Official Biochemical and Statistical Evidence 100% confirms Moderna created Covid-19

expose-news.com/2022/07/04/proof-moderna-created-covid/

By The Exposé July 4, 2022

Evidence has emerged which proves beyond a reasonable doubt that the pharmaceutical giant Moderna, the company that has made billions through the sale of an experimental Covid-19 injection, actually created the Covid-19 virus.

On February 23 the Daily Mail ran an article showing that Moderna has patented the 19 base letter (nucleotide) sequence which codes for the Furin Cleavage site in Covid-19.

By a concerned reader

They cited a Paper by Scientists in India, Switzerland, Italy and the US (cautiously entitled: MSH3 Homology and Potential Recombination Link to SARS-CoV-2 Furin Cleavage Site) in which they calculated that the chances of a 19 nucleotide sequence patented by Moderna randomly appearing in Covid-19 in circumstances where it does not appear anywhere else in nature are 1 in 3 trillion.

But they failed to make the obvious deduction there from. Had they made said obvious deduction I fear that might have been the last scientific deduction they ever got published!

They decided to investigate the RNA sequence for the Furin cleavage site in the Covid-19 Spike Protein to see if it occurred anywhere else in nature. .

Fortunately the NCBI/NIH have produced the wonderful BLAST database which catalogues every gene sequence in nature known to man and every synthetic patented gene sequence known to the patent office.

The researchers chose the Furin Cleavage sequence because it is the only continuous gene letter sequence (nucleotide sequence) in Covid-19 with more than 3 nucleotides, that differs from the respective letters in its closest natural relative the Bat Coronavirus RaTG13 (all other differences are 3 letters or less long). So it was by far the best candidate for determining whether or not Covid-19 was man made.

The reader might consider it more likely that a Furin Cleavage Site would appear in the Sun than in the Daily Mail. But this cleavage refers to the separation of spike from virus rather than pillow from pillow.

Furthermore the Furin Cleavage Site is key to the pathogenicity of Covid-19. So if there was to be some man made gain of function included in the virus, this is where one might expect to find it.

The Amino Acid sequence of the Furin Cleavage Site is PRRA (Proline Argenine Argenine Alanine). Each Amino Acid is coded for by a Codon, consisting of 3 nucleotides (genetic sequence letters). So all the differences in the genetic code between Covid-19 and RaTG13 are at most one Codon long, one amino acid long, other than the Furin Cleavage Sequence, which is…

CCT CGG CGG GCA

The complimentary sequence (the opposing DNA strand of the double helix is (GGAGCCGCCCGT) because C binds with G and A binds with T

The reverse compliment (the same thing written backwards) is therefore TGCCCGCCGAGG

The researchers did a BLAST (Basic Local Alignment Search Tool) alignment search (which means they search for the gene sequence, the reverse gene sequence, the complimentary gene sequence and the reverse complimentary gene sequence) through every gene sequence in nature known to man for CTCCTCGGCGGGCACGTAG which is the 19 nucleotide sequence containing the Furin Cleavage Sequence, which also appears in Covid-19, and which is found actually in the reverse compliment form CTACGTGCCCGCCGAGGAG patented by Moderna.

Their search results can be found here.

Table 1 shows that it does exist in the 5 US patents cited below…

US9149506B2: Modified polynucleotides encoding septin-4 – https://patents.google.com/patent/US9149506B2/en

Inventor: Tirtha Chakraborty, Antonin de Fougerolles
Current Assignee: ModernaTx Inc

2012-04-02 Priority to US201261618953P
2013-12-16 Application filed by Moderna Therapeutics Inc
2014-05-22 Publication of US20140141067A1
2015-10-06 Publication of US9149506B2
2015-10-06 Application granted
2020-01-10 First worldwide family litigation filed

US9216205B2: Modified polynucleotides encoding granulysin – https://patents.google.com/patent/US9216205B2/en

Inventor: Tirtha Chakraborty, Antonin de Fougerolles
Current Assignee: ModernaTx Inc

2012-04-02 Priority to US201261618873P
2013-12-16 Application filed by Moderna Therapeutics Inc
2014-04-24 Publication of US20140113960A1
2015-12-22 Publication of US9216205B2
2015-12-22 Application granted

US9255129B2: Modified polynucleotides encoding SIAH E3 ubiquitin protein ligase 1 – https://patents.google.com/patent/US9255129B2/en

Inventor: Tirtha Chakraborty, Antonin de Fougerolles
Current Assignee: ModernaTx Inc

2012-04-02 Priority to US201261618868P
2013-12-16 Application filed by Moderna Therapeutics Inc
2014-05-22 Publication of US20140141068A1
2016-02-09 Application granted
2016-02-09 Publication of US9255129B2

US9301993B2: Modified polynucleotides encoding apoptosis inducing factor 1 – https://patents.google.com/patent/US9301993B2/en

Inventor: Tirtha Chakraborty, Antonin de Fougerolles
Current Assignee: ModernaTx Inc

2012-04-02 Priority to US201261618957P
2013-12-16 Application filed by Moderna Therapeutics Inc
2014-04-17 Publication of US20140107189A1
2016-04-05 Application granted
2016-04-05 Publication of US9301993B2
2020-01-10 First worldwide family litigation filed

US9587003B2: Modified polynucleotides for the production of oncology-related proteins and peptides – https://patents.google.com/patent/US9587003B2/en

Inventor: Stephane Bancel, Tirtha Chakraborty, Antonin de Fougerolles, Sayda M. Elbashir, Matthias John, Atanu Roy, Susan Whoriskey, Kristy M. Wood, Paul Hatala, Jason P. Schrum, Kenechi Ejebe, Jeff Lynn Ellsworth, Justin Guild

Current Assignee: ModernaTx Inc

2012-04-02 Priority to US201261618868P
2016-02-04 Application filed by ModernaTx Inc
2016-06-02 Publication of US20160152678A1
2017-03-07 Publication of US9587003B2
2017-03-07 Application granted

So Moderna first applied for a patent for the 19 nucleotide sequence in 2013 on December 16. Perhaps December25 would have been more appropriate since it was destined to become the Crown of Thorns of Mathew27, Mark15 and John19

Table2: Shows that the sequence occurs in Covid-19 from nucleotide 23601 to 23619.

Table3: Shows that this gene sequence does not exist in nature (but 14 nucleotide parts of it do).

I decided to check their work. Yes. I fact checked them (I will send an invoice to the globalists). This turned out to be a bit of an epic journey. The Google patent page for **US9587003B2** does not contain the gene sequence. The pdf of the patent does not contain the gene sequence and is not searchable from pages 101-304. But it does have a link to a lengthy 'Sequence Listing" section which link one cannot copy. So I manually transcribed it in my fair hand – http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US09587003B2

From that page you can enter the Sequence ID quoted in the paper as 11652 and get to https://seqdata.uspto.gov/?pageRequest=viewSequence&DocID=US09587003B2&seqID=11652 which has the following at Nucleotides 2751-2733 reading backwards…

gccctgatca ccatcatggc ccagatcggc ag**ctacgtgc ccgccgagga g**gccaccatc 2760

CTACGTGCCCGCCGAGGAG patented by Moderna is the reverse compliment of CTCCTCGGCGGGCACGTAG, the 19 nucleotide sequence which appears in Covid-19 DNA from nucleotide 23601-23619 (which would therefore be covered by their patent).

Likewise you can search for the sequence in **US9149506B2** by going to https://seqdata.uspto.gov/?pageRequest=viewSequence&DocID=US09149506B2&seqID=11652, whereupon you will find the same thing again

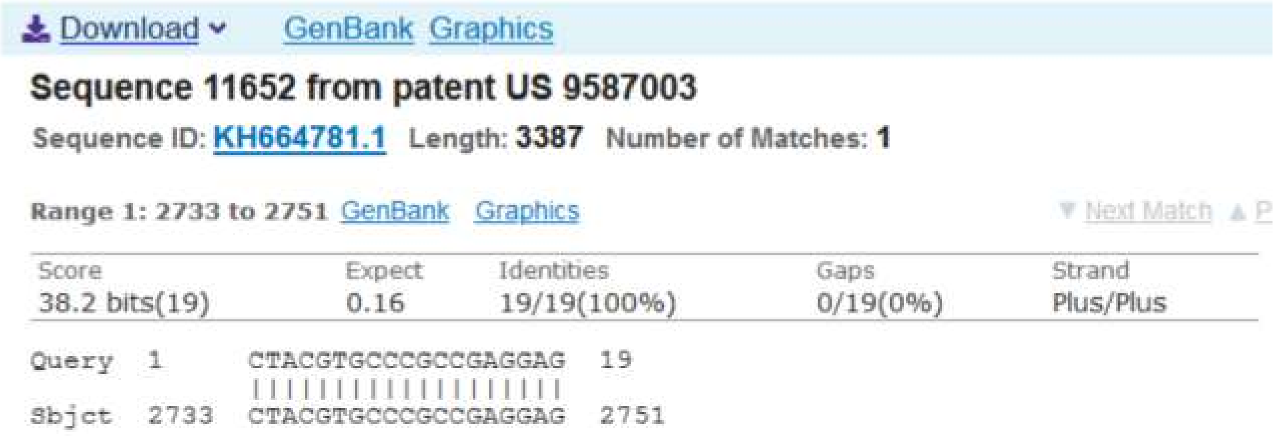
gccctgatca ccatcatggc ccagatcggc ag**ctacgtgc ccgccgagga g**gccaccatc   2760

I then searched the gene sequence of Wuhan Hu1 (alpha) at https://www.ncbi.nlm.nih.gov/nuccore/NC_045512 and found

23581 ttatcagact cagactaatt **ctcctcggcg ggcacgtag**t gtagctagtc aatccatcat from https://www.ncbi.nlm.nih.gov/nuccore/NC_045512

Which has the 19 nucleotide sequence CTCCTCGGCGGGCACGTAG from 23601-23619 as described in table 3.

I then ran my own non aligned blast search of all patented gene sequences for the reverse compliment directly (or perhaps for a back handed compliment) and got the same results as the researchers



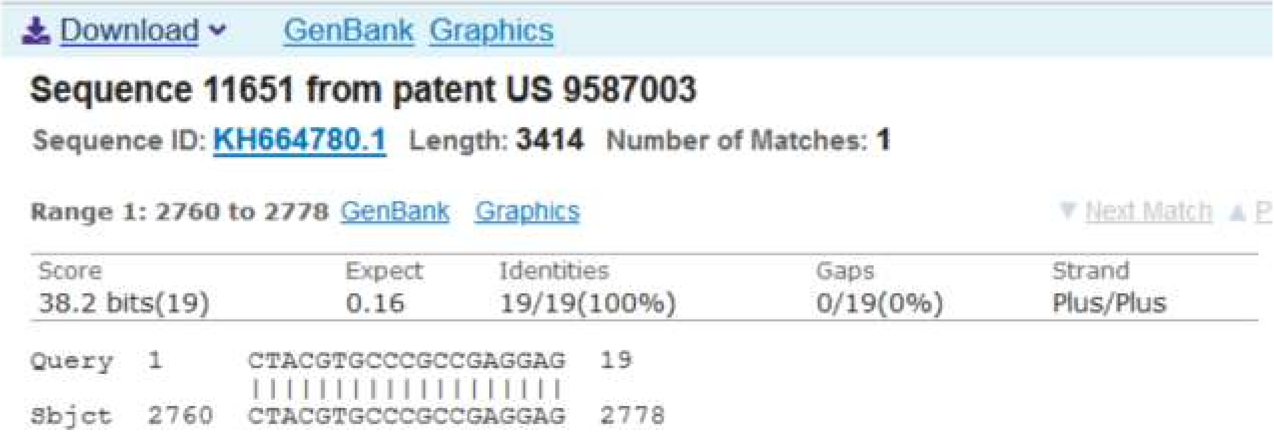
Sequence 11652 from patent US 9587003

Sequence ID: KH664781.1 **Length:** 3387 **Number of Matches:** 1

Range 1: 2733 to 2751

Score	Expect	Identities	Gaps	Strand
38.2 bits(19)	0.16	19/19(100%)	0/19(0%)	Plus/Plus

```
Query  1     CTACGTGCCCGCCGAGGAG  19
             |||||||||||||||||||
Sbjct  2733  CTACGTGCCCGCCGAGGAG  2751
```



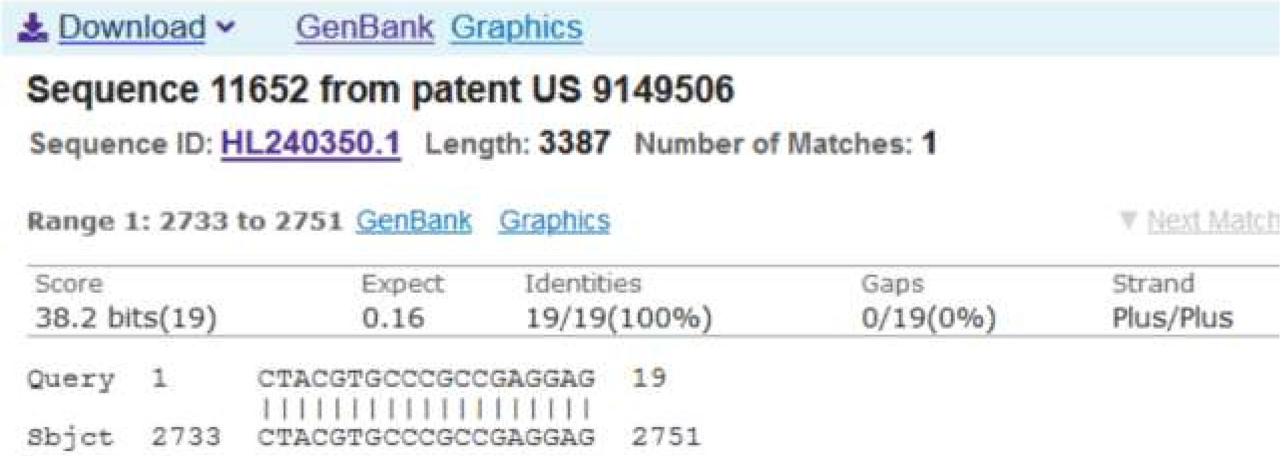
Sequence 11651 from patent US 9587003

Sequence ID: KH664780.1 **Length:** 3414 **Number of Matches:** 1

Range 1: 2760 to 2778

Score	Expect	Identities	Gaps	Strand
38.2 bits(19)	0.16	19/19(100%)	0/19(0%)	Plus/Plus

```
Query  1     CTACGTGCCCGCCGAGGAG  19
             |||||||||||||||||||
Sbjct  2760  CTACGTGCCCGCCGAGGAG  2778
```



Sequence 11652 from patent US 9149506

Sequence ID: HL240350.1 Length: 3387 Number of Matches: 1

Range 1: 2733 to 2751 GenBank Graphics ▼ Next Match

Score	Expect	Identities	Gaps	Strand
38.2 bits(19)	0.16	19/19(100%)	0/19(0%)	Plus/Plus

```
Query  1     CTACGTGCCCGCCGAGGAG  19
             |||||||||||||||||||
Sbjct  2733  CTACGTGCCCGCCGAGGAG  2751
```

Sequence 11651 from patent US 9149506

Sequence ID: HL240349.1 Length: 3414 Number of Matches: 1

Range 1: 2760 to 2778 GenBank Graphics ▼ Next Match

Score	Expect	Identities	Gaps	Strand
38.2 bits(19)	0.16	19/19(100%)	0/19(0%)	Plus/Plus

```
Query  1     CTACGTGCCCGCCGAGGAG  19
             |||||||||||||||||||
Sbjct  2760  CTACGTGCCCGCCGAGGAG  2778
```

And the same for the other 3 US patents.

So I can confirm, and the reader can confirm using the links above, that Moderna did apply for a Patent not only on the reverse compliment of the 12 nucleotide Furin Cleavage Site in Covid-19 but actually on the 19 nucleotide sequence containing it as described above.

Furthermore they did not merely apply for a patent on 2016 February 4 with **US9587003B2:** as reported in the Daily Mail. They actually applied on 2013 December 16 for 4 patents with **US9149506B2, US9216205B2, US9255129B2, US9301993B2**:as well.

So Moderna had developed the 19 nucleotide gene sequence containing the Furin Cleavage Site which gives Covid19 its infectivity to humans by patented gain of function research as early as 2013, 6 years before the Wuhan outbreak took place. Not 3 as reported in the Mail and virally elsewhere..

So now we look at the chances of this occurring naturally. The paper calculates the probability of this particular 19 nucleotide sequence occurring randomly in a 30,000 nucleotide virus as

$(30{,}000-18) \times (1/4)^{19} = 1.09 \times 10^{-7}$

Which is correct because there are 30,000-18 places to start the sequence given that it needs a further 18 more letters to complete it. But there are actually 29,904 nucleotides in Wuhan HU1 (alpha). So a more accurate calculation would be

$(29{,}904-18) \times (1/4)^{19} = 1.087 \times 10^{-7}$

Then they calculate the chances that the 19 nucleotide sequence occurs in the patented library of 24,712 sequences with a mean length of 3300 nucleotides. But that calculation is irrelevant because the sequence did not randomly appear in 5 Moderna Patent applications. The sequence was known to code for a Furin Cleavage Site, which is known to provide gain of function to Coronaviruses.

It was put there deliberately and patented due to its infecting power in humans, which we shall see, later in the article, results from the normal viral Arginine (R) codon AGA (used in 45% of viral Arginine codons) being replaced by the human Arginine codon CGG (used in 0% of viral Arginine codons) in the furin cleavage site.

All we are tying to work out here is what the chances are of a 19 nucleotide sequence patented by Moderna turning up in Covid-19 through natural causes, the natural mutations of Bat Coronavirus RaTG13 or some other virus.

The nucleotides form Codons which are triplets. So there are 64 possible triplets of the 4 DNA nucleotides ACGT (4x4x4 = 64). But all triplets do occur. 61 code for 20 amino acids redundantly and 3 are stop codons which tell the ribosome to stop making the protein.

But things are not this simple because the Furin cleavage site appears in the spike protein where it needs to be and the spike protein only has 1273×3 = 3819 nucleotides. The chances of the 19 nucleotide Furin Cleavage sequence appearing in the spike protein are

$(3{,}819-18) \times (1/4)^{19} = 1.389 \times 10^{-8}$

Or 1 in 72 million. So those would be the chances that one particular variant, say the first Covid-19 variant, had the 19 nucleotide sequence in the right place (the spike). And it did. So certainly by the balance of probabilities, and certainly beyond a reasonable doubt (1 in 72 million being an unreasonable doubt) Moderna made Covid-19.

100% Biochemic Proof that Covid19 was Man Made

The Double CGG Codon used in the Moderna Specific Furin Cleavage site does not occur in any other Furin cleavage site in any other virus in nature. Furin cleavage sites do occur in other viruses but NOT at all in other betacoronaviruses like Covid-19 and NOT at all with the double CGG codon.

Arginine (R), can be encoded by any of the 6 triplets: AGG, AGA, CGA, CGC, CGG, CGT. In Covid-19, the furin site (PRRA), has 12 nucleotides (3 x 4). In Covid-19, the RR doublet of the furin site is encoded by CGG-CGG.

Two Biochemists Prof Antonio R. Romeu and Assistant Prof Enric Ollé analysed the RR doublet from a large sample of furin cleavage sites of several kinds of viruses. They found that there were no RR doublets encoded by the CGG-CGG codons in any virus in nature. They observed that the AGA triplet was the majority codon involved in these viral RR doublets.

In all genetic recombination (where a part of one genome merges with another genome), the donor code is passed to the acceptor. But there is simply NO KNOWN VIRUS with a Moderna Specific Furin Cleavage Site (having the CGG-CGG codon pair) that exists to donate a Moderna Specific furin cleavage site to Covid19. So the only way that sequence could get into Covid-19 is from Moderna. Moderna was the donor. Nature was not. QED. Case Closed..

But it gets worse.

The Spanish Profs decided to analyse the arginine codon usage in every single protein in Covid-19. The found the following…
AGG (13%)
AGA (45%)
CGA (5%)
CGC (10%)
CGG (3%)
CGT (24%).

So the AGA codon triplet was the majority, and interestingly, CGG was the minority codon for Arginine in the virus.

But it gets worse still.

In the specific case of S protein, of the 42 Arginines (R) it has, 20 are encoded by AGA, and only 2 by CGG. These 2 of course, are the two in the Moderna Specific Furin Cleavage Site.

So the only Arginine in the spike protein that is encoded a la Moderna are in the Furin Cleavage site. The other 40 instances do not use CGG at all.

They then go on to comment that each individual species in nature has its own codon preferences. Obviously viruses like AGA, and do not like CGG at all, in nature.

But guess which species does use CGG for Arginine more than the other 5 competing codons – yes its jolly old homo sapiens. Our coding preferences for Arginine are

AGG (20%)
AGA (20%)
CGA (11%)
CGC (19%)
CGG (21%)
CGT (9%).

So the CGG codon in the furin cleavage site WILL have come about through Chimeric (human animal combination) gain of function research.

Could Somebody other than Moderna have made Covid-19 using the Moderna Specific Furin Cleavage Site?

"New documents show that just 18 months before the first Covid-19 cases appeared, researchers had submitted plans to release skin-penetrating nanoparticles and aerosols containing "novel chimeric spike proteins" of bat coronaviruses into cave bats in Yunnan, China. They also planned to create chimeric viruses, genetically enhanced to infect humans more easily, and requested $14million from the Defense Advanced Research Projects Agency (Darpa) to fund the work.

Papers, confirmed as genuine by a former member of the Trump administration, show they were hoping to introduce "human-specific cleavage sites" to bat coronaviruses which would make it easier for the virus to enter human cells.
When Covid-19 was first genetically sequenced, scientists were puzzled about how the virus had evolved such a human-specific adaptation at the cleavage site on the spike protein, which is the reason it is so infectious." – the Telegraph

I can see all of the great journalists at the Daily Mail and the Telegraph (not to mention scientists around the world) doing all of this research into Covid19 and reaching the inevitable logical conclusion that there was either an accidental or a deliberate lab leak and then having to word their conclusions in such a way as to label that strong probablity as a weak possibility.

But here above we have proved it as a fact (since the Moderna Specific Furin Cleavage Sequence CGG codon does not occur in any furin cleavage site in any natural virus and therefore it cannot have been the result of natural genetic recombination. So it has to be the result of man made genetic insertion.

In theory a further party involved with the NAIAD or the NIH could have used the furin cleavage site patented by Moderna and made Covid19 themselves. This would not have broken any patent of Moderna. The Furin cleavage site itself is not patentable having been known since at least 2004

US7223390B2: Insertion of furin protease cleavage sites in membrane proteins and uses thereof
2004-05-07 Application filed by Research Development Foundation
2004-11-11 Publication of US20040224391A1
2007-05-29 Application granted

Although Moderna could actually have patented the Moderna Specific (CGG for AGA) encoding of the furin cleavage site which was is not known in nature even today (if we accept that Covid-19 is man made).

But given that the lab leak (deliberate or accidental) came from Wuhan, and given the Chinese cover up and given the Fauci denials exposed by Senator Rand Paul, and given the NIH, NIAID cover ups and the US Intelligence services cover up, when their 3 month long report into the origin of Covid-19 ordered by presidential impersonator Biden yielded nothing, and given the relationships between the NIAID, the NIH, the WIV, the EcoHealth Alliance, the University of North Carolina and Moderna, I cannot see any room for anyone else.

Furthermore the entire unholy cabal of bad actors started developing the Moderna Vaccine before the pandemic struck – https://www.infowars.com/posts/must-watch-nih-claimed-joint-ownership-of-moderna-mrna-vaccine-began-development-weeks-ahead-of-pandemic/

But things are not as simple as that because nature has had certainly 100,000 years to make human viruses and it never once put a Moderna specific (CGG for AGA) furin cleavage site into anything, nor did it put the 19 nucleotide sequence in anything before.

Yet within 6 years of Moderna patenting it, we find it in Covid-19 in circumstances where Moderna is working with that virus. So just there the probability is not 100,000 to 6 or 16,666 to 1 that Moderna is responsible rather than nature. No it is 100% because nature has not done it. It never has and there is no evidence that it ever will.

It is man the mixes up human and viral Arginine codons not nature.

Pro Luc Montagnier spent the last years of his life proving that COVID-19 was man made and containing much of the HIV1 genetic code

Prof Luc Montagnier, before he died on 2022February8, did a total assassination of the concept that Covid-19 evolved naturally by showing that it had massive equivalence to HIV. The diagram below shows a 275 nucleotide region of Covid-19 which has 200 nucleotides from HIV/SIV (Simian ImmunoVirus) in it. And remember there are 61 codons specifying 20 amino acids. So one can say the same thing in on average 3 different ways with codons.

You can download a pdf of his study here and the supplementary materials here. It is very technical. But he did win the Nobel prize for discovering the HIV virus. So if anyone would know if Covid had been boosted with HIV, it would be him. He pointed out that Covid-19 was man made early in the pandemic and was himself assassinated by the press and the fact checkers as a result. Every single fact checker who attacked him was wrong.

There was no scientific basis to any of their fact checking. These outfits are not fact checkers at all of course. They are globalist disinformation agencies, sons of Goebbels, fact chuckers and science deniers. They are about as trustworthy as an American election. I can check a fact for myself thank you very much. I don't need a brainwashed woke madrassa student telling me their opinion about a subject that they never studied at University.

So, to summarize: a contiguous region representing 2.49% of the whole COVID-19 genome is 40.99% made up of 12 diverse EIE originating from various strains of HIV SIV retroviruses.

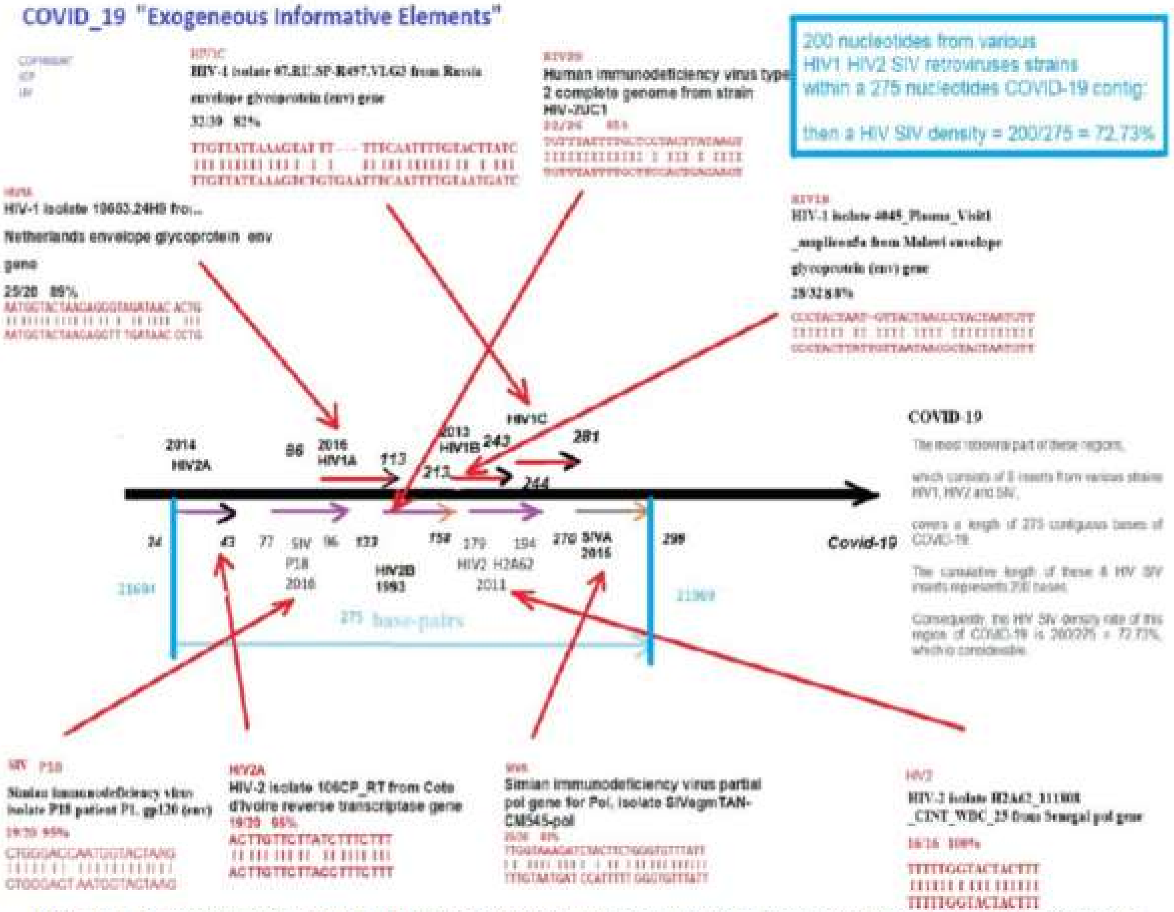


Figure 2: Summary chart of the 8 HIV/SIV EIE from region "B". This summary chart demonstrating how 200bases from various HIV SIV retroviral strains within a concentrated 275bases COVID-19 contig have a density rate equal to 72.73%.

Since we have proven beyond a reasonable doubt (beyond a 1 in 72 million doubt statically and with 100% certainly biochemically from the Moderna Specific Furin Cleavage Site) that Moderna made Covid-19. And since Moderna and Fauci have not admitted to having made it and have in fact covered up evidence to that effect, it may be the case that they are hiding something else as well.

Because the only two theories now left are the accidental lab leak theory and the deliberate lab leak theory. I mean the vast majority of political leaks are not accidents. They are deliberate strategies to provide advantage to the leaker or his paymaster. It is well known in the IT industry that viruses appear when antivirus sales are needed. Why would things be any different with human viruses, now that they can be man made too? Especially when you consider the massive role of Bill Gates and his foundation and GAVI and GVAP in he global vaccination business.

The only reason that Moderna would make Covid-19 is to release it. Otherwise the entire exercise would be financially futile, commercially pointless

The reason adduced by Fauci for doing gain of function research is that man needs to be ahead of nature or bad actors in order to have a vaccine in good time if a disease mutates or is genetically modified by the Chinese or the Russians to be lethal.

But in order to believe that one has to believe that Moderna are interested in the saving people’s lives. I am sorry. All their actions show to me that they are interested in vaccinating people knowing how likely that is to cost them their lives.

They are interested in profit, the profit that comes from a pandemic. They are not saviours of mankind as they represent. They are our exploiters and our abusers.

They produced the virus in order to leak it, in order to pose as our saviours from their own leak. These are not the activities of a saviour figure. Luc Montagnier was trying to be our saviour from them and he was assassinated (professionally) by their groupies. Moderna were doing gain of function research in order to release the virus and force a vaccine for it in a manner which would maximise their profits. That is not a conspiracy theory. It is what happened precisely. Their share price went up by 20x.

They released it in order to sell their vaccines and to destroy the immune systems of their customers because our immune systems reduce their profits. That is Big Pharma business.

The reason that the writer is so confident that Moderna or their agents made and leaked Covid-19 and the reason I called it as such at the start of the pandemic to almost as much ridicule as Prof Montagnier received (God bless him) is that the scriptures say in Matthew27, Mark15 and John19 that.

29 And they (the soldiers of the governor of verse 27) platted a crown of thorns and put it upon his head, and a reed in his right hand; and they kneeled down before him, and mocked him, saying, Hail, King of the Jews!

30 And they spat upon him, and took the reed and smote him on the head. (Matthew 27 ASV)

May I therefore beg your indulgence whilst I interpret these words:

The US department of defence funded the gene splicing of the Coronavirus of Spike Proteins (Covid-19) through NIH and NIAID and DARPA which first infected Jesus, through his fiance, the New Covenant Saints, just after he became the secular King, Caesar to those saints, the antitypical Jews, those covenanted to be angelic sons of Jacob, the born agains angelically.

We calculated that the malediction which prevented Jesus becoming Caesar to the saints ended in 2019Tishri15 (October17/18). Glenn Beck did a documentary showing that 10 hospitals in Wuhan took cases with Covid19 symptoms in October 2019. Yes Folks. Covid-19 is a proof that Jesus is now secular King over the saints, the antitypical Jews, the Jews by angelic salvation covenant, at the least.

But then the soldiers spat upon him. For that is how Covid19 is transferred, through small aerosol droplets exhaled out of the mouth. The soldiers deliberately spat upon him. It was not a SALIVA LEAK! They smote Jesus on the head because the saints are the head of the church and they caught Covid19 not by random chance infection but by a deliberate smiting with a read, a biological weapon, a deliberate weaponised attack. For more on this see here.

So what Prof Montagnier saw with his virology expertise, I saw with my theological expertise. Showing that whilst fact checkers and science are mutually exclusive, science and theology actually agree, when properly understood (and that is one big caveat). Prof M taught us that the vaccines cause the variants. Indeed basic virology forbids mass vaccination during a pandemic for that very reason. He said the the curve of deaths follows the curve of vaccinations. Mind you, paradoxically, if the vaccines caused Omicron, then they saved us from themselves!

The Time has Come to hold People and Organisations to Account

The Covid19 makers, the genetic vaccine makers. their funders and their promoters, which include almost every government and public sector and health service in the world, are therefore guilty of Genocide and crimes against humanity. They have pushed genetic rape and sickness and death onto half of the population of the world in order to enrich the pockets of Pharmaceutical Companies. Governments and Public sectors around the world have abandoned their health service regulation to billionaires and heartless corporations

In the UK, all of the income tax we pay goes to the health service and all of its protocols are determined by its regulators and all of its regulators are controlled and funded by Big Pharma who seek to damage then manage our health for their profit.

So every penny we spend in income tax brings us one step closer to sickness, to death and to drug dependency.

So why did Prof Montagnier choose to spend the last years of his life proving that Covid-19 was man made and that the spike proteins, and therefore the vaccines, were an existential threat to the species? What did he have left to prove to himself or to anybody else at 87-89? He certainly did not do it to increase his reputation in the profession.

No, he was driven by the same passion that drove him to discover HIV. A passion to SAVE mankind from viruses and those who would engineer them to damage us. And why did he give up the ghost in February 2022? Because he knew that Omicron had the vaccines beat. His job was done by a greater virologist even than him. He could therefore rest in peace and go see some people who understood the magnitude of his contribution.

Covid-19 was not made in 2019. It was made from the 19 nucleotide Moderna specific chimeric (CGG for AGA) furin cleavage site which does not occur anywhere in nature. And every Covid death and every Covid vaccine death is parked squarely on the doorstep of ModeRNA waiting for justice.

But we shall not execute that justice fast enough. And therefore the final plague upon mankind of Revelation 6:8, delivered by the 4th horseman of the apocalypse, which plague Bill Gates himself has prophesied, will arrive later this year (after War and after Famine, the 2nd and 3rd horsemen).

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