Exhaustive proof Moderna made Covid-19

Description

By a concerned reader who is a qualified cell biologist via Daily Exposé.uk

STEP 0: The genome, the complete genetic code of Covid19 is found here – *https://www.ncbi.nlm.nih.gov/nuccore/NC_045512.2/* The genome of Bat Coronavirus RaTG13 is found here – *https://www.ncbi.nlm.nih.gov/nuccore/MN996532*

One can compare these two genomes, letter by letter using the BLAST Genome alignment comparison tool at *https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastSearch&BLAST_SPEC=blast2seq&LINK_LOC*

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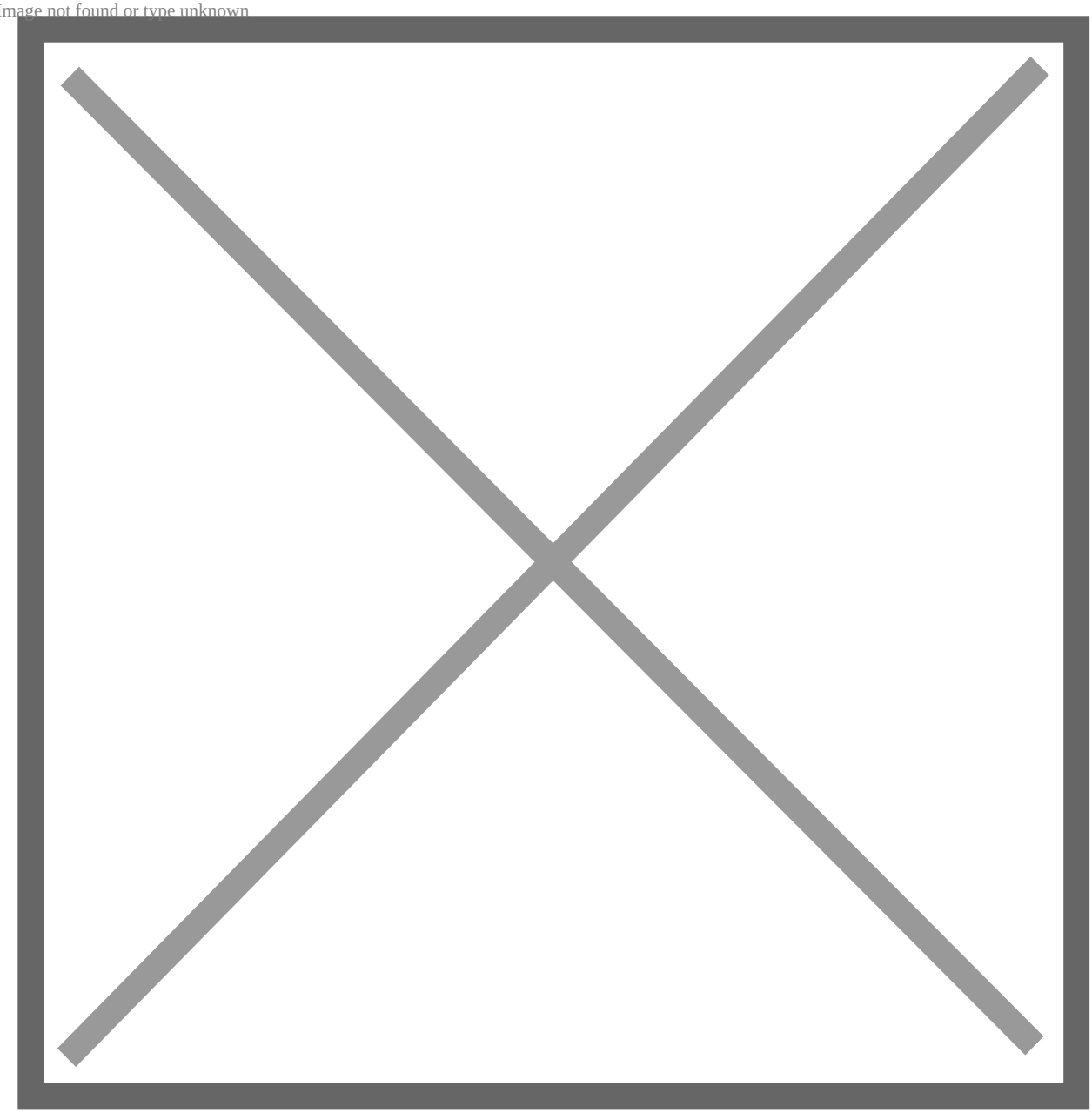

Just put NC_045512.2 in the Query Sequence Box and MN996532 in the Subject Sequence Box. Then choose the radio button:: More dissimilar sequences (discontinguous megablast). Then hit BLAST. Then when the results appear (a few second later) choose the Alignments tab and you will see both genomes compared perfectly. For the entire comparison see here

A is the base Adeninie
C is the base Cytosine
G is the base Gaumine
T is the base Thymine (not Thiamine which is a Vitamin added to Cornflakes)

The two genomes (full genetic codes) are 96% Identical. Here are all the differences…

There are 995 instances of a 1 letter mismatch
There are 24 instances of a 2 letter mismatch
There are 4 instances of a 3 letter mismatch
There are no further mismatches

There are 2 instances of a 1 letter omission at lines numbered 27341 and 29800.
There are 2 instances of a 2 letter omission at lines numbered 22981 and 23038
There are 2 instances of a 3 letter omission at lines numbered 3301 and 26504
There is one instance of a 12 letter omission at line numbered 23576
There are no further omissions.

Here are all the omissions –

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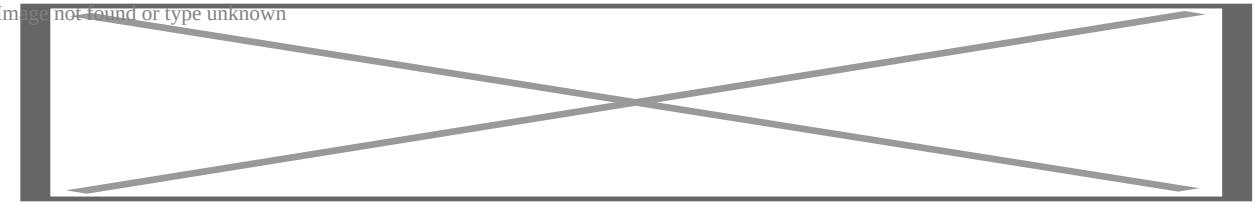

And that is it. There are no further differences. The overall match is 28723 letters out of 29877(96%). The total numbers of gap letters is 24 (12+3+3+2+2+1+1).

Natural mutations normally occur one letter at a time. So to determine whether or not Covid19 is man made we just have to look at the 12 letter gap, which is way too large for a series of random mutations that just happened to occur right next to each other in a 29877 letter genome, and all in the 6 years between 2013 (when RatG13 was sequenced) and 2019 when Covid-19 appeared. So the extra 12 letters, the extra 12 bases, the extra 12 nucleotides (base + sugar + phosphate) were inserted from another genome, either by nature or by man.

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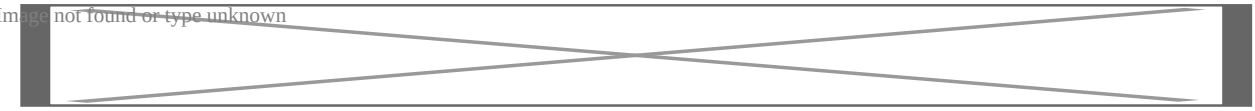

Each 3 letter group (called a codon) codes for one amino acid. So the inserted group in whole codons is actually…

TCT CCT CGG CGG GCA which codes for SPRRA (Serine, Proline, aRginine, aRginine, Alanine).

But the Furin Cleavage Site is PRRAR which includes the next Codon CGT which also codes for aRginine (R).

So the only difference between Covid-19 and RaTG13 which involves more than 3 nucleotides (more than one complete 3 letter Codon) is the Furin Cleavage Site which involves 12 nucleotides and parts of 5 Codons (15 nucleotides).

STEP 1: Run a BLAST virus search *https://www.ncbi.nlm.nih.gov/labs/virus/vssi/#/* to see if this sequence (TCTCCTCGGCGGGCA) occurs in any virus in nature other than Covid19. Answer: It does not.

Search also for CTCCTCGGCGGGCA – Answer: It does not occur in any natural virus.. One cannot search just for the 12 letters CCTCGGCGGGCA because the search must have 14 letters minimum for some reason.

Search also for CCTCGGCGGGCACGT which codes for PRRAR, the famous Furin Cleavage site, which gives Covid-19 its gain of function infectivity – Answer: It does not occur in any natural virus.

STEP 2: Run a Patent BLAST *(Basic Local Alignment Search Tool https://blast.ncbi.nlm.nih.gov/Blast.cgi choose 'Blastn' and make sure 'align 2 or more sequences' is unchecked and choose patent sequences)* search of every patent application for the 14 nucleotide sequence CTCCTCGGCGGGCA which is the 12 nucleotide insert plus the rest of the final 3 letter codon, the next two letters. We have to do this because the BLAST searches need a minimum of 14 letters. You cannot do a BLAST search for 12 nucleotides. In the Algorithm Parameters section set max targets to 5000.

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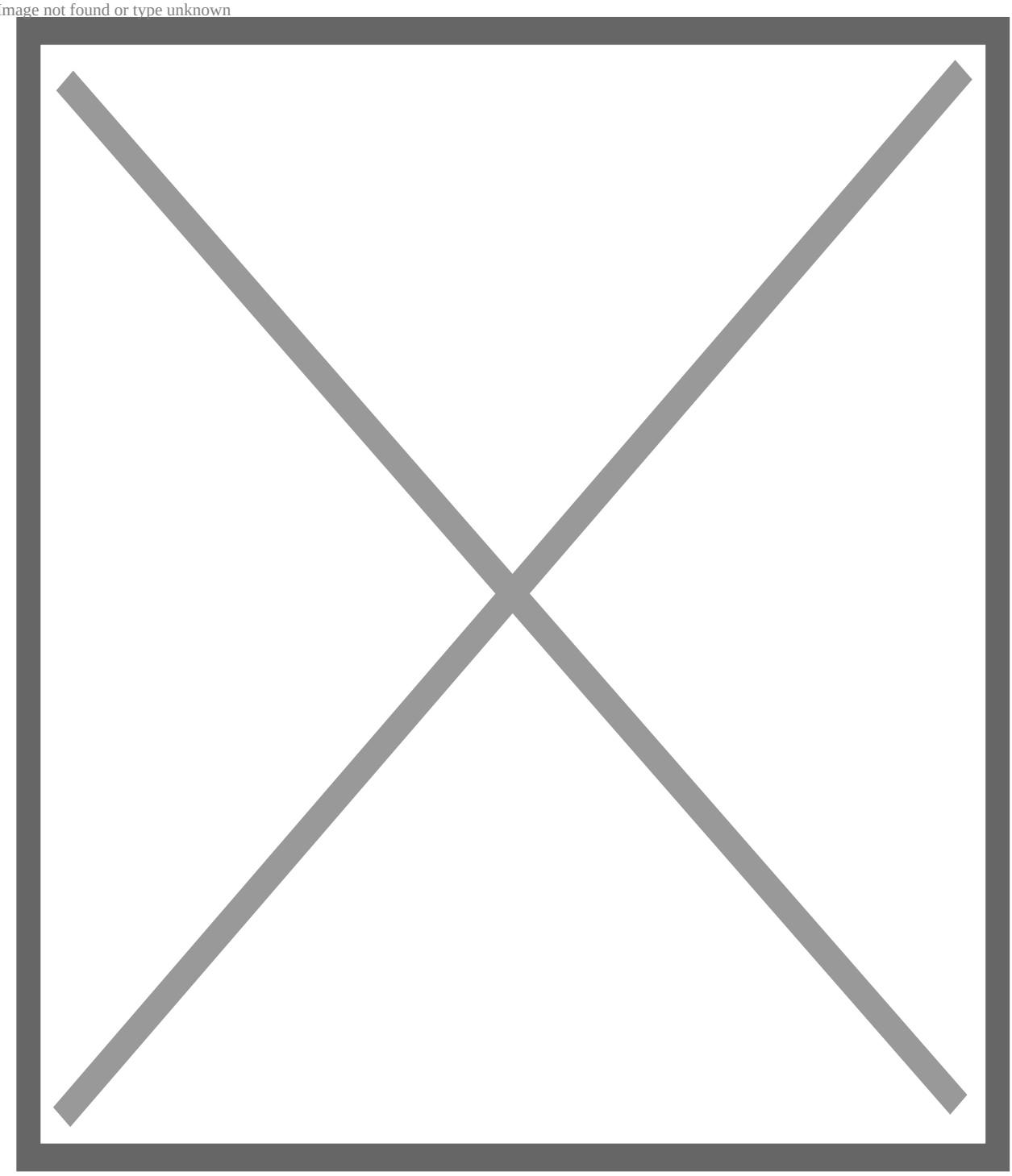

Here are the results…

US5606032A: Process for preparing glial mitogenic factors
Description: The most disgusting imaginable method of obtaining a 745 base pair sequence of DNA from Bovine pituitary glands which has the wonderful capability of stimulating the division of rat Schwann cells in when resident in fetal calf blood plasma.

Inventor: Andrew Goodearl, Paul Stroobant, Luisa Minghetti, Michael Waterfield, Mark Marchioni, Mario S. Chen, Ian Hiles
Current Assignee: Ludwig Institute for Cancer Research Ltd, Acorda Therapeutics Inc

1991-04-10: Priority to GB919107566A
1995-06-06: Application filed by Ludwig Institute for Cancer Research Ltd, Cenes Pharmaceuticals Inc
1997-02-25: Application granted and published
2017-02-25: PATENT EXPIRED

So the first patented appearance of the 14 nucleotide insertion was in a 745 nucleotide sequence extracted from Cow's pituitary glands and published in 1997 at the beginning of the public internet!

US5958721A: Methods for screening of substances for therapeutic activity and yeast for use therein
Inventor: Christopher John Marshall, Alan Ashworth, David Anthony Hughes
1993-04-07: Priority to British Patent GB9307250
1994-03-31: Application filed by Cancer Research Campaign Technology Ltd
1999-09-28: Application granted and published
2099-09-28: PATENT EXPIRED

Description: Candidate pharmaceuticals for use in treatment of cancer, inflammatory disorders, cardio-vascular disorders or neurological disease. – Pretty much all the side effects of mRNA vaccines !

They used the mammalian MAPKK (Mitogen Activated Protein Kinase Kinase) gene sequence (containing the 14 nucleotide insert sequence) in yeast to screen for anti cancer capability. They did not use it in a virus.

US6074828A: Amino acid transporters and uses
Description: DNA encoding human amino acid transporters.

Inventor: Susan G. Amara, Jeffrey L. Arriza
Current Assignee: Oregon Health Science University

1998-03-17: Application filed by Oregon Health Science University
2000-06-13: Application granted and published
2020-06-13: PATENT EXPIRED

So the 14 nucleotide sequence exists in humans as well as cows.

US6833447B1: Myxococcus xanthus (a bacterium) genome sequences and uses thereof
Inventor: Barry S. Goldman, Gregory J. Hinkle, Steven C. Slater, Roger C. Wiegand,
2001-07-10: Application filed by Monsanto Technology LLC
2002-01-11: Assigned to MONSANTO TECHNOLOGY LLC
2004-12-21: Application granted and published

So the 14 nucleotide gene sequence exists in humans, in cows, and in bacteria. And it has been used in yeast.

Patent monopolies last for 20 years. So some of these monopolies granted on a novel use of naturally occurring DNA from humans, cows and bacteria, expired before Covid19 came along. But it was actually the British who started isolating and using DNA containing the 14 base pair insert first – woops!

STEP 3: In order to make the sequence into a Furin cleavage site which gives the virus its infectivity, we must add the final Arginine codon CGT and get the 17 nucleotide sequence CTCCTCGGCGGGCACGT, which we call the double CGG coded furin cleavage site insert.

We now run a BLAST *(Basic Local Alignment Search Tool https://blast.ncbi.nlm.nih.gov/Blast.cgi choose 'Blastn' make sure 'align 2 or more sequences' is unchecked and choose patent sequences)* of every patent application for the 17 nucleotide Furin Cleavage Site sequence CTCCTCGGCGGGCACGT. Here are all the 100% match results (dated before the arrival of Covid19 in October 2019.

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
2017-03-07 Application granted and published

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
2013-12-16 Application filed by Moderna Therapeutics Inc
2016-04-05 Application granted and published
2020-01-10 First worldwide family litigation filed

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
2013-12-16 Application filed by Moderna Therapeutics Inc
2016-02-09 Application granted and published

US9216205B2: Modified polynucleotides encoding granulysin – *https://patents.google.com/patent/US9216205B2/en*
Inventor: Tirtha Chakraborty, Antonin de Fougerolles
Current Assignee: ModernaTx Inc
2013-12-16 Application filed by Moderna Therapeutics Inc
2015-12-22 Application granted and published

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

Inventor: Tirtha Chakraborty, Antonin de Fougerolles
Current Assignee: ModernaTx Inc
2013-12-16 Application filed by Moderna Therapeutics Inc
2015-10-06 Application granted and published
2020-01-10 First worldwide family litigation filed

Sequence 11651 from patent US 9149506
Sequence ID: HL240349.1
Range 1: 2762 to 2778
Plus/Minus (this means the match is for the reverse compliment of the sequence which is CTCCTCGGCGGGCACGT because A bonds with T and C bonds with G.

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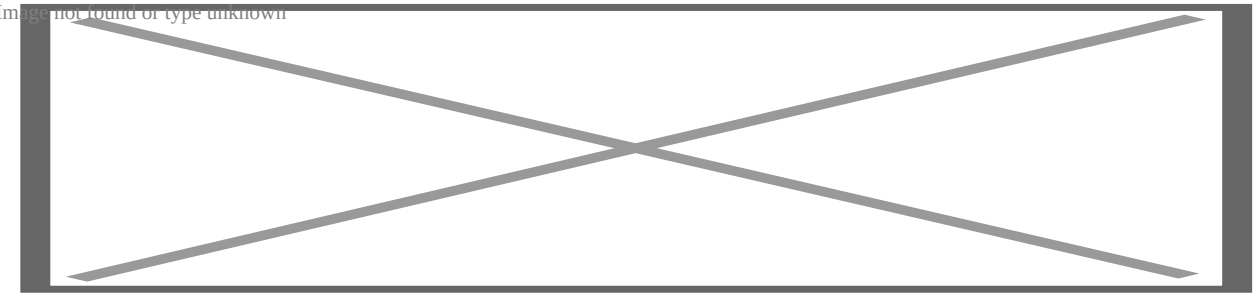

US9024113B2: Polynucleotides for expression of microbial starch branching enzymes in plants for production of plants with improved yield
Inventor: Yongwei Cao, Gregory J. Hinkle, Steven C. Slater, Xianfeng Chen, Barry S. Goldman,
Current Assignee: Monsanto Technology LLC
2007-10-29: Application filed by Monsanto Technology LLC
2014-04-18: Assigned to MONSANTO TECHNOLOGY LLC
2015-05-05: Application granted and published

Monsanto used the sequence to genetically modify plants, not humans.

US8952217B2: Process for decreasing verbascose in a plant by expression of a chloroplast-targeted fimD protein
Inventor: Piotr Puzio, Birgit Wendel, Michael Manfred Herold, Ralf Looser, Astrid Blau, Gunnar Plesch, Beate Kamlage, Florian Schauwecker
Current Assignee: BASF Metabolome Solutions GmbH
2006-09-06: Application filed by Metanomics GmbH
2015-02-10: Application granted and published

BASF used the gene sequence for the Genetic Modification of plants.

US8372601B2: Compositions and methods for the synthesis of APPA-containing peptides (as antibiotics)
Inventor: William W. Metcalf, Wilfred A. van der Donk, Junkal Zhang, Benjamin T. Circello, Svetlana A. Borisova
Current Assignee: University of Illinois at Urbana Champaign
2011-01-21: Application filed by University of Illinois at Urbana Champaign
2011-02-28: Assigned to NATIONAL INSTITUTES OF HEALTH (NIH), U.S. DEPT. OF HEALTH AND HUMAN
SERVICES (DHHS), U.S. GOVERNMENT
2011-05-13: Assigned to UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN
2013-02-12: Application granted and published

“Exemplary vectors suitable for replication in mammalian cells may include viral replicons, or sequences that ensure integration of an embodiment of the isolated nucleic acid of the present disclosure into the host genome. Suitable vectors may include, for example, those derived from simian virus SV40, retroviruses, bovine papilloma virus, vaccinia virus, and adenovirus”

“Expression of proteins encoded by an embodiment of the isolated nucleic acid of the present disclosure then occurs in cells or animals which are infected with the live recombinant vaccinia virus.”

This patent is about manufacturing proteins containing the amino acid sequence APPA. Covid19 does contain that sequence but not in the spike protein, which has the furin cleavage site. The patent claims DNA similar to Patent gene sequences 2,3,4 and 5-13. Whereas the Furin Cleavage site occurs in Patent gene sequence 14. So it is incidental to the patent.

US7635798B2: Nucleic acid compositions conferring altered metabolic characteristics
Description: This invention encompasses the identification and isolation genes and gene fragments that confer altered metabolic characteristics in Nicotiana benthamiana plants, when expressed using GENEWARE™ viral vectors.
Inventor: Thaddeus Weglarz, Daniel Gachotte, Beth Blakeslee, Ignacio Larrinua, David A. McCrery, Randy J. Pell, J. Vincent B. Oriedo, Barbara A. Miller, Avutu S. Reddy, Vipula Shukla, Rodney Crosley
2002-08-30: Application filed by Dow AgroSciences LLC
2004-10-01: Assigned to DOW CHEMICAL COMPANY, THE
2005-01-14: Assigned to DOW AGROSCIENCES LLC
2009-12-22: Application granted and published

Dow Agrisciences was using viruses to Genetically modify Tobacco plants.

US7314974B2: Expression of microbial proteins in plants for production of plants with improved properties

Inventor: Yongwei Cao, Gregory J. Hinkle, Steven C. Slater, Xianfeng Chen, Barry S. Goldman
2003-02-20: Application filed by Monsanto Technology LLC
2003-08-25: Assigned to MONSANTO TECHNOLOGY LLC
2008-01-01: Application granted and published

Monsanto used the gene sequence in their genetic modification of plants not humans or viruses.

US6869788B2: DNA encoding novel D-aminoacylase and process for producing D-amino acid by using the same
Inventor: Masami Osabe, Katsuyuki Takahashi, Toshifumi Yamaki, Teruo Arii, Toshihiro Oikawa
2002-02-01: Application filed by Mitsui Chemicals Inc
2002-09-30: Assigned to MITSUI CHEMICALS, INC.
2005-03-22: Application granted and published

Not to do with viruses.

STEP 4: Run a BLAST (Basic Local Alignment Search Tool https://blast.ncbi.nlm.nih.gov/Blast.cgi chose Blastn make sure 'align 2 or more sequences' is unchecked and chose patent sequences) of every patent application for the 15 nucleotide Furin Cleavage Site sequence CCTCGGCGGGCACGT, which codes for PRRAR, Here are all the 100% new match results.

US6833447B1: Myxococcus xanthus (a bacterium) genome sequences and uses thereof
Inventor: Barry S. Goldman, Gregory J. Hinkle, Steven C. Slater, Roger C. Wiegand,
2001-07-10: Application filed by Monsanto Technology LLC
2002-01-11: Assigned to MONSANTO TECHNOLOGY LLC
2004-12-21: Application granted and published

The usual Monsanto team. So the CGG coded Furin Cleavage Site does exist in bacteria in nature, but not in viruses in nature.

US6912470B2: Genes and proteins involved in the biosynthesis of enediyne ring structures
Inventor: Chris M. Farnet, Alfredo Staffa, Emmanuel Zazopoulos,
Current Assignee: Thallion Pharmaceuticals Inc
2002-05-21: Application filed by Ecopia Biosciences Inc
2005-06-28: Application granted and published

Enediyne rings are cancer torpedoes. Ecopia were trying to improve the functionality and production of these torpedoes, which are not proteins. .

US7314974B2: Expression of microbial proteins in plants for production of plants with improved properties (Transgenic Plants)

Inventor: Yongwei Cao, Gregory J. Hinkle, Steven C. Slater, Xianfeng Chen, Barry S. Goldman
2003-02-20: Application filed by Monsanto Technology LLC
2003-08-25: Assigned to MONSANTO TECHNOLOGY LLC
2008-01-01: Application granted and published

US7750207B2: Transgenic plants:
Inventor: Kunsheng Wu, Santanu Dasgupta, Targolli L Jayaprakash, Shoba Cherian
Current Assignee: Monsanto Technology LLC
2006-09-01: Application filed by Monsanto Technology LLC
2010-07-06: Application granted and published

US7834146B2: Recombinant Polypetides Associated with Plants
Description: The Polypeptides may be promoted in the plants through Plant viruses such as the Cauliflower Mosaic Virus.
Inventor: David K. Kovalic, Yihua Zhou, Yongwei Cao, Scott E. Andersen, Michael D. Edgerton, Jingdong Liu
Current Assignee: Monsanto Technology LLC
2004-01-29: Application filed by Monsanto Technology LLC
2010-11-16: Application granted and published

So Ecopia was the first to file a human therapeutic use of the double CCG Furin Cleavage site insert in the form of better Enediyne ring cancer torpedoes on 2002May21
Dow Agrisciences was the first to file a patent to use it in a plant virus in 2002August30
The University of Illinois was the first to file a patent for the use the double CGG Furin Cleavage Site insert in a human virus on 2011January21. But they were trying to make APPA containing proteins as antibiotics. The Furin Cleavage Site was incidental to their patent.
Moderna is the only other outfit to file a human use of the insert before 2019. They filed 5 patents using the insert from 2013December16 to 2016February4. They were the last 5 patents filed using it before Covid19 broke out in October 2019.

STEP 5: Run a BLAST (Basic Local Alignment Search Tool https://blast.ncbi.nlm.nih.gov/Blast.cgi chose Blastn make sure ‘align 2 or more sequences’ is unchecked and chose all genomes and choose complete genomes) search of microbes for the 15 nucleotide Furin Cleavage Site sequence CCTCGGCGGGCACGT, which codes for PRRAR. It finds more than a thousand bacteria known to have this gene sequence! Myxococcus Xanthus has it 209 times!

So over a thousand bacteria have multiple copies of it. Humans have it. Cows have it. Plants have it. But no viruses have it at all except Covid19.

If nature was going to give it to viruses it would have done it by now, like it did with humans, like it did with cows, like it did with bacteria and like it did with plants..

Covid-19 was Man Made

The final codon completed inserted gene sequence CTCCTCGGCGGGCA does not exist in natural viruses and neither does the CGG coded Furin Cleavage site CCTCGGCGGGCACGT which codes for PRRAR. But they do exist naturally in bacteria and in humans and in cows and in plants. Viruses can invade bacteria and insert their genes into the them. But bacteria cannot insert their genes into viruses. So the only way for bacterial DNA to end up in a virus is by human intervention. So Covid19 must have been man made.

Profs Romeu and Olle

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 man.

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.

Was it Moderna or Someone else?

From our exhaustive patent searches we see that only Moderna and the University of Illinois and Ecopia Biosciences Inc were involved in human virus research using the double CGG Furin cleavage site. The University of Illinois was interested in the sequence APPA not PRRAR and they did not claim anything from the genome containing the double CGG coded PRRAR sequence.

Ecopia Biosciences was making Enediyne rings which are not proteins, but are cancer torpedoes which can be delivered by viruses . Whereas we know the Moderna's research led to their mRNA vaccines against Covid19. So they are the only candidate doing research in precisely the right area. They filed their first patent containing the double CGG coded Furin Cleavage site on 2013December16 and they filed the last 5 patents citing the double CGG insert before the Covid19 pandemic began.

Furthermore of all the patents citing the insert, only the Moderna Patents match the entire 19 nucleotide sequence CTCCTCGGCGGGCACGTAG in Covid19. No other patents filed before Covid19 arrived have the entire 19 letter sequence.

Moderna cite 7 patents on their website at https://www.modernatx.com/patents for their gene therapy mRNA-1273 (amino acid chain) vaccine…
US 10,703,789 filed January 12 2019
US 10,702,600 filed February 28 2020
US 10,577,403 filed June 12 2019
US 10,442,756 filed December 18 2017
US 10,266,485 filed June 11 2018
US 10,064,959 filed April 21 2017
US 9,868,692 filed July 27, 2017

The 2nd patent, filed on February 28 2020 was a continuation of an earlier patent application number 16/368,270 which was filed on March 28, 2019

So they had all 7 patents applied for by June12, 2019, which is quite impressive given that the WHO was only informed of a pneumonia type outbreak in Wuhan on December 31, 2019.

So all the patents needed to protect Moderna's particular vaccine monopoly were applied for 4 months before the outbreak of the disease that the vaccine is supposed to be curing.

Nature has had certainly 100,000 years to make human viruses and it never once put a double CGG

furin cleavage site into any virus. Yet within 6 years of Moderna referring to it in their patents, we find it in Covid-19 in circumstances where Moderna is working on a vaccine for 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 in a virus. It never has and there is no evidence that it ever will.

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

US 10,703,789 Here is what the patent claims: Claim1: A pharmaceutical composition comprising: a plurality of lipid nanoparticles comprising a cationic lipid, a neutral lipid, a cholesterol, and a PEG (polyethylene glycol) lipid, wherein the plurality of lipid nanoparticles has a mean particle size of between 80 nm and 160 nm; and wherein the lipid nanoparticles comprise an mRNA encoding a polypeptide, wherein the mRNA comprises:
(i) at least one 5?-cap structure;
(ii) a 5?-UTR (UnTranslated Region);
(iii) an open reading frame encoding the polypeptide and consisting of nucleotides including N1-methyl-pseudouridine (fake Uracil), cytosine, adenine, and guanine;
(iv) a 3?-UTR; and
(v) a poly-A region of least 100 nucleotides in length.

Claim1 is basically the finished vaccine. So in October 2019, just 4 months after 2019June12 when they got the N1 Methyl Pseudouridine (fake Uracil) patent filed, 10 hospitals in Wuhan had Coronavrius cases according to Glenn Beck's documentary.

"We do know just about 12 months later in Wuhan – where Peter Daszak, Dr. Shi, the bat lady, and Dr Baric were all doing research on coronaviruses – about a year later, there's an outbreak, and the outbreak actually begins according to documents that we have that have been smuggled out of China that there were 10 hospitals involved by October with patients that were now, we now know, are corona-like virus symptoms. They didn't know what was going on. Now, that was in October". – Glenn Beck – https://thelibertydaily.com/glenn-beck-drops-bombshells-on-tucker-nih-claims-joint-ownership-of-moderna-vaxx-started-working-on-it-long-before-pandemic/

So the writer can confirm, and the reader can confirm using the links above, that Moderna did apply for a Patent on the reverse compliment of the double CGG coded 15 nucleotide Furin Cleavage Site in Covid-19 and 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. But the bat coronavirus RaTG13 from which Covid19 was derived was also discovered in 2013. Well, what a coincidence!

Covid Prophets?

The reason that the writer is so confident that Moderna or their agents made and leaked Covid-19 and

the reason he 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, those born again 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 may have 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 profit drunk 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 having won the Nobel Prize for discovering the HIV virus?

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 their doorstep 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).

Wikipedia Disinformation

A certain professor from a UK Teaching Hospital wrote to me as follows

“You aught to read this from the Wikipedia article

Furin cleavage site
Some claims of bioengineering focus on the presence of two sequential cytosine-guanine-guanine (CGG) codons in the virus’ RNA, more precisely in the crucial furin cleavage site.[9][74] The CGG codon is one of several codons that translates into an arginine amino acid, and it is the least common arginine codon in human pathogenic betacoronaviruses.[105] Partially, this lack of CGG codons in human pathogenic coronaviruses is due to natural selection: B-cells in the human body recognize areas on virus genomes where C and G are next to each other (so-called CpG islands).[15][106] The CGG codon makes up 5% of the arginine codons in the SARS-CoV-1 genome, and it makes up 3% of the arginine codons in the SARS-CoV-2 genome.[9]

Proponents of an engineered virus, including journalist Nicholas Wade, claim that two such uncommon codons in a row are evidence for a laboratory experiment; because of the low chance of a CGG codon pair occurring in nature, and in contrast, the common usage of CGG codons for arginine in genetic engineering work.[9][74]

This has been disputed by scientists, who note that the CGG codon is also present (and even more frequent) in other coronaviruses, including MERS-CoV,[107] and that a codon being rare does not mean it cannot be present. In addition, the presence of the furin cleavage site, which is responsible for

a significant increase in transmissibility, largely outweighs the disadvantageous immune responses from B-cells triggered by the genetic sequences which code for it.[106][15]

You are unlikely to gain support from people who are actually involved in genetic engineering and evolutionary studies like myself.

I will delete this thread and block your email after sending.

xxx – not easily taken in – xxxxx “

So I looked up the paper by the plurality of “scientists” as opposed to the singular “journalist” Nicholas Wade – reference 107. And wrote the following response and checked that his email server did accept my email…

‘***Dear Prof XXX***,

Thanks for your email. If you can prove my reasoning wrong I would be happy to write a correction in my next article.

I read the one reference cited in Wikipedia for MERS-CoV having the CGG Codon and that paper states explicitly and emphatically…

“All human coronaviruses analyzed in this study did not use two synonymous codons (CGC, CGG) for arginine as well as CCG for proline and UGA for stop codon at all. ” – https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7487440/

My argument is very simple.

No virus in nature uses the CGG codon for Arginine in a furin cleavage site. I did check that in the blast database. I did the search. Nothing came up.

Please therefore show me a naturally occurring virus (preferably one that appeared before Moderna appeared) with a furin cleavage site containing two CGG codons and you will defeat my argument.

I am afraid you were taken in XXX – not by me, but by Wikipedia !

Regards….‘

I got no response from the Professor. But strangely Wikipedia changed the reference number from 107 to 116 in the article above. Yet it still links to the same paper? So Wikipedia is falsely inferring that “scientists”, as opposed to one lone journalist, dispute that there is a low chance of double CGG occurring in nature, by noting that the CGG codon occurs in MERS citing a paper which explicitly declares that none of the human coronaviruses analysed within it used a double CGG codon, No true scientist can dispute the low chance of a sequence occurring in viruses by analysing viruses in which said sequence does not occur. Wikipedia is providing disinformation which just happens to protect the interests of pharmaceutical companies

But all of this is – dare I say it – academic. Because there are absolutely no viruses which have a CGG doublet in a Furin Cleavage site (PRRAR) except Covid-19 and except plant viruses which Dow

Agroscience, Monsanto, or the like, have modified. And whether you are a journalist or a cell biologist or both (like myself) or neither, this article gives you the tools to check that FACT for yourself.

https://www.ncbi.nlm.nih.gov/labs/virus/vssi/#/ Search for CCTCGGCGGGCACGT which codes for PRRAR.