

## SARS-CoV-2 similarity to bat-SARS-ZXC21

22-Jan-2023

I thought you might find this interesting. I spent a full week in August 2022 looking over various RNA sequences in GenBank of the NIH. I found a very close match of COVID-19 to a bat virus with the exception of the spike coding region. COVID-19 appears to have been made from replacing the spike protein in the bat-SARS-ZXC21 with a spike toxic to humans. That spike is unique and does not match anything submitted to GenBank including MERS or SARS-CoV. The first figure shows how similar the amino acid sequences are between these two viruses at the beginning of the genome sequence. The second figure shows the similarity of SARS-CoV-2 to ZXC21, SARS-CoV and MERS at the region where the spike protein code begins. I obtained all the genetic codes from the acquisition codes listed from the NIH. I would not expect such a drastic change in matches right at the point where the spike protein begins.

Tools Bat\_SARS\_ZXC21.pdf x SARS\_CoV\_2\_Wuha... Tools Bat\_SARS\_ZXC21.pdf SARS\_CoV\_2\_Wuha... x

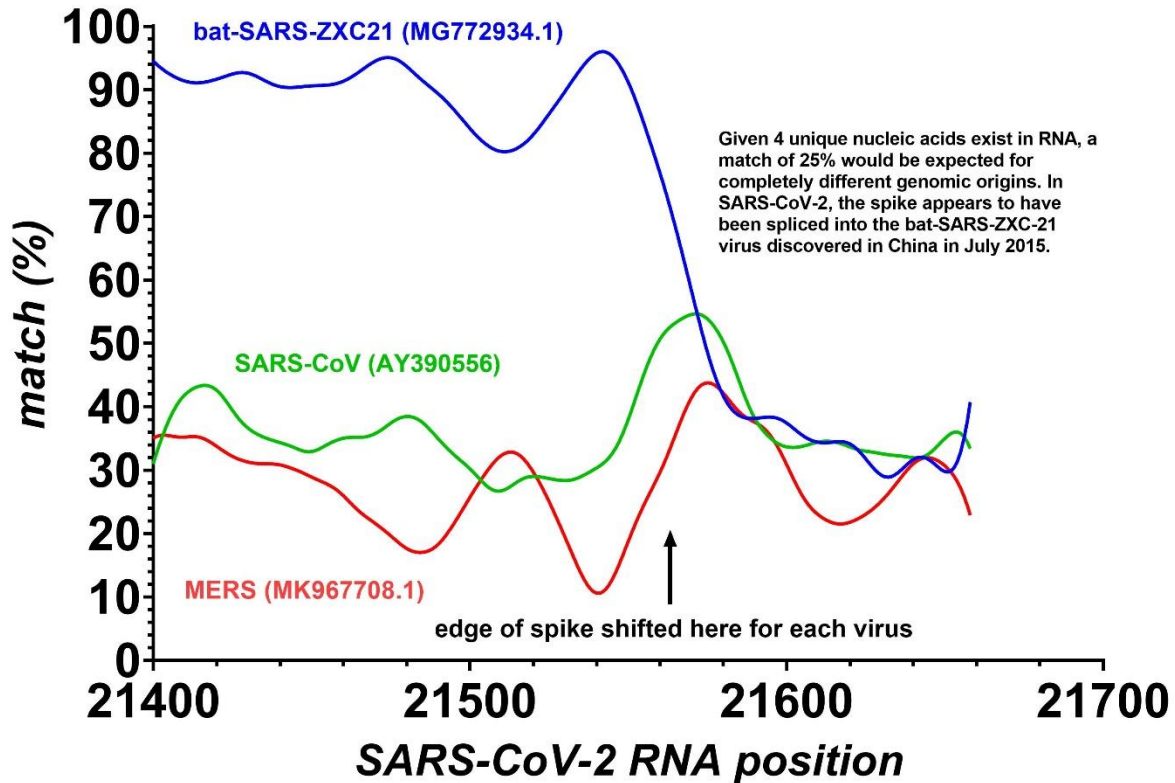
2 / 17 99% 3 / 26 99%

View: This file originated from a potentially unsafe location, and most features have been disabled tView: This file originated from a potentially unsafe location, and most features have been disabled to

```
-----  
/protein_id="AVF78041.1"  
  
/translation="MESLVPGFNEKTHVQLSLPVLQVCDVLVIRGFGDSVEEALSEARQ  
HLKDGTCGLVEVEKGVLPQLEQPYVPIKRS DARTAHGHVMVELVAELDGIQYGRSGE  
TLGVLPVPHVGEVFPVAYRKVLLRKNKNGKAGGHSYGADLKSFDLGDDELGTDPIEDFQEN
```

```
-----  
/protein_id="YP_009724389.1"  
/db_xref="GeneID:43740578"  
  
/translation="MESLVPGFNEKTHVQLSLPVLQV RDVLVIRGFGDSVEEVLSEARQ  
HLKDGTCGLVEVEKGVLPQLEQPYVPIKRS DARTAFHGHVMVELVAELGIIQYGRSGE  
TLGVLPVPHVGEIPVAYRKVLLRKNKNGKAGGHSYGADLKSFDLGDDELGTDPIYEDFQEN
```

## SARS-CoV-2 Similarity to Other SARS Viruses



Also find the link below to a very interesting paper where a number of Chinese bat viruses were characterized and genomic sequences sent to the NIH GenBank in 2018.

<https://pubmed.ncbi.nlm.nih.gov/30209269/>

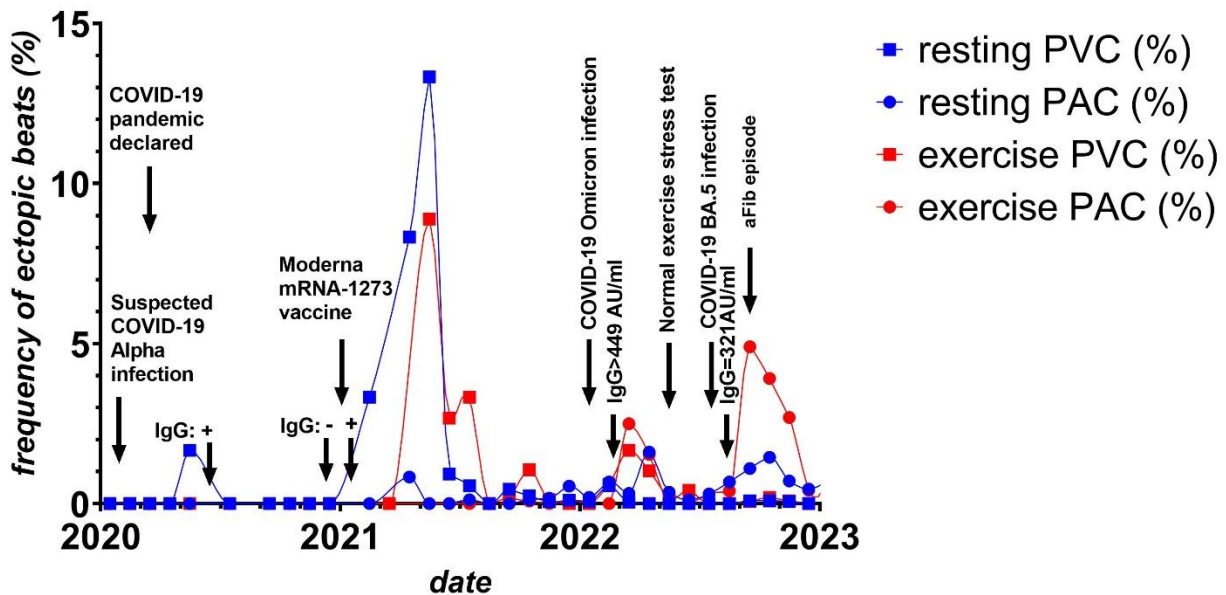
Take a look on Page 9 of that paper. It reads "Preparation of rabbit antiserum against two peptides. To obtain the polyclonal antibody of bat SL-CoV ZC45 N protein, two partial peptides with 15-amino acid residues of N protein were synthesized (Sangon Biotech, Shanghai, China) after a homology search according to the bioinformatics analysis and prediction of signal peptide (SignalIP-4.1), hydrophilicity and antigenicity of N protein..."

I suspect that the Chinese selected the ZXC21 (identical to ZC45 at the N protein region shown in Fig 1 of this paper) as a base template for COVID-19 because **they learned how to produce antibodies to target the N protein in the base template** rather than the spike protein. Presumably antibodies to this N protein would be a treatment for COVID-19 since this protein is the same for both infections. Antibodies to the spike protein of COVID-19 is possibly causing many of the problems patients develop following COVID-19 infections and/or mRNA vaccinations. At this time, China's military is guarding the cave where this bat virus was discovered. It is their vaccine for the current strains plus future strains developed in their labs.

<https://www.businessinsider.com/china-policing-bat-caves-scientists-hope-coronavirus-clues-inside-2020-12>

Each time a person is exposed to the spike antigen, changes in the heart conduction can occur with the cardiac effect peaking at 3 months post exposure. The figure below shows changes in the ectopic heart beats following each exposure to the spike protein antigen. Similar effects also occur with other diseases including Rheumatic Fever and Chagas. Unfortunately, our vaccines are targeting the wrong part of the genetic sequence of COVID-19. They should be targeting the N protein. It cannot be ruled out that this virus may have been designed so that the spikes would lead to autoimmune responses.

## Ectopic Heart Beat Frequencies



Protecting yourself from severe COVID-19 infections

China has show that it had the ability to move spikes between different viruses as far back as 2004. The following paper shows China moved the spike from the original SARS virus to the HIV particle in 2004.

<https://pubmed.ncbi.nlm.nih.gov/15358126/>

The purpose of this research was to create a slowly replicating highly infectious virus that entered cells via the ACE2 receptor site in order to determine if the entry rate depended on the pH of the endosome. It is unclear if the spike placement made this virus airborne. Page 998 of this paper did report that the entry of viruses into the ACE2 receptor site is pH dependent with an increased entry rate with low endosomal pH. This provides a clue to protecting yourself from viruses such as COVID-19 that enter the cells via the ACE2 receptor site. Low pH is associated with poor mitochondrial health which forces the production of ATP from the anaerobic lactic acid producing pathway. Improving mitochondrial health is best achieved from encouraging low deuterium energy metabolism. This is best achieved by regular exercise and low deuterium food intake and avoidance of vitamin/mineral deficiencies. The following paper discusses techniques for assessing foods for low deuterium content.

<https://esmed.org/MRA/mra/article/view/2833>

In sum, the overall strategy is to avoid excessive carbohydrates and consume more seafoods and grass-fed animal meats. The best oils to include in the diet include olive oil, coconut and avocado oils.

Furthermore, deuterium has also been reported to stabilize viruses. A slide from a conference in Feb 2021 shows research groups are studying the effect of deuterium on viral infections.

## Viruses are stabilized by excess deuterium!

- The nucleocapsid protein in SARS-CoV-2 starts to unfold at 35 degrees Centigrade (95 degrees Fahrenheit) and is completely denatured at 55 degrees Centigrade (131 degrees Fahrenheit)\*
  - A fever is a natural defense against the virus
- Viruses take up deuterium and trap it in their protein coat and in their internal single strand of RNA\*\*
  - Deuterium stabilizes the viral protein and protects from temperature denaturation
  - The virus removes deuterium from the body fluids
- When the deuterium level in the body fluids is high, the virus becomes more stable

\*Milan Surjit and Sunil K Lal. Infection, Genetics and Evolution 8 (2008) 397-405.

\*\*Jiangsen MAO et al., Chinese Science Bulletin 2004 Vol. 49 No. 3 253-257.

Since we currently do not have any vaccines targeting the N protein of SARS-CoV-2 and those vaccines targeting the spike protein appear to lead to autoimmune responses, our best defense to these viruses include 1.a proper low carbohydrate, low deuterium diet with ample vitamins and minerals and 2. regular exercise.

In October 2022, I stumbled on the following Exposé article dated March 14, 2022 <https://expose-news.com/2022/03/14/documents-published-confirming-moderna-created-covid/> I confirmed the facts in this article and summarized them below. This article reveals the possible origin of the spike coding region for COVID-19.

Moderna has five U.S. Patents containing the proprietary genetic sequence CTACGTGCCCGCCGAGGAG. These patents are **US9149506B2**, **US9216205B2**, **US9255129B2**, **US9301993B2** and **US9587003B2**. The first four were filed for patent on 16-Dec-2013 and the last one on 4-Feb-2016. The reverse complement of this sequence is CTCCTCGGCGGGCACGTAG which can be found in the spike coding region of COVID-19 between bases 23501-23519(\*). This sequence codes for a Furin cleavage site. This match took some time to identify because it is the reverse complement that was patented. This is because their patent is listed as a DNA sequence and COVID-19 is the reverse complement mRNA of that DNA sequence. Also note that the patent sequence clearly indicates this sequence is an “Artificial Sequence” indicating it was generated in a laboratory.

The statistical chance that this sequence might occur randomly in SARS-CoV-2 is one in  $4^{19} / 30,000 = 9.1$  million where 4 is the number of nucleic acids (A,T,C,G), 19 is the length of the matching sequence above and 30,000 is the number of bases in the COVID-19 genome.

(\*) one sample has this at 23483-23501 due to a mutation in that sample.

Here is one example of that sequence in SEQ ID 11652 of US Patent 9587003 B2. The NIH Blast search results are attached.

**US Patent # US 9587003 B2 filed by Moderna and granted on Mar. 7, 2017.**

**SOURCE: <https://seqdata.uspto.gov/?pageRequest=viewSequence&DocID=9587003B2&seqID=11652>**

**Notice the 19 pair DNA sequence ctacgtgc cgcggagga g that is bolded and underlined below. Search for this DNA sequence using the NIH BLAST tool link below:**

**[https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE\\_TYPE=BlastSearch&LINK\\_LOC=blasthome](https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome)**

**The results are all SARS-CoV-2 entries! More specifically, these matches are to the "Furin Cleavage site" in the spike protein! Moderna has a total of 5 patents containing this DNA sequence dating back to patent applications made on Dec 16, 2013.**

SEQ ID NO 11652

LENGTH: 3387

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic coding sequence

SEQUENCE: 11652

```
atgagcagaa gaaagcccgc cagcggcggc ctggccgccca gcagcagcgc ccccgccaga 60
caggccgtgc tgagcagatt cttccagagc accggcagcc tgaagagcac cagcagcagc 120
accggcgccg ccgaccaggt ggaccccggc gccgcgcgcc cgcccgcccc ccccgcccc 180
gccttcccc cccagctgcc cccccacatc gccaccgaga tcgacagaag aaagaagaga 240
cccctggaga acgacggccc cgtgaagaag aaggtgaaga aggtgcagca gaaggagggc 300
ggcagcgacc tgggcatgag cggcaacagc gagcccaaga agtgcctgag aaccagaaac 360
gtgagcaaga gcctggagaa gctgaaggag tctgctgctg acagcgcctt gccccagagc 420
agagtgcaga ccgagagcct gcaggagaga ttccgctgct gcaccaagtg caccgacttc 480
gacgacatca ccctgctgca cgccaagaac gccgtgagca gcgaggacag caagagacag 540
atcaaccaga aggacaccac cctgttcgac ctgagccagt tcggcagcag caacaccagc 600
cacgagaacc tgcagaagac cgccagcaag agcgcacaaca agagaagcaa gagcatctac 660
acccccctgg agctgcagta catcgagatg aagcagcagc acaaggacgc cgtgctgtgc 720
gtggagtgcg gctacaagta cagattcttc ggcgaggacg ccgagatcgc cgccagagag 780
ctgaacatct actgccacct ggaccacaac ttcatgaccg ccagcatccc caccacagaa 840
ctgttcgtgc acgtgagaag actggtggcc aagggctaca aggtgggctt ggtgaagcag 900
accgagaccg ccgccctgaa ggccatcggc gacaacagaa gcagcctgtt cagcagaaag 960
ctgaccgccc tgtacaccaa gagcaccctg atcggcgagg acgtgaacct cctgatcaag 1020
ctggacgacg ccgtgaacgt ggacgagatc atgaccgaca ccagcaccag ctacctgctg 1080
tgcacagcgc agaacaagga gaacgtgaga gacaagaaga agggcaacat cttcatcggc 1140
atcgtgggcg tgcagcccgc caccggcgag gtggtgttcg acagcttcca ggacagcgc 1200
agcagaagcg agctggagac cagaatgagc agcctgcagc ccgtggagct gctgctgccc 1260
agcgccttga gcgagcagac cgaggccctg atccacagag ccaccagcgt gagegtgcag 1320
gacgacagaa tcagagtgga gagaatggac aacatctact tcgagtacag ccacgccttc 1380
caggccgtga ccgagttcta cgccaaggac accgtggaca tcaagggcag ccagatcatc 1440
agcggcatcg tgaacctgga gaagcccgtg atctgcagcc tggccgcat catcaagtac 1500
ctgaaggagt tcaacctgga gaagatgctg agcaagcccg agaacttcaa gcagctgagc 1560
```

```

agcaagatgg agttcatgac catcaacggc accaccctga gaaacctgga gatcctgcag 1620
aaccagaccg acatgaagac caagggcagc ctgctgtggg tgctggacca caccaagacc 1680
agcttcggca gaagaaagct gaagaagtgg gtgaccagc ccctgctgaa gctgagagag 1740
atcaacgcca gactggacgc cgtgagcgag gtgctgcaca gcgagagcag cgtggtcggc 1800
cagatcgaga accacctgag aaagctgccc gacatcgaga gaggcctgtg cagcatctac 1860
cacaagaagt gcagcaccca ggagttcttc ctgatcgtga agacctgtga ccacctgaag 1920
agcgagtcc aggccatcat ccccgcctgtg aacagccaca tccagagcga cctgctgaga 1980
accgtgatcc tggagatccc cgagctgctg agccccgtgg agcactacct gaagatcctg 2040
aacgagcagg ccgccaaggt gggcgacaag accgagctgt tcaaggacct gagcgacttc 2100
cccctgatca agaagagaaa ggacgagatc cagggcgtga tcgacgagat cagaatgcac 2160
ctgcaggaga tcagaaagat cctgaagaac cccagcgcgc agtacgtgac cgtgagcggc 2220
caggagtcca tgatcgagat caagaacagc gccgtgagct gcatccccac cgactgggtg 2280
aaggtgggca gcaccaaggc cgtgagcaga ttccacagcc ccttcatcgt ggagaactac 2340
agacacctga accagctgag agagcagctg gtgctggact gcagcgcga gtggctggac 2400
ttcctggaga agttcagcga gcactaccac agcctgtgca aggccgtgca ccacctggcc 2460
accgtggact gcatcttcag cctggccaag gtggccaagc agggcgacta ctgcagacc 2520
accgtgcagg aggagagaaa gatcgtgatc aagaacggca gacaccccgt gatcgacgtg 2580
ctgctgggcg agcaggacca gtacgtgccc aacaacaccg acctgagcga ggacagcgag 2640
agagtgatga tcatcaccgg ccccaacatg ggcggcaaga gcagctacat caagcaggtg 2700
gccctgatca ccatcatggc ccagatcggc agctacgtgc ccgccgagga ggccaccatc 2760
ggcatcgtgg acggcatctt caccagaatg ggcgcgccg acaacatcta caagggccag 2820
agcaccttca tggaggagct gaccgacacc gccgagatca tcagaaaggc caccagccag 2880
agcctggtga tcctggacga gctgggcaga ggcaccagca cccacgacgg catcgccatc 2940
gcctacgcca ccctggagta cttcatcaga gacgtgaaga gcctgaccct gttcgtgacc 3000
cactaccccc ccgtgtgcga gctggagaag aactacagcc accaggtggg caactaccac 3060
atgggcttcc tggtgagcga ggacgagagc aagctggacc ccggcgccgc cgagcaggtg 3120
cccgaacttcg tgaccttctt gtaccagatc accagaggca tcgccgccag aagctacggc 3180
ctgaacgtgg ccaagctggc cgacgtgccc ggcgagatcc tgaagaaggc cgcccacaag 3240
agcaaggagc tggagggcct gatcaacacc aagagaaaga gactgaagta cttcgccaag 3300
ctgtggacca tgcacaacgc ccaggacctg cagaagtgga ccgaggagt t caacatggag 3360
gagacccaga ccagcctgct gcactag

```

In summary, COVID-19 appears to have been made by inserting a laboratory generated weapons grade spike protein on the bat-SARS-ZXC21. The spike protein contains proprietary genetic sequences found in five separate U.S. pharmaceutical company patents. China's Wuhan laboratory then placed this spike onto the bat-SARS-ZXC21 since that unaltered virus can produce antibodies to the N-protein which is left unchanged once the spike is replaced. This allowed China to have a vaccine before the virus was released. However as of now, it is unclear if the release was accidental or deliberate. It is also unclear if the Chinese had a spy working for Moderna where the Furin cleavage site was developed. Finally, the best defense to protecting yourself from COVID-19 is a low deuterium diet with regular exercise which maintains a proper functioning immune system.

### December 2022 Update

A paper published in June 2022 did reveal that mutations are occurring within the nucleocapsid N-protein which no longer allows the bat-SARS-ZXC21 to provide immunity to SARS-CoV-2.

<https://pubmed.ncbi.nlm.nih.gov/35728038/>

As of December 2022, China has been experiencing an upsurge in COVID-19 cases. However, they are refusing Western Vaccines possibly because they know the spike proteins induce autoimmune responses against our organs. <https://www.reuters.com/world/china/chinas-xi-unwilling-accept-vaccines-despite-threat-protests-us-intel-2022-12-04/>

### **January 2023 Update**

By January 2023, China reported that 80% of their population was infected with COVID-19.

<https://www.cnn.com/2023/01/21/china-says-covid-outbreak-has-infected-80percent-of-population.html>

### **February 26, 2023 Update**

The U.S. Department of Energy (DOE) concludes that the COVID-19 virus was made in a laboratory.

<https://www.washingtonexaminer.com/policy/healthcare/coronavirus-most-likely-originated-lab>

### **September 12, 2023 Update**

A CIA whistleblower came forth to report that CIA agents studying the origin of COVID-19 were bribed to report that it was not of a laboratory origin. The CIA agents reportedly believed that the origin was the WUHAN laboratory.

<https://www.msn.com/en-us/news/other/cia-whistleblower-s-bombshell-claim-about-covid-conspiracy/ar-AA1gCpui>