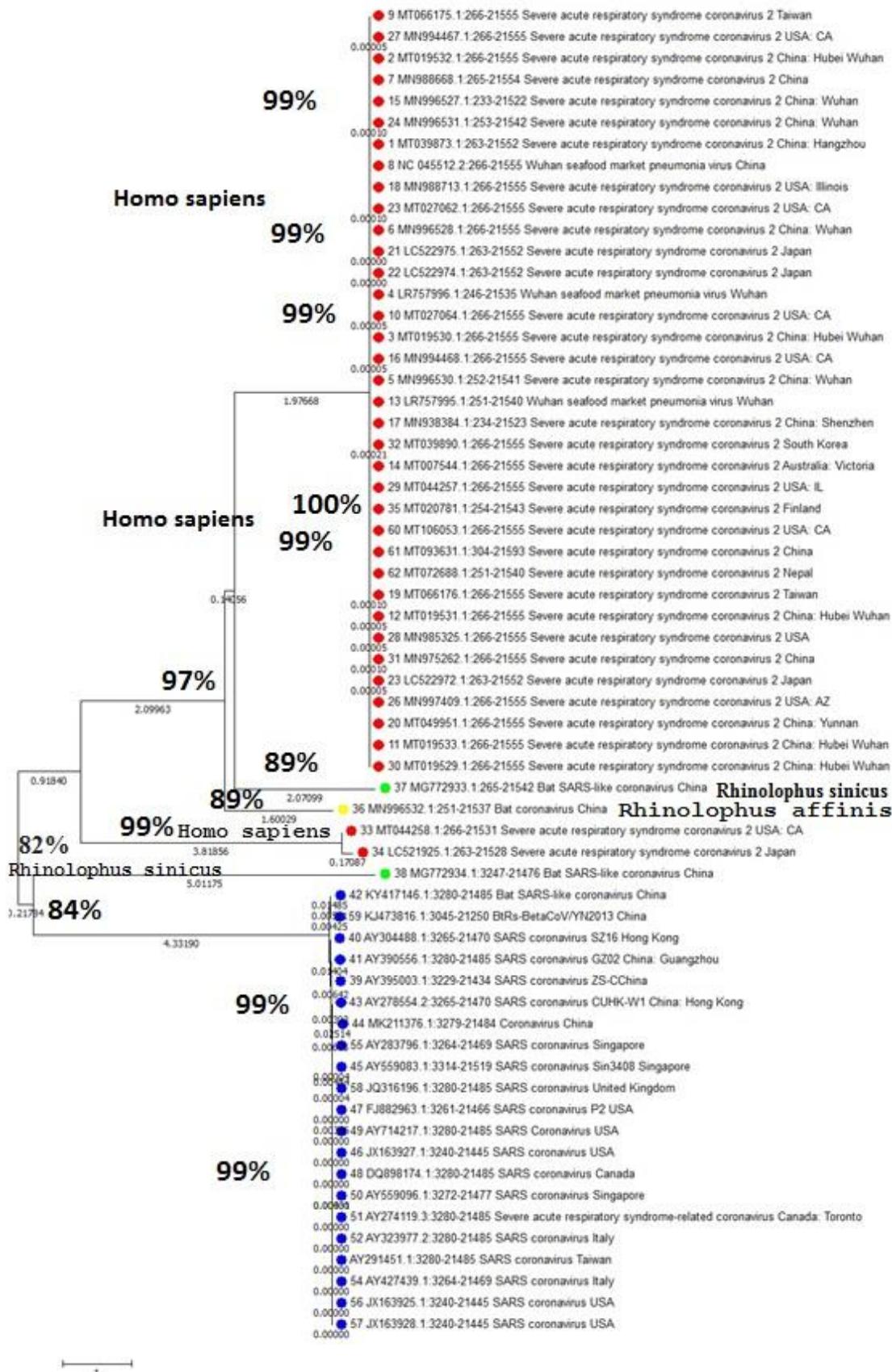


Figure 1. Neighbor-joining tree of Coronavirus

Query	1	MESLVPGFNEKTHVQLSLPVQVRDVLVRGFGDSVEEVLSARQHLDGTGLVEVKGVLQLEQPYVFIKRSARTAPHGVMVELVAELEGIQYGRSGETLGVLPVGEIPVAY
YP_009725295_1	1	
QIA20043_1	1	
OHU79172_1	1	
OHRE63289_1	1	
QIE07480_1	1	
OHU79171_1	1	
OH787591_1	1	
Homosapiens		
2020		
HR63299_1		
Rhinolophus affinis		
2013		
AVP78030_1		
ATD16715_1		
AT098204_1		
ALK02469_1		
AT098131_1		
AT098119_1		
AT098180_1		
AT098107_1		
AGC74171_1		
AAR23244_1		
AAR87533_1		
ARO76381_1		
APP51226_1		
ACZ72223_1		
Query	361	VLLRKNGKAGGHSYGAIDLKSFDLGLDELTGDPYDFQENWNTKHSSGVTRLEMRELNGGAYTRYVDNNFCGPDPGYPLECIKDLARAGKASCLTSEQLDFIDTKRGVYCCEHEHEI
YP_009725295_1	121	
QIA20043_1	121	
OHU79172_1	121	
OHRE63289_1	121	
QIE07480_1	121	
OHU79171_1	121	
OH787591_1	116	
Homosapiens		
2020		
HR63299_1		
Rhinolophus affinis		
2013		
AVP78030_1		
ATD16715_1		
AT098204_1		
ALK02469_1		
AT098131_1		
AT098119_1		
AT098180_1		
AT098107_1		
AGC74171_1		
AAR23244_1		
AAR87533_1		
ARO76381_1		
APP51226_1		
ACZ72223_1		
Query	721	YTERSEKSYELOTPFEIKLAKKFDTFNGECPNFVFLNSIIKKTIPRVEKKLDGFMSGTRCSVVPASPIECHQICLSTLHKCDHGETSWQTGDFVKATCEFCGTENLTKEGATTG
YP_009725295_1	241	
QIA20043_1	241	
OHU79172_1	241	
OHRE63289_1	241	
QIE07480_1	241	
CO-19	241	
OHU79171_1	241	
OH787591_1	233	
HR63299_1		
Rhinolophus affinis		
2013		
AVP78030_1		
ATD16715_1		
AT098204_1		
ALK02469_1		
AT098131_1		
AT098119_1		
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AT098107_1		
AGC74171_1		
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AAR87533_1		
ARO76381_1		
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ACZ72223_1		
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OHU79172_1	361	
OHRE63289_1	361	
QIE07480_1	361	
OHU79171_1	361	
OH787591_1	353	
HR63299_1		
Rhinolophus affinis		
2013		
AVP78030_1		
ATD16715_1		
AT098204_1		
ALK02469_1		
AT098131_1		
AT098119_1		
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APP51226_1		
ACZ72223_1		
Query	1441	SASTSAFVETVKGLDYKAFQIQVESCGNFKVTKGAKKGAWNIGEQKSILSPPLYAFASEAARVRSIFSRTLEAQNSVRVLQKAATILDGISQYSRLIDAMMFTSDLATINLVM
YP_009725295_1	481	
QIA20043_1	481	
OHU79172_1	481	
OHRE63289_1	481	
QIE07480_1	481	
OHU79171_1	481	
OH787591_1	473	
HR63299_1		
Rhinolophus affinis		
2013		
AVP78030_1		
ATD16715_1		
AT098204_1		
ALK02469_1		
AT098131_1		
AT098119_1		
AT098180_1		
AT098107_1		
AGC74171_1		
AAR23244_1		
AAR87533_1		
ARO76381_1		
APP51226_1		
ACZ72223_1		

Query YP_009725295_1	1801	ITGGVQQLTSQWLTNIFGTVYKEKPVLDWLEEKFKEGVEFLRGWEIVKFISTCAEIVGGQIVTCAKEIKEVESQTFKLVNLFLACDADSIIIGGAKLKALNLLGETFVTHSKGLYR
OIA20043_1	601	.
OHU79172_1	601	.
OHRE63289_1	601	.
OIE07480_1	601	.
OHU79171_1	601	.
OHZ87591_1	593	.
HR63299_1	601	Q.
AVP78030_1	601	M.
AID16715_1	601	LSPAGEINV
AT098204_1	601	V...L..OI...S..L..TV...R..IFA..I..A..LSA...K..A..L..L..GVPD..K..QVASDN..DC..KC..IDV...A..EM..I..QVT..A...RS...V..IAQ..
ALK02469_1	601	V...L..OI...S..L..TV...R..IFA..I..A..LSA...K..A..L..L..GVPD..K..QVASDN..DC..KC..IDV...A..EM..I..QVT..A...RS...V..IAQ..
AT098131_1	601	V...L..OI...S..L..TV...R..IFA..I..A..LSA...K..A..L..L..GVPD..K..QVASDN..DC..KC..IDV...A..EM..I..QVT..A...RS...V..IAQ..
AT098119_1	601	V...L..OI...S..L..TV...R..IFA..I..A..LSA...K..A..L..L..GVPD..K..QVASDN..DC..KC..IDV...A..EM..I..QVT..A...RS...V..IAQ..
AT098180_1	601	V...L..OI...S..L..TV...R..IFA..I..A..LSA...K..A..L..L..GVPD..K..QVASDN..DC..KC..IDV...A..EM..I..QVT..A...RS...V..IAQ..
AT098107_1	601	V...L..OI...S..L..TV...R..IFA..I..A..LSA...K..A..L..L..GVPD..K..QVASDN..DC..KC..IDV...A..EM..I..QVT..A..V..RS...V..IAQ..
AGC74171_1	601	V...L..OV...S..LV..SAV...R..FA..V..SRSD...K..A..L..L..LIRGMFD..R..QVTSNDN..C..KS..IDVI...A..EM..I..YVT..A..T..RS...V..IAQ..
AAR23244_1	601	V...L..OV...S..LV..SAV...R..FA..V..SRSD...K..A..L..L..LIRGMFD..R..QVTSNDN..C..KS..IDVI...A..EM..I..YVT..A..T..RS...V..IAQ..
AAR87533_1	601	V...L..OV...S..LV..SAV...R..FA..V..SRSD...K..A..L..L..LIRGMFD..R..QVTSNDN..C..KS..IDVI...A..EM..I..YVT..A..T..RS...V..IAQ..
AR076381_1	601	V...L..OV...S..LV..SAV...R..FA..V..SRSD...K..A..L..L..LIRGMFD..R..QVTSNDN..C..KS..IDVI...A..EM..I..YVT..A..T..RS...V..IAQ..
AAP51226_1	601	V...L..Q...S..L..TV...R..IFA..I..A..LSA...K..A..L..L..GVPD..K..QVASDN..DC..KC..IDV...A..EM..I..QVT..A...RS...V..IAQ..
ACZ72223_1	601	V...L..Q...S..L..TV...R..IFA..I..A..LSA...K..A..L..L..GVPD..K..QVASDN..DC..KC..IDV...A..EM..I..QVT..A...RS...V..IAQ..
Query YP_009725295_1	2881	EFGATSAALXXXXXXXXXXXXXXTVGQDGSEDNXXXXXXXXXEVQQLEMELTPVQTEVENSFGYKLTDNVYTKNADIVEEAKVKPTVVVIAANIVYLHGGVAGALNKA
OIA20043_1	961	.
OHU79172_1	961	.
OHRE63289_1	961	.
OIE07480_1	961	.
OHU79171_1	961	.
OHZ87591_1	953	.
HR63299_1	961	VTP...L...V.E.D..V...IT.S.A...P...I...
AVP78030_1	966	FSSSSQ..EQ.EDWLES---DS.Q.TAVEENKIPS..P.V.QV.S...E.S.Q.N.T...F...
AID16715_1	957	...STET-----PHVEEEEEEE.WLD...--VI..T...--EPEPEPLPEEP..Q.V...A..CI..K..QSA..I..TH..
AT098204_1	964	...STE...-MQUEEEEE.WLG...-ATELSEHEPEPELTTEEP..T...A..CV..K..QAN..I..IH..
ALK02469_1	964	...STEQUEE..E..DWLG...-AT..LSE...-HEPEPELTTEEP..T...A..CV..K..QAN..I..IH..
AT098131_1	964	...STE...-MQUEEEEE.WLG...-ATELSEHEPEPELTTEEP..T...A..CV..K..QAN..I..IH..
AT098119_1	964	...STE...-MQUEEEEE.WLG...-ATELSEHEPEPELTTEEP..T...A..CV..K..QAN..I..IH..
AT098180_1	964	...STE...-MQUEEEEE.WLG...-ATELSEHEPEPELTTEEP..T...A..CV..K..QAN..I..IH..
AT098107_1	964	...STE...-MQUEEEEE.WLG...-ATELSEHEPEPELTTEEP..T...A..CV..K..QAN..I..IH..
AGC74171_1	964	...STETV..V...-MQUEEEEE.WLG...-ATELSEHEPEPELTTEEP..T...A..CV..K..QAN..I..IH..
AAR23244_1	963	...SAETRV..-EEEEEE.WLD..TTE...-SET..P..PE..PTPEEP..T...A..CV..K..QAN..I..IH..
AAR87533_1	963	...SAETRV..-EEEEEE.WLD..TTE...-SET..P..PE..PTPEEP..T...A..CV..K..QAN..I..IH..
AR076381_1	964	...STET..V...-EEEEEE.WLD..TTE...-SET..P..PE..PTPEEP..T...A..CV..K..QAN..I..IH..
AAP51226_1	963	...SAETRV..-EEEEEE.WLD..TTE...-SET..P..PE..PTPEEP..T...A..CV..K..QAN..I..IH..
ACZ72223_1	963	...SAETRV..-EEEEEE.WLD..TTE...-SET..P..PE..PTPEEP..T...A..CV..K..QAN..I..IH..
Query YP_009725295_1	3241	NAMQVESDYYIATNGPLKVGGSCVLSGHNLAHKHLVVGPNVNKGEDIQLLKSAHENFNQHEVLLAPLLSAGIFGADPHIHSRLRVCVDTRHTVLYAVFDKILYDKLVSSFLEMKSEQ
OIA20043_1	1081	.
OHU79172_1	1081	.
OHRE63289_1	1081	.
OIE07480_1	1081	.
OHU79171_1	1081	.
OHZ87591_1	1073	.
HR63299_1	1080	H...G...N...R...D...V...
AVP78030_1	1076	G...N..E..RL..T..L..EK..L..A..V..R..SQD..K..LQ..KM..E..Q..N..S..QTILDY.DSLKP..
AID16715_1	1051	G...N..E..RL..T..L..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
AT098204_1	1059	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
ALK02469_1	1059	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
AT098131_1	1059	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
AT098119_1	1059	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
AT098180_1	1059	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
AT098107_1	1059	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
AGC74171_1	1060	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
AAR23244_1	1059	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
AAR87533_1	1059	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
AR076381_1	1060	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
AAP51226_1	1059	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
ACZ72223_1	1059	G...N..K..KL..T..L..K..L..A..A..SQDT..K..L..Q..Q..Q..I..N..A..EQV..MDY..DSLPRV
Query YP_009725295_1	4681	SREVRTIKVFTTVVDNINLHTQVDMMSMTYGOQGPYTYLGADPVTIKPHNSHEGKTFVLPNDDTLRVEAFYEYHTTDPSSLGRYMSALNHTKKWQPVNLTSIKWADNNCYLAT
OIA20043_1	1561	.
OHU79172_1	1561	.
OHRE63289_1	1561	.
OIE07480_1	1561	.
OHU79171_1	1561	.
OHZ87591_1	1553	.
HR63299_1	1560	K...
AVP78030_1	1557	...N...
AID16715_1	1529	...K...T..HI..P...I...
AT098204_1	1538	...K...T..L...
ALK02469_1	1538	...K...T..L...
AT098131_1	1538	...K...T..L...
AT098119_1	1538	...K...T..L...
AT098180_1	1538	...K...T..L...
AT098107_1	1538	...K...T..L...
AGC74171_1	1539	...K...T..L...
AAR23244_1	1538	...K...T..L...
AAR87533_1	1538	...K...T..L...
AR076381_1	1538	...K...T..L...
AAP51226_1	1538	T...K...T..L...
ACZ72223_1	1538	...K...
Query YP_009725295_1	5041	LTLQQIELKFNPPLQDAYYRARAGEAANFCALIAYCNKTVGELGDVRETMISLQFHANLDSCKRVLNVVCKTCGQQTTLKGVEAVMMGTLSYEFKKGVQPCCTGKQATKYLV
OIA20043_1	1681	.
OHU79172_1	1681	.
OHRE63289_1	1681	.
OIE07480_1	1681	.
OHU79171_1	1681	.
OHZ87591_1	1673	.
HR63299_1	1680	..N..L..Q..
AVP78030_1	1677	..I..N..L..Q..
AID16715_1	1649	..V..V..A..E..D..S..L..E..A..H..KT..R..DEL..T..SV..V..CN..Q..
AT098204_1	1658	..V..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..
ALK02469_1	1658	..V..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..
AT098131_1	1658	..V..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..
AT098119_1	1658	..V..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..
AT098180_1	1658	..V..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..
AT098107_1	1658	..V..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..
AGC74171_1	1659	..V..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..
AAR23244_1	1658	..V..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..
AAR87533_1	1658	..L..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..
AR076381_1	1658	..L..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..
AAP51226_1	1658	..L..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..
ACZ72223_1	1658	..L..V..A..E..D..S..L..E..A..H..KT..T..DNL..T..S..V..RD..Q..

Query	5401	ESPFVMSAPPAYQELKHGHTCASEYTGNYQCGHVKHTSKETLYCIDGALLTKSSEYKGPITDVFYKENSFTTICKPVTKLDGVCTEIDPKLDNYYKKDNSYTFEQPIDLVPQ
YP_009725295.1	1801
QIA20043.1	1801
OHU79172.1	1801
OHRE63289.1	1801
QIE07480.1	1801
OHU79171.1	1801
OHZ87591.1	1793
QHR63299.1	1800
AVP78030.1	1797
AID16715.1	1769
AT09284.1	1778
ALK02469.1	1778
AT098131.1	1778
AT098119.1	1778
AT098180.1	1778
AT098107.1	1778
AGC74171.1	1779
AAR23244.1	1778
AAR87533.1	1778
AR076381.1	1778
AAP51226.1	1778
AC272223.1	1778
Query	6121	CEDLKPVSEEVNPNTIQKDVLCECNKTTVEVGDILKPAANSLKITEEVGHTDLMAAYVDNSLTIKKPNELSRLVGLKLATHGLAAVISVPWDTIANYAKPFLNKVSTTNIVT
YP_009725295.1	2041
QIA20043.1	2041
OHU79172.1	2041
OHRE63289.1	2041
QIE07480.1	2041
OHU79171.1	2041
OHZ87591.1	2033
QHR63299.1	2040
AVP78030.1	2037
AID16715.1	2009
AT09284.1	2018
ALK02469.1	2018
AT098131.1	2018
AT098119.1	2018
AT098180.1	2018
AT098107.1	2018
AGC74171.1	2019
AAR23244.1	2018
AAR87533.1	2018
AR076381.1	2018
AAP51226.1	2018
AC272223.1	2018
Query	6481	LNRVCNTNMPYXXXXXXXXXXXXXRSNTNSRIKASMPPTIAKNTVKSGVKFCLEASFNSYKSPNFSKLINIIWFLLSVCLGLSIYSTAALGVLSMSNLGMPSYCTGYREGYLNSTNIVT
YP_009725295.1	2161
QIA20043.1	2161
OHU79172.1	2161
OHRE63289.1	2161
QIE07480.1	2161
OHU79171.1	2161
OHZ87591.1	2153
QHR63299.1	2160
AVP78030.1	2157
AID16715.1	2129
AT09284.1	2138
ALK02469.1	2138
AT098131.1	2138
AT098119.1	2138
AT098180.1	2138
AT098107.1	2138
AGC74171.1	2139
AAR23244.1	2138
AAR87533.1	2138
AR076381.1	2138
AAP51226.1	2138
AC272223.1	2138
Query	6841	YCTGSIPCSVCLSGLDSLTDYPSLETIQITISSFKWDLTAGLVAEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIIINLVQMAPISAMVRMYIFFASFYVWKSY
YP_009725295.1	2281
QIA20043.1	2281
OHU79172.1	2281
OHRE63289.1	2281
QIE07480.1	2281
OHU79171.1	2281
OHZ87591.1	2273
QHR63299.1	2280
AVP78030.1	2277
AID16715.1	2249
AT09284.1	2258
ALK02469.1	2258
AT098131.1	2258
AT098119.1	2258
AT098180.1	2258
AT098107.1	2258
AGC74171.1	2259
AAR23244.1	2258
AAR87533.1	2258
AR076381.1	2258
AAP51226.1	2258
AC272223.1	2258
Query	7201	VDGCSNSTCCMCMYKRNRATRVECTTIVNGVRRSFVYANGKGFKFLHNWNVCNCDFTCAGSTFSIDEVARDLSQLQFKRPINPTDQSSYIVDSVTKNGSIHYLFDKAGQKTYERHS
YP_009725295.1	2401
QIA20043.1	2401
OHU79172.1	2401
OHRE63289.1	2401
QIE07480.1	2401
OHU79171.1	2401
OHZ87591.1	2393
QHR63299.1	2400
AVP78030.1	2397
AID16715.1	2369
AT09284.1	2378
ALK02469.1	2378
AT098131.1	2378
AT098119.1	2378
AT098180.1	2378
AT098107.1	2378
AGC74171.1	2379
AAR23244.1	2378
AAR87533.1	2378
AR076381.1	2378
AAP51226.1	2378
AC272223.1	2378

Query YP_009725295_1	7561	FVNLDNLRANNTKGSLPINVIVFDGXXXXXXXXXXXXVYYSQLMCQPILLDQALVSDVGDSAEAVKMFADYVNTFSSTFNVPMEKLTVATAEALAKNSLDNVLFSTAAR
OIA20043_1	2521	
OHU79172_1	2521	
OHRE63289_1	2521	
OIE07480_1	2521	
OHU79171_1	2521	
OHZ87591_1	2513	
OHRE63299_1	2520	
AVP78030_1	2517	
ATD16715_1	2489	
AT098204_1	2498	
ALK02469_1	2498	
AT098131_1	2498	
AT098119_1	2498	
AT098180_1	2498	
AT098107_1	2498	
AGC74171_1	2499	
AAR23244_1	2498	
AAR87533_1	2498	
AR076381_1	2498	
AAP51226_1	2498	
ACZ72223_1	2498	
Query YP_009725295_1	9001	SGRWVLNNNDYRSRSPGVFCGVDAVILLTNMFTPLIOPIGALDXXXXXXXXXXXCLAYYFMRFRRAFGEYSHVVAFTNLLFLMSFTVLCLTPVYSFLPGVSVIYLTFYLTN
OIA20043_1	3001	
OHU79172_1	3001	
OHRE63289_1	3001	
OIE07480_1	3001	
OHU79171_1	3001	
OHZ87591_1	2993	
OHRE63299_1	3000	
AVP78030_1	2997	
ATD16715_1	2969	
AT098204_1	2978	
ALK02469_1	2978	
AT098131_1	2978	
AT098119_1	2978	
AT098180_1	2978	
AT098107_1	2978	
AGC74171_1	2979	
AAR23244_1	2978	
AAR87533_1	2978	
AR076381_1	2978	
AAP51226_1	2978	
ACZ72223_1	2978	
Query YP_009725295_1	9361	SFLAHTQIMMFTPLVPTWITTAIYIIC1STKHFYWFSNYKRRVVFGVSFTEEAACLCTFLINKEMYLKLRSDVLLPLTQNYRLALYNYKYSGAHDTTSYREAACCHLAKAL
OIA20043_1	3121	
OHU79172_1	3121	
OHRE63289_1	3121	
OIE07480_1	3121	
OHU79171_1	3121	
OHZ87591_1	3113	
OHRE63299_1	3120	
AVP78030_1	3117	
ATD16715_1	3089	
AT098204_1	3098	
ALK02469_1	3098	
AT098131_1	3098	
AT098119_1	3098	
AT098180_1	3098	
AT098107_1	3098	
AGC74171_1	3099	
AAR23244_1	3098	
AAR87533_1	3098	
AR076381_1	3098	
AAP51226_1	3098	
ACZ72223_1	3098	
Query YP_009725295_1	9721	FSNSGSDVLYOPPQTSITSAVLQSGFRKMAFPSGVCEGMVQTCGTTLNLWLDVVYCPRHVICTSEDMLNPNEYDLIRKSNHNFLVQAGHVLQRVIGHSMQNCVLLKVDTAN
OIA20043_1	3241	
OHU79172_1	3241	
OHRE63289_1	3241	
OIE07480_1	3241	
OHU79171_1	3241	
OHZ87591_1	3233	
OHRE63299_1	3240	
AVP78030_1	3237	
ATD16715_1	3209	
AT098204_1	3218	
ALK02469_1	3218	
AT098131_1	3218	
AT098119_1	3218	
AT098180_1	3218	
AT098107_1	3218	
AGC74171_1	3219	
AAR23244_1	3218	
AAR87533_1	3218	
AR076381_1	3218	
AAP51226_1	3218	
ACZ72223_1	3218	
Query YP_009725295_1	10081	TPKYKFVRIQPGQTSVLAGYNGPSGVYQCAMRPNFTIKGSFLNGSCSGVGFNIDYDCVSFCYMHMELPTGVHAGTDLEGNFYGPVDRQTAQAAGTDTTITVNVLAWLYAAVING
OIA20043_1	3361	
OHU79172_1	3361	
OHRE63289_1	3361	
OIE07480_1	3361	
OHU79171_1	3361	
OHZ87591_1	3353	
OHRE63299_1	3360	
AVP78030_1	3357	
ATD16715_1	3329	
AT098204_1	3338	
ALK02469_1	3338	
AT098131_1	3338	
AT098119_1	3338	
AT098180_1	3338	
AT098107_1	3338	
AGC74171_1	3339	
AAR23244_1	3338	
AAR87533_1	3338	
AR076381_1	3338	
AAP51226_1	3338	
ACZ72223_1	3338	

Query	12241	KNTCDGTTFTYASALWEIQVVDADSKIVQLSEISMDSNPNLAWPLIVTALRANSAVKLQNNELSPVALRQMSCAAGTTQACTDDNALAYNTKGGRFVLALLSDLQDLKWARFPK
YP_009725295_1	4081
QIA20043_1	4081
QHU79172_1	4081
QHR63289_1	4081
QIE07480_1	4081
QHU79171_1	4081
QHZ87591_1	4073
QHR63299_1	4080
AVP78030_1	4077N.....
AID16715_1	4049N.....
AT098204_1	4058N.....
ALK02469_1	4058N.....
AT098131_1	4058N.....
AT098119_1	4058N.....
AT098180_1	4058N.....
AT098107_1	4058N.....
AGC74171_1	4059N.....
AAR23244_1	4058N.....
AAR87533_1	4058N.....
AR076381_1	4058N.....
AAP51226_1	4058N.....
ACZ72223_1	4058N.....

Query range 37: 4321 to 4405		
Query	12961	FGGASCLLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPVGFTLKNITVCTVGMWKGYGCSCDQLREPMILQSADAQSFNLNGFAV
YP_009725295_1	4321
QIA20043_1	4321
QHU79172_1	4321
QHR63289_1	4321
QIE07480_1	4321
QHU79171_1	4321
QHZ87591_1	4313
QHR63299_1	4320
AVP78030_1	4317V.....
AID16715_1	4288R.....
AT098204_1	4298R.....
ALK02469_1	4298R.....
AT098131_1	4298R.....
AT098119_1	4298R.....
AT098180_1	4298R.....
AT098107_1	4298R.....
AGC74171_1	4299R.....
AAR23244_1	4298R.....
AAR87533_1	4298R.....
AR076381_1	4298I.R.....
AAP51226_1	4298R.....
ACZ72223_1	4298R.....

Figure 2. Sequence amino acid analysis of Coronavirus isolate by NCBI.

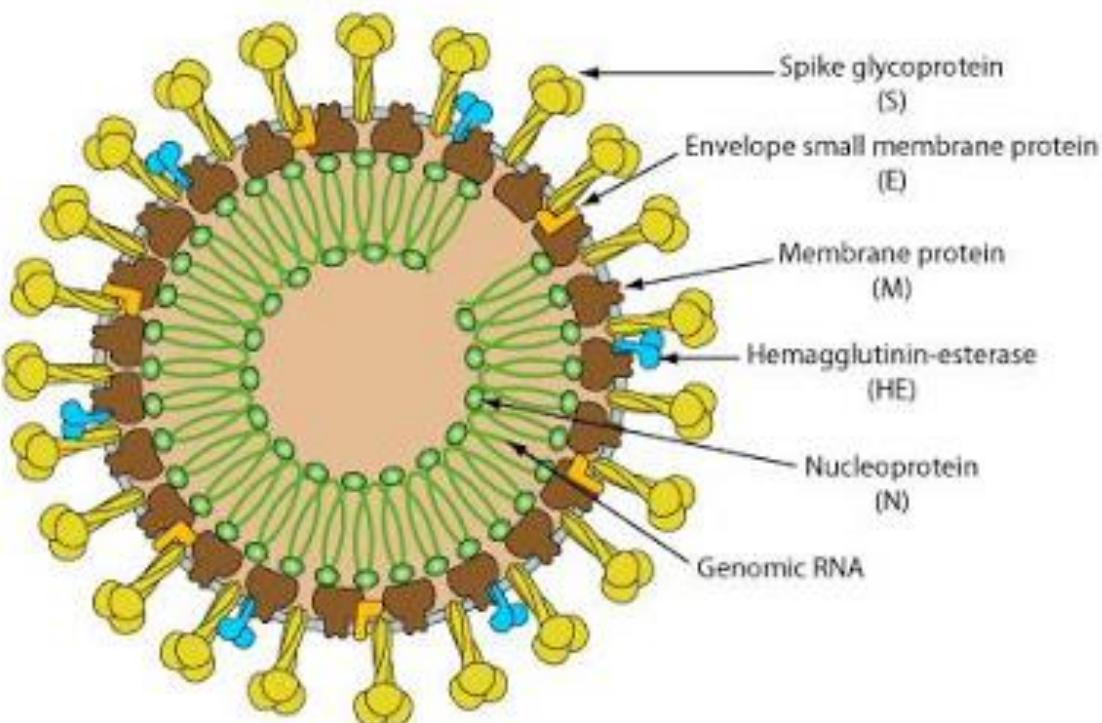


Figure 3. Diagram of a coronavirus structure.

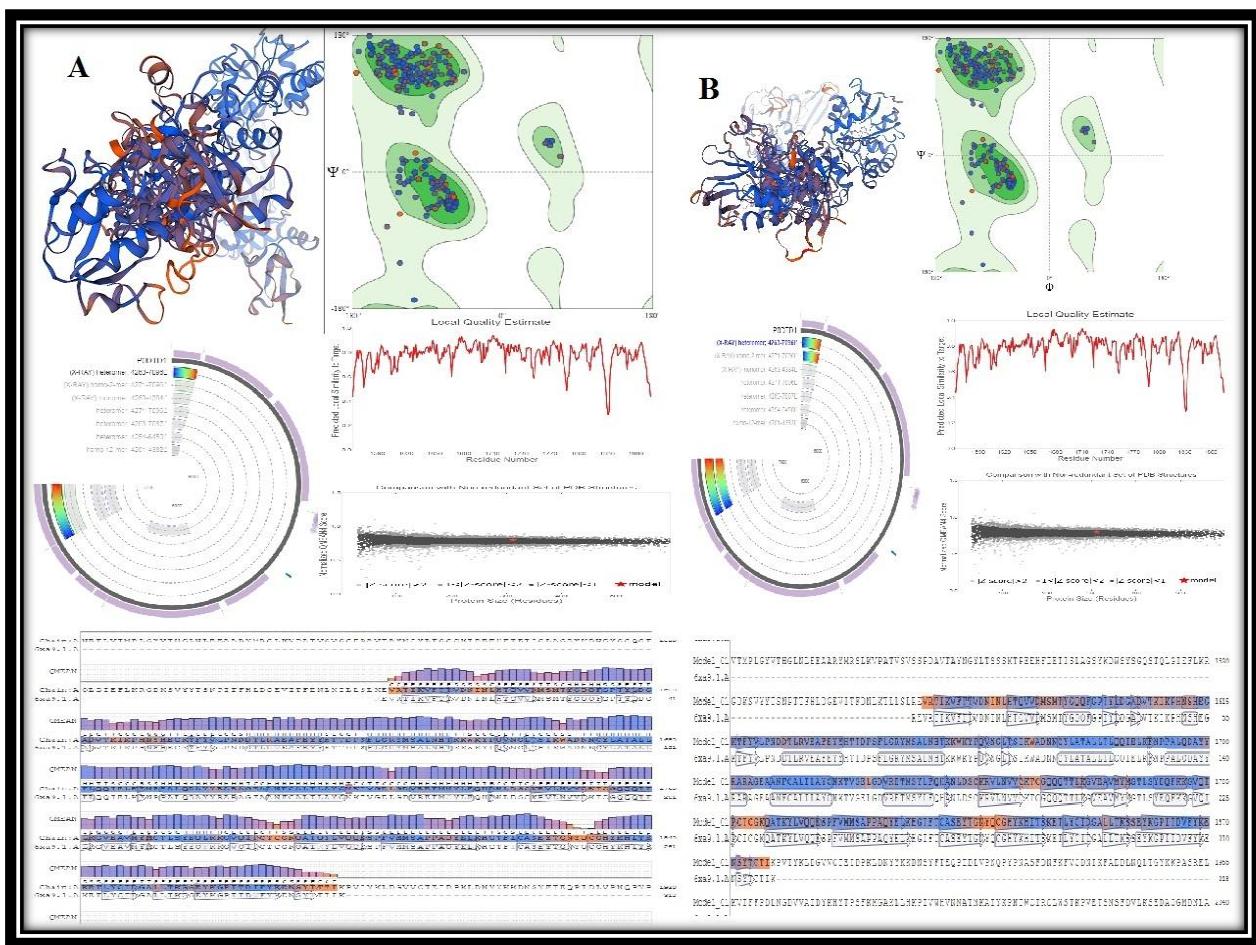


Figure 4. Conformation of protein from COVID-19, (A: Bat Coronavirus and B:human coronavirus).

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تطور الخريطة الجينية لشجرة الوراثية لفيروس كورونا (كوفيد -19) : المراجعة

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الخلاصة

يشتبه في أن فيروس كورونا (كوفيد -19) نشاً من مضيف حيواني (مشترك) متبعاً بانتقال من إنسان إلى إنسان، والهدف من مقالة المراجعة هو معرفة الشجرة الوراثية وشكل البروتين للفيروس التاجي. من خلال دراسة التسلسل الجيني، كما هو موضح في تصميم شجرة التطورية والتغيرات الجينية، فإن السبب الرئيسي لـ COVID-19 هو فيروس Bat Coronavirus RaTG13 (SARS) في ID: MG772933.1 و ID: MN996532.1 (SARS) في 24 تموز (يوليو) 2013 وشباط (فبراير) 2017، حيث يظهر تطور الفيروس التاجي من 2003-2013 إلى 2020، والذي أصبح الذروة الأكثر فتكاً في البشر، إذ تطور الفيروس من تأثير الخفافيش على البشر. إذ أظهرت نتائج تحليل البروتين هنالك 98 تغيير في الأحماض الأمينية من RaTG13 إلى COVID-19 Homo sapiens. وهذا، فقد زادت هذه الدراسة من فهمنا للتنوع الجيني لـ COVID-19، كذلك نستنتج أن تركيب وشكل البروتين متطابق بين الخفافيش والإنسان.

الكلمات المفتاحية: السارس، كوفيد -19، التطور الجيني، الخفافيش.