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SARS-COV2 VARIANTS AND VACCINES MRNA SPIKES FIBONACCI NUMERICAL UA/CG METASTRUCTURES

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ABSTRACT

In this paper, we suggest a biomathematical numerical method for analysing mRNA nucleotides sequences based on UA/CG Fibonacci numbers proportions.

This method is used to evaluate then compare the spike genes related to the main SARS-CoV2 VARIANTS currently circulating within the world population.

The 10 main results proposed to be reproduced by peers are:

1) SARS-CoV2 genome and spike evolution in one year 2020-2021.
2) SARS-CoV2 Origins.
3) Comparing 11 reference variants spikes.
4) Analysing 32 CAL.20C California variant patients' spikes.
5) Toward a meta mRNA Fibonacci gene end message code.
6) Analysing S501 UK, S484 South Africa and « 2 mutations » INDIA variants.
7) Suggesting a possible variants spike mRNA palindrome symmetry metastructure improving mRNA stability then infectiousness.
8) Analysing Fibonacci Metastructures in the mRNA coding for the vaccines PFIZER and MODERNA.
9) Does the CG-rich modification of the synonymous codons of the spikes of the 2 mRNA vaccines affect the expression and quantity of SARS-CoV2 antibodies?
10) The exceptional case of the Brazilian variant P.1.

Particularly, we suggest the following conjecture at mRNA folding level:

CONJECTURE of SARS-CoV2 VARIANTS:

The growth of long Fibonacci structures in the shape of "podiums" for almost all of the variants studied (UK, California, South Africa, India, etc.) suggests the probable folding of the Spike mRNA in the form of a "hairpin", which can strengthen the cohesion and the lifespan of this mRNA.

Finally, we show that these kinds of Fibonacci matastructures disapear TOTALLY by analysing the published mRNA sequences of PFIZER and MODERNA vaccines. One fact is certain, the two mRNAs of the Moderna and Pfizer vaccines will result in a low functionality of the spike vaccine. This is because their designers by seeking greater stability, have doped to build CG rich sequences which, as soon as they are inserted into the human host, will, paradoxically, seek to mutate, like SARS-CoV2 variants, towards CG ==> UA forms in order to improve their STABILITY and LIFETIME. We conclude using new biomathematics theoretical methods (Master code and numerical standing waves), and comparing the Spikes of the two vaccines Moderna and Pfizer, that there will be very probable differences in stability and shelf life of the two respective mRNAs vaccines. However, "State of the Art" analyzes will disclose that their two protein sequences are strictly identical. By modified their synonymous codons using different strategies, no one can guarantee that the quantity of antibodies generated will be identical in the two cases.

We wish to draw attention to the great ADAPTATION power - at the global scale of their genomes - of the most infectious VARIANTS, such as the BRAZIL 20J / 501Y.V3 variant (P.1). This is very worrying for the VACCINES <==> VARIANTS run: We demonstrate how the Brazilian variant P.1 which becomes uncontrollable in Brazil in April 2021 has a level of organization of long metastructures of 17,711 bases covering the genome which is 3.6 more important than that of the 2 reference genomes SARS-CoV2 and worldwide D614G. We suggest that this high level of overall structure of this variant contributes to the stability of this genome and, might explain its greater contagiousness.

To complete this article, an ADDENDUM by Nobelprizewinner Luc Montagnier vas added at the end of this paper.

1. INTRODUCTION

Thirty years ago, after pioneering in A.I (Perez, 1988, 1991), we published in a paper entitled "chaos, DNA, and neuro computers: the golden link" (Perez, 1991), presenting a numerical method to analyse DNA sequences based on Fibonacci numbers. In 2017 (Perez, 1997, 2017, 2019), we revisited this method to démonstrate application of this method in mtDNA mutations involved on Human cancers.

Fiftyeight years ago, (Montagnier L. § Kingsley Sanders F., 1963) Luc Montagnier described the isolation of an infectious double helix RNA in cells infected with a picornavirus. It is perhaps likely that there is an analogous form in the coronavirus, specifically on VARIANTS mRNA spikes. This structure is very stable, resistant to RNase, and can therefore retain the genetic information of the virus for a long time. The palindromic structures detected here could constitute a "hairpin" double stranded RNA form.

2. METHODS AND DATA SOURCES

2.1. COMPUTING FIBONACCI METASTRUCTURES

Consider the sequence of Fibonacci numbers

0 1 1 2 3 5 8 13 21 34 55 89 144 233 377 610 **987 1597 2584** 4181 6765 10946 17711 28657 46368 75025 121393 196418 317811 514229 832040 1346269 2178309 3524578 5702887...

Example of the SPIKE from Wuhan reference genome, this mRNA SPIKE is 3822 bases UCAG in length.
Recall Wuhan reference https://www.ncbi.nlm.nih.gov/nuccore/NC_045512

Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome NCBI Reference Sequence: NC_045512.2

the longest Fibonacci structures would therefore measure 2584 bases.
When looking for such structures, the first one found is in 1200 location:
therefore, the bases located between 1201 and 3784 (1200 + 2584):
These 2584 bases are broken down respectively into:
1597 bases UA
et 987 bases CG

Here are the first 20 basics that the reader can easily check:
SPIKREF [1200+¼20]

```
G U A A U U A G A G G U G A U G A A G U
0 1 1 1 1 1 1 0 1 0 0 1 0 1 1 0 1 1 0 1.../...
  U A A U U A   A     U    A U    A A     U     1597 bases UA

G U A A U U A G A G G U G A U G A A G U
1 0 0 0 0 0 0 1 0 1 1 0  1 0 0 1 0 0 1 0.../...
G             G   G G   G     G     G        987 bases CG
```

The SPIKE analyzes of this Wuhan-Hu-1 reference genome reports 63 metastructures of this type if we close the sequence on itself (as in mtDNA or bacteria) and 7 metastructures and if we consider the mRNA sequence in its linear form, as will be the case throughout this study.

2.2. ANALYZES OF REFERENCE VARIANTS

We analysed 5 tracks of variants:
UK variant N501Y
South Africa variant E484K
Brazil variant N501Y + E484K
California variant L452R
India variant E484Q + L452R
Main data source: https://covariants.org/

- **VARIANT South Africa MUTATIONS:**

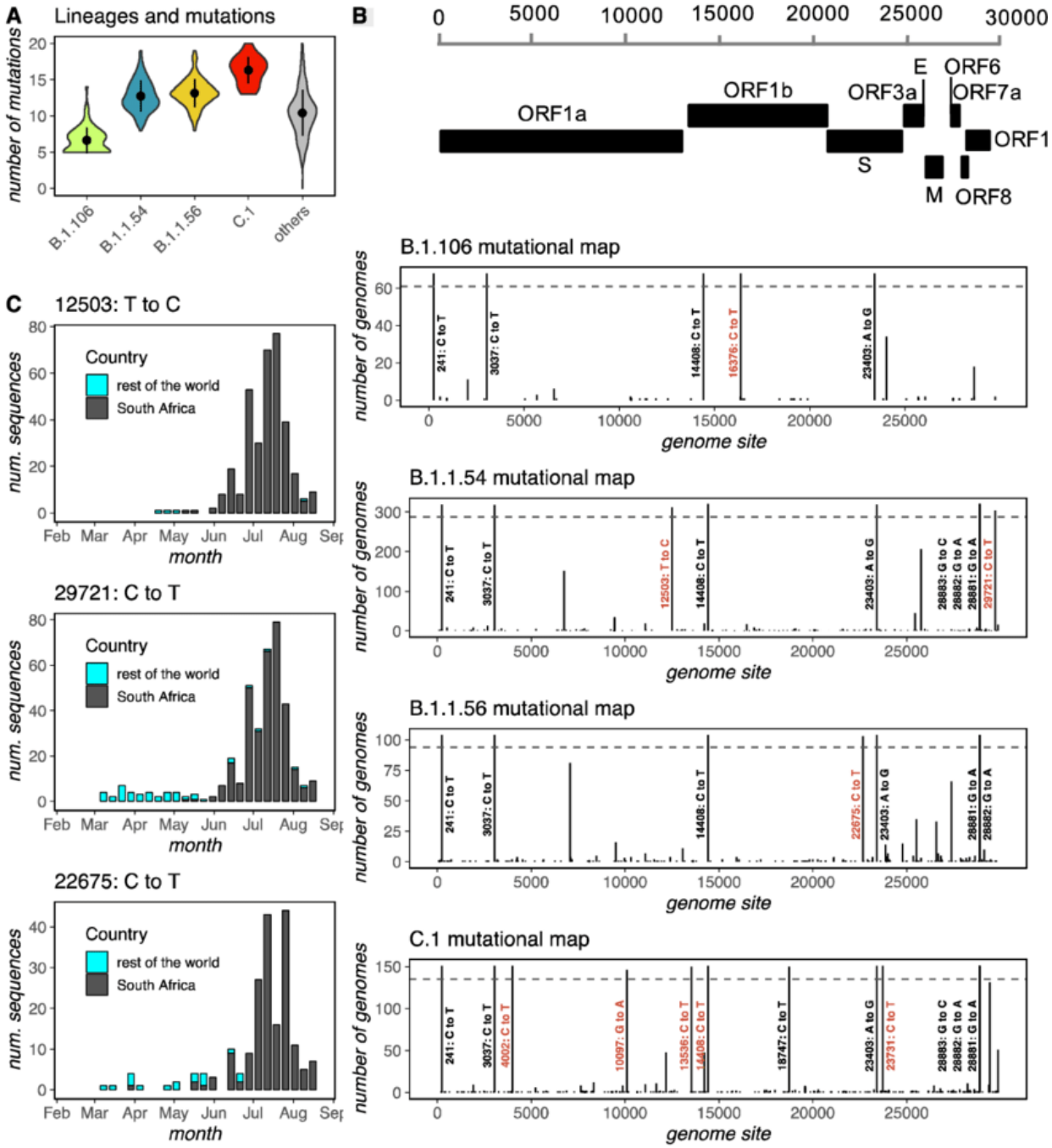


Figure 1: Mutations of the four reference variants from South Africa.

- **VARIANT U.K. MUTATIONS:**

Source (Da Silva Filipe et al, 2020), https://www.nature.com/articles/s41564-020-00838-z

Table 1: Mutations in U.K. variant

Gene	Nucleotide	Amino Acid
ORF1ab	C3267T	T1001I
	C5388A	A1708D
	T6954C	I2230T
	11288-11296 deletion	SGF 3675-3677 deletion
Spike	21765-21770 deletion	HV 69-70 deletion
	21991-21993 deletion	Y144 deletion
	A23063T	N501Y
	C23271A	A570D
	C23604A	P681H
	C23709T	T716I
	T24506G	S982A
	G24914C	D1118H
Orf8	C27972T	Q27stop
	G28048T	R52I
	A28111G	Y73C
N	28280 GAT->CTA	D3L
	C28977T	S235F

- **VARIANT BRAZIL MUTATIONS:**

Sources

First reference:

VARIANTS BRAZIL JAPAN (Naveca F et al, 2021)

https://virological.org/t/phylogenetic-relationship-of-sars-cov-2-sequences-from-amazonas-with-emerging-brazilian-variants-harboring-mutations-e484k-and-n501y-in-the-spike-protein/585

Phylogenetic relationship of SARS-CoV-2 sequences from Amazonas with emerging Brazilian variants harboring mutations E484K and N501Y in the Spike protein

second reference: (Gröhs Ferrareze P. A., et al, 2021),

E484K as an innovative phylogenetic event for viral evolution: Genomic analyzes of the E484K spike mutation in SARS-CoV-2 lineages from Brazil. https://www.biorxiv.org/content/10.1101/2021.01.27.426895v1

Genomic Region	Nucleotide / Amino acid		
	B.1.1.28-AM-II	B.1.1.28(K417T/E484K/N501Y)	B.1.1.28(E484K)
ORF1a		T733C C2749T C3828T / ORF1a:S1188L A5648C / ORF1a:K1795Q	C100T
	A6319G A6613G	A6319G A6613G	
		C12778T	T10667G / ORF1a:L3468V C11824T C12053T / ORF1a:L3930F
ORF1b		C13860T G17259T / ORF1b:E1264D	
Spike		C21614T / S:L18F C21621A / S:T20N C21638T / S:P26S G21974T / S:D138Y G22132T / S:R190S A22812C / S:K417T G23012A / S:E484K A23063T / S:N501Y C23525T / S:H655Y C24642T / S:T1027I	G23012A / S:E484K
	G25088T / S:V1176F	G25088T / S:V1176F	G25088T / S:V1176F
ORF3a	T26149C / ORF3a:S253P	T26149C / ORF3a:S253P G28167A / ORF8:E92K	C28253T
N/ORF9b		C28512G / N:P80R, ORF9b:Q77E A28877T / N:R203K G28878C / N:R203K	G28628T / N:A119S

Figure 2: Mutations of 3 Brazil variants

- **VARIANT CAL.20C from California Mutations (L452):**

It is possible that S13I increases the efficiency of cleavage on the 12 amino-peptide terminals, which may increase the volume of S-protein on the host cell.

CAL.20C has three unique amino acid substitutions in its spike protein. The spike protein is the part of the virus that interacts and locks into proteins from the human host cell, essentially the key to open the host to the virus. Among these are S13I and W152C in the N-terminal domain, and L452R in the receptor-binding domain.

Reference (Wenjuan Zhang et al, 2021)
https://www.medrxiv.org/content/10.1101/2021.01.18.21249786v1.full.pdf+html

- **ANALYZING W152C Mutation:**

Among these are S13I and W152C in the N-terminal domain, and L452R in the receptor-binding domain.

Other general source:
https://www.forbes.com/sites/williamhaseltine/2021/02/03/concerns-grow-over-the-newly-discovered-southern-

california-covid-19-variant/

32 California patients' genomes from GenBank:

CA1ID: MW433772.1 California 5 January

CA3ID: MW433769.1 California 5 January 2021

CA5ID: MW433764.1 California 5 January 2021

CA6ID: MW433763.1 California 5 January 2021

CA8ID: MW433758.1 California 5 January 2021

CA10ID: MW433752.1 California 5 January 2021

CA11ID: MW505197.1 California 2 February 2021

CA17ID: MW505189.1 California 22 January 2021

CA19ID: MW505187.1 California 2February 2021

CA20ID: MW505186.1 California 2February 2021

CA25ID: MW505149.1 California 22 January 2021

CA27ID: MW505147.1 California 22 January 2021

CA51ID: LR883179.1 netherland 25 January 2021

CA52ID: MW525111.1 California 26 January 2021

CA53ID: MW525040.1 USA MO 26 January 2021

CA54ID: MW525020.1 USA FL 26 January 2021

CA55ID: MW524999.1 USA NY 26 January 2021

CA56ID: MW524976.1 USA CA 26 January 2021

CA57ID: MW524942.1 USA CA 26 January 2021

CA58ID: MW523875.1 USA CA 26 January 2021

CA59ID: MW523873.1 USA CA 26 January 2021

CA60ID: MW523867.1 USA TX 26 January 2021

CA61ID: MW523795.1 USA CA 26 January 2021

CA62ID: MW523792.1 USA CA 26 January 2021

CA63ID: MW519791.1 USA NV 25 January 2021

CA64ID: MW519755.1 USA AZ 25 January 2021

CA65ID: MW519751.1 USA AZ 25 January 2021

CA66ID: MW519739.1 USA CA 25 January 2021

CA67ID: MW519738.1 USA CA 25 January 2021

CA68ID: MW519725.1 USA CA 25 January 2021

CA69ID: MW519715.1 USA CA 25 January 2021

CA70ID: MW519708.1 USA CA 25 January 2021

- **Indian « two mutations » variant:**

Samples with the E484Q and L452R, soient South Africa + California variants

Sources:
https://www.bbc.com/news/world-asia-india-56507988
and
https://pib.gov.in/PressReleaseIframePage.aspx?PRID=1707177

We must note that variant is E484K while Indian variant is E484Q.

	U	C	A	G	
G	Valine Val - V	Alanine Ala - A	Aspartic acid Asp - D	Glycine Gly - G	U
			Glutamic acid Glu - E		C
					A
					G
C	Leucine Leu - L	Proline Pro - P	Histidine His - H	Arginine Arg - R	U
			Glutamine Gln - Q		C
					A
					G
A	Isoleucine Ile - I	Threonine Thr - T	Asparagine Asn - N	Serine Ser - S	U
					C
	Methionine Met - M		Lysine Lys - K	Arginine Arg - R	A
					G
U	Phenylalanine Phe - F	Serine Ser - S	Tyrosine Tyr - Y	Cysteine Cys - C	U
					C
	Leucine Leu - L		STOP codon	STOP codon	A
				Tryptophan Trp - W	G

Figure 3: Recall Universal Genetic Code Table.

3. RESULTS and DISCUSSION

3.1. SARS-COV2 GENOME AND SPIKE EVOLUTION IN ONE YEAR 2020-2021.

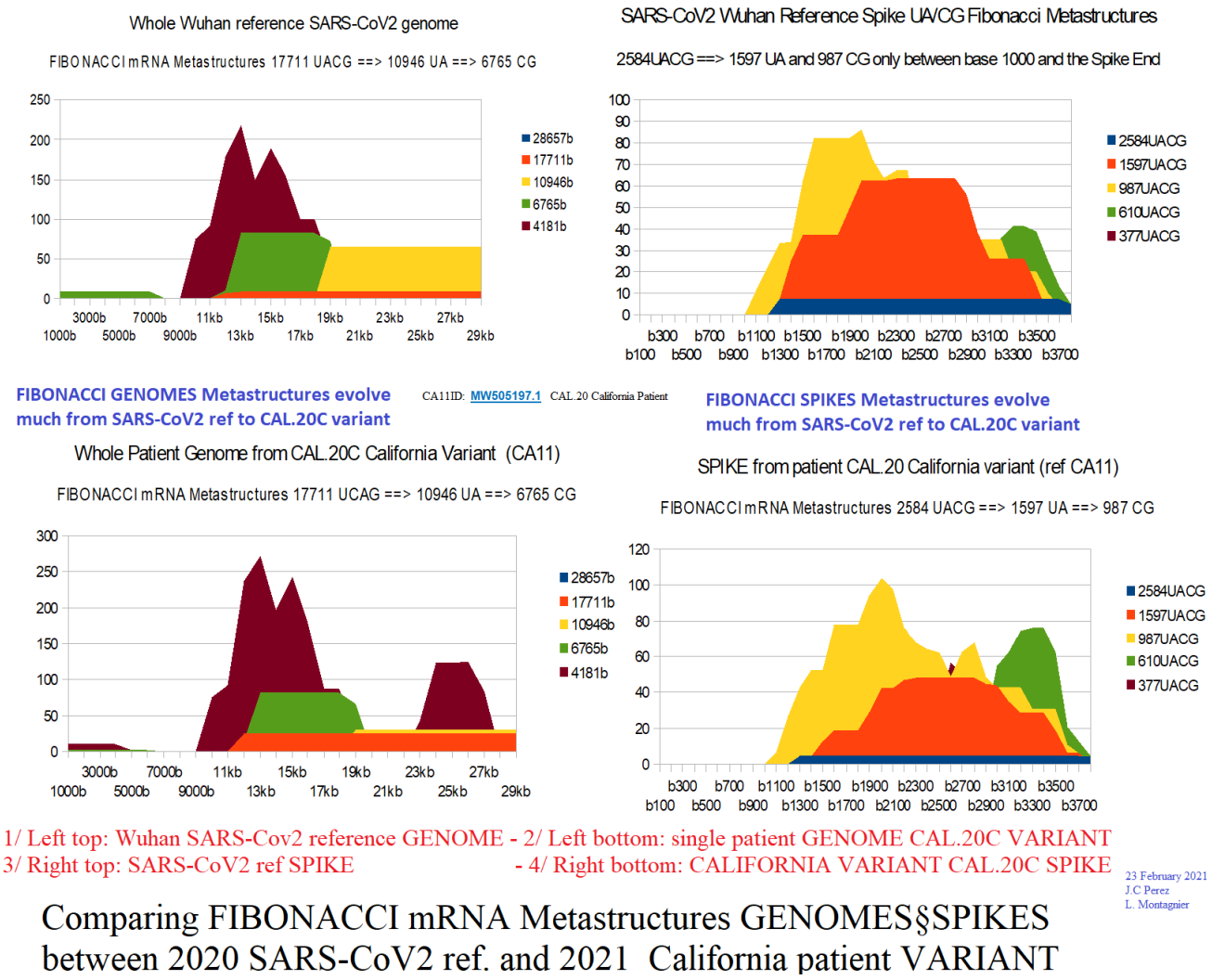


Figure 4: comparing SARS-CoV2 genome and spike evolution between Wuhan strain (january 2020) and CAL.20C variant (january 2021).

At the level of the genomes, the very long Fibonacci metastructures (17711nt) increase considerably, which means a reinforcement of the overall mRNA structure of the genome.

On the contrary, the overall metastructure of the spike seems to be reduced, although this variant has evolved at the level of amino acid mutations (mutations in CAL.20C california

L452R, S13I, W152C).

3.2. SARS-COV2 ORIGINS

Fibonacci metastructures "shed a radically new light on" the relationships already recognized or suspected "between the four Sars-CoV2 Wuhan (1/2020), SARS-covZC45 (2017), SARS-covZXC21 (2015) and bat RATG13 genomes (2013) revealing evidence of manipulation of CODONS synonymous with Spike of one or the other between SARS-CoV2 and beats RATG13, giving rise to the question "which of the two was manipulated?" (Perez, 2020),

(Perez§Montagnier, 2020), (Castro-Chavez, 2020). We can assert that it is the SARS-Cov2 spike that has been manipulated to modify synonymous CODONS while retaining the functionality of the same amino acids. We believe that this manipulation will most certainly have attenuated the virulence and pathogenicity of SARS-CoV2 opposite bat RATG13 * (blue regions of the 2 images of their Spikes).

Moreover, if at the level of the four respective genomes, the strong neighborhoods between SARS-CoV2 and bat RATG13 on one hand, and ZC45 and ZXC21 on the other, are confirmed by these Fibonacci metastructures (vertical analogies in the image). A less expected bi-duality is highlighted at the level of their four respective spikes: on one hand, this obvious neighborhood between ZXC21 and bat RATG13, and, on the other , although less obvious, this other neighbour

==> ZXc21

https://www.google.com/url?sa=t&source=web&rct=j&url=https://www.ncbi.nlm.nih.gov/nuccore/MG772934&ved=2ahUKEwi63MmXkIfvAhVPrxoKHc7rBkAQFjAAegQIBBAD&usg=AOvVaw2DaPGodhGxK_sv2JPdNU29

Bat SARS-like coronavirus isolate bat-SL-CoVZXC21, complete genome

GenBank: MG772934.1

/collection_date="Jul-2015"

21483..25220

/note="S"

/codon_start=1

/product="spike

==> Bat Ratg13

https://www.google.com/url?sa=t&source=web&rct=j&url=https://www.ncbi.nlm.nih.gov/nuccore/MN996532&ved=2ahUKEwjO1KKqkIfvAhVlx4UKHYypB4oQFjABegQIARAC&usg=AOvVaw1NImUic0dN6Ke140Hf408t

Bat coronavirus RaTG13, complete genome

GenBank: MN996532.2

Go to:

LOCUS MN996532 29855 bp RNA linear VRL 24-NOV-2020

COMMENT On Oct 13, 2020 this sequence version replaced MN996532.1.

/isolation_source="fecal swab"

/collection_date="24-Jul-2013"

/gene="S"

CDS 21560.25369

/gene="S"

==> ZC45

https://www.google.com/url?sa=t&source=web&rct=j&url=https://www.ncbi.nlm.nih.gov/nuccore/MG772933&ved=2ahUKEwig_s_0j4fvAhUPKBoKHe_oD44QFjAAegQIBBAD&usg=AOvVaw0IPCwtlOcZJxs4SzfZhzPu

Bat SARS-like coronavirus isolate bat-SL-CoVZC45, complete genome

GenBank: MG772933.1

/collection_date="Feb-2017"

SPIKE

CDS 21549.25289

/note="S"

/codon_start=1

The following SARS-CoV2 "quadrille", bat RATG13, ZC45 and ZXC21 is remarkable for its enigmatic nature over the actual origins of SARS-CoV2. Indeed, when the first two are supposed to be of natural origin, we have the certainty and the evidence that the last two were read to the point - and published - by military laboratories.

Fibonacci analyzes of these four genomes and their Spike genes will reveal links, subfamilies and correlations two to two between these four key genomes in the history and genesis of the COVID-19 pandemic.

Genome's scale analyzes:

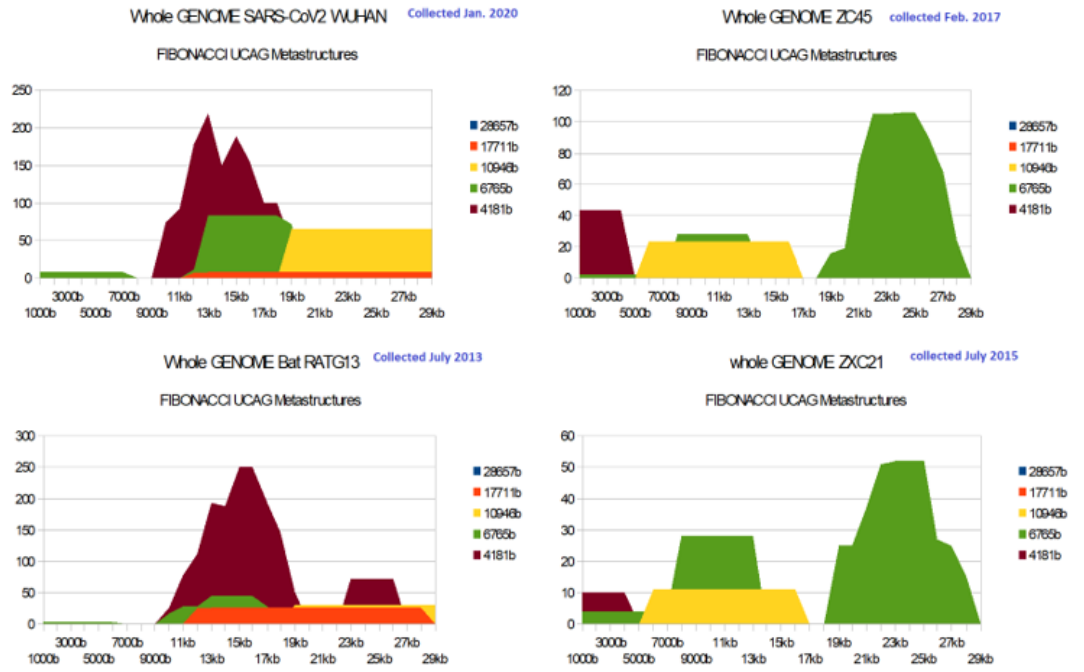


Figure 5: remarkable vertical analogies (SARS-CoV2 vs bat RaTG13). Spike's scale analyzes:

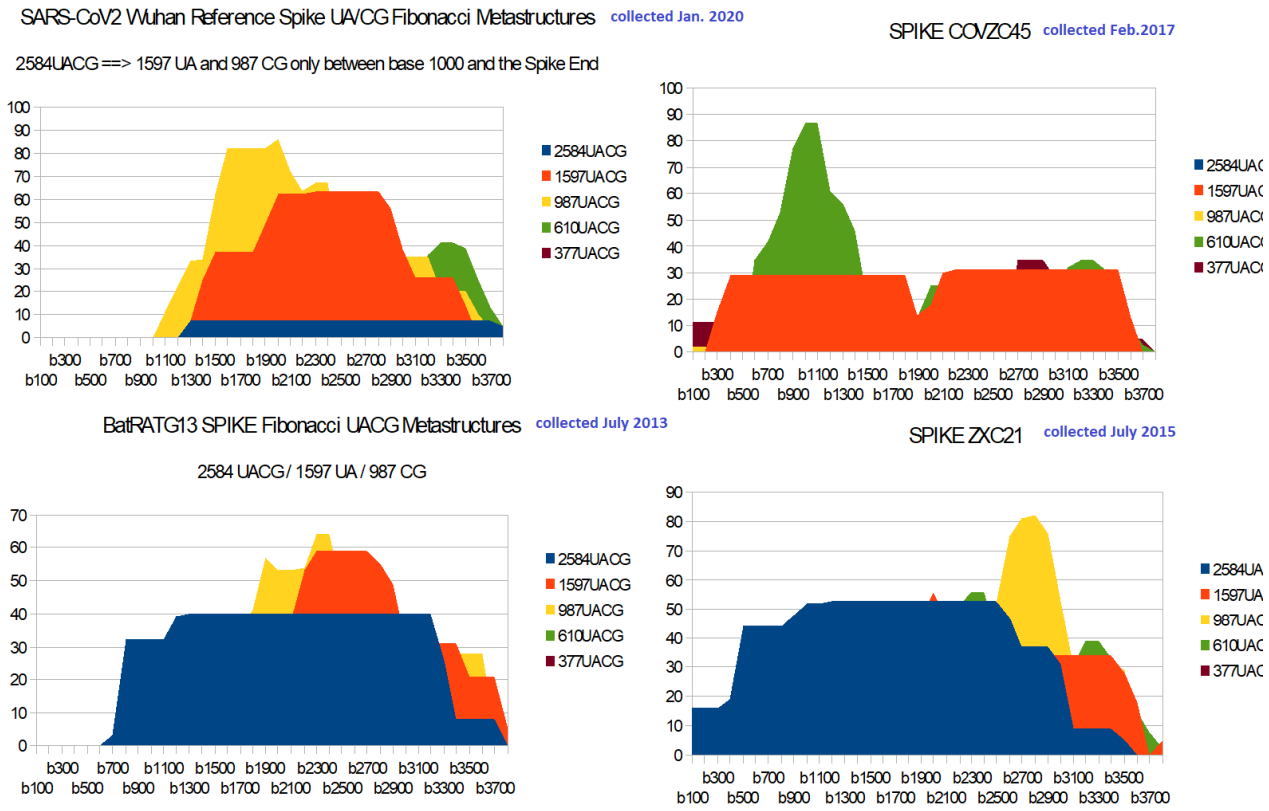


Figure 6: remarkable horizontal analogies (Bat RATG13 vs ZXC21).

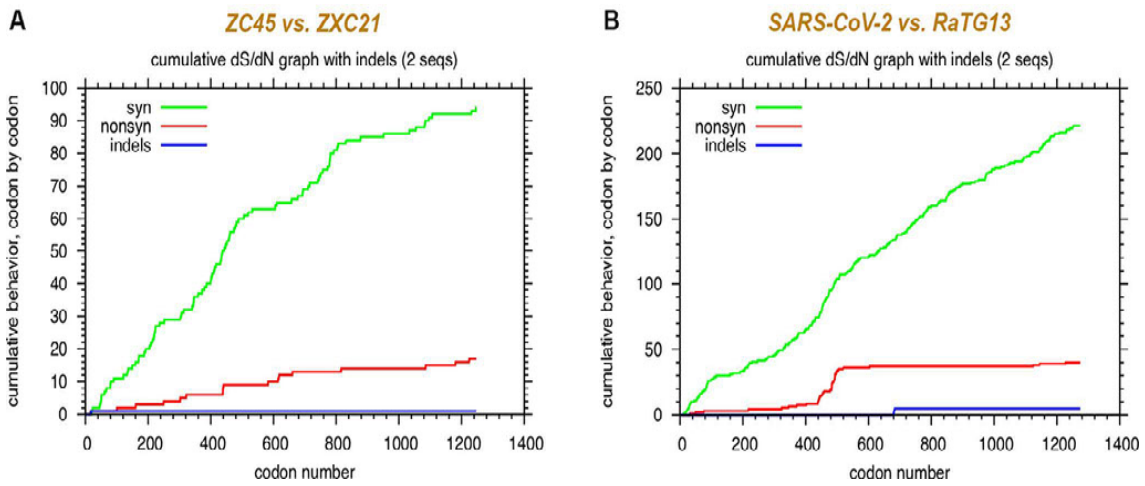


Figure 7: Evidence of patterns analogies at Synonimes/non synonimes codons.

FIGURE. 7 concerning the abnormal number of synonymous codons between SARS-CoV2 and bat RATG13 on the one hand and ZXC21 and ZC45 on the other hand confirms and reinforces the dichotomy which has just been revealed here by the Fibonacci analyzes.

Particularly, both bat RATG13 and ZXC21 Spikes provide a high level of Fibonacci long range UA/CG resonances (blue coloured in Fig7). For us, that is the proof of natural evolutionary contraints contrarly the 2 remaining spikes SARS-CoV2 and ZC45.

Let us summarize the respective results of figures 5, 6 and 7: figure 5 (genomes) confirms the above dichotomy natural versus laboratory. indeed, a double vertical analogy clearly classifies these four genomes into two + two by the clear graphic correlation of their Fibonacci images.

On the contrary (figure 6 spikes), the comparative analyzes of the four spikes clearly shows a horizontal dichotomy between SARS-CoV2 and ZC45 on the one hand and bat RATG13 and ZCX21 on the other hand. Does this mean that ZC45 would have served as a "model" for SARS-CoV2 while ZXC21 would have "inspired" bat RATG13, or perhaps the reverse if we take into account the respective dates: bat RATG13 (2013/2020) ZXC21 (2015) ZC45 (2017) SARS-CoV2 (2019/2020).

SARS-Cov2 is directly linked to RaTG13 as ZC45 is linked to ZXC21 and the reduction or even disappearance of the 2584 UACG metastructures in SARS-Cov2 and ZC45 shows that practically ZC45 is “made from” ZXC21 like SARS-Cov2 from RaTG13.

3.3. COMPARING 11 REFERENCE VARIANTS SPIKES

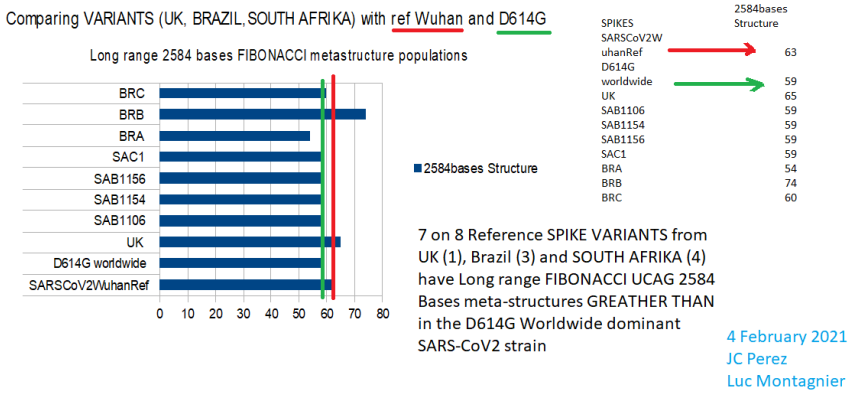


Figure 8: Comparing CIRCULAR Fibonacci metastructures between reference variants and Wuhan and D614G worldwide spikes.

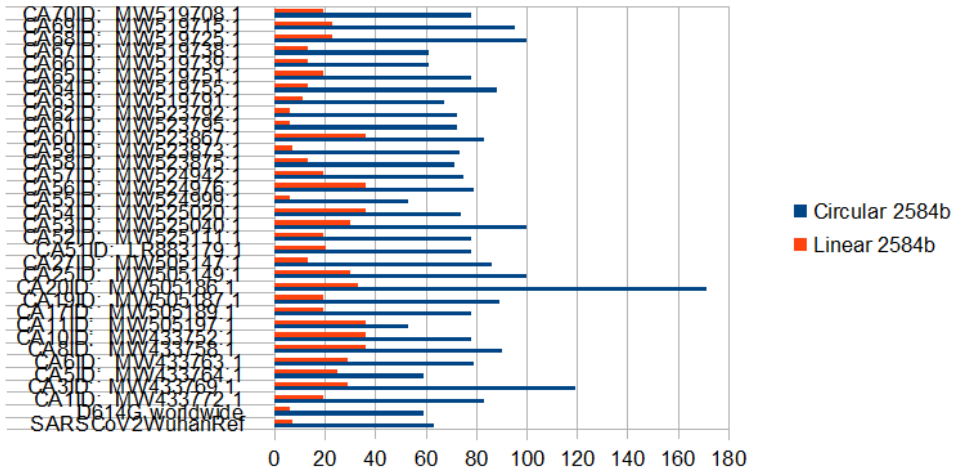


Figure 9: Comparing CIRCULAR and LINEAR Fibonacci metastructures between 32 CAL.20C Sample patients spikes variants and Wuhan and D614G worldwide spikes.

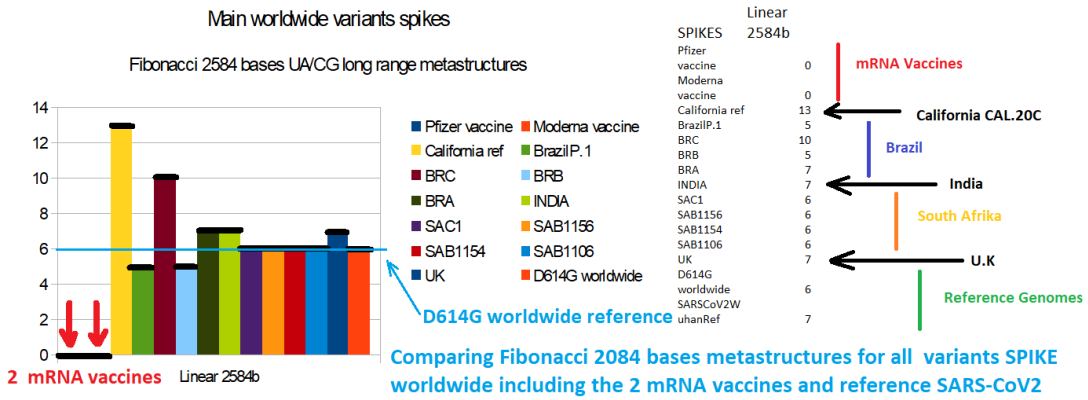


Figure 10: Comparing LINEAR Fibonacci metastructures between reference variants and Wuhan and D614G worldwide spikes, note: The cases of mRNA vaccines are discussed in §8 and 9.

Table 2: Comparing LINEAR Fibonacci metastructures between reference variants and Wuhan and D614G worldwide spikes.

SPIKES variants or vaccines	Linear 2584 bases
Pfizer vaccine	0
Moderna vaccine	0
California CAL20C reference	13
Brazil P1	5
Brazil C	10
Brazil B	5
Brazil A	7
INDIA	7
South Afrika SAC1	6
South Afrika SAB1156	6

South Afrika SAB1154	6
South Afrika SAB1106	6
UK	7
D614G worldwide	6
SARS-CoV2 Wuhan	7

In this paragraph 3, we attempt to answer the question: "Do the variants strengthen or reduce the level of Fibonacci metastructures of the Spikes vis-à-vis the original Wuhan and worldwide D614G strains?".

We carry out two types of additional analyzes: on the one hand by considering the mRNA spike looped back on itself (ring like: figures 8 and 9), which is inaccurate here but nevertheless provides information which makes sense, and corresponds to the actual situation (figure 10 and table 2).

Globally, it appears that there is a significant increase in Fibonacci structures for the variants, but these variants are only theoretical sequences; we will see in the following that the increase in metastructure of the variant spikes is much more pronounced in the case of patients (see study of CAL.20C variant patients).

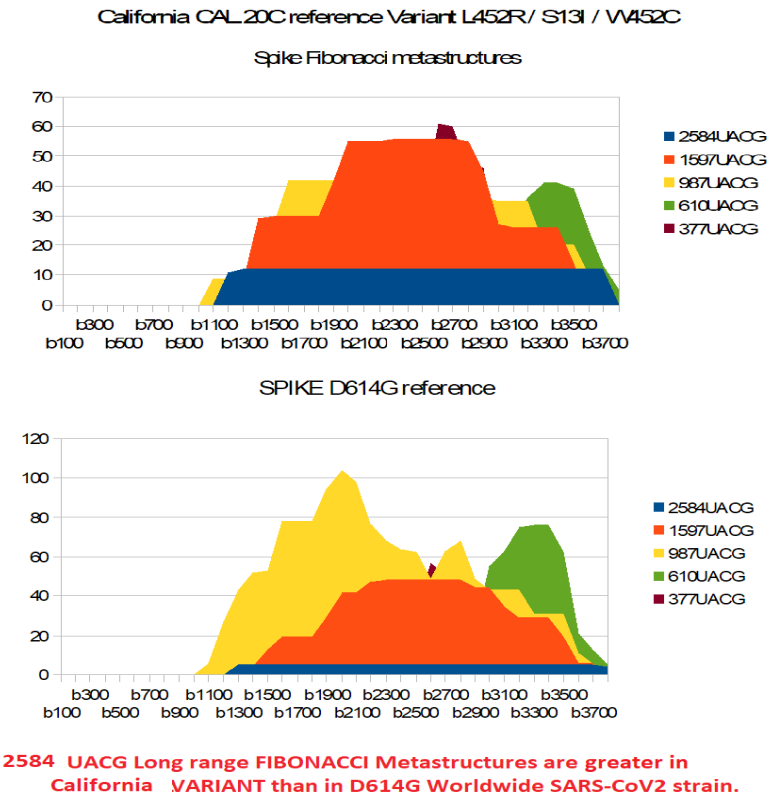


Figure 11: Comparing reference variant CAL.20C Fibonacci metastructures with worldwide spike D614G.

3.4. ANALYSING 32 CAL.20C CALIFORNIA VARIANT PATIENTS' SPIKES

This section analyzes the genomes and spikes of thirtytwo patients with the California variant CAL.20C. Figure 11 and tables 4 to 6 summarize two major results:

- the very great diversity of the results.
- the very clear trend of an increase in the number of Fibonacci structures compared to the reference genome D614G.

But the newest and most remarkable is the one which will be the subject of the next & 5 ...

Data sources: GenBank.

Table 3: Variant California CAL.20C: 32 individual patients spikes

32 L452R variants	**S13I California variant mutation**			**W152C California variant mutation**			**2584 UCAG FIBONACCI circular matastructures population D614G spike: 59**	**2584 UCAG FIBONACCI linear matastructures population D614G spike: 5**	***"mRNA checksum natural law" SPIKE***	**17711 UCAG FIBONACCI linear matastructures population D614G genome: 8**
	AGU regular (S13)	**AUU variant (I13I)**	**Other (deletions)**	**UGG regular (W152)**	**UGU variant (152C)**	**Other (deletions)**				
CA1		AUU			UGU		83	19	1597 1597	5
CA3		AUU				GCA	119	29	1597 1595	21
CA5			UAA			UGA	59	25	1597 1598	11
CA6			UAC			ACU	79	29	1597 1595	31
CA8		AUU				AUG	90	36	1597 1596	8
CA10			UAC			ACA	78	36	1597 1594	9
CA11		**AUU**				**GGU**	**53 <==**	**36**	**1597 1594**	**25**
CA17		AUU			UGU		78	19	1597 1597	9
CA19		AUU			UGU		89	19	1597 1597	39
CA20			UAG			CUU	171	33	1597 1597	39
CA25		AUU			UGU		100	30	1597 1596	28
CA27		AUU			UGU		86	27	1597 1598	28
CA51			UCA			UAU	78	20	1597 1598	47
CA52		AUU			UGU		78	19	1597 1597	8
CA53		AUU			UGU		100	30	1597 1596	29

CA54		AUU				AUU	74	36	1597 1592	9
CA55	**AGU**			**UGG**			**53 <==**	**6**	**1597 1599**	**12**
CA56			CUA			ACC	79	36	1597 1595	35
CA57		AUU			UGU		75	19	1597 1597	33
CA58	AGU			UGG			71	13	1597 1598	43
CA59			UCA			GAU	73	7	1597 1601	43
CA60			GCA			GAA	83	36	1597 1589	39
CA61		AUU			UGU		72	6	1597 1599	39
CA62		AUU			UGU		72	6	1597 1599	13
CA63		AUU			UGU		67	11	1597 1597	33
CA64		AUU			UGU		88	12	1597 1598	26
CA65		AUU			UGU		78	19	1597 1597	28
CA66		AUU			UGU		61	12	1597 1598	33
CA67		AUU			UGU		61	12	1597 1598	40
CA68		AUU				GAA	100	22	1597 1597	12
CA69		AUU				GAA	95	22	1597 1597	33
CA70		AUU			UGU		78	19	1597 1597	3

Table 4: VARIANT L452R and variability S13I California CAL.20C vs HIV/SIV « EIE » (July 2020: Perez, J. C., & Montagnier, L. (2020). COVID-19, SARS AND BATS CORONAVIRUSES GENOMES PECULIAR HOMOLOGOUS RNA SEQUENCES. International Journal of Research -GRANTHAALAYAH, 8(7), 217-263. https://zenodo.org/record/3975589).

California VARIANT S13I	AGU regular (S13)	AUU variant(I13I)	Other (deletions)	Total (L452R)

Number of strains	2	22	8	32
% of strains	6,00%	69,00%	25,00%	100,00%
Nota		94% mutations or deletions where HIV/SIV « EIE » Perez§Montagnier article are involved		

Note: for information, a first mutation is located in the HIV zone (S13I). 3 bases after Kenya (1 in chart) and 8 bases before the second HIV (2 in chart). See Perez§Montagnier 2020.

We analyzed (table 3) the genomes and spikes of thirtytwo patients with the California variant CAL.20C. The result is very interesting:

For the circular structures analyzes of the spike, thirty out of thirtytwo cases increase the metastructures 2584 AU / CG vis-à-vis the reference D614G (column 8).

For the linear structures analyzes of the spike (column 9), the integrity of the thirtytwo cases increases these same metastructures 2584 AU / CG.

At the level of whole genomes, the 17711 UA / CG metastructures (column 11) increase in thirty out of thirtytwo cases with respect to the reference genome D614G.

We can only conclude that the reference variants are only textbook cases, much less rich in synonymous mutations than the genomes of real patients. We conclude that a large number of synonymous mutations specific to each patient reinforce the overall structure of genomes and spikes, it suffices to observe the diversity of the results for each of the thirtytwo patients.

Another remark, if all thirtytwo patient cases have the L452R, for the two remaining mutations characterizing CAL.20C, there is a large diversity of individual cases for mutations S13I and W152C: someone has one or other or none between these mutations. There are also cases with deletions overlaping these S13I or W152C crucial mutations. Finally, we must conclude that the key of variants evolution and pathogenicity knowledge provides more from individual patients sequences full analyzes than that from theoretical reference variants description.

Table 5: VARIANT L452R and variability W152C California CAL.20C vs HIV/SIV « EIE » (July 2020: Perez, J. C., & Montagnier, L. (2020). COVID-19, SARS AND BATS CORONAVIRUSES GENOMES PECULIAR HOMOLOGOUS RNA SEQUENCES. International Journal of Research -GRANTHAALAYAH, 8(7), 217-263. https://zenodo.org/record/3975589).

W152C California variant mutation	**UGG regular (W152)**	**UGU variant (152C)**	**Other (deletions)**	**Total (L452R)**
Number of strains	2	16	14	32
% of strains	6,00%	50,00%	44,00%	100,00%
Nota		94% mutations or deletions just after where HIV/SIV « EIE » Perez§Montagnier article are involved		

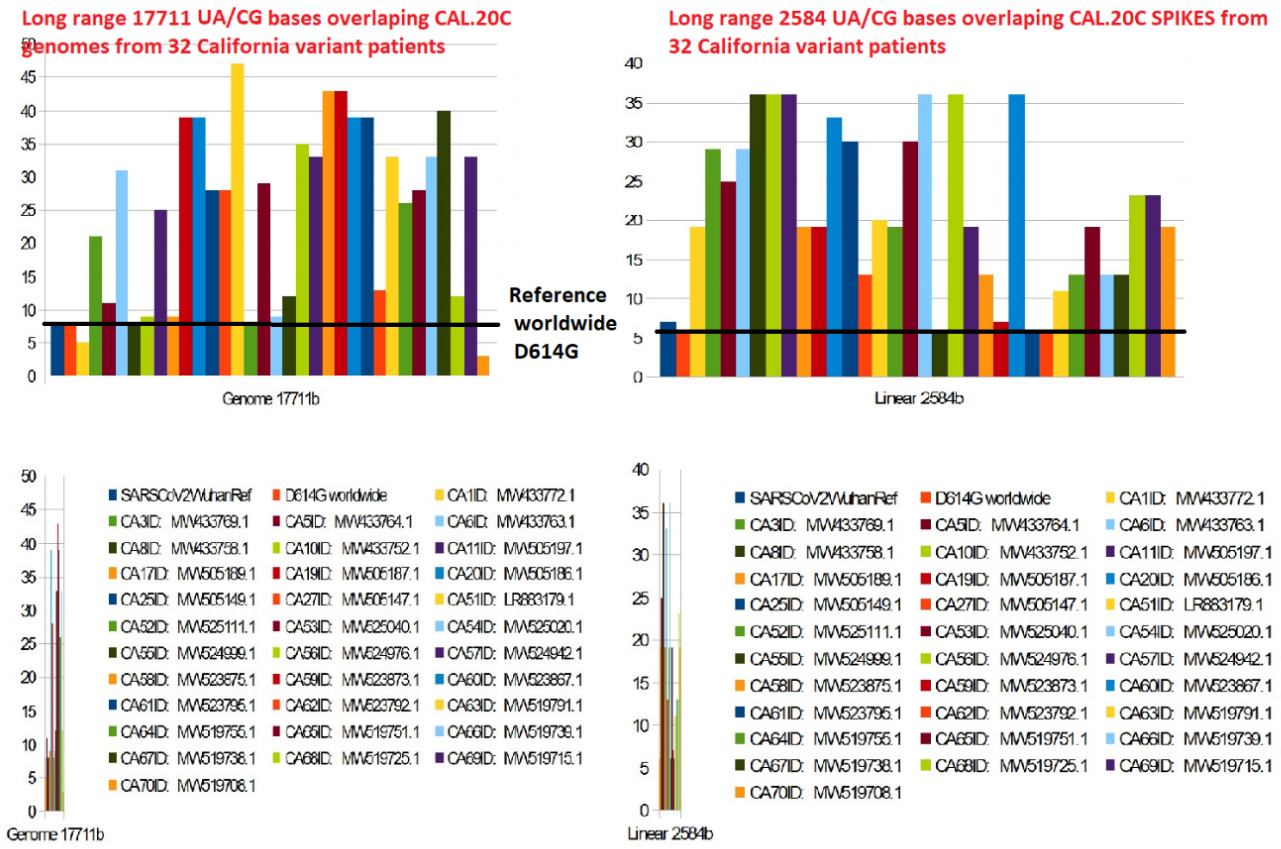


Figure 12: Comparing genome and spike between 32 CAL.20C patients and ref Wuhan and D614G worldwide reference.

Table 6: Comparing genome and spike between 32 CAL.20C patients and ref Wuhan and D614G worldwide reference.

SPIKES references, Genbank link and dates	Linear GENOME Fibonacci UA/CG 17711 bases	Linear SPIKE Fibonacci UA/CG 2584 bases
SARS-CoV2 Wuhan reference	8	7
D614G worldwide	8	6
CA1ID: MW433772.1 California 5 January 2021	5	19
CA3ID: **MW433769.1** California 5 January 2021	21	29
CA5ID: **MW433764.1** California 5 January 2021	11	25
CA6ID: **MW433763.1** California 5 January 2021	31	29
CA8ID: **MW433758.1** California 5 January 2021	8	36

CA10ID: MW433752.1 California 5 January 2021	9	36
CA11ID: MW505197.1 California 2 February 2021	25	36
CA17ID: MW505189.1 California 22 January 2021	9	19
CA19ID: MW505187.1 California 2February 2021	39	19
CA20ID: MW505186.1 California 2February 2021	39	33
CA25ID: MW505149.1 California 22 January 2021	28	30
CA27ID: MW505147.1 California 22 January 2021	28	13
CA51ID: LR883179.1 netherland 25 January 2021	47	20
CA52ID: MW525111.1 California 26 January 2021	8	19
CA53ID: MW525040.1 USA MO 26 January 2021	29	30
CA54ID: MW525020.1 USA FL 26 January 2021	9	36
CA55ID: MW524999.1 USA NY 26 January 2021	12	6
CA56ID: MW524976.1 USA CA 26 January 2021	35	36
CA57ID: MW524942.1 USA CA 26 January 2021	33	19
CA58ID: MW523875.1 USA CA 26 January 2021	43	13
CA59ID: MW523873.1 USA CA 26 January 2021	43	7
CA60ID: MW523867.1 USA TX 26 January 2021	39	36
CA61ID: MW523795.1 USA CA 26 January 2021	39	6
CA62ID: MW523792.1 USA CA 26 January 2021	13	6
CA63ID: MW519791.1 USA NV 25 January 2021	33	11
CA64ID: MW519755.1 USA AZ 25 January 2021	26	13
CA65ID: MW519751.1 USA AZ 25 January 2021	28	19
CA66ID: MW519739.1 USA CA 25 January 2021	33	13
CA67ID: MW519738.1 USA CA 25 January 2021	40	13

CA68ID: MW519725.1 USA CA 25 January 2021	12	23
CA69ID: MW519715.1 USA CA 25 January 2021	33	23
CA70ID: MW519708.1 USA CA 25 January 2021	3	19

3.5. TOWARD A META MRNA FIBONACCI GENE END MESSAGE CODE

This point is at a level of fundamental research of mechanisms unknown to biology. Indeed, we demonstrate how, beyond and above the STOP codon which commands the protein manufacturing machinery to end the process, there would exist a sort of "end of gene message", which would be addressed, on the scale of messenger RNA, to this "code" and would be digital in nature, carried by the ultimate UA / CG metastructure of Fibonacci. We observe that this message would be of Nature GIGOGNE, constituted like the Russian dolls of a nesting of proportions all ending on one of the three bases of the STOP codon. This discovery is validated in this article on fortythree Spikes from UK, South Africa, BRAZIL and California variants. Of these Spikes, thirtytwo were from real patients.

In each box of the penultimate column of table 3, there are two very close numbers: the first number 1597 is the optimal number of UA bases with a final resonance of 2584 UACG which would end in the immediate vicinity of the codon stop UAA of the Spike. The second number (ie. 1598) is the real number of UA bases contained among these last 2584 bases of the spike. Remember that 2584 bases cover 2/3 of the spike which has about 3800 bases. It is therefore a strong meta-structure which would control the relative proportions of nucleotides in the spike.

Table 7: Distribution of cases around the three bases of the UAA stop codon of the spike.

1597 Fibonacci UA bases	Base number	Number cases
	1594	2
	1595	3
	1596	3
1597 A (stop codon)	1597	11
1598 A (stop codon)	1598	8
1599 U (stop codon)	1599	8
	1600	3
	1601	2
	1602	1
Others		2

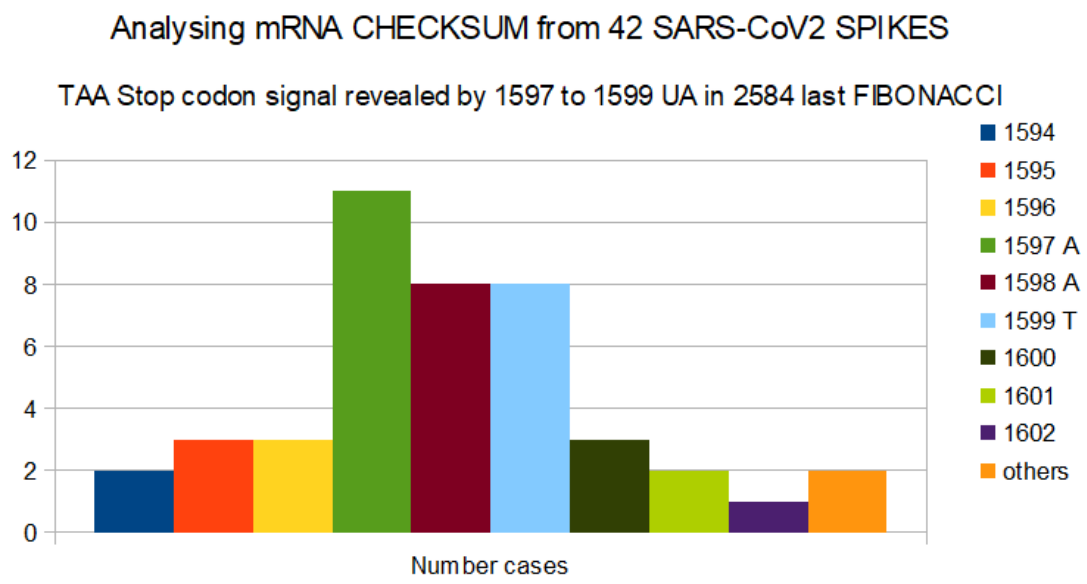


Figure 13: histogram perfectly illustrating the "bell" concentration of cases around the 3 bases of the UAA stop codon of the spike.

Table 7 and the histogram of FIG. 13 illustrate this remarkable phenomenon of "end-of-gene meta-structure" generalized to the thirty two spike strains of CAL.20C patients plus eleven spikes of reference variants, for a total of forty three cases. The histogram perfectly illustrates the "bell" concentration of cases around the three bases of the UAA stop codon of the spike.

3.6. ANALYSING S501 UK, S484 SOUTH AFRICA, AND LAST "TWO MUTATIONS" INDIAN VARIANTS

N501 UK VARIANTS

Mutation Information

- S:N501 has appeared multiple times independently: each can be associated with different accompanying mutations
- Amino-acid changes are S:N501Y (nucleotide mutation A23063T), S:N501T (nucleotide mutation A23064C), and S:N501S (nucleotide mutation A23064G)

½SN501Y„SN501T„SN501S„SPIKD614G
3822
SN501Y [1500+ 1 2 3]
AAT
SN501Y [1500+ 1 2 3] ='TAT'
SN501T [1500+ 1 2 3] ='ACT'
SN501S [1500+ 1 2 3] ='AGT'

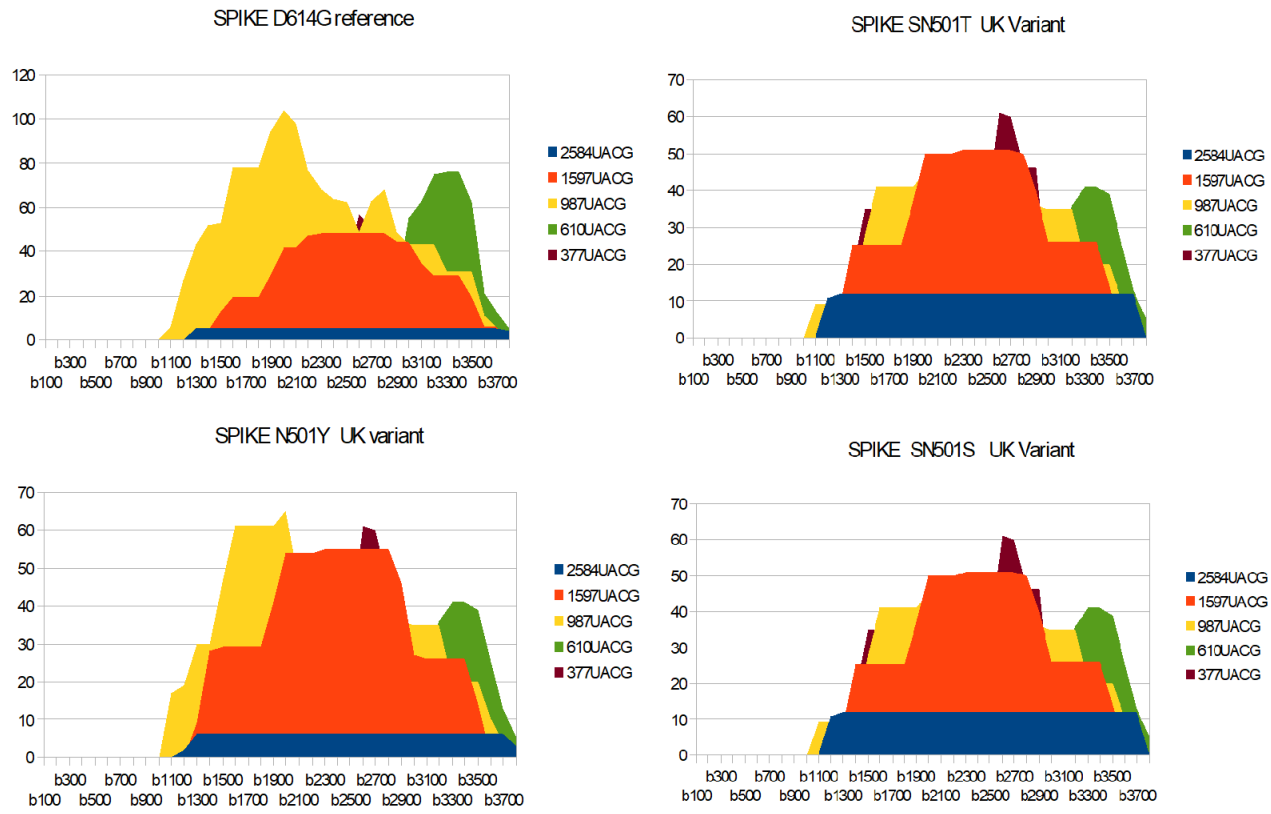


Figure 14: Comparing 3 UK variants Spike codon 501 mutations with reference D614G spike.

For the English variant (Figure 14), we see that at least two of the three mutations significantly increase the long metastructures of 2584 UACG bases (blue regions in Figure 14). This can generate better stability and life of the mRNA of the spine of these variants, and therefore correspond to the increase in infectivity and pathogenicity observed in patients who are victims of this English variant.

South Africa VARIANT

20H/501Y.V2

Also known as B.1.351

Announced in December 2020, 501Y.V2 originated and/or initially expanded in South Africa (Tegally et al., medRxiv).

501Y.V2 is associated with multiple mutations in Spike, including: S:N501Y (see S N501 page), S:E484K, S:K417N, and S:D80A. Additionally, there is a deletion at 242-245. There is also a mutation in Nucleocapsid: N:T205I and a deletion in ORF1a(Nsp6) at positions 3675-3677 (also seen in 501Y.V1 and 501Y.V3).

GAA ==> AAA E484K
AAG ==> AAU K417N
GAU ==> GCU D80A
SE484K [237+1 2 3] = 'GCT' SE484K [1248+1 2 3] = 'AAT' SE484K [1449+1 2 3] = 'AAA'

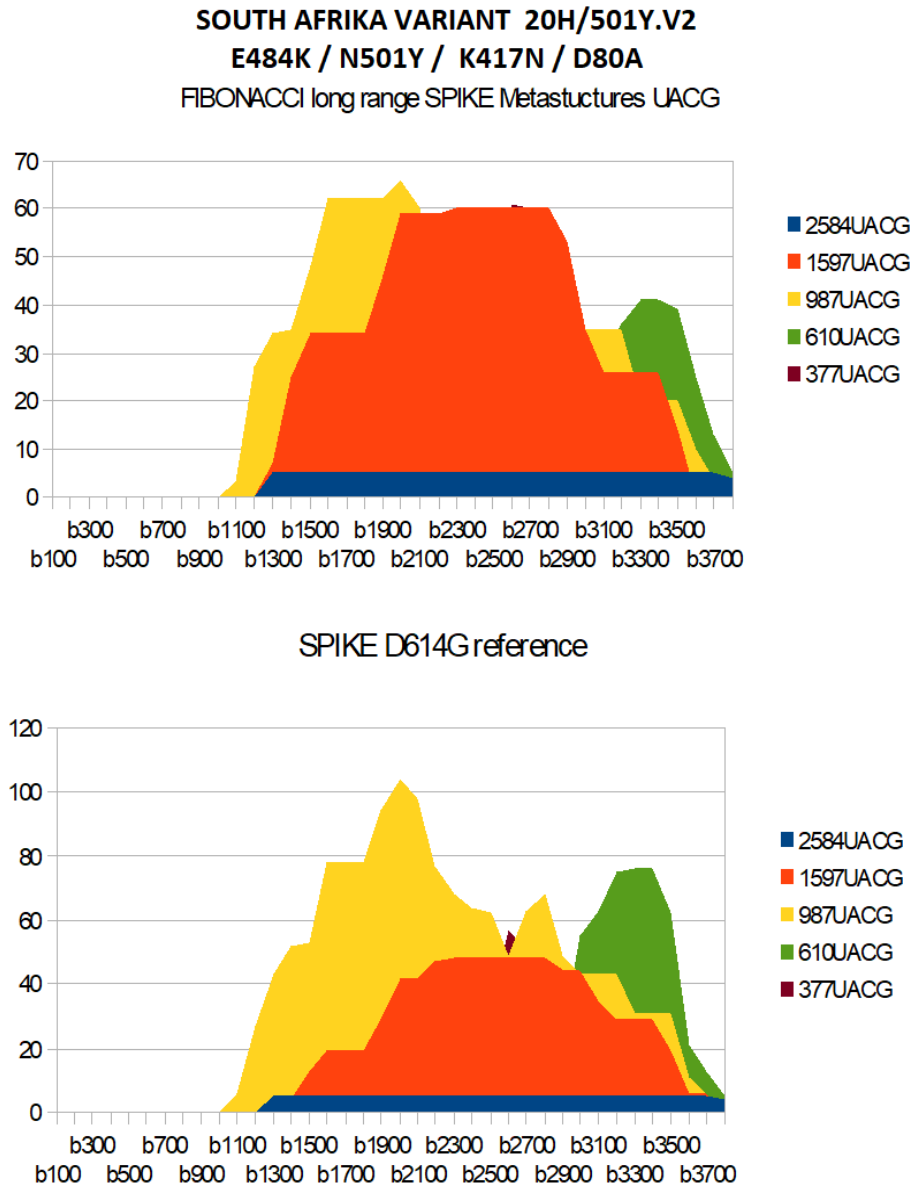


Figure 15: Comparing South Africa variant spike with reference D614G spike.

For this South African variant (figure 15), we see above all a strong increase in metastructures 1597 UACG (orange in figure 15).

On the other hand, the "podium" shape, already observed for the English variant, becomes very clear here. This enigmatic form will be the subject of the next and last paragraph & 7 ...

Indian « two mutations » variant:

We analyse here two cases:
Basic variant
Full variant
See also (Govinarajan, 2020a) and (Govinarajan, 2020b).
In BASIC VARIANT, we modify spike D614G only with these two mutations: E484Q and L452R.

In FULL VARIANT, we manage the fusion between South Africa variant, California variant and the small change vs. South Africa variant doing E484Q.

SINDIABASIC

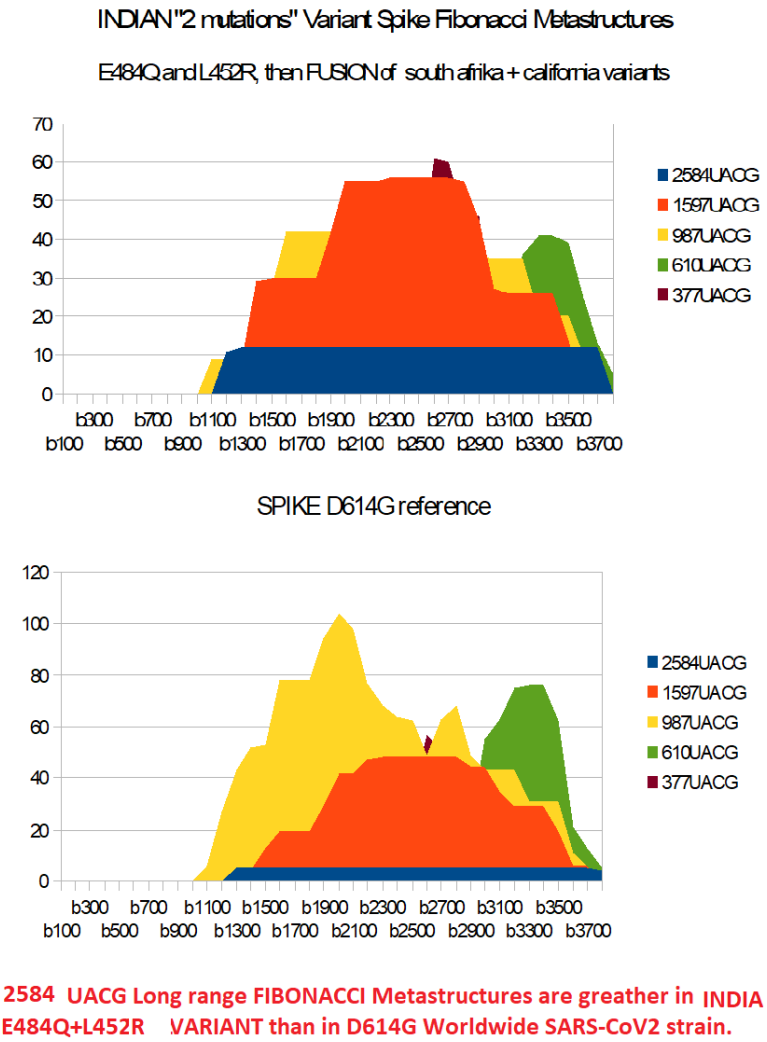


Figure 16: Analysing INDIAN variant Basic (only with 2 mutations E484Q and L452R

SINDIAFULL:

We run following process:

SINDIAFULL = SPIKD614G

Dim SE484K 3822 bases

Dim S614CALREF 3822 bases

Locations of differences in nucleotides between SINDIAFULL and S614CALREF:

38 456 1355

Values of mutations to do in SINDIAFULL:

TTG

SINDIAFULL [38 456 1355] = 'TTG'

Locations of differences in nucleotides between SE484K South Africa and S614CALREF:

239 1251 1450 1501

Values of mutations to do in SINDIAFULL:

CTAT

SINDIAFULL [239 1251 1450 1501] = 'CTAT'

Manage difference E484K to E484Q:
SINDIAFULL [1355] = 'G'

Control:
cumulate SINDIAFULL different SPIKD614G
7
cumulate SINDIAFULL different INDIABASIC
6

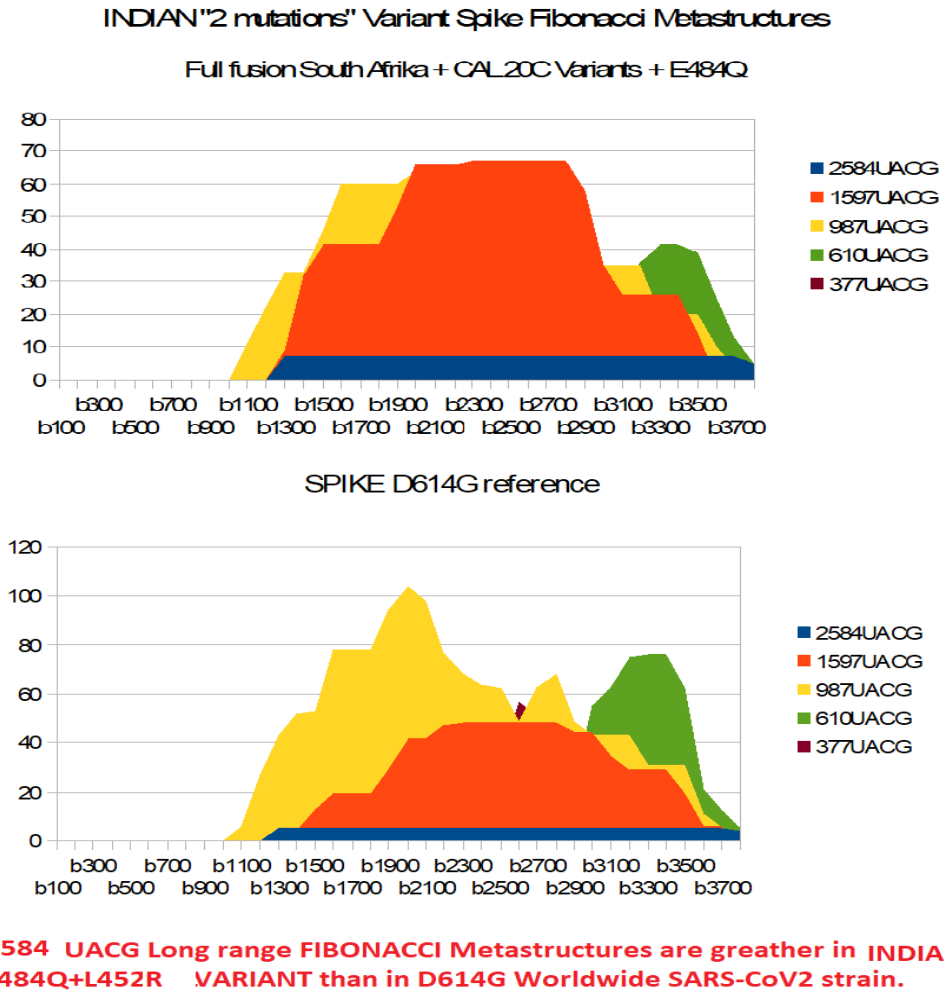


Figure 17: Analysing INDIAN variant Full (fusion CAL.20C and South Africa + difference with South Africa E484Q) Samples with the E484Q and L452R, then South Africa + California variants
https://www.bbc.com/news/world-asia-india-56507988
https://pib.gov.in/PressReleaseIframePage.aspx?PRID=1707177

3.7. SUGGESTING A POSSIBLE VARIANTS SPIKE MRNA PALINDROME SYMMETRY METASTRUCTURE IMPROVING MRNA STABILITY THEN INFECTIOUSNESS

Here, we have gathered several pieces of evidence showing that, as they evolve, the variants would constitute and reinforce a kind of Palindrome-type symmetry based on "Russian doll" interlocking of their mRNA, which could lead to a double strand of the "hairpin" type, thus reinforcing the stability and the lifespan of the Spike mRNA, thus certainly the increasing contagiousness of the variant virus.

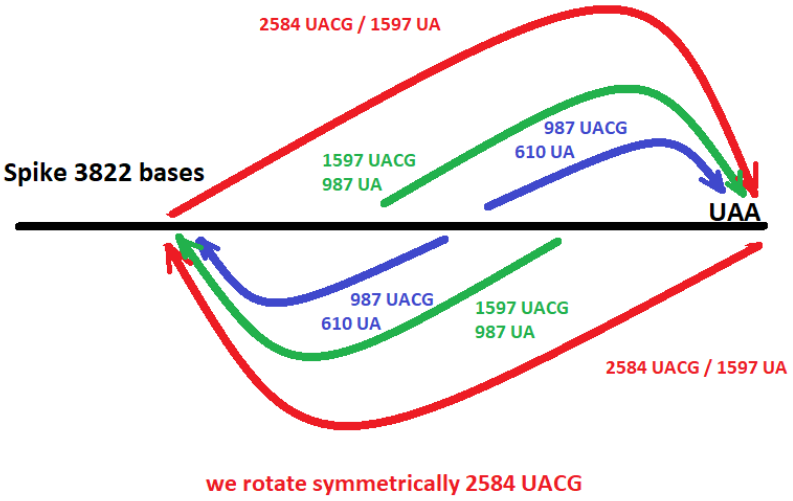


Figure 18: « Fibonacci GLOBAL PALINDROMES » scenario test.

Clearly more pronounced "PODIUM-like" structures appear in these UK, South Africa, India, California (figures 14 to 17) variants than in the strain D614G Spike.

The structures in orange 1597UACG form a curious "PODIUM" ...

Is this the sign of a PALINDROME TYPE SYMMETRY BETWEEN 2 STRUCTURES

FIBONACCI 1597 UACG?

FIBONACCI PALINDROMES EFFECT?

It would seem that in these UK variants, (especially Figure 14, the 2 on the right, particularly right, bottom: Spike UK SN501S variant), a kind of

phenomenon FIBONACCI PALINDROMES (Symmetry) as presented and schematized

in handwritten graph (part in orange STRUCTURES 1597 UACG)

Addresses first and last STRUCTURES of 1597UACG:

First: 1111+1597 = 2708 end of the first 1597 structure.

Last: 1973+1597 = 3570 end of the last 1597 structure.

Then, we considere now area between 1973 and 2708.

The first structure: V1 = SN501S [1111 on 1597]

The last structure: V2 = SN501S [1973 on 1597]

Building the symmetrical palindrome of V2: V2 = rotate V2

Now, we test « hypothetical global palindrome nature » matching on various dimensions:

Comparing matching between the 100 first bases of V1 and the 100 first bases of V2.

In fact, this is similar with comparing the 100 first bases of the first 1597 structure with the 100 last bases of the last 1507 structure...

100 bases test:

V1[on 100] = 'UA' ==> 66 bases

V2[on 100] = 'UA' ==> 61 bases

Then, we continue:

200 bases test:

V1[on 200] = 'UA' ==> 129 bases

V2[on 200] = 'UA' ==> 129 bases

Then, we continue:

300 bases test:
V1[on 300] = 'UA' ==> 198 bases
V2[on 300] = 'UA' ==> 192 bases
Then, we continue:

400 bases test:
V1[on 400] = 'UA' ==> 258 bases
V2[on 400] = 'UA' ==> 249 bases
Then, we continue:

500 bases test:
V1[on 500] = 'UA' ==> 324 bases
V2[on 500] = 'UA' ==> 308 bases
Then, we continue:
…/...
800 bases test:
V1[on 800] = 'UA' ==> 501 bases
V2[on 800] = 'UA' ==> 495 bases
Then, we continue:

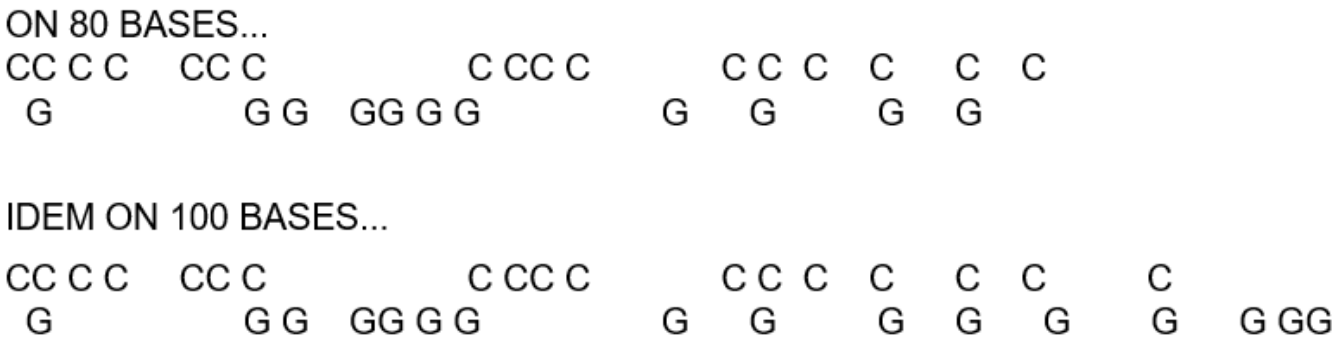
1000 bases test:
V1[on 1000] = 'UA' ==> 613 bases
V2[on 1000] = 'UA' ==> 615 bases
Then, we continue:

1200 bases test:
V1[on 1200] = 'UA' ==> 743 bases
V2[on 1200] = 'UA' ==> 742 bases
Then, we continue:
…/...
1400 bases test:
V1[on 1400] = 'UA' ==> 877 bases
V2[on 1400] = 'UA' ==> 872 bases
Then, we continue:

1500 bases test:
V1[on 1500] = 'UA' ==> 934 bases
V2[on 1500] = 'UA' ==> 936 bases
Then, we continue:

FULL 1597 bases test:
V1[on 1597] = 'UA' ==> 987 bases
V2[on 1597] = 'UA' ==> 987 bases

Then 987 UA and 610 CG
Globally, the palindrome like mRNA folding is good...
Palindrome symmetry test on the first eighty bases of the first 1597 UACG and the first eighty bases of the symmetrical of the last 1597 UACG. They are superimposed face to face like Palindrome.
It does appear C <==> G relations on the hypothetical double strand of mRNA.



Nota: « » is a U or A nucleotide (space).

Particularly, we suggest the following conjecture at mRNA folding level (Mengwen et al, 2006):

CONJECTURE of SARS-CoV2 VARIANTS:

The growth of long Fibonacci structures in the shape of "podiums" for almost all of the variants studied (UK, California, South Africa, India, etc.) suggests the probable folding of the Spike mRNA in the form of a "hairpin", which can strengthen the cohesion and the lifespan of this mRNA.

3.8. ANALYSING FIBONACCI METASTRUCTURES IN THE MRNA CODING FOR THE VACCINES PFIZER AND MODERNA

Stanford University team published and provide experimental sequence information for the RNA components of the initial Moderna (https://pubmed.ncbi.nlm.nih.gov/32756549/) and Pfizer/BioNTech (https://pubmed.ncbi.nlm.nih.gov/33301246/) COVID-19 vaccines (Dae Eun Jeong et al, 2021).

Then we analysed using the same method the hypothetic metastructure of this mRNA vaccine...

Here are the results:

Dim VACCINPFIZER = 4175 bases.
Dim VACCINMODERNA = 4004 bases.

Figure 1 : Spike-encoding contig assembled from BioNTech/Pfizer BNT-162b2 vaccine.

GAGAATAAACTAGTATTCTTCTGGTCCCCACAGACTCAGAGAGAACCCGCCACC***ATGTTCGTGTTCCTGGTGCTGCTGCCTCTGGTGT***
CCA GCCAGTGTGTGAACCTGACCACCAGAACACAGCTGCCTCCAGCCTACACCAACAGCTTTACCAGAGGCGTGTACTACCCCGACAAGGTGTT
CAGATCCAGCGTGCTGCACTCTACCCAGGACCTGTTCCTGCCTTTCTTCAGCAACGTGACCTGGTTCCACGCCATCCACGTGTCCGGCACC
AATGGCACCAAGAGATTCGACAACCCCGTGCTGCCCTTCAACGACGGGGTGTACTTTGCCAGCACCGAGAAGTCCAACATCATCAGAGGCT
GGATCTTCGGCACCACACTGGACAGCAAGACCCAGAGCCTGCTGATCGTGAACAACGCCACCAACGTGGTCATCAAAGTGTGCGAGTTCCA
GTTCTGCAACGACCCCTTCCTGGGCGTCTACTACCACAAGAACAACAAGAGCTGGATGGAAAGCGAGTTCCGGGTGTACAGCAGCGCCAAC
AACTGCACCTTCGAGTACGTGTCCCAGCCTTTCCTGATGGACCTGGAAGGCAAGCAGGGCAACTTCAAGAACCTGCGCGAGTTCGTGTTTA
AGAACATCGACGGCTACTTCAAGATCTACAGCAAGCACACCCCTATCAACCTCGTGCGGGATCTGCCTCAGGGCTTCTCTGCTCTGGAACC
CCTGGTGGATCTGCCCATCGGCATCAACATCACCCGGTTTCAGACACTGCTGGCCCTGCACAGAAGCTACCTGACACCTGGCGATAGCAGC
AGCGGATGGACAGCTGGTGCCGCCGCTTACTATGTGGGCTACCTGCAGCCTAGAACCTTCCTGCTGAAGTACAACGAGAACGGCACCATCA
CCGACGCCGTGGATTGTGCTCTGGATCCTCTGAGCGAGACAAAGTGCACCCTGAAGTCCTTCACCGTGGAAAAGGGCATCTACCAGACCAG
CAACTTCCGGGTGCAGCCCACCGAATCCATCGTGCGGTTCCCCAATATCACCAATCTGTGCCCCTTCGGCGAGGTGTTCAATGCCACCAGA
TTCGCCTCTGTGTACGCCTGGAACCGGAAGCGGATCAGCAATTGCGTGGCCGACTACTCCGTGCTGTACAACTCCGCCAGCTTCAGCACCT
TCAAGTGCTACGGCGTGTCCCCTACCAAGCTGAACGACCTGTGCTTCACAAACGTGTACGCCGACAGCTTCGTGATCCGGGGAGATGAAGT
GCGGCAGATTGCCCCTGGACAGACAGGCAAGATCGCCGACTACAACTACAAGCTGCCCGACGACTTCACCGGCTGTGTGATTGCCTGGAAC
AGCAACAACCTGGACTCCAAAGTCGGCGGCAACTACAATTACCTGTACCGGCTGTTCCGGAAGTCCAATCTGAAGCCCTTCGAGCGGGACA
TCTCCACCGAGATCTATCAGGCCGGCAGCACCCCTTGTAACGGCGTGGAAGGCTTCAACTGCTACTTCCCACTGCAGTCCTACGGCTTTCA
GCCCACAAATGGCGTGGGCTATCAGCCCTACAGAGTGGTGGTGCTGAGCTTCGAACTGCTGCATGCCCCTGCCACAGTGTGCGGCCCTAAG
AAAAGCACCAATCTCGTGAAGAACAAATGCGTGAACTTCAACTTCAACGGCCTGACCGGCACCGGCGTGCTGACAGAGAGCAACAAGAAGT
TCCTGCCATTCCAGCAGTTTGGCCGGGATATCGCCGATACCACAGACGCCGTTAGAGATCCCCAGACACTGGAAATCCTGGACATCACCCC
TTGCAGCTTCGGCGGAGTGTCTGTGATCACCCCTGGCACCAACACCAGCAATCAGGTGGCAGTGCTGTACCAGGACGTGAACTGTACCGAA
GTGCCCGTGGCCATTCACGCCGATCAGCTGACACCTACATGGCGGGTGTACTCCACCGGCAGCAATGTGTTTCAGACCAGAGCCGGCTGTC
TGATCGGAGCCGAGCACGTGAACAATAGCTACGAGTGCGACATCCCCATCGGCGCTGGAATCTGCGCCAGCTACCAGACACAGACAAACAG
CCCTCGGAGAGCCAGAAGCGTGGCCAGCCAGAGCATCATTGCCTACACAATGTCTCTGGGCGCCGAGAACAGCGTGGCCTACTCCAACAAC
TCTATCGCTATCCCCACCAACTTCACCATCAGCGTGACCACAGAGATCCTGCCTGTGTCCATGACCAAGACCAGCGTGGACTGCACCATGT
ACATCTGCGGCGATTCCACCGAGTGCTCCAACCTGCTGCTGCAGTACGGCAGCTTCTGCACCCAGCTGAATAGAGCCCTGACAGGGATCGC
CGTGGAACAGGACAAGAACACCCAAGAGGTGTTCGCCCAAGTGAAGCAGATCTACAAGACCCCTCCTATCAAGGACTTCGGCGGCTTCAAT
TTCAGCCAGATTCTGCCCGATCCTAGCAAGCCCAGCAAGCGGAGCTTCATCGAGGACCTGCTGTTCAACAAAGTGACACTGGCCGACGCCG
GCTTCATCAAGCAGTATGGCGATTGTCTGGGCGACATTGCCGCCAGGGATCTGATTTGCGCCCAGAAGTTTAACGGACTGACAGTGCTGCC
TCCTCTGCTGACCGATGAGATGATCGCCCAGTACACATCTGCCCTGCTGGCCGGCACAATCACAAGCGGCTGGACATTTGGAGCAGGCGCC
GCTCTGCAGATCCCCTTTGCTATGCAGATGGCCTACCGGTTCAACGGCATCGGAGTGACCCAGAATGTGCTGTACGAGAACCAGAAGCTGA
TCGCCAACCAGTTCAACAGCGCCATCGGCAAGATCCAGGACAGCCTGAGCAGCACAGCAAGCGCCCTGGGAAAGCTGCAGGACGTGGTCAA
CCAGAATGCCCAGGCACTGAACACCCTGGTCAAGCAGCTGTCCTCCAACTTCGGCGCCATCAGCTCTGTGCTGAACGATATCCTGAGCAGA
CTGGACCCTCCTGAGGCCGAGGTGCAGATCGACAGACTGATCACAGGCAGACTGCAGAGCCTCCAGACATACGTGACCCAGCAGCTGATCA
GAGCCGCCGAGATTAGAGCCTCTGCCAATCTGGCCGCCACCAAGATGTCTGAGTGTGTGCTGGGCCAGAGCAAGAGAGTGGACTTTTGCGG
CAAGGGCTACCACCTGATGAGCTTCCCTCAGTCTGCCCCTCACGGCGTGGTGTTTCTGCACGTGACATATGTGCCCGCTCAAGAGAAGAAT
TTCACCACCGCTCCAGCCATCTGCCACGACGGCAAAGCCCACTTTCCTAGAGAAGGCGTGTTCGTGTCCAACGGCACCCATTGGTTCGTGA
CACAGCGGAACTTCTACGAGCCCCAGATCATCACCACCGACAACACCTTCGTGTCTGGCAACTGCGACGTCGTGATCGGCATTGTGAACAA
TACCGTGTACGACCCTCTGCAGCCCGAGCTGGACAGCTTCAAAGAGGAACTGGACAAGTACTTTAAGAACCACACAAGCCCCGACGTGGAC
CTGGGCGATATCAGCGGAATCAATGCCAGCGTCGTGAACATCCAGAAAGAGATCGACCGGCTGAACGAGGTGGCCAAGAATCTGAACGAGA
GCCTGATCGACCTGCAAGAACTGGGGAAGTACGAGCAGTACATCAAGTGGCCCTGGTACATCTGGCTGGGCTTTATCGCCGGACTGATTGC
CATCGTGATGGTCACAATCATGCTGTGTTGCATGACCAGCTGCTGTAGCTGCCTGAAGGGCTGTTGTAGCTGTGGCAGCTGCTGCAAGTTC

GACGAGGACGATTCTGAGCCCGTGCTGAAGGGCGTGAAACTGCACTACACA**TGATGA**CTCGAGCTGGTACTGCATGCACGCAATGCTAGCT
GCCCCTTTCCCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCACCTGCCCCACTCACCACCTCTGC
TAGTTCCAGACACCTCCCAAGCACGCAGCAATGCAGCTCAAAACGCTTAGCCTAGCCACACCCCCACGGGAAACAGCAGTGATTAACCTTT
AGCAATAAACGAAAGTTTAACTAAGCTATACTAACCCCAGGGTTGGTCAATTTCGTGCCAGCCACACCCTGGAGCTAGCA

Cyan : Putative 5' UTR Green : Start Codon Yellow : Signal Peptide Orange : Spike encoding region Red : Stop codon(s) Purple : 3' UTR Blue : Start of polyA region (incomplete)

Figure 19: Spike-encoding contig assembled from BioNTech/Pfizer BNT-162b2 vaccine.

Figure 2 : Spike-encoding contig assembled from Moderna mRNA-1273 vaccine.

GGGAAATAAGAGAGAAAAGAAGAGTAAGAAGAAATATAAGACCCCGGCGCCGCCACC***ATGTTCGTGTTCCTGGTGCTGCTGCCCCTGG***
TGAGCAGCCAGTGCGTGAACCTGACCACCCGGACCCAGCTGCCACCAGCCTACACCAACAGCTTCACCCGGGGCGTCTACTACCCCGACAAGG
T GTTCCGGAGCAGCGTCCTGCACAGCACCCAGGACCTGTTCCTGCCCTTCTTCAGCAACGTGACCTGGTTCCACGCCATCCACGTGAGCGGC
ACCAACGGCACCAAGCGGTTCGACAACCCCGTGCTGCCCTTCAACGACGGCGTGTACTTCGCCAGCACCGAGAAGAGCAACATCATCCGGG
GCTGGATCTTCGGCACCACCCTGGACAGCAAGACCCAGAGCCTGCTGATCGTGAATAACGCCACCAACGTGGTGATCAAGGTGTGCGAGTT
CCAGTTCTGCAACGACCCCTTCCTGGGCGTGTACTACCACAAGAACAACAAGAGCTGGATGGAGAGCGAGTTCCGGGTGTACAGCAGCGCC
AACAACTGCACCTTCGAGTACGTGAGCCAGCCCTTCCTGATGGACCTGGAGGGCAAGCAGGGCAACTTCAAGAACCTGCGGGAGTTCGTGT
TCAAGAACATCGACGGCTACTTCAAGATCTACAGCAAGCACACCCCAATCAACCTGGTGCGGGATCTGCCCCAGGGCTTCTCAGCCCTGGA
GCCCCTGGTGGACCTGCCCATCGGCATCAACATCACCCGGTTCCAGACCCTGCTGGCCCTGCACCGGAGCTACCTGACCCCAGGCGACAGC
AGCAGCGGGTGGACAGCAGGCGCGGCTGCTTACTACGTGGGCTACCTGCAGCCCCGGACCTTCCTGCTGAAGTACAACGAGAACGGCACCA
TCACCGACGCCGTGGACTGCGCCCTGGACCCTCTGAGCGAGACCAAGTGCACCCTGAAGAGCTTCACCGTGGAGAAGGGCATCTACCAGAC
CAGCAACTTCCGGGTGCAGCCCACCGAGAGCATCGTGCGGTTCCCCAACATCACCAACCTGTGCCCCTTCGGCGAGGTGTTCAACGCCACC
CGGTTCGCCAGCGTGTACGCCTGGAACCGGAAGCGGATCAGCAACTGCGTGGCCGACTACAGCGTGCTGTACAACAGCGCCAGCTTCAGCA
CCTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTCACCAACGTGTACGCCGACAGCTTCGTGATCCGTGGCGACGA
GGTGCGGCAGATCGCACCCGGCCAGACAGGCAAGATCGCCGACTACAACTACAAGCTGCCCGACGACTTCACCGGCTGCGTGATCGCCTGG
AACAGCAACAACCTCGACAGCAAGGTGGGCGGCAACTACAACTACCTGTACCGGCTGTTCCGGAAGAGCAACCTGAAGCCCTTCGAGCGGG
ACATCAGCACCGAGATCTACCAAGCCGGCTCCACCCCTTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCTCTGCAGAGCTACGGCTT
CCAGCCCACCAACGGCGTGGGCTACCAGCCCTACCGGGTGGTGGTGCTGAGCTTCGAGCTGCTGCACGCCCCAGCCACCGTGTGTGGCCCC
AAGAAGAGCACCAACCTGGTGAAGAACAAGTGCGTGAACTTCAACTTCAACGGCCTTACCGGCACCGGCGTGCTGACCGAGAGCAACAAGA
AATTCCTGCCCTTTCAGCAGTTCGGCCGGGACATCGCCGACACCACCGACGCTGTGCGGGATCCCCAGACCCTGGAGATCCTGGACATCAC
CCCTTGCAGCTTCGGCGGCGTGAGCGTGATCACCCCAGGCACCAACACCAGCAACCAGGTGGCCGTGCTGTACCAGGACGTGAACTGCACC
GAGGTGCCCGTGGCCATCCACGCCGACCAGCTGACACCCACCTGGCGGGTCTACAGCACCGGCAGCAACGTGTTCCAGACCCGGGCCGGTT
GCCTGATCGGCGCCGAGCACGTGAACAACAGCTACGAGTGCGACATCCCCATCGGCGCCGGCATCTGTGCCAGCTACCAGACCCAGACCAA
TTCACCCCGGAGGGCAAGGAGCGTGGCCAGCCAGAGCATCATCGCCTACACCATGAGCCTGGGCGCCGAGAACAGCGTGGCCTACAGCAAC
AACAGCATCGCCATCCCCACCAACTTCACCATCAGCGTGACCACCGAGATTCTGCCCGTGAGCATGACCAAGACCAGCGTGGACTGCACCA
TGTACATCTGCGGCGACAGCACCGAGTGCAGCAACCTGCTGCTGCAGTACGGCAGCTTCTGCACCCAGCTGAACCGGGCCCTGACCGGCAT
CGCCGTGGAGCAGGACAAGAACACCCAGGAGGTGTTCGCCCAGGTGAAGCAGATCTACAAGACCCCTCCCATCAAGGACTTCGGCGGCTTC
AACTTCAGCCAGATCCTGCCCGACCCCAGCAAGCCCAGCAAGCGGAGCTTCATCGAGGACCTGCTGTTCAACAAGGTGACCCTAGCCGACG
CCGGCTTCATCAAGCAGTACGGCGACTGCCTCGGCGACATAGCCGCCCGGGACCTGATCTGCGCCCAGAAGTTCAACGGCCTGACCGTGCT
GCCTCCCCTGCTGACCGACGAGATGATCGCCCAGTACACCAGCGCCCTGTTAGCCGGAACCATCACCAGCGGCTGGACTTTCGGCGCTGGA
GCCGCTCTGCAGATCCCCTTCGCCATGCAGATGGCCTACCGGTTCAACGGCATCGGCGTGACCCAGAACGTGCTGTACGAGAACCAGAAGC
TGATCGCCAACCAGTTCAACAGCGCCATCGGCAAGATCCAGGACAGCCTGAGCAGCACCGCTAGCGCCCTGGGCAAGCTGCAGGACGTGGT
GAACCAGAACGCCCAGGCCCTGAACACCCTGGTGAAGCAGCTGAGCAGCAACTTCGGCGCCATCAGCAGCGTGCTGAACGACATCCTGAGC
CGGCTGGACCCTCCCGAGGCCGAGGTGCAGATCGACCGGCTGATCACTGGCCGGCTGCAGAGCCTGCAGACCTACGTGACCCAGCAGCTGA
TCCGGGCCGCCGAGATTCGGGCCAGCGCCAACCTGGCCGCCACCAAGATGAGCGAGTGCGTGCTGGGCCAGAGCAAGCGGGTGGACTTCTG
CGGCAAGGGCTACCACCTGATGAGCTTTCCCCAGAGCGCACCCCACGGAGTGGTGTTCCTGCACGTGACCTACGTGCCCGCCCAGGAGAAG
AACTTCACCACCGCCCCAGCCATCTGCCACGACGGCAAGGCCCACTTTCCCCGGGAGGGCGTGTTCGTGAGCAACGGCACCCACTGGTTCG
TGACCCAGCGGAACTTCTACGAGCCCCAGATCATCACCACCGACAACACCTTCGTGAGCGGCAACTGCGACGTGGTGATCGGCATCGTGAA
CAACACCGTGTACGATCCCCTGCAGCCCGAGCTGGACAGCTTCAAGGAGGAGCTGGACAAGTACTTCAAGAATCACACCAGCCCCGACGTG
GACCTGGGCGACATCAGCGGCATCAACGCCAGCGTGGTGAACATCCAGAAGGAGATCGATCGGCTGAACGAGGTGGCCAAGAACCTGAACG
AGAGCCTGATCGACCTGCAGGAGCTGGGCAAGTACGAGCAGTACATCAAGTGGCCCTGGTACATCTGGCTGGGCTTCATCGCCGGCCTGAT
CGCCATCGTGATGGTGACCATCATGCTGTGCTGCATGACCAGCTGCTGCAGCTGCCTGAAGGGCTGTTGCAGCTGCGGCAGCTGCTGCAAG

TTCGACGAGGACGACAGCGAGCCCGTGCTGAAGGGCGTGAAGCTGCACTACACC**TGATAATAG**GCTGGAGCCTCGGTGGCCTAGCTTCTTG
CCCCTTGGGCCTCCCCCCAGCCCCTCCTCCCCTTCCTGCACCCGTACCCCCGTGGTCTTTGAATAAAGTCTGAGTGGGCGGCAAAAAAAAA

Cyan : Putative 5' UTR Green : Start Codon Yellow : Signal Peptide Orange : Spike encoding region Red : Stop codon(s) Purple : 3' UTR Blue : Start of polyA region (incomplete)

Figure 20: Spike-encoding contig assembled from Moderna mRNA-1273 vaccine.

It is interesting to note that the starting region of the Spike was modified in both vaccines. We show i (Perez§Montagnier 2020) that this crucial region contains « EIE » HIV like inserts, particularly HIV1 Kenya.

Recall the 100 first bases of SARS-CoV2 Spike:
ATGTTTGTTTTTCTTGTTTTATTGCCACTAGTCTCTAGTCAGTGTGTTAATCTTACAACCAGAACTCAATTACCCCCTG
CATACACTAATTCTTTCACAC

It is interesting comparing this region with the same areas in both vaccines (bold).

What should we conclude about this total absence of Fibonacci metastructures in the mRNAs of these 2 vaccines?

This implies that, although functional, these mRNAs will have a short lifespan and their overall physical structure will be very weak. These mRNAs will be able to split rather quickly into separate fragments which will risk combining with other mRNAs present in their environment.

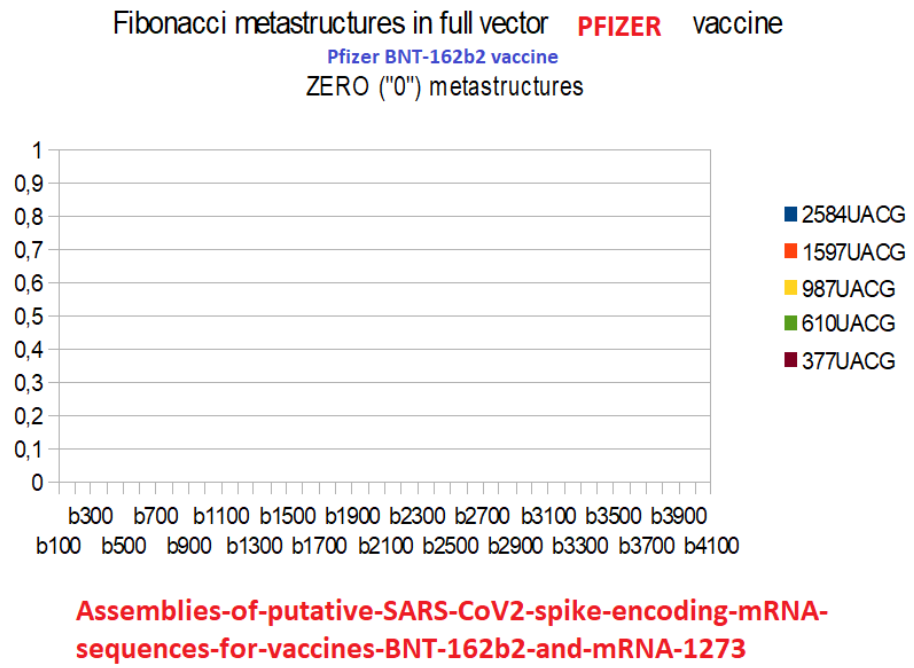


Figure 21: Flat response for Fibonacci Metastructures from **BioNTech/Pfizer BNT-162b2 vaccine**.

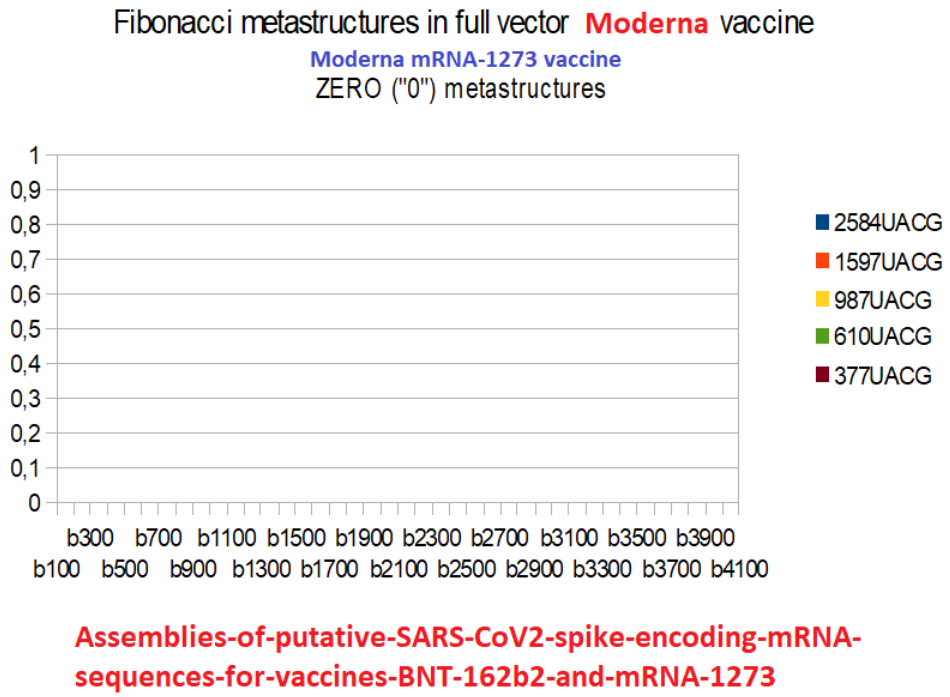


Figure 22: Flat response for Fibonacci Metastructures from **Moderna mRNA-1273 vaccine**.

We will now explain the technological reasons which, in the design of these two vaccines, led to such differences between the Fibonacci structures of real SARS-CoV2, their variants and these two mRNA vaccines.

A necessary but not sufficient condition for the possible emergence of Fibonacci UA / CG metastructures is that the ratio between the total number of UA and CG bases of the analyzed sequence is> 1 and, ideally, close to the optimum Phi = 1.618, the "Golden ratio".

Let us calculate these ratios for certain SARS-CoV2 genomes and spikes various variants, then for the two mRNAs of the Moderna and Pfizer vaccines.

Table 8 below demonstrates how the entire genomes as well as the spikes and the different variants all have an AU / CG ratio very close to 1.618. The maximum error is less than 4%. On the contrary, the two of the Pfizer and Moderna mRNA vaccines have radically INVERTED ratios such as CG> UA.

Table 8: Comparing various UA/CG ratios from 20 SARS-CoV2, variants, and mRNA vaccines.

MRNA sequence	Ratio UA/CG	Error 1.618 – ratio UA/CG
Whole Genomes		
SARS-CoV2 ref	1.633465434	**-0.01543144473**
SARSCOV2 D614G	1.633233533	**-0.01519954393**
Bat RATG13	1.629006692	**-0.0109727035**
CoVZC45	1.570467483	**0.04756650582**
CoVZXC21	1.575760201	**0.04227378801**
VCA19 (patient California variant ref Table4)	1.633710647	**-0.01567665833**
Spikes		
Spike SARS-CoV2 ref	1.680224404	**-0.06219041493**
D614G	1.678346181	**-0.0603121918**
Bat RaTG13	1.661774983	**-0.04374099353**
CoVZC45	1.600834492	**0.01719949665**
CoVZXC21	1.627988748	**-0.009954759242**
SCA19 (patient California variant ref Table4)	1.682105263	**-0.06407127416**
Variant UK SN501Y	1.678346181	**-0.0603121918**
Variant UK SN501T	1.676470588	**-0.05843659924**
Variant UK SN501S	1.676470588	**-0.05843659924**
Variant South Africa SE484K	1.680224404	**-0.06219041493**
Variant INDIABASIC (ref §3.6)	1.676470588	**-0.05843659924**
Variant INDIAFULL (ref §3.6)	1.682105263	**-0.06407127416**
mRNA vaccines		
Pfizer	0.7593763169	**0.8586576721**
Moderna	0.6132151491	**1.00481884**

Faced with such a distortion between the real and "humanized" SARS-CoV2 strains and its variants on the one hand, and the mRNAs of the two vaccines on the other hand, we will now try to answer two essential questions:

1) Is there a mutation "strategy" governing the adaptation of the virus and its variants to its host? This strategy, if it exists, will ALSO constitute a strong mutation constraint for the two mRNAs of the Moderna and Pfizer vaccines? Table 10 below will answer this key question.

2) For what technological reasons did the designers of the two mRNA vaccines decide to "dope" the sequences constituting their vaccines in CG bases?

Does this predominance of AU / CG ratios located around Phi = 1.618 extend to other SARS-CoV2 genes?

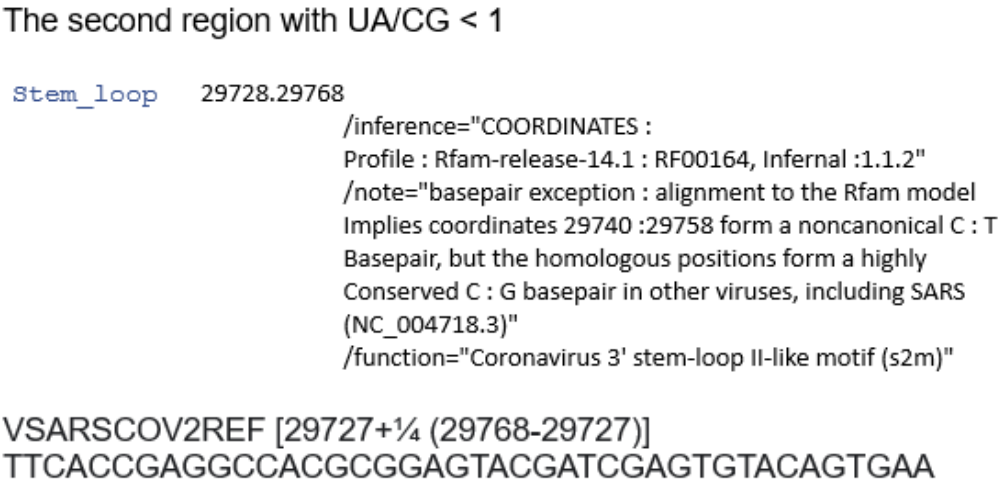
In Table 9, we demonstrate this generalization. Only two sequences, very short, have a UA / CG ratio <1. We find that the entire genome, the large ORF1ab gene, the spike gene, as well as the average of all genes closely obey this law. The average cumulative error over all genes is .03. (1.85%)

Particularly, the gene ORF1ab17 with a ratio <1 is a very short quasi palindrome mRNA sequence:

Coronavirus frameshifting stimulation element
stem-loop 1"

Semi palindrome

The second region with UA/CG < 1



This sequence is also very short.

Recall SARS-CoV2 Wuhan references
https://www.ncbi.nlm.nih.gov/nuccore/NC_045512

Table 9: Computing UA/CG ratio for all SARS-CoV2 Wuhan reference genes.

MRNA sequence	Ratio UA/CG	Error 1.618 – ratio UA/CG
Whole Genomes		
SARS-CoV2 ref	1.633465434	**¯0.01543144473**
Genes		
5 UTR	1.245762712	**0.3722712771**
ORF 1AB	1.669927264	**¯0.05189327461**
ORF1 ab1	1.061068702	**0.5569652867**
ORF1 ab2	1.508519004	**0.1095149851**
ORF1 ab3	1.785202864	**¯0.167168875**
ORF1 ab4	1.742230347	**¯0.1241963583**
ORF1 ab5	1.742230347	**¯0.1241963583**

ORF1 ab6	1.740112994	**-0.1220790054**
ORF1 ab7	1.621052632	**-0.003018642579**
ORF1 ab8	1.605263158	**0.01277083111**
ORF1 ab9	1.492647059	**0.1253869302**
ORF1 ab10	1.355932203	**0.2621017856**
ORF1 ab11	1.682341651	**-0.06430766167**
ORF1 ab12	1.620639535	**-0.002605545884**
ORF1 ab13	1.61322314	**0.004810848504**
ORF1 ab14	1.940509915	**-0.322475926**
ORF1 ab15	1.820189274	**-0.2021552854**
ORF1 ab16	1.650491277	**-0.03245728832**
ORF1 ab17 §	0.6470588235	**0.9709751655**
ORF1 ab18	+1.750000000	**-0.131966011**
SPIKE	1.680224404	**-0.06219041493**
ORF3a	1.532110092	**0.08592389726**
Gene E (ref Yan Li Meng)	1.620689655	**-0.002655666172**
Gene M	1.347368421	**0.2706655679**
ORF6	1.347368421	**0.2706655679**
ORF7a	1.614285714	**0.003748274714**
ORF7b	2.219512195	**-0.6014782061**
ORF8	1.79389313	**-0.1758591408**
Gene N	1.117647059	**0.5003869302**
ORF10a	+1.925000000	**-0.306966011**
ORF10b	1.769230769	**-0.1511967802**
ORF10c	2.222222222	**-0.6041882332**
3UTR	1.726190476	**-0.1081564872**
Coordinates	0.7826086957	**0.8354252933**
AVERAGE	**1.588022181**	**0.03001180791 (1.85%)**
MRNA vaccines		
Pfizer	0.7593763169	**0.8586576721**
Moderna	0.6132151491	**1.00481884**

Table 10: Comparing UA ==> CG and CG ==> UA mutations in fifteen worldwide SARS-CoV2 variants (source https://covariants.org/).

Variant reference	UA ==> CG	CG ==> UA
20E(EU1) https://covariants.org/variants/20A.EU1	1	1
20A.EU2	1	3

https://covariants.org/variants/20A.EU2		
20I/501Y.V1 https://covariants.org/variants/S.501Y.V1	1	6
20H/501Y.V2 https://covariants.org/variants/S.501Y.V2	0	4
20J/501Y.V3 https://covariants.org/variants/S.501Y.V3	3	5
20C/S:452R https://covariants.org/variants/S.L452R	2	2
20C/S:484K https://covariants.org/variants/20C.S.484K	1	2
20A/S :484K https://covariants.org/variants/20A.S.484K	4	8
20A/S:439K https://covariants.org/variants/20A.S.484K	0	1
S:677H.Robin1 https://covariants.org/variants/S.Q677H.Robin1	1	4
S:677P.Pelican https://covariants.org/variants/S.Q677P.Pelican	1	3
20A/S:98F https://covariants.org/variants/S.S98F	0	1
20C/S:80Y **https://covariants.org/variants/S.D80Y**	**0**	**8**
20B/S:626S https://covariants.org/variants/S.A626S	0	0
20B/S:1122L https://covariants.org/variants/S.V1122L	0	0
Total	**15**	**48**

Let out of the fifteen variants referenced > three times more CG ==> UA than UA ==> CG.

A very marginal residual number consists of U / A or C / G.

Morality: variants, by synonymous mutations most often seek to optimize (ie. "NATURALIZE")

the mRNA of the genome by privileging the UA, and probably the ratio UA / CG close to phi 1.618, this is what the Fibonacci analyzes shows on the variants by means of our curves.

As for the MODERNA and PFIZER mRNAs, they are MAJORITY in CG, therefore Fibonacci UA / CG NULS.

Now, what about the second question:

« For what technological reasons did the designers of the two mRNA vaccines decide to "dope" the sequences constituting their vaccines in CG bases? »

In (Jackson et al, 2020), we could read: «Last, codon optimization and modification of nucleotides have contributed to translation efficiency. For example, optimization of guanine and cytosine (GC) content can have a significant impact (Kudla et al, 2016) and has been well established with DNA vaccines ».

(Kudla et al, 2016) detailed this « CG rich manufacturing technology »: « Mammalian genes are highly heterogeneous with respect to their nucleotide composition, but the functional consequences of this heterogeneity are not clear. In the previous studies, weak positive or negative correlations have been found between the silent-site guanine and cytosine (GC) content and expression of mammalian genes. However, previous studies disregarded differences in the genomic context of genes, which could potentially obscure any correlation between GC content and expression. In the present work, we directly … »

This leads to a new question:

"Can we distinguish between natural variants and variants triggered by vaccines?"

This D80Y spike variant would be a good candidate for this variant for this vaccine question because it has a high number of syn C ==> U mutations.

We recall here this detailed variant:

Dedicated 20C/S:80Y Nextstrain build

Defining mutations

Nonsynonymous:

S:D80Y

N:S186Y

N:D377Y

ORF1a:T945I

ORF1a:T1567I

ORF1a:Q3346K

ORF1a:V3475F

ORF1a:M3862I

ORF1b:P255T

- ORF7a:R80I

Synonymous :

G4960T

C6070T

C7303T

C7564T

C10279T

C10525T

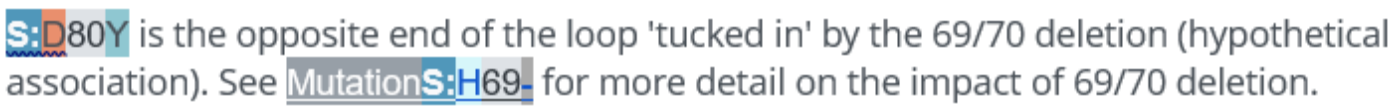
C10582T

- C27804T

Of full list of eighteen nucleotide mutations, fifteen are mutations to T (possibly related to APOBEC-like editing within host, see (Simmonds, 2020).

This variant is found in at least 10 countries across Europe.

S: D80Y



This strain is present everywhere in Europe.

Quite rightly, Professor Luc Montagnier asks me:

"I put my question again in another form: all the variants that you have studied have in the sequence of their Spike proteins a Fibonacci YES series? Why? Because it is a rule of harmonization of Nature that is followed by the variants during their passage through their successive hosts. The m-RNA sequences of vaccines were chosen by technologists ignoring these laws, which only had the aim of increasing the stability of their messages."

This is why I researched and found what technological reasons led them to make mRNA CG rich.

But another more speculative question then arises:

Between these two disjointed universes, mRNA and proteins, would having a HYPER STRUCTURED mRNA be able to transmit "a certain dynamic energy during the passage into amino acids" to the future protein, which would make it more stable? more functional?

If so, can our Fibonacci methods be used for that? One fact is certain, the two mRNAs of the Moderna and Pfizer vaccines will result in a low functionality of the spike vaccine because by doping these sequences in CG rich, their designers, in search of greater STABILITY of these RNAs will have built, sequences that, as soon as they are inserted into the human host, will seek to mutate, like SARS-CoV2 variants, towards CG ==> UA forms in order to improve, paradoxically, their STABILITY and their LIFETIME.

3.9. DOES THE CG-RICH MODIFICATION OF THE SYNONYMOUS CODONS OF THE SPIKES OF THE 2 MRNA VACCINES AFFECT THE EXPRESSION AND QUANTITY OF SARS-COV2 ANTIBODIES?

Analyzing Master Code fractal structure and stationary waveforms differences between Moderna and Pfizer Spikes mRNA.

In (Perez, 2015 and Perez, 2018), we present a unifying theoretical method, from the atomic masses of their bioatoms C O N H S P, the three biological universes of RNA, DNA and proteins. We published various articles involving applications based on this basic research (Perez, 2017b, Perez, 2017c).

The Master Code of the sequence can be applied indistinctly to all DNA or RNA sequences, irrespective of whether they are coding proteins or not, and to all protein sequences. To every nucleotide triplet (codon), or amino acid (AA), there can be associated a cypher comprising of between -3 and +7. These cyphers are established in relation with the atomic masses of the chemical elements C, N, O, H, S, P constituting the nitrogen bases (purines and pyrimidines) and the amino acids. They allow a simple numerical translation of the sixtyfour codons and twenty amino acids. Exposing here the concepts leading to this code goes beyond the scope of this article and we refer the budding mathematicians to the article (Perez, 2018) “Six Fractal Codes of Biological Life: perspectives in Exobiology and Artificial Intelligence Biomimetism Decisions Making, 2018”. One could oppose the criticism that this representation reduces too drastically the physico-chemical reality of the translated sequences. However, it allows their underlying geometrical reality to be measured. This mathematical conversion has the advantage to reduce the complexity of the problem. We can cite here the great mathematician and physicist Von Neumann who used to say with humor “There's no sense in being precise when you don't even know what you're talking about”.

Although the amino acid sequences of the spikes of the two mRNA vaccines are identical, it is interesting to analyze with these biomathematic methods their nucleotide sequences which are very different. Indeed (& 3.8), we have seen that these two sequences were doped with CG rich nucleotides at the level of the synonymous codons coding for the same amino acid, therefore without affecting the sequence of the spike protein.

In Figure 23 below, we see that, while the two Moderna and Pfizer protein sequences (blue proteomics curves) are identical, their respective Genomics curves (red curves) are very different. We observe in particular a completely chaotic fractal roughness in the case of Pfizer spike. In fact, in the case of the two spikes of these vaccines, a large number of synonymous codons were modified in order to dope these sequences in CG bases without altering the amino acid sequence. We believe that this exceptional fractal roughness could affect the stability and the lifespan of

the RNA, whereas the CG emphasis sought by the designers of Pfizer-BionTech was, precisely, to increase the stability of these RNAs. One advantage will be that these RNAs will be quickly destroyed (around ten days). On the other hand, the fragility of these RNAs could lead to “breaks” of the RNA strand, with the risk of erratic combinations (HERV retrovirus for example, naturally present in the cell).

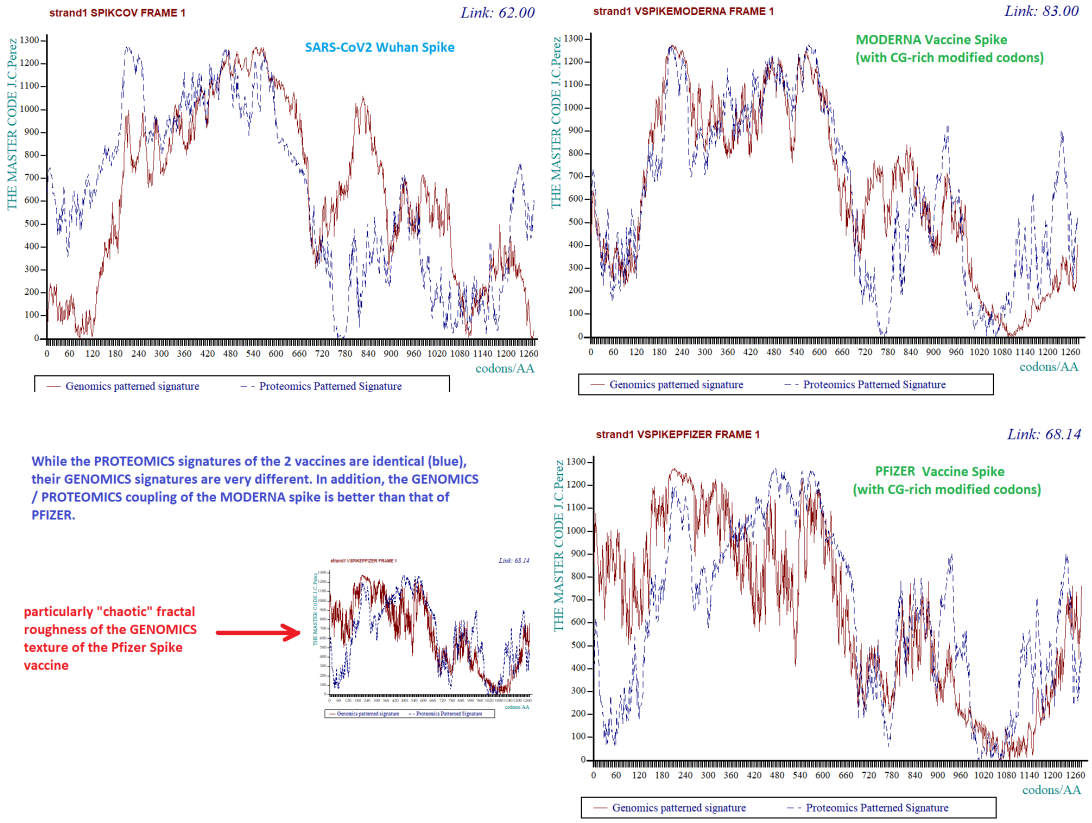


Figure 23: Comparing Master Code Genomics/Proteomics between SARS-CoV2 Wuhan, Moderna and Pfizer spikes.

Computing Standing waves:

In (Perez,2018), we describe this biomathematical method associating with any Genomics sequence periodic waves (numerical where period is a number of nucleotides).

The Genomics master code is generalized to meta-codons that no longer have three nucleotides as a codon, but four, five, ... one hundred nucleotides. Then we analyze the textures by the undulatory code. It then appears dissonances and resonances that will reveal periods of discrete waves, resonances, and standing waves.

This method provides a global analyzes of the roughness or fractal texture of the DNA sequences at the whole sequence scale. To do this, we generalize the method of numerical analyzes of the "Master Code". Thus, we restructure the sequence into different generic sequences based on "meta codons", no longer triplets of three nucleotides, but values ranging from one to a hundred nucleotides. This method of analyzes will then reveal, in most cases, discrete waves or interferences, most often dissonances resulting from Genomics Master code texture. However, sometimes there will emerge kinds of resonances where all scales of analyzes appear to be in symbiosis.

The following Figure 24 shows this kind of waveforms in the three cases of spike sequences provided by the SARS-CoV2 Wuhan reference, Moderna vaccine and Pfizer vaccine.

Figure 24 below illustrates and confirms, as before, standing waves of eight nucleotides quite similar for SARS-CoV2 and Moderna spikes. On the contrary, the Spike Pfizer is characterized by a different frequency: period of seven nucleotides.

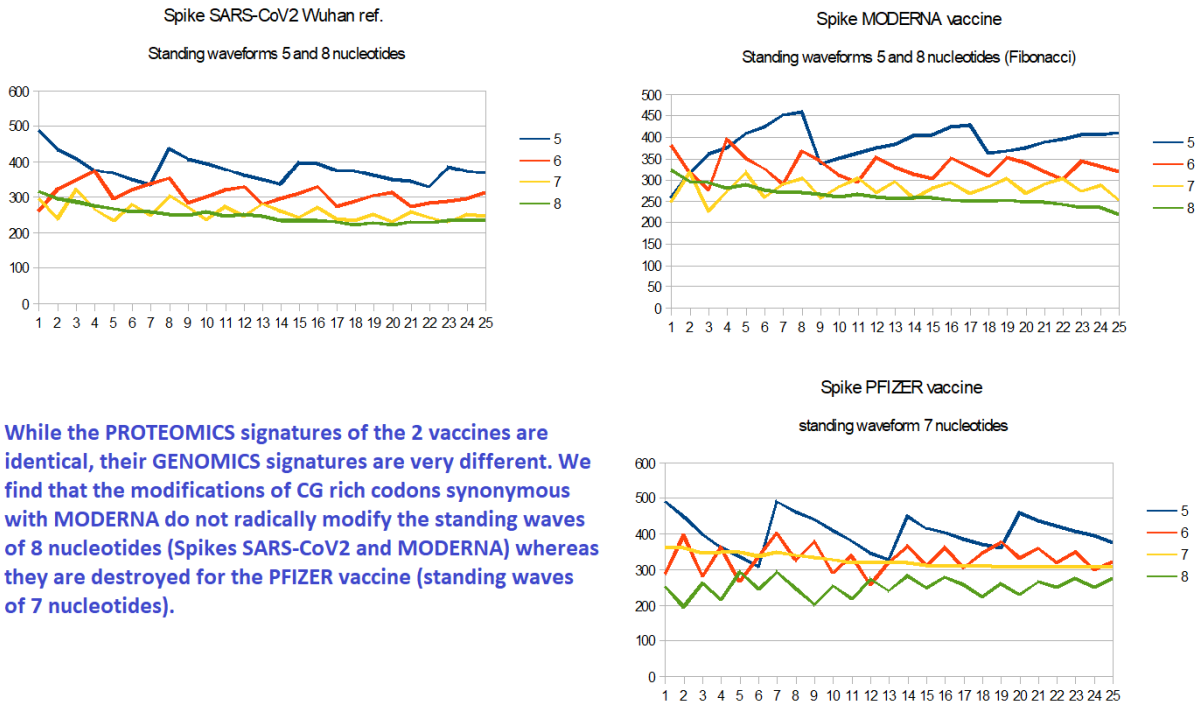


Figure 24: Comparing numerical « Standing waves » between SARS-CoV2 Wuhan, Moderna and Pfizer spikes.

From this comparison of the spikes of the two vaccines Moderna and Pfizer, we conclude a very probable difference in stability and shelf life of the two respective mRNAs of these two vaccines. However, conventional "State of the Art" analyzes will only rveal that their two protein sequences are strictly identical. By having modified their synonymous codons using different strategies, no-one can guarantee that the quantity of antibodies generated will be identical in the two cases.

No-one can affirm that this difference in the two mRNAs will not have contributed to the dynamic formation of the spike protein. This is all the more complex since these mRNAs contain certain modified U / T bases. Professor Roland Baker (Molecular Genetics, U.C. Berkeley) stated that: " T is for thymine used in DNA. U is for uracil used instead of T for mRNA. The mRNA vaccines made by Moderna and Pfizer use neither. Instead, they use 1-methyl-3'-pseudouridylyl which either shows a m1Ψ or simply Ψ. 1-methyl-3'-pseudouridylyl is used to increase the half-life of the mRNA. Otherwise, it degrades too quickly. "

One might wonder why such a period of eight nucleotides is important? We observe that the spikes of SARS-CoV2 (and all its variants), as well as the Moderna spike, retain this period 8, unlike the Pfizer spike.

8 is a Fibonacci number, and Figure 25 below illustrates how these Fibonacci periods (8 13 21 34 55 89 ...) are conserved at the scale of whole genomes SARS-CoV2 Wuhan, but also in this variant CAL 21C collected from a Californian patient (Table3, CA51). It even appears that these Fibonacci standing wave periods at the scale of the entire genome would be "reinforced" in the case of the Californian variant (Figure 25) even though these two genomes are significantly different (29903nt for SARS-CoV2 and 29754nt for CA51).

CA51 contains one deletion encompassing S13I and another deletion encompassing W152C (see Table3), two of the three characteristic mutations of the California variant CAL.20C. However, despite this high level of deletions of the CAL.20C genome, the level of Fibonacci standing waves is preserved and even reinforced. At the same time, the number of Fibonacci UA / CG metastructures (Table3) is also reinforced with respect to the reference genome.

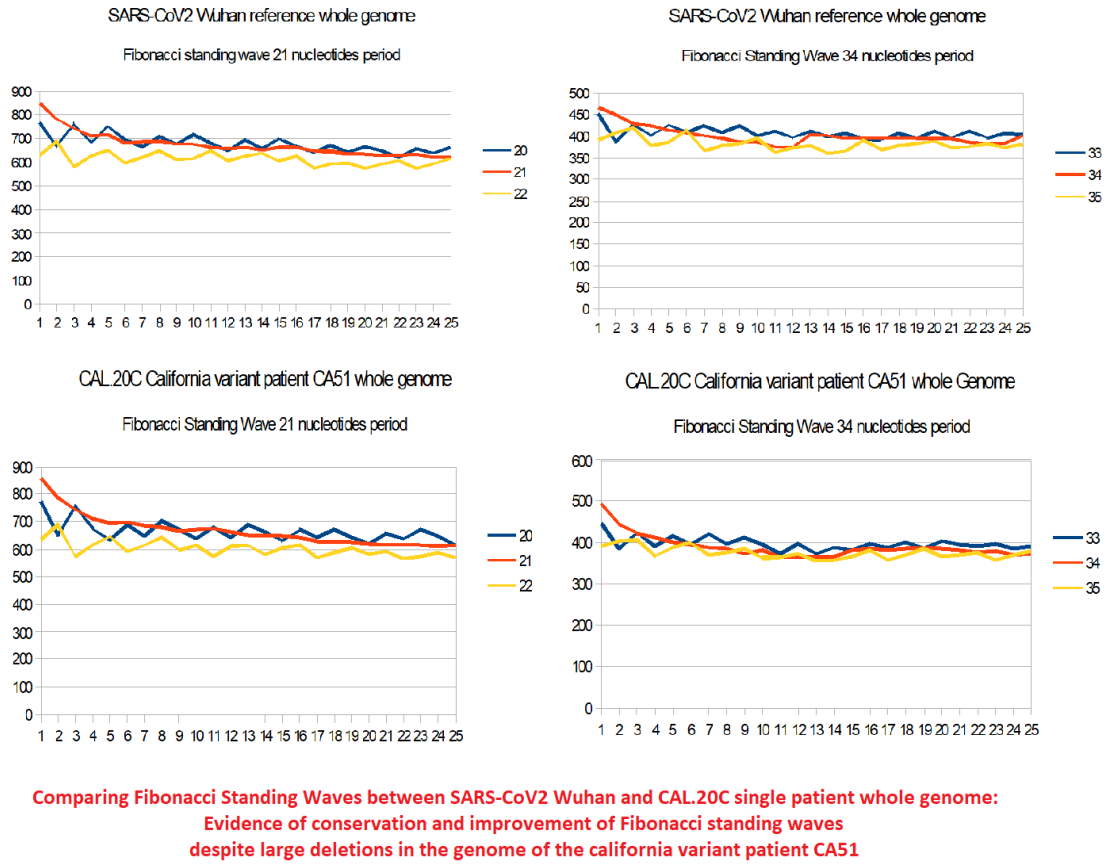


Figure 25: Comparing Fibonacci Standing Waves between SARS-CoV2 Wuhan and CAL.20C single patient whole genomes.

10. The exceptional case of the Brazilian variant P.1.

Although having appeared in Brazil (Manhaus) at the end of 2020, this P.1 variant has become almost uncontrollable in this country during April 2021. As shown by the mutations below, this P.1 variant accumulates the mutations of the majority of other variants. It seemed necessary to us to analyze its genome and its spike using the various biomathematic tools which were presented in this article.

Mutations on the SARS-CoV2 Wuhan reference genome recall. https://www.ncbi.nlm.nih.gov/nuccore/NC_045512

Recall locations of the 3 genes with mutations involved in in Brazil P.1:
266..21555
/gene="ORF1ab"

28274..29533
/gene="N"

21563..25384
/gene="S"

P.1 is the variant name associated with variant
20J/501Y.V3
Defining mutations

Nonsynonymous :

- S:L18F
- S:K417T
- S:E484K
- S:N501Y
- S:H655Y
- ORF1a:S3675-
- ORF1a:G3676-
- ORF1a:F3677-
- N:P80R
- N:R203K
- N:G204R

Synonymous :

- C241T
- T733C
- C2749T
- C3037T
- A6319G
- A6613G
- C12778T
- C13860T
- A28877T
- G28878C

This variant is one of three 3 "Variants of Concern" reported at the end of 2020/beginning of 2021, in:

- The UK (20I/501Y.V1 or B.1.1.7)
- South Africa (20H/501Y.V2 or B.1.351)
- Brazil (20J/501Y.V3 or P.1)

See a list of shared mutations for these variants. More information on each of these variants can be found by visiting the links above.

View data generation scripts

20I/501Y.V1 (B.1.1.7)	20H/501Y.V2 (B.1.351)	20J/501Y.V3 (P.1)	20B/S.484K (P.2)	20C/S.452R (B.1.427/9)	20C/S.484K (B.1.526)	20A/S.484K (B.1.525)
Shared mutations Sort by:Commonness Position						
	S:L18F	S:L18F				
S:H69-						S:H69-
S:V70-						S:V70-
S:Y144-						S:Y144-
	S:K417N	S:K417T				
	S:E484K	S:E484K	S:E484K		S:E484K	S:E484K
S:N501Y	S:N501Y	S:N501Y				
S:D614G	S:D614G	S:D614G	S:D614G	S:D614G	S:D614G	S:D614G
	S:A701V				S:A701V	
		S:V1176F	S:V1176F			
Other mutations						
S:A570D	S:D80A	S:T20N		S:S13I	S:L5F	S:Q52R
S:P681H	S:D215G	S:P26S		S:W152C	S:T95I	S:A67V
S:T716I	S:L241-	S:D138Y		S:L452R	S:D253G	S:Q677H
S:S982A	S:L242-	S:R190S				S:F888L
S:D1118H	S:A243-	S:H655Y				
		S:T1027I				

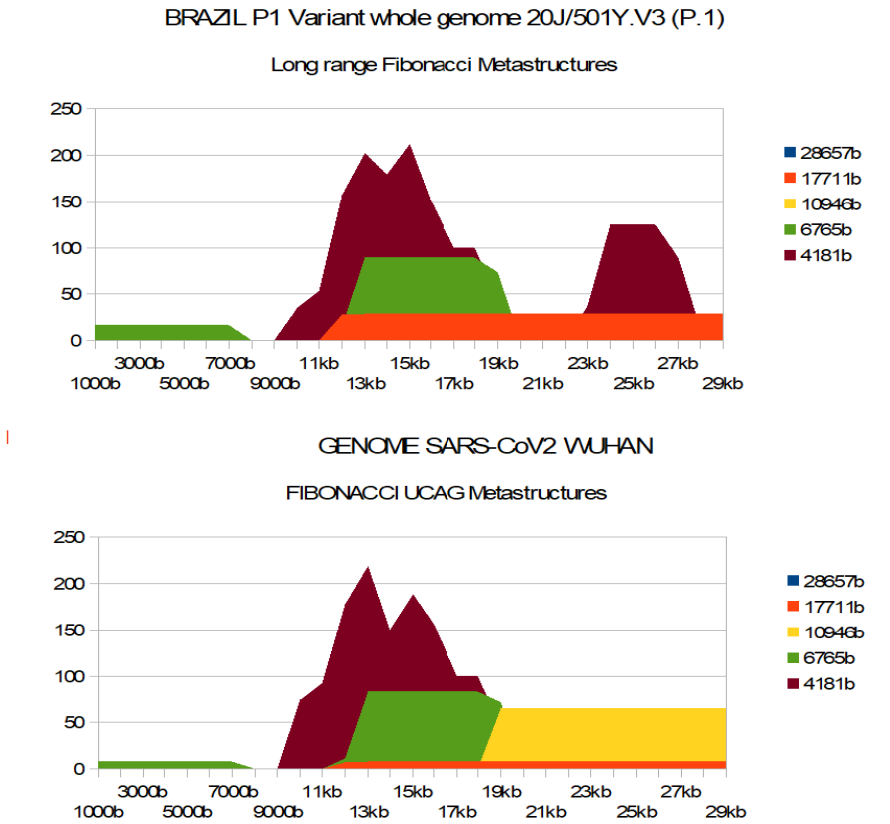


Figure 26: Evidence of an increasing long range metastructure in the whole Brazil P.1 variant.

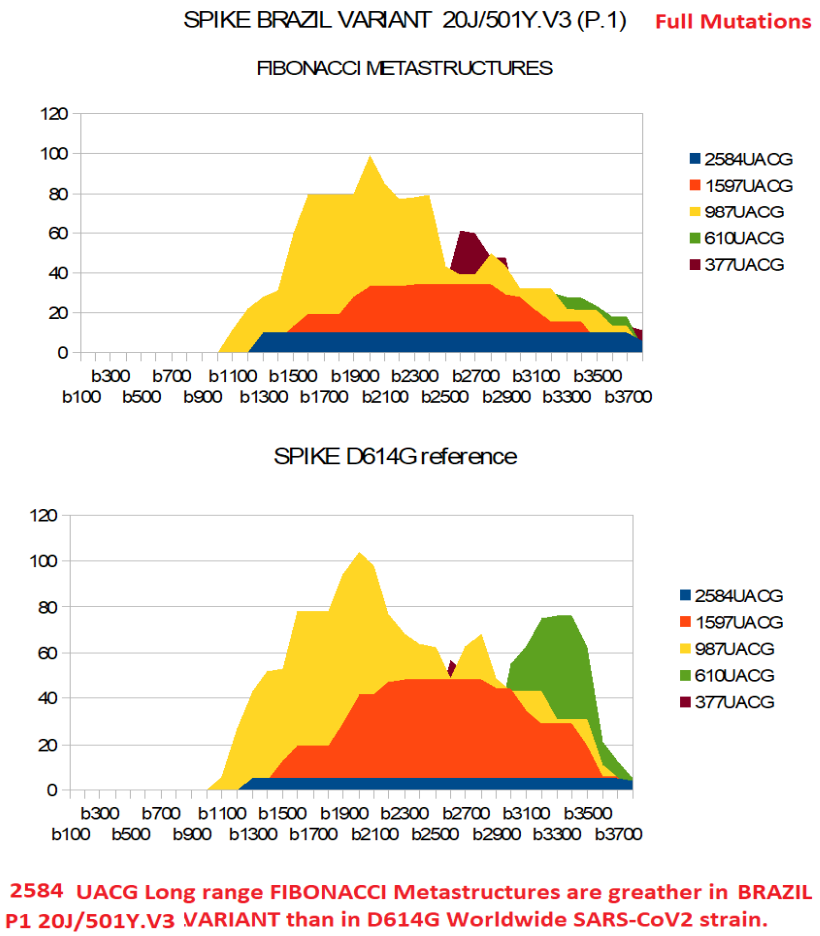


Figure 27: Evidence of an increasing long range metastructure in the Brazil P.1 variant spike.

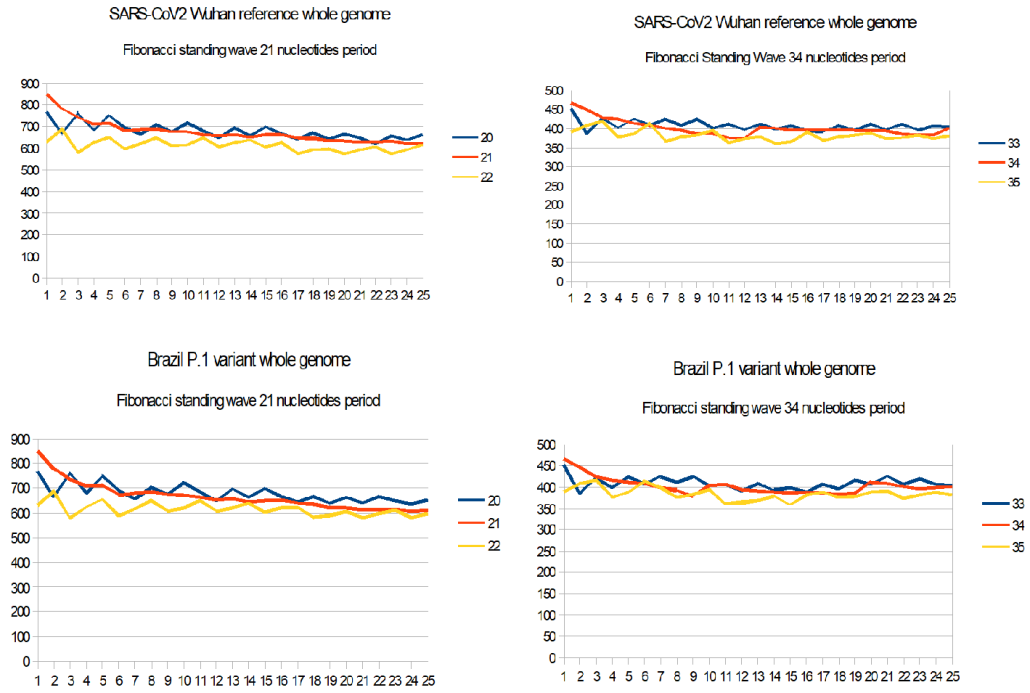


Figure 28: Evidence of long-range Fibonacci standing waves structuring the Brazil P.1 variant whole genome.

We note that the analyzes of the number of Fibonacci metastructures of 17711 base for the genome is considerable: 29 against 8 for the dominant strain D614G and for the original strain SARS-CoV2 Wuhan, that is to say nearly 3.62 times.

Secondly, the long-range Fibonacci standing waves 2 3 5 8 13 21 34 (here 21 and 34 in Fugure 28) remain conserved despite the high level of mutations of this variant:

-12 mutations on Spike.

- 3 mutations on ORF1a.

- 3 mutations on gene N.

- 10 synonymous mutations.

4. CONCLUSIONS

First, this study of spikes by Fibonacci metastructures highlights four primary conclusions:

- **It presents a clarification by the image of links already suspected by multiple researchers between the spikes of bat RATG13, ZXC21, ZC45 and SARS-CoV2.**
- **As we had predicted and already verified (WA state USA) in (Perez & Montagnier 2020), some variants deleted as a priority our predicted « EIE » HIV-like fragments from the dense HIV region at the start of the spike. This is the case with the English variant but also with several patients of the California variant CAL.20C.**
- **Overall, the reference spikes of all the variants studied here have a reinforcement of the most significant Fibonacci structures (2584 bases). But this phenomenon is amplified and confirmed when we analyze the spikes of patients (32 CAL.20C patients).**
- **We note the total absence of Fibonacci metastructures in the mRNAs of both mRNA vaccines PFIZER and MODERNA. This means that, although functional, these mRNAs will have a short lifespan and their overall physical structure will be very weak. These mRNAs will be able to split rather quickly into separate fragments which will risk combining with other mRNAs present in their environment.**
- **We demonstrate how the Brazilian variant P.1 which becomes uncontrollable in Brazil in April 2021 has a level of organization of long metastructures of 17,711 bases covering the genome which is 3.6 more important than that of the 2 reference genomes SARS-CoV2 Wuhan and worldwide D614G. We suggest that this high level of overall structure of this variant contributes to the stability of this genome and, possibly, to its greater contagiousness.**

We will also conclude the tendency of the variant spikes to strengthen their overall structure, which may be correlated with their greater cohesion and lifespan of their mRNA spike, and probably the greater infectivity and pathogenicity of the variants.

Of the ten clusters of results presented here, three deserve to be revisited, reproduced and extended more deeply:

1) point -II-

Fibonacci metastructures "shed a radically new light on" the relationships already recognized or suspected "between the four Sars-CoV2 Wuhan (1/2020), SARS-covZC44 (2017), SARS-covPZXC2P1 (2015) and bat RATG13 genomes (2013). Added to this is evidence of manipulation of CODONS synonymous with spike of one or the other between SARS-CoV2 and beats RATG13, to the question "which of the 2 was manipulated?". We can assert that it is the SARS-CoV2 spike that has been manipulated to modify synonymous CODONS while retaining the functionality of the same amino acids. We believe that this manipulation will most certainly have attenuated the virulence and pathogenicity of SARS-CoV2 opposite bat RATG13 * (blue regions of the 2 images of their Spikes).

Moreover, if at the level of the four respective genomes, the strong neighborhoods between SARS-CoV2 and bat RATG13 on one hand, and ZC45 and ZXC21 on the other are confirmed by these Fibonacci metastructures (vertical analogies in the image), a less expected bi-duality is highlighted at the level of their four respective spikes: on one hand, this obvious neighborhood between ZXC21 and bat RATG13, and, on the other , although less obvious, the neighborhood between ZC45 and SARS -CoV2 (horizontal analogies in the image).

2) the point -V-

This point is at a level of fundamental research of mechanisms unknown to biology. Indeed, we demonstrate how, beyond and above the STOP codon which commands the protein manufacturing machinery to end the process, there would exist a sort of "end of gene message", which would be addressed, on the scale of messenger RNA, to this "code" and would be digital in nature, carried by the ultimate UA / CG metastructure of Fibonacci. We observe that this message would be the of Nature GIGOGNE, constituted like the Russian dolls of a nesting of proportions all ending on one of the three bases of the STOP codon. This discovery is validated in this article on fortythree spikes from UK, South Africa, BRAZIL and California variants. Of these spikes, thirtytwo were from real patients.

3) point -VII-

Here, we have gathered several pieces of evidence showing that, as they evolve, the variants would constitute and reinforce a kind of Palindrome-type symmetry based on "Russian doll" interlocking of their mRNA, which could lead to a double strand. of the "hairpin" type, thus reinforcing the stability and the lifespan of the spike mRNA, thus increasing the contagiousness of the variant virus.

In (Demongeot § Henrion-Caude, 2020), Alexandra Henrion-Caude and Jacques Demongeot proposed in 2020 a possible universel starting RNA 22 nucleotides sequence which could be a candidate bootstrap at origins of Life in a RNA primitive world.

Professor Luc Montagnier observes that these authors attribute an essential role in the origin of life to a circular RNA of 22 nucleotides. This is the length of our “EIE” (Exogenous Insertion Elements) in SARS-CoV2 genome published in https://zenodo.org/record/3975578

Particularly, this hyper constrainst circular 22nt sequence codes for the twenty amino acids + codon stop + only one redundant amino acid (MET). We found this archaic mRNA sequence using BLASTn long (14nt) contiguous sequences in HIV mRNA genomes... and also in SARS-CoV2 Wuhan reference mRNA genome!

But consider the circular character of this primitive RNA 22 nucleotides long UCAG. So, here is our original result on its multiple and SYSTEMATIC Fibonacci proportions as soon as it is a CIRCULAR RNA sequence ...

5' AUGGUACUGCCAUUCAAGAUGA 3'
AUGGUACUGCCAUUCAAGAU G ==> A 13AU 8CG
AUGGUACUGCCAUUCAA G ==> AUGA 13AU 8CG
AUGGUACUGCCAUU C ==> AAGAUGA 13AU 8CG
AUGGUACUGC C ==> AUUCAAGAUGA 13AU 8CG
AUGGUACUG C ==> CAUUCAAGAUGA 13AU 8CG
AUGGUACU G ==> CCAUUCAAGAUGA 13AU 8CG
AUGGUA C ==> UGCCAUUCAAGAUGA 13AU 8CG
AUG G ==> UACUGCCAUUCAAGAUGA 13AU 8CG
AU G ==> GUACUGCCAUUCAAGAUGA 13AU 8CG

Seen from the point of view of the autopoiesis Francisco Varela theory (ref Varela), autonomy of Indoor vs. Outdoor systems, these results could be interpreted as the rest of the loop of 21 UACG (outdoor) "seen" from a base C or G (indoor). So, the perceived signal is a kind of Fibonacci resonance ... By virtue of Francisco Varela's theory of autopoiesis (Varela § Maturana, 1980) that we applied to Artificial Intelligence in the 1980s by creating the “fractal chaos” artificial neural network (Perez 1988). Thus, the Fibonacci numbers, therefore the optimal proportion of the Golden Tatio would perhaps have already been present from the first moments of life on earth, a life for which they would have served as a "matrix" …

"If I followed correctly, the circular RNA sequence obeys the Fibonacci rule. If we extrapolate, we can think that Life was formed (or was created, according to our religion) from this RNA according to a mathematical principle? " (Luc Montagnier)?

Actually, the RNA sequence proposed by the article by Alexandra Henrion-Caude, which seems to "spring" from nowhere can only intrigue the reader. Indeed, what is certain with this sequence is that God, or panspermia, or self-organization are indeed Mathematicians ...

Indeed: They already know how to count 4 + 5 + 6 + 7 = 22.

I meant 4C, 5G, 6U, 7A

Let C + G = 9

U + A = 13

We are already very close to the 13/8 = Phi ratio, the same one that we can verify in all SARS-CoV2 genomes. But also, pyrimidine purines:

4C+6U=10UC

5G+7A=12AG

10=2x5

12=2x6

5 and 6 are the two key numbers associated with the harmonious but unstable shape of the Pentagon (5) and the harmonious but stable form of the Hexagon (6).

It is no coincidence that Nature (flowers) or religions - also - have invented stars with 5 or 6 branches ....

And the structure of RNA and DNA are built around Pentagons and Hexagons ...And "Pollack's Water Fourth state" structure of WATER (https://www.pollacklab.org/), also built around the hexagon ...

So, EVERYTHING seems to be potentially written in these 22 nucleotides ...

We also note 2x6 = 12 bases in primers of palindromes or mirror series:

AUGGUA mirror and UCAAGA quasi palindrome.

Finally, we will note cs 5 triplets of consecutive nucleotides:

GAA UGG GCC AUU CAA

Symetries purines pyrimidines on 4 of the 5 TRIPLETS

UGG CAA

GCC AUU

Finally, we must recall this open question:

CONJECTURE of SARS-CoV2 VARIANTS:

The growth of long Fibonacci structures in the shape of "podiums" for almost all of the variants studied (UK, California, South Africa, India, etc.) suggests the probable folding of the spike mRNA in the form of a "hairpin", can strengthen the cohesion and the lifespan of this mRNA.

Three final conclusions:

One fact is certain, the two mRNAs of the Moderna and Pfizer vaccines will result in a low functionality of the spike vaccine because by doping these sequences in CG rich, their designers, in search of greater STABILITY of these RNAs will have built sequences which, as soon as they are inserted into the human host, will seek to mutate, like SARS-CoV2 variants, towards CG ==> UA forms in order to improve their STABILITY and their LIFETIME...

Secondly, using new biomathematics theoretical methods (Master code and numerical standing waves), and comparing the spikes of the two vaccines of Moderna and Pfizer, we conclude a very probable difference in stability and shelf life of the two respective mRNAs of these two vaccines. However, current "State of the Art" analyzes will only reveal that their two protein sequences are strictly identical. By having modified their synonymous codons using different strategies, no-one can guarantee that the quantity of antibodies generated and sensitivity to variants will be identical in the two cases (Kustin et al, 2021).

Despite the immense progress of Biology, the RNA universe remains today full of unexplained mysteries. However, it is said, as we will see, that it could have constituted the first crucible of life. This is why we will have to exercise the greatest caution, on one hand in the face of an mRNA virus such as SARS-CoV2, but even more in the face of the unpredictable evolution of new vaccines, themselves based on RNA.

We must note the great ADAPTATION power - at the global scale of their genomes - of the most infectious VARIANTS such as the BRAZIL 20J / 501Y.V3 variant (P.1). This is very worrying for the VACCINES <==> VARIANTS run: We demonstrate how the Brazilian variant P.1 which becomes uncontrollable in Brazil in April 2021 has a level of organization of long metastructures of 17,711 bases covering the genome which is 3.6 more important than that

of the 2 reference genomes SARS-CoV2 Wuhan and worldwide D614G. We suggest that this high level of overall structure of this variant contributes to the stability of this genome and, possibly, to its greater contagiousness.

Finally, we could propose a causal link between vaccines and variants as suggested in (Megawaty Tan et al, 2021).

5. ADDENDUM BY PROFESSOR LUC MONTAGNIER

For the first time the work of JC Perez allows the detection of numerical series in the natural sequence evolution of new variants of Covid-19 Corona virus.

Long Fibonacci séries are described by him in the variants which are the most spreading in the human population.

This would indicate a natural selection of more stable structures also possibly more transmissible.

This evolution is in contrast with the path followed by the vaccine makers:

to make the synonymous codons enriched in G-C in order to increase their m-RNA vaccine stability.

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CONFLICT OF INTEREST

The author have declared that no competing interests exist.

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