Wuhan nCoV-2019 SARS Coronaviruses Genomics Fractal Metastructures Evolution and Origins

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Wuhan COVID-19 and SARS Coronaviruses Genomics Fractal Metastructures Evolution and Partially Synthetic Origins

"Where there is matter, there is geometry."
Johannes Kepler

Jean-claude PEREZ,
PhD Maths § Computer Science Bordeaux University, RETIRED interdisciplinary researcher (IBM Emeritus, IBM European Research Center on Artificial Intelligence), **7 avenue de terre-rouge F33127 Martignas Bordeaux metropole France, phone 33 0781181112 jeanclaudeperez2@gmail.com**

ABSTRACT :
The main result of this updated release is the formal proof that 2019-nCoV coronavirus is partially a SYNTHETIC genome. We proof the CONCENTRATION in a small région of wuhan New genome (300bp) of 3 different régions from HIV1 ENVELOPPE gene and 3 others from HIV2 and SIV (ENV and POL RT). All this is remarkable and bears the mark of a desire for organization of a human nature: LOGIC, SYMETRIES.
In this article, we demonstrate also that there is a kind of global human hosts adaptation strategy of SARS viruses as well as a strategy of global evolution of the genomes of the different strains of SARS which have emerged, mainly in China, between years 2003 first SARS genomes and the last 2019 COVID-19 Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome.
This global strategy, this temporal link, is materialized in our demonstration by highlighting stationary numerical waves controlling the entire sequence of their genomes.
Curiously, these digital waves characterizing the 9 SARS genomes studied here are characteristic whole numbers: the "Fibonacci numbers", omnipresent in the forms of Nature, and which our research for several decades has shown strong links with the proportions of nucleotides in DNA.
Here we demonstrate that the complexity and fractal multiplicity of these Fibonacci numerical waves increases over the years of the emergence of new sArs strains.
We suggest that this increase in the overall organization of the SARS genomes over the years reflects a better adaptation of SARS genomes to the human host.
The question of a link with pathogenicity remains open.
However, we believe that this overall strategy for the evolution of the SARS genomes ensures greater unity, consistency and integrity of the genome.
Finally, we ask ourselves the question of a possible artificial origin of this genome, in particular because of the presence of fragments of HIV1, HIV2 and SIV retroviruses.

Keywords : SARS ; Wuhan COVID-19 ; Fibonacci numbers ; Fractal genome ; Numerical stationary periodic waves; HIV1 ;HIV2 ; SIV,; synthetic genomes.

1. Introduction

Since the SARS coronavirus emergence 18 years ago, a large number of severe acute respiratory syndrome related coronaviruses (SARSr-CoV) have been discovered in their natural host, bats. Some of those bat SARSr-CoVs have the potential to infect humans. In january 2020, Wuhan China megacity was the origin of a Novel SARS disease entitled by OMS « COVID-19 » [6]. This novel coronavirus (COVID-19) caused an epidemic of respiratory syndrome in humans, in Wuhan, China then in other World countries (Iran South Korea, Italia...). As show in the following figures, we analyse in this article 9

whole SARS genomes with the goal to discover a possible strategy of SARS GENOMES EVOLUTION from 2003 original viruses to the 2020 WUHAN virus.

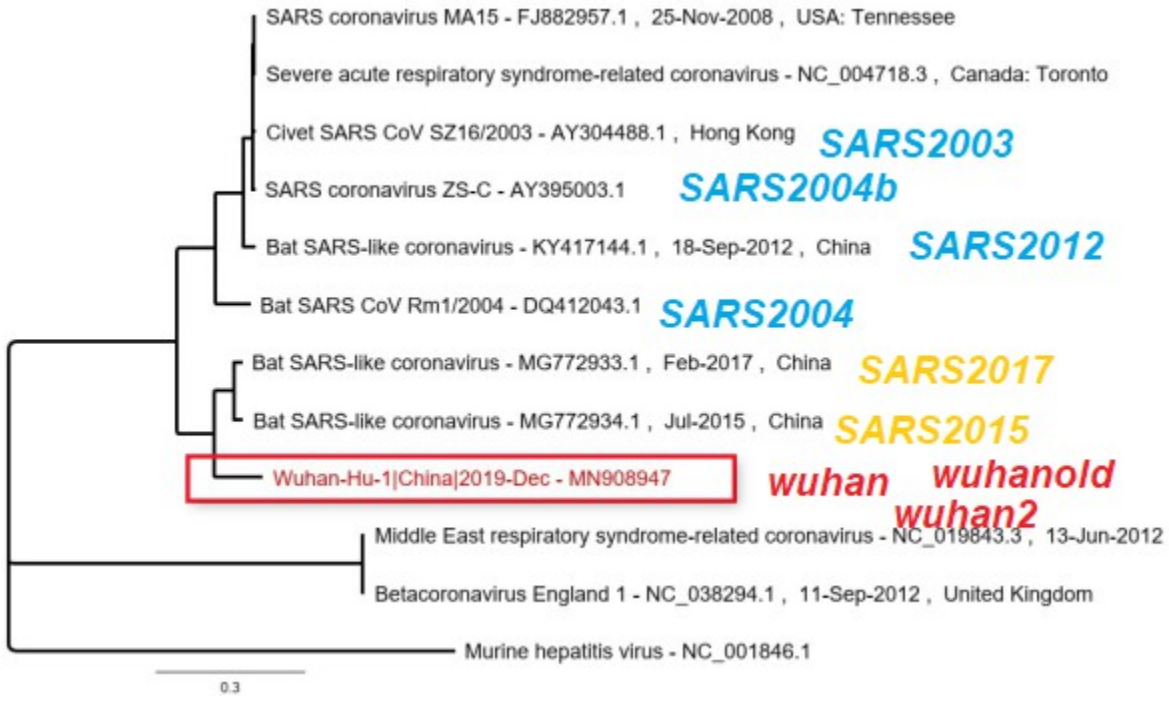


Figure 1 from NCBIinsights 2020. Coloured references are our 9 analysed SARS/Wuhan genomes.

Secondly, for about 30 years, we have been looking for possible global, even digital, structures that would organize DNA, genes, chromosomes, and even whole genomes [27, 28 , 30, 50, 51].

owever, it is only by deepening the notion of "fractal periodicity", outlined in [7, 38], and we will highlight here that we have re-discovered the major role of **Fibonacci fractal stationary waves** at both scales of each whole individual chromosomes and whole genome. We then demonstrate a sort of "hierarchical classification" of the 24 chromosomes. In this hierarchy, the chromosome4 seems to play a major and privileged role.

By comparing chromosome chromosome the 3 reference genomes of Neanderthal, Sapiens BUILD34 of 2003 and Sapiens HG38 of 2013, we demonstrate the evidence of « fractal periods » and « Resonance periods» characterizing each of the 24 human chromosomes [47]. As illustrated in Figure1 below, these resonances make it possible to differentiate the respective genomes of Neanderthal and Sapiens on the global scale of the chromosome (here chromosome 4). Here, a resonance of 34 nucleotides is common to both chromosomes 4 of Sapiens and Neanderthal, however, the respective forms of these resonance curves are radically different.

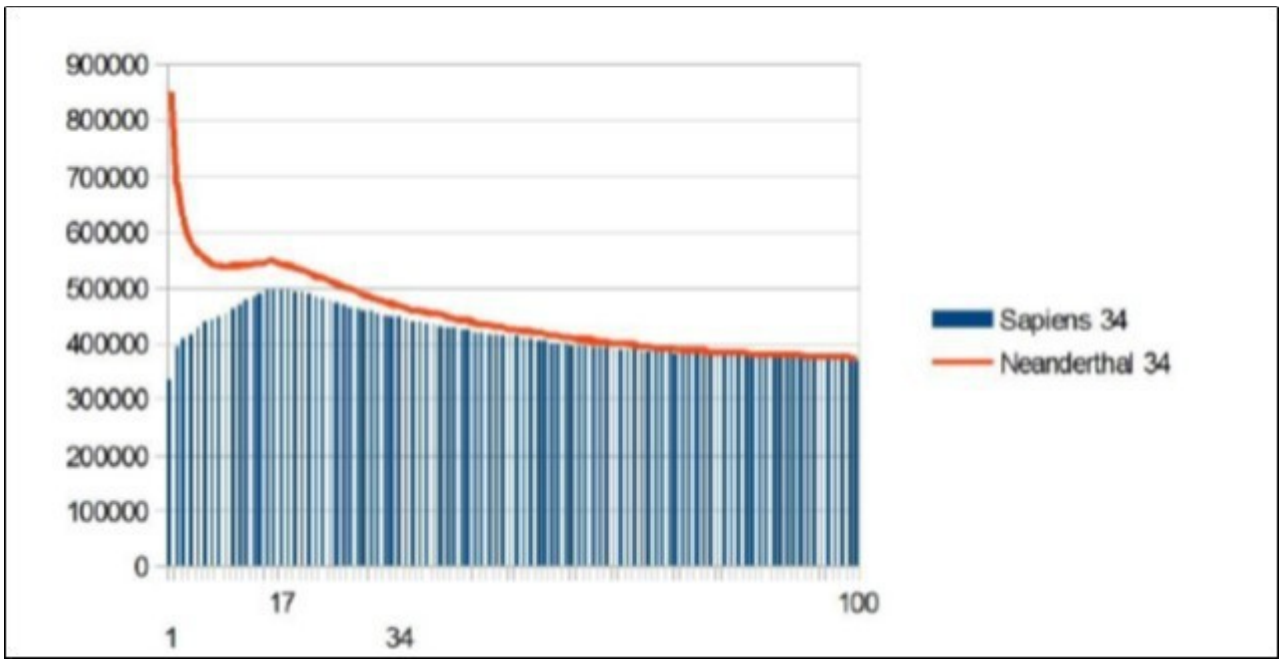


Figure 2. As will be demonstrated here, the 2 respective Chromosomes 4 of Neanderthal and Sapiens HG38 share a "resonance" of 34 bp, however, these two radically different resonance curves illustrate a major differentiation of the 2 human species at the GLOBAL scale of chromosome 4.

2. Methods

The 9 analysed genomes :

SARS2003 **SARS coronavirus SZ16, complete genome**
https://www.ncbi.nlm.nih.gov/nuccore/Ay304488

SARS2004 **Bat SARS coronavirus Rm1, complete genome**
https://www.ncbi.nlm.nih.gov/nuccore/DQ412043

SARS2004b **SARS coronavirus ZS-C, complete genome**
https://www.ncbi.nlm.nih.gov/nuccore/AY395003

SARS2012 **Bat SARS-like coronavirus isolate Rs4084, complete genome - Nucleotide - NCBI. Ky417144.1**
https://www.ncbi.nlm.nih.gov/nuccore/KY417144.1

SARS2015 **Bat SARS-like coronavirus isolate bat-SL-CoVZXC21, complete genome**
https://www.ncbi.nlm.nih.gov/nuccore/Mg772934

SARS2017 **Bat SARS-like coronavirus isolate bat-SL-CoVZC45, complete genome**
https://www.ncbi.nlm.nih.gov/nuccore/Mg772933

WUHANOLD (first genome sequenced 12 january 2020) **Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome**
https://www.ncbi.nlm.nih.gov/nuccore/MN908947.1

WUHAN2 (second improved sequenced genome 14 january 2020) **Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome** GenBank: MN908947.2
https://ncbiinsights.ncbi.nlm.nih.gov/2020/01/13/novel-coronavirus/
https://www.ncbi.nlm.nih.gov/nuccore/MN908947.3?report=fasta

WUHAN (23 january 2020) **Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome** GenBank: MN908947.3
https://www.ncbi.nlm.nih.gov/nuccore/MN908947.3

Computing Fractal Periods and Resonances Summary:

The complete description of this method can be found in [47], Six Fractal Codes of Biological Life: perspectives in Exobiology, Cancers Basic Research and Artificial Intelligence Biomimetism Decisions Making Making. Preprints 2018, 2018090139 (doi: 10.20944/preprints201809.0139.v1). https://www.preprints.org/manuscript/201809.0139/v1

We introduce here a method of global analysis of the roughness or fractal texture of the DNA sequences at the chromosome scale. To do this, we generalize the method of numerical analysis of the "Master Code of Biology" [39-42, 44]. Thus, we restructure the sequence into different generic sequences based on "meta codons" no longer triplets of 3 nucleotides but values ranging from 17 to 377 nucleotides, ie 360 simulations. This method of analysis will then reveal, in most cases, discrete waves or interferences, most often dissonances. However, sometimes there will emerge kinds of resonances where all scales of analysis appear to be in symbiosis.

FUNCTION:
The Genomics master code (-II-) is generalized to meta-codons that no longer have 3 nucleotides as a codon, but 4, 5, ... 377 nucleotides. Then we analyze the textures by the undulatory code (-IV-). It then appears dissonances and resonances that will reveal periods of discrete waves, resonances, and standing waves. The Genomics Binary code analysis (-III-) confirms these periods using a complementary independant method.
INPUTS: Double strand DNA sequence Pi-mass grouped by meta-codons (each Pi-mass is = -1 times number of « G » bases in meta-codon double strand or also = -1 times number of « C+G » bases in single strand meta-codon.
OUTPUTS: Peiod and resonance standing wave computed by two complementary methods.
SUMMARY :
We introduce here a method of global analysis of the roughness or fractal texture of the DNA sequences at the chromosome scale. To do this, we generalize the method of numerical analysis of the "Master Code" [47 -II-]. Thus, we restructure the sequence into different generic sequences based on "meta codons", no longer triplets of 3 nucleotides, but values ranging from 17 to 377 nucleotides, ie 360 simulations. This method of analysis will then reveal, in most cases, discrete waves or interferences, most often dissonances (based on Genomics Undulatory waves described here in [47 -II-]. However, sometimes there will emerge kinds of resonances where all scales of analysis appear to be in symbiosis.

PROCESS:
The discrete interferences fields resulting from the analysis of an entire chromosome are therefore a three- dimensional space: Dim y (vertical) restructuring in meta codons of lengths 17 to 377 nucleotides *(or in this Coronavirus article meta codons 1bp to 100bp)* Dim x (horizontal) Leibnitz differentiations such that prmary 1/2 secondary 1/3... 1/4 ... 1 / n Dim z cumulated populations from the "Master code" operators. The + 1 / -1 derivatives will be of type increase, ie +1 if derivative increasing and will be of type decrease, ie -1 if derived decreasing. In this context we will explore these 3D spaces in 2 forms:
-Horizontally [47 -IV-], meta codons dimension: curves for a given meta codon dimension, see in the example "resonances" below (see **Figure 3** and **Figure 4**).
-Vertically [47 -III-], spectral differentiation: discrete series d2-d1 is +1 if increase and -1 if decrease (see **Figure 5**). We represent in top the +1 and in low the -1, (see **Figure 5**).

Table 1 – Computing the periodic standing waves and resonances for various metacodons

Genomics Master code...

Dim x	d1	d2		…/... d100	
Dim y					
0	1	2	3	4	5
17	1298833	1181005	1133041	1103633	1087486
18	1029171	1074033	960839	1000920	1028712
19	1091521	982429	937709	912626	975473
20	878537	903906	914801	922094	927631
21	933380	834734	893561	848319	885361
22	761233	774174	779102	783714	786854
23	809977	837877	764596	791545	755377
24	852758	779786	750287	735631	726226
25	710190	727911	736109	742027	699579
…/...	377				

Horizontal scan : exp. meta codons of 22 bases : 22 761233 774174 779102 783714 786854 …/...
(see **Figure 3**)
Vertical scan example derivations of first order: 1 if d2>d1 and -1 if d2<d1 then : -1 1 -1 1 -1 1 1 -1 1 -1 1 1 …/...
(see **Figure 4** and **Figure 5**).

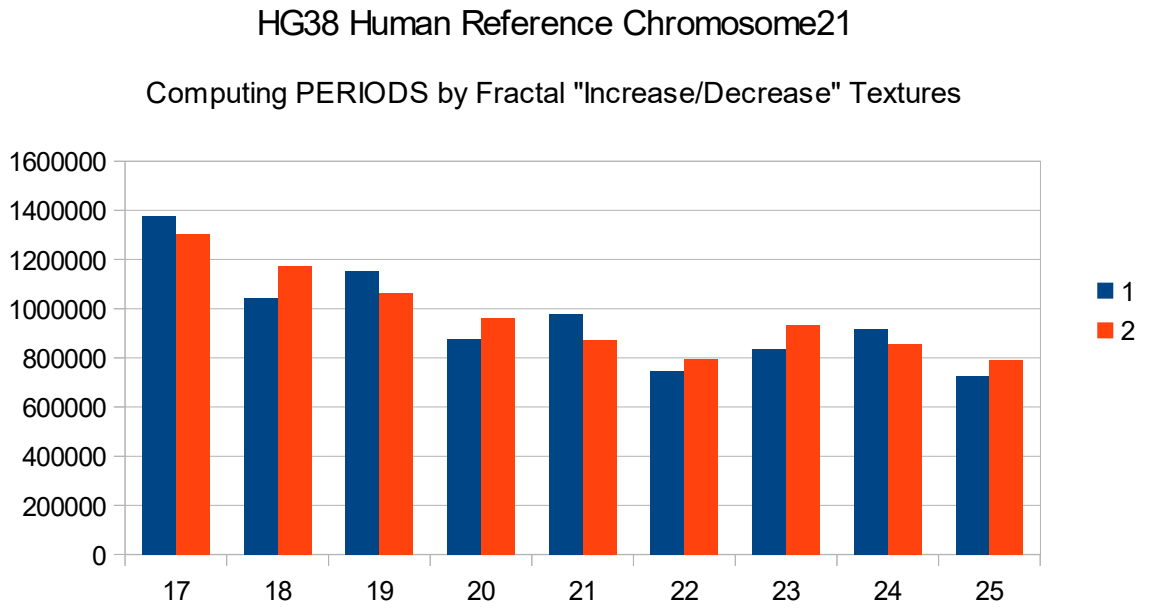


Figure 3 - zoom on vertical scan method revealing PERIOD = 22 from HG38 reference chromosome21.

These two independent methods lead in all the cases analyzed to the same period value: here, for example, the period "horizontal scan" is a resonance of 22bp **(Figure 4)** and the period "vertical scan" is a period of repeatability of 22bp also **(Figure 5)**.

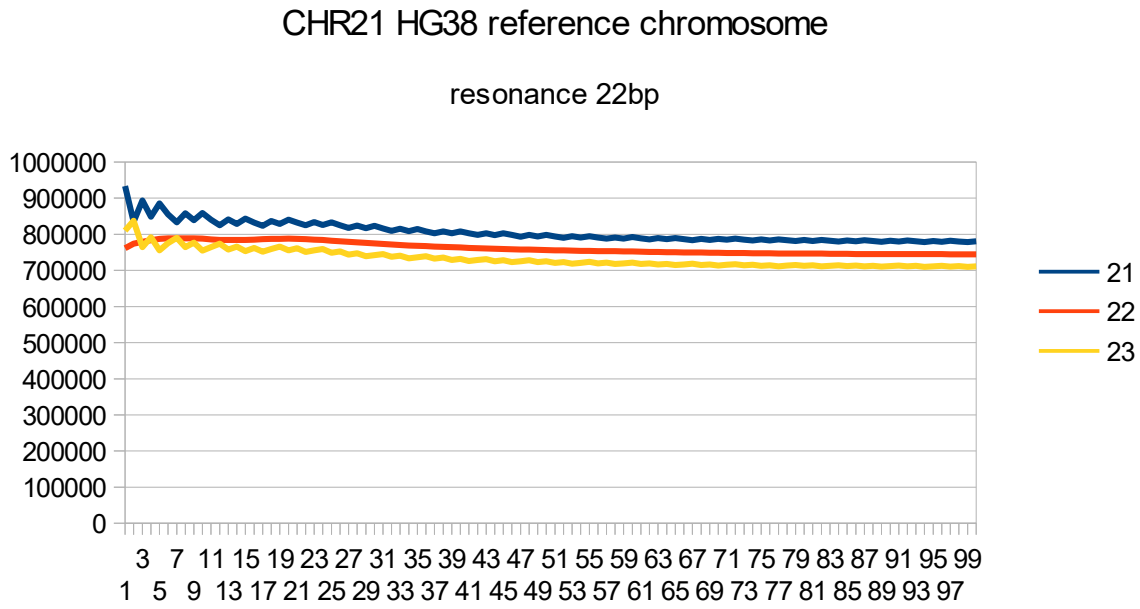


Figure 4 - Evidence of a resonance of 22bp period in the whole HG38 human reference chromosome21

(see **Figure 4** and **Figure 5**), [47 -IV-].

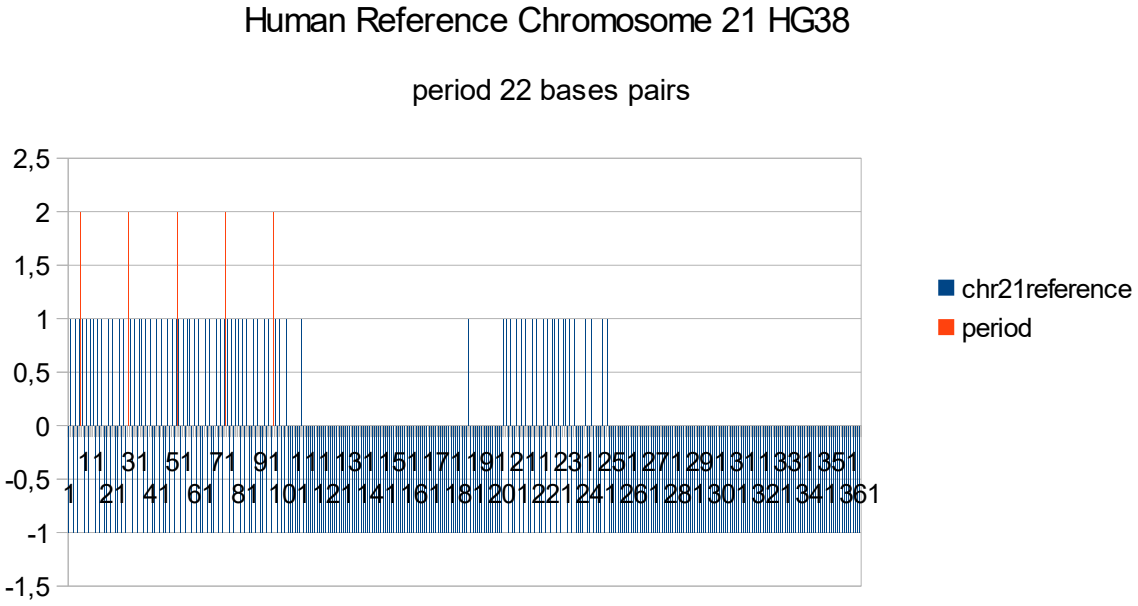


Figure 5 - Confirmation of a 22bp period in the whole HG38 human reference chromosome21 [47 -IV-].

A third complementary method is presented here: knowing the period determined and confirmed by the two previous methods, we segment the complete sequence of the chromosome by consecutive segments according to this period, for example here for the chromosome21, we will "cut" the entire

sequence of the chromosome in successive sections of 22 bases, the length of the period discovered. Then we record for each segment the C + G populations on the one hand and T + A on the other hand. We then represent the cumulative distribution curve of these different CG and TA populations throughout the chromosome sequence.
We then represent the cumulative distribution curve of these different CG and TA populations throughout the chromosome sequence (Table2).

Table 2. This table shows a C+G top for 8 bases value within 22 bases segments distribution.

7	8	9
205735	230173	219804
46083	75340	10683

The **Figure 6** shows a C+G top for 8 bases value within 22 bases segments distribution.
segmented by 22 bases periods.

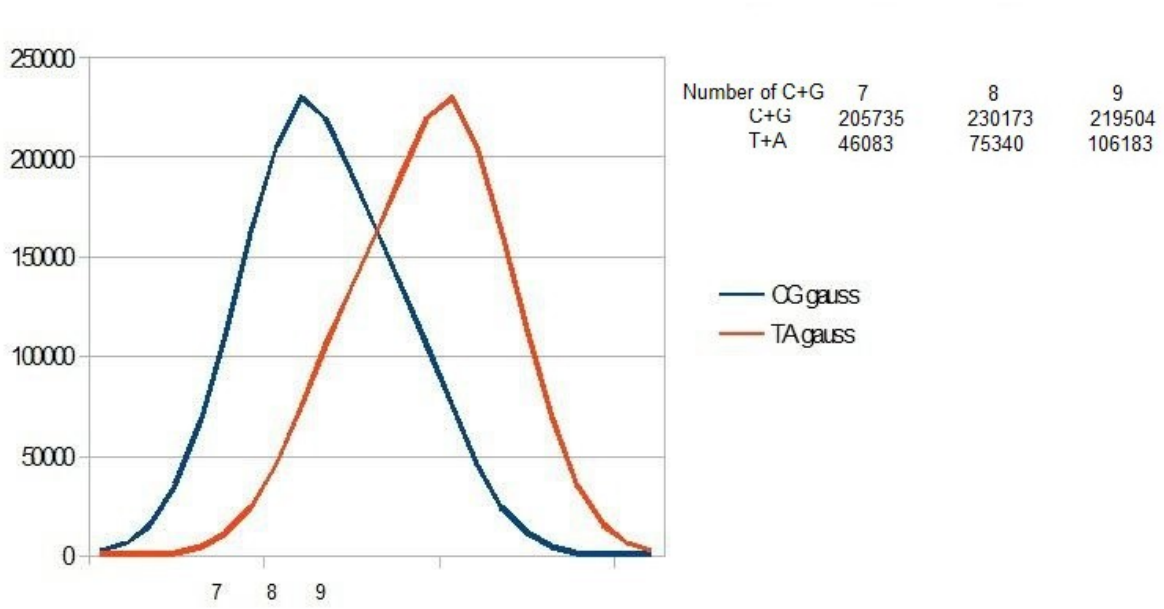


Figure 6 - Gauss like CG / TA distribution within the whole human HG38 chromosome21.

3. Results and Discussion

SARS2003

SARS coronavirus SZ16, complete genome

https://www.ncbi.nlm.nih.gov/nuccore/Ay304488

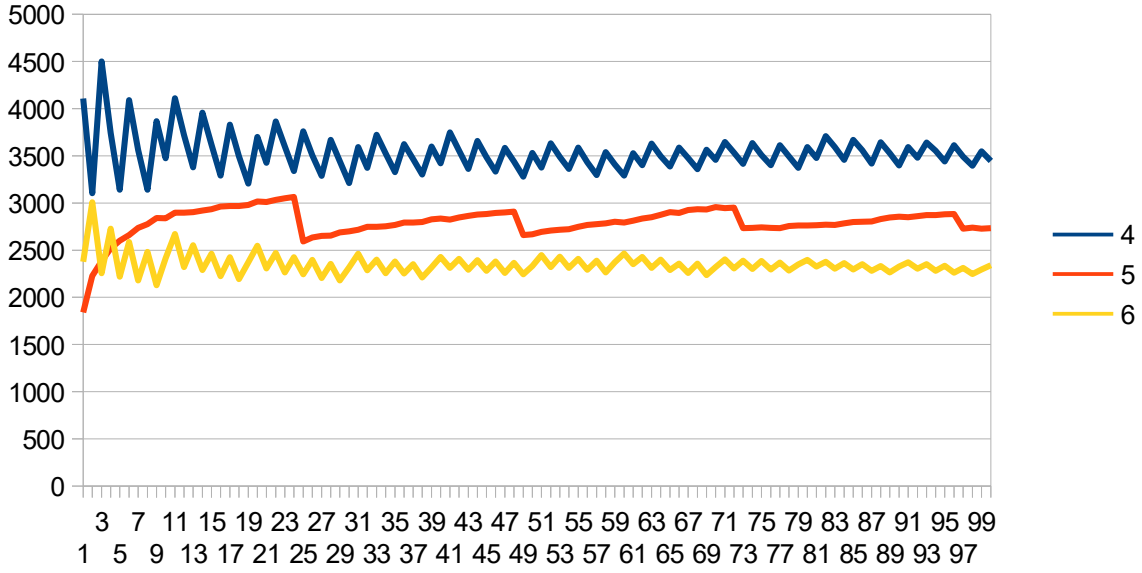


Figure 7 : Stationary wave 5bp ON

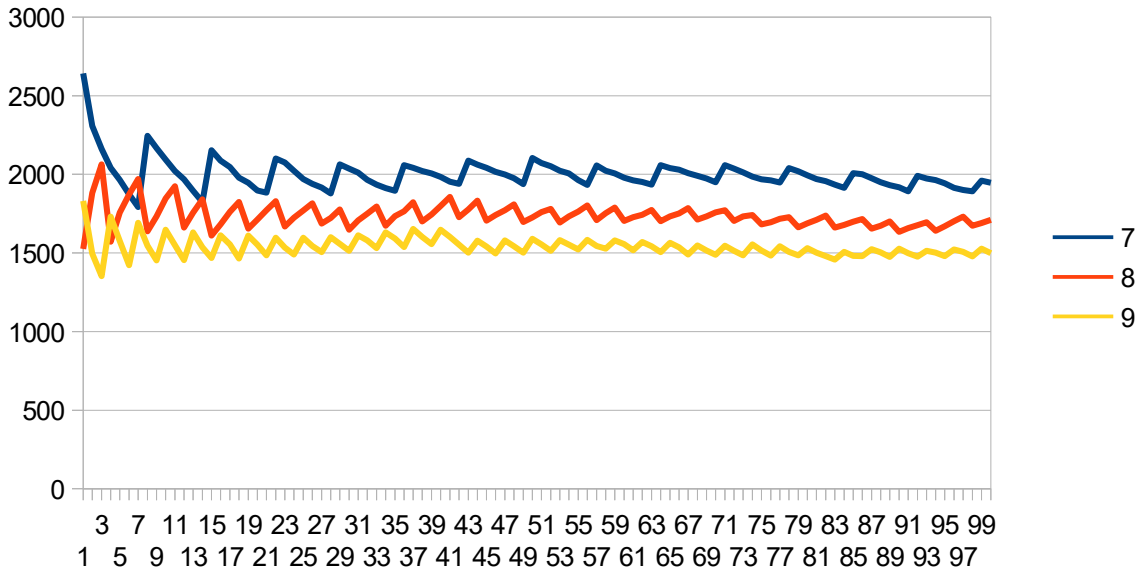


Figure 8 : Stationary wave 8bp OFF

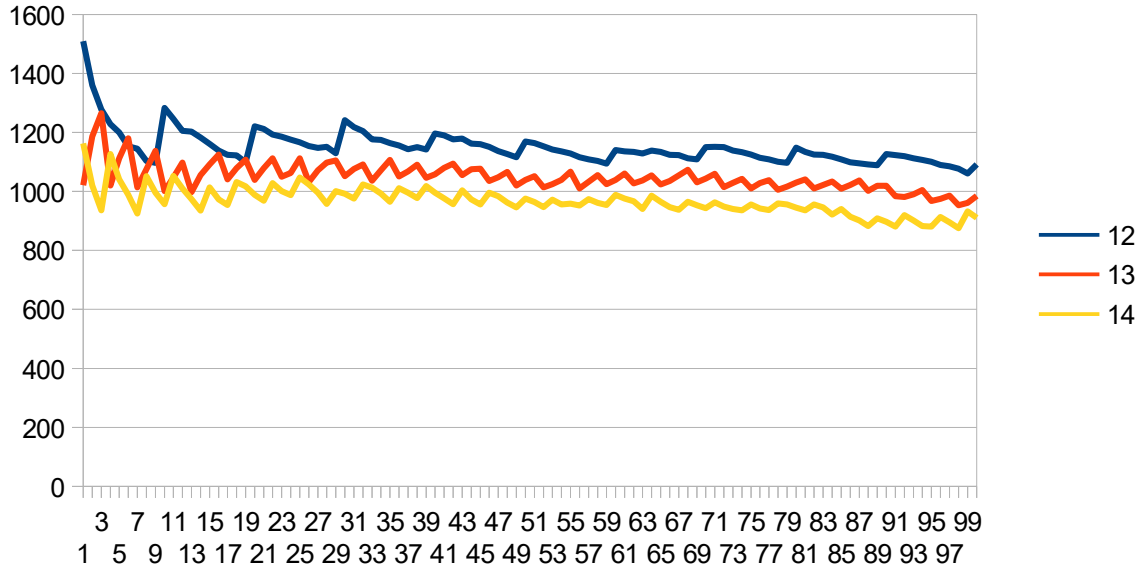


Figure 9 : Stationary wave 13bp OFF

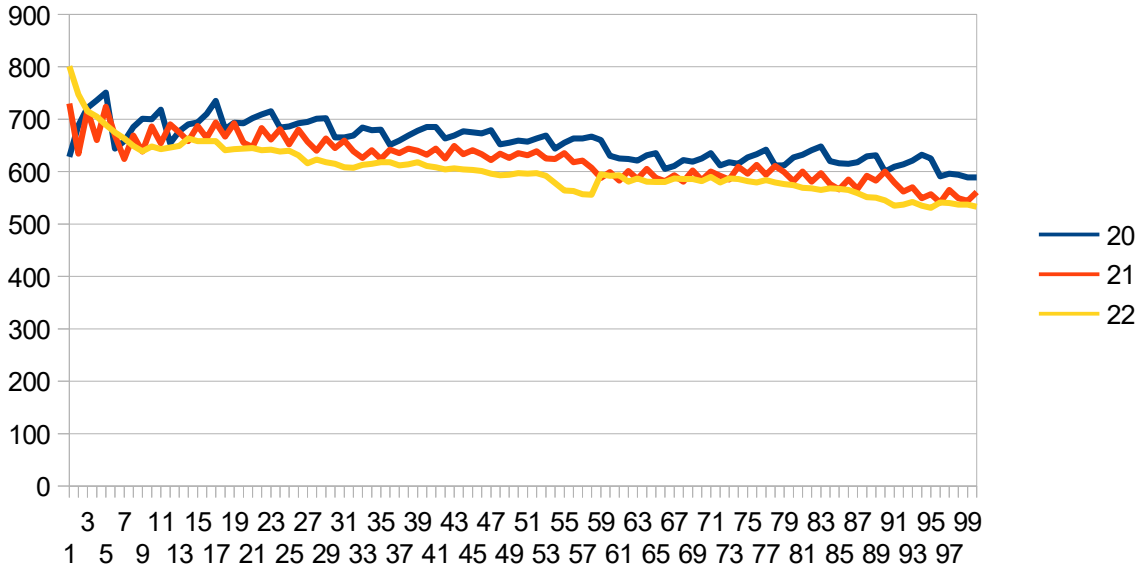


Figure 10 : Stationary wave 21bp OFF

In this initial SARS2003 genome, we find only the Fibonacci stationary wave 5bp (Figure 7). All other fractal waves 8,13, 21 bp are absent.

SARS2004

Bat SARS coronavirus Rm1, complete genome

https://www.ncbi.nlm.nih.gov/nuccore/DQ412043

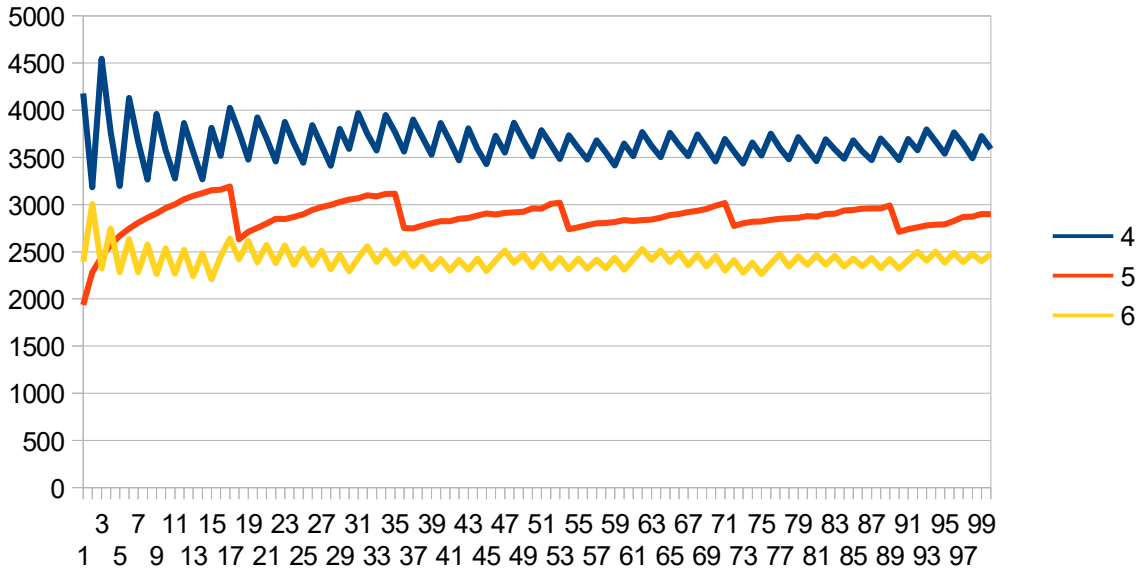


Figure 11 : Stationary wave 5bp ON

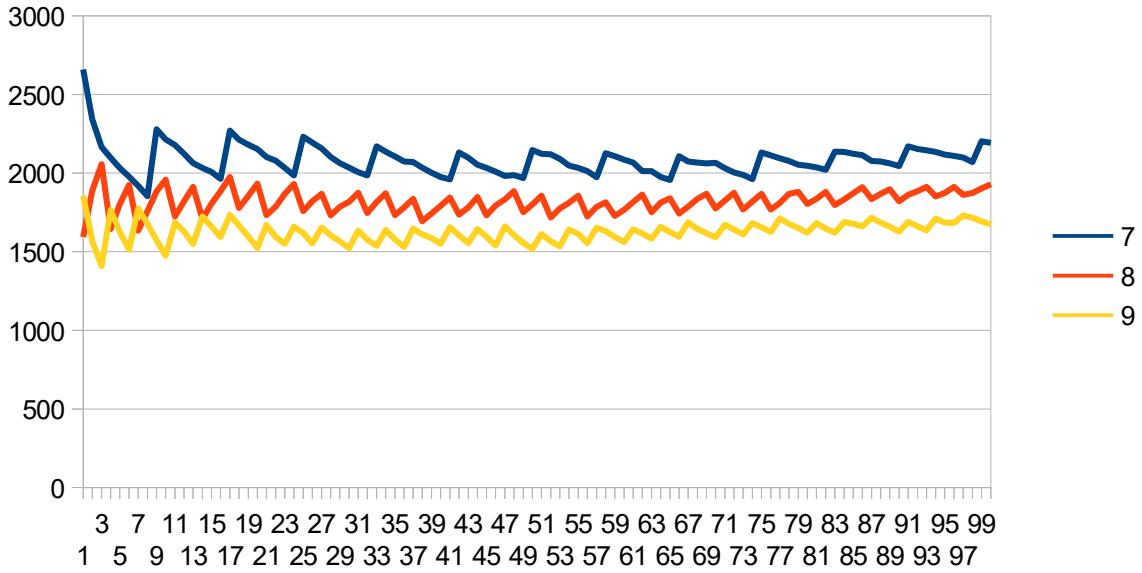


Figure12 : Stationary wave 8bp OFF

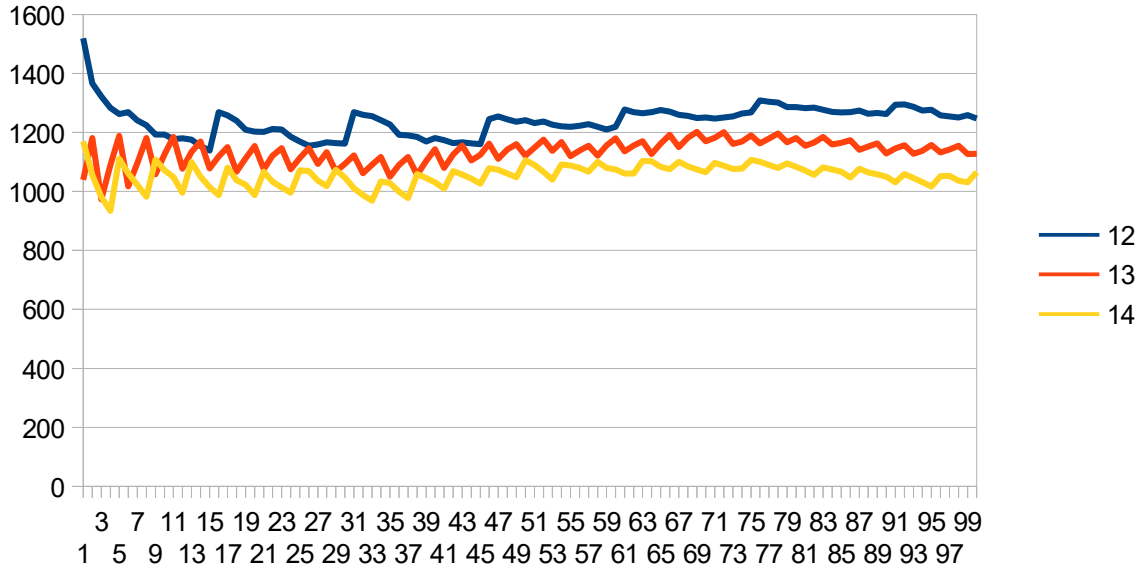


Figure 13 : Stationary wave 13bp OFF

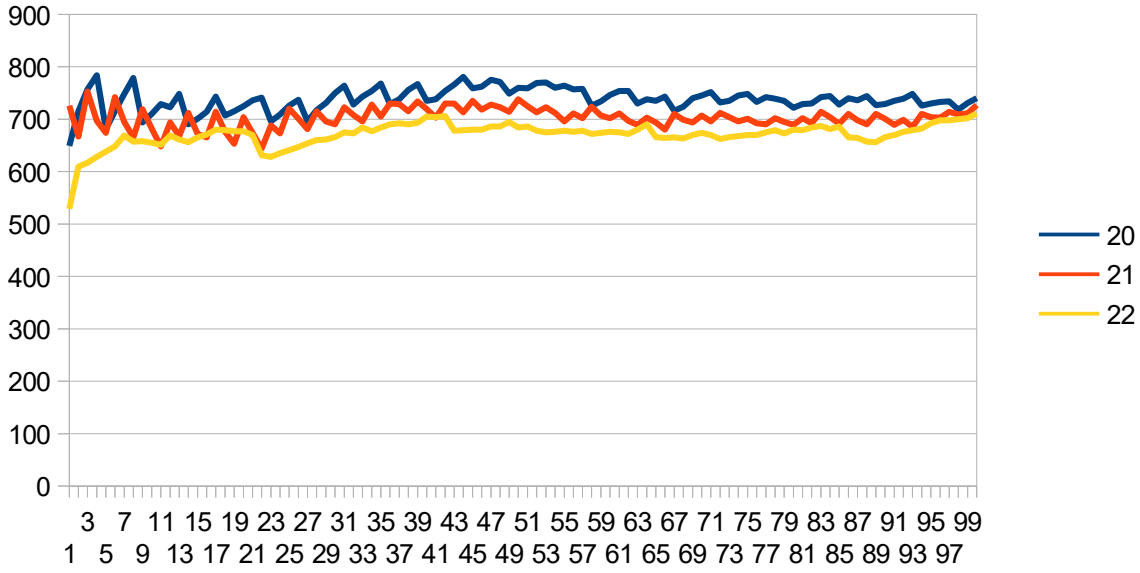


Figure 14 : Stationary wave 21bp OFF

In this second SARS2004 genome, we find only the Fibonacci stationary wave 5bp (Figure 11). All other fractal waves 8,13, 21 bp are absent.

SARS2004b

SARS coronavirus ZS-C, complete genome

https://www.ncbi.nlm.nih.gov/nuccore/AY395003

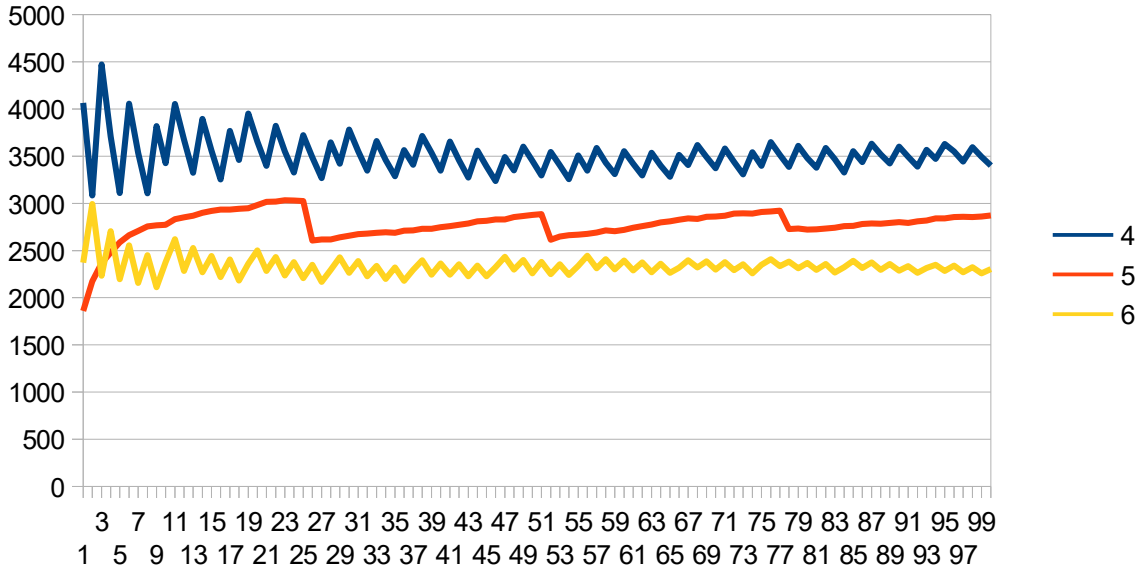


Figure 15 : Stationary wave 5bp ON

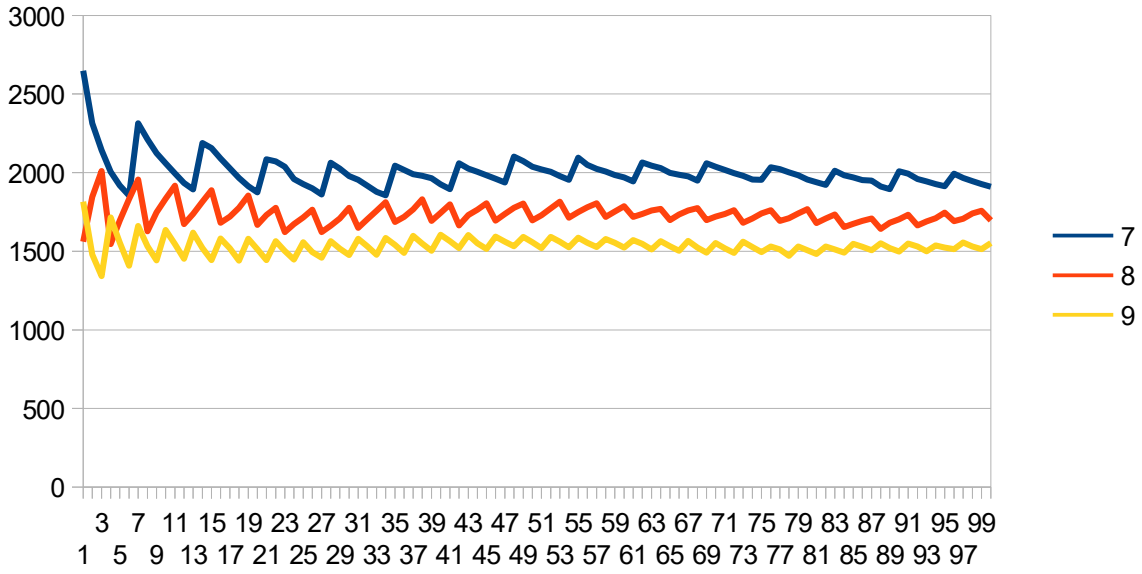


Figure 16 : Stationary wave 8bp OFF

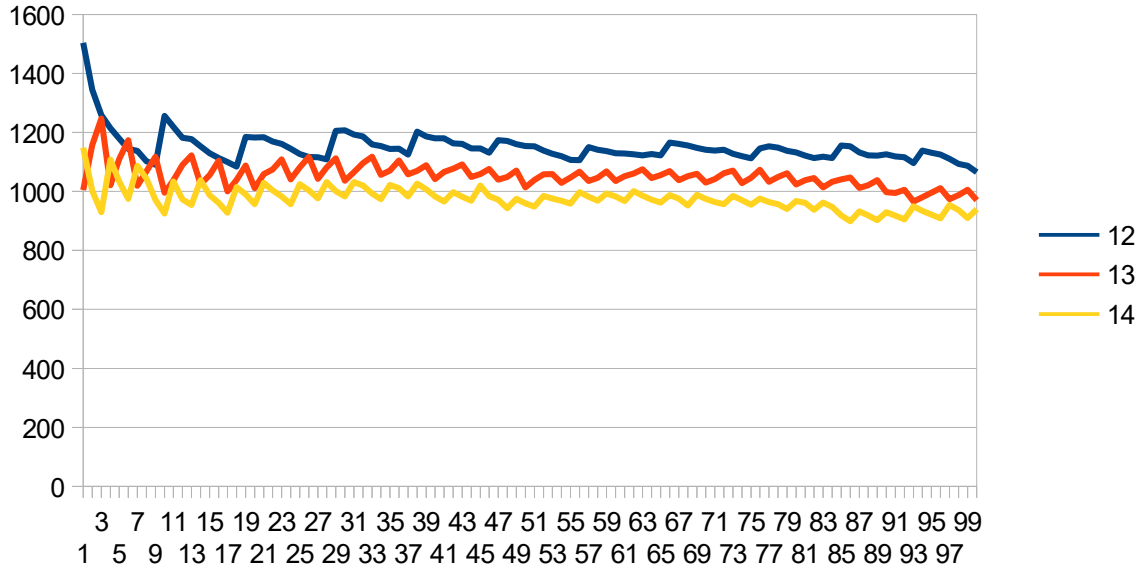


Figure 17 : Stationary wave 13bp OFF

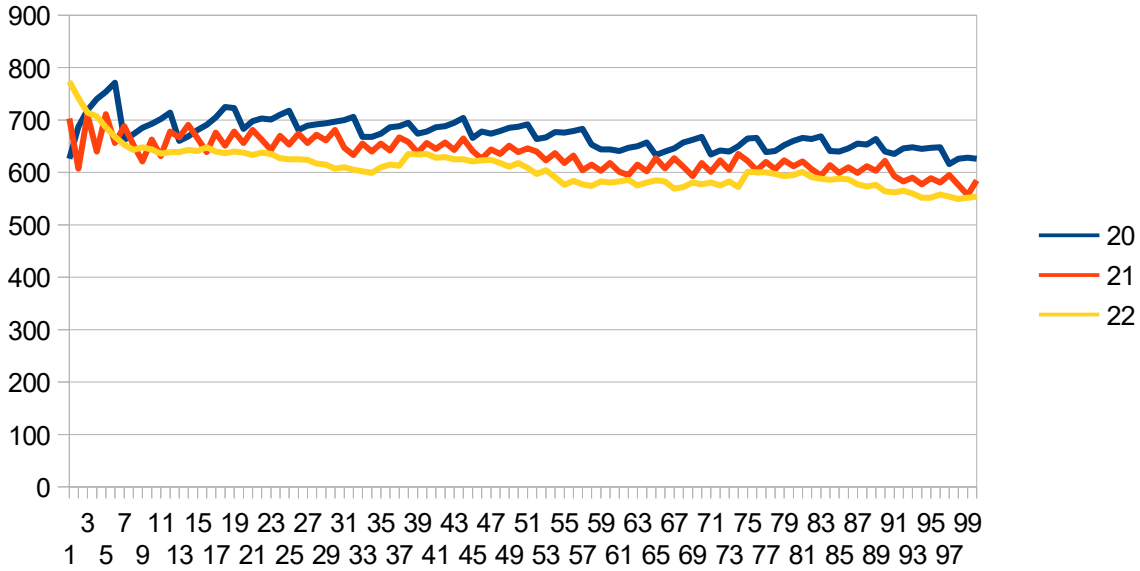


Figure 18 : Stationary wave 21bp OFF

In this third SARS2004b genome, we find only the Fibonacci stationary wave 5bp (Figure 15). All other fractal waves 8,13, 21 bp are absent.

SARS2012

Bat SARS-like coronavirus isolate Rs4084, complete genome - Nucleotide - NCBI. Ky417144.1

https://www.ncbi.nlm.nih.gov/nuccore/KY417144.1

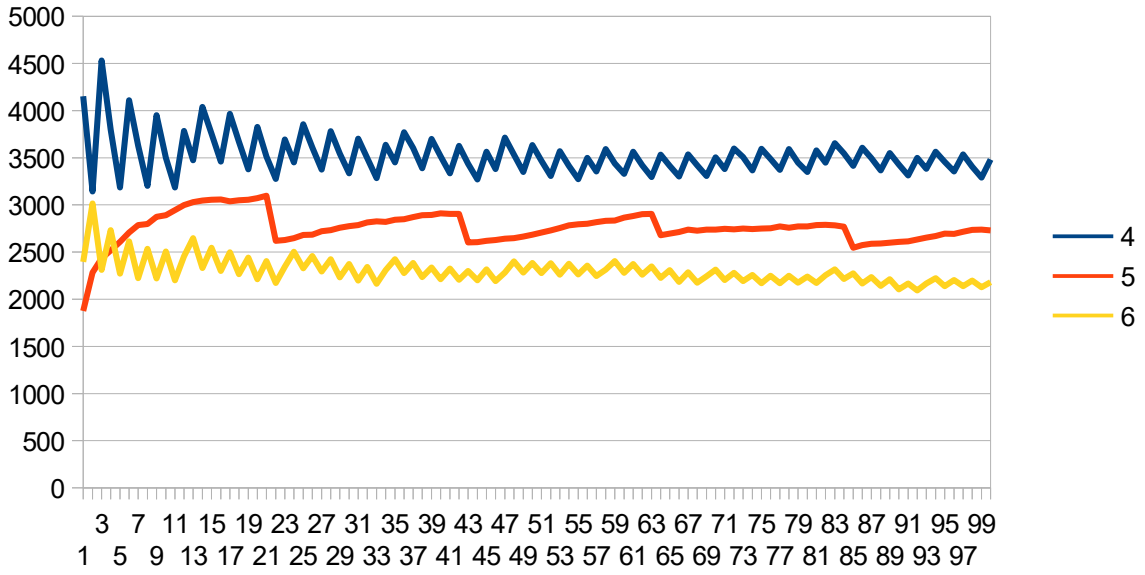


Figure 19 : Stationary wave 5bp ON

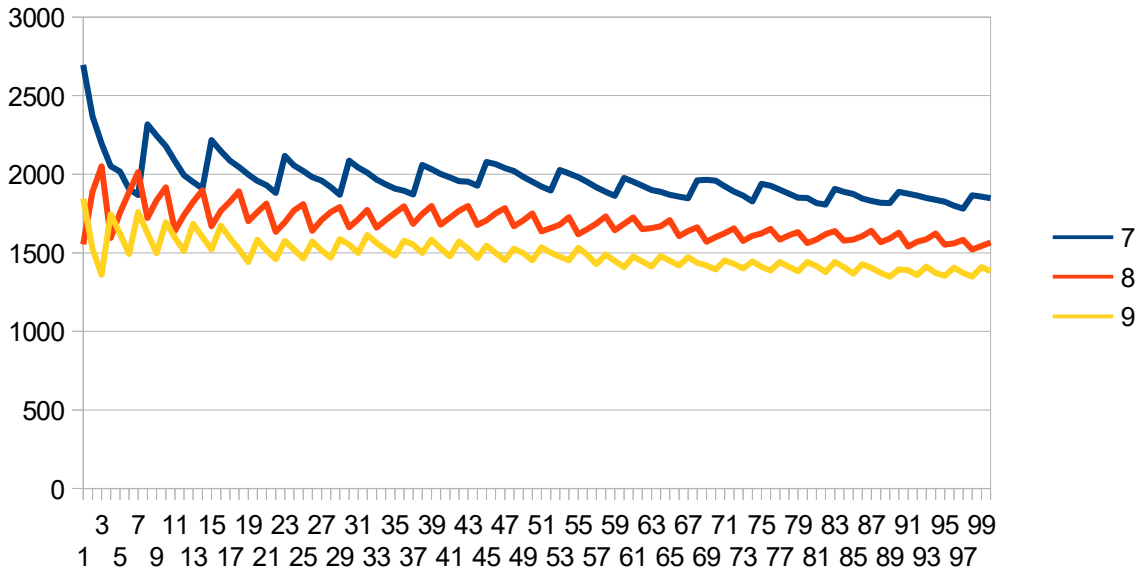


Figure 20 : Stationary wave 8bp OFF

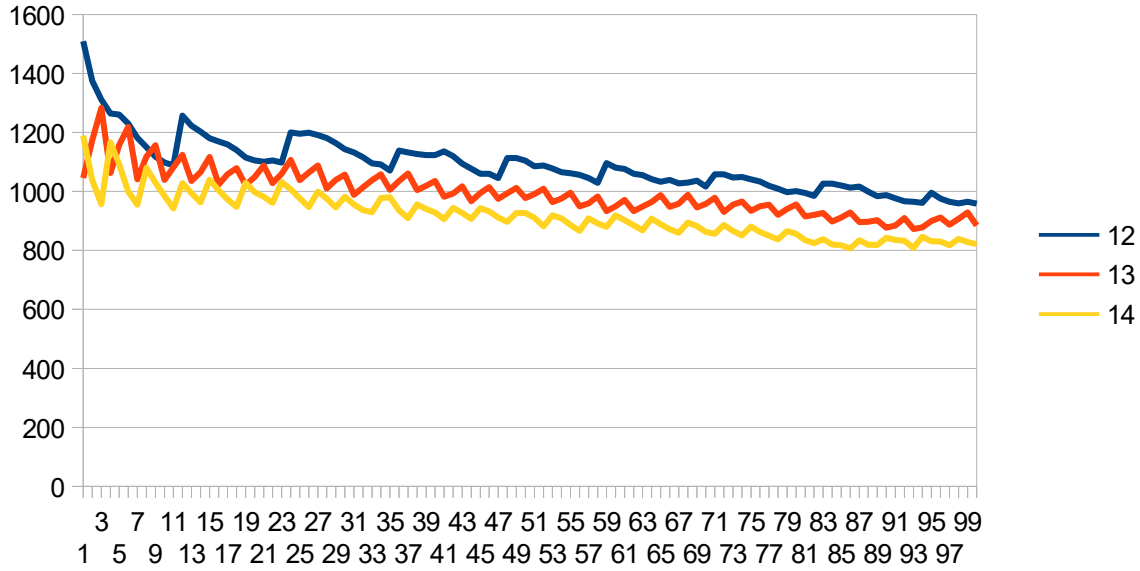


Figure 21 : Stationary wave 13bp OFF

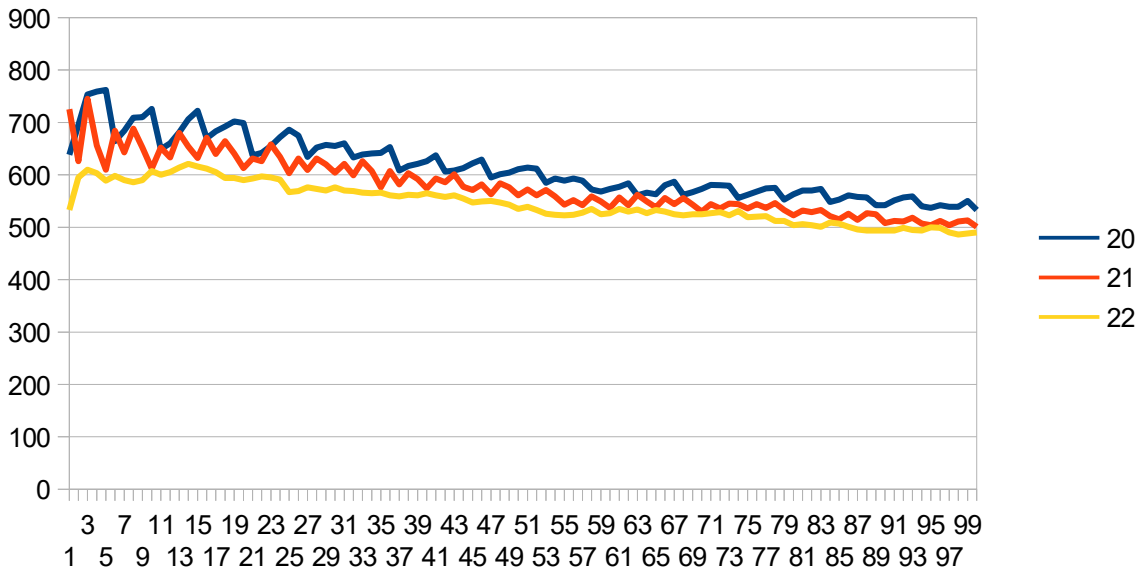


Figure 22 : Stationary wave 21bp OFF

In this fourth SARS2012 genome, we find only the Fibonacci stationary wave 5bp (Figure 19). All other fractal waves 8,13, 21 bp are absent.

SARS2015

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

https://www.ncbi.nlm.nih.gov/nuccore/Mg772934

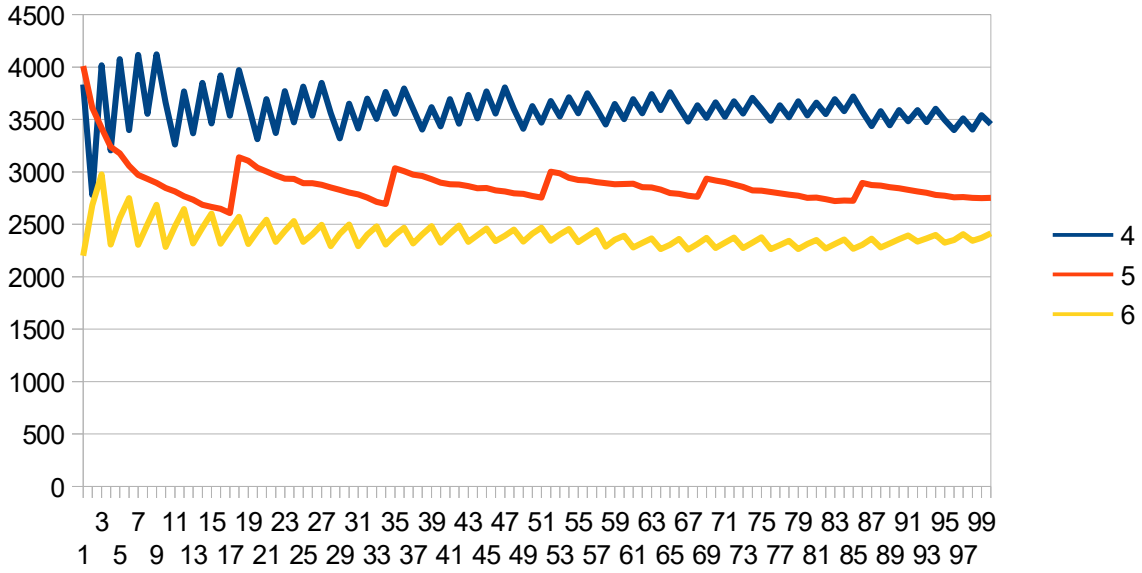


Figure 22 : Stationary wave 5bp ON

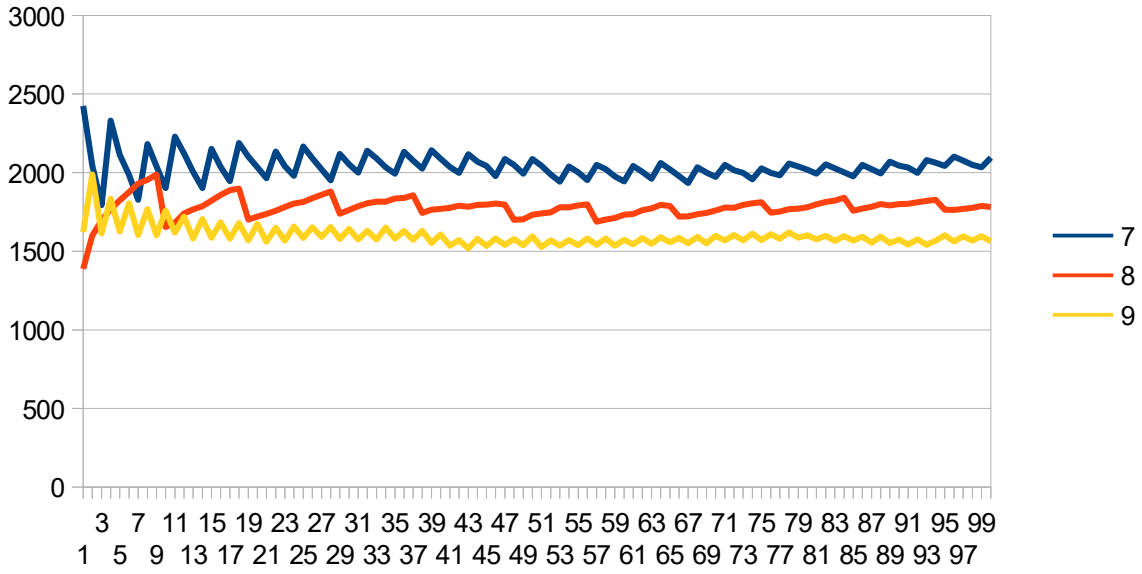


Figure 23 : Stationary wave 8bp ON

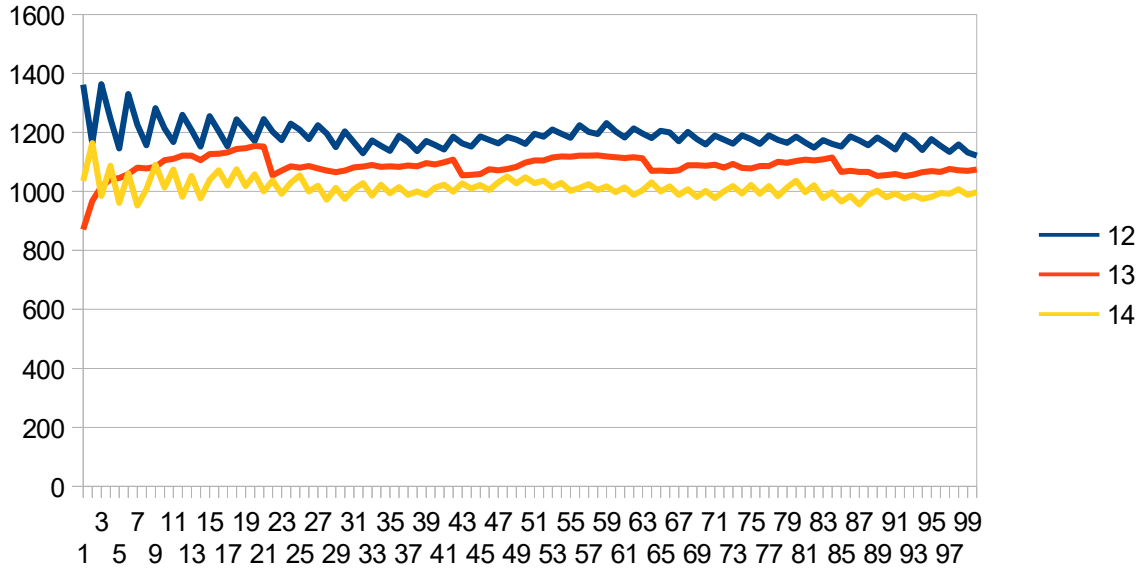


Figure 24 : Stationary wave 13bp ON

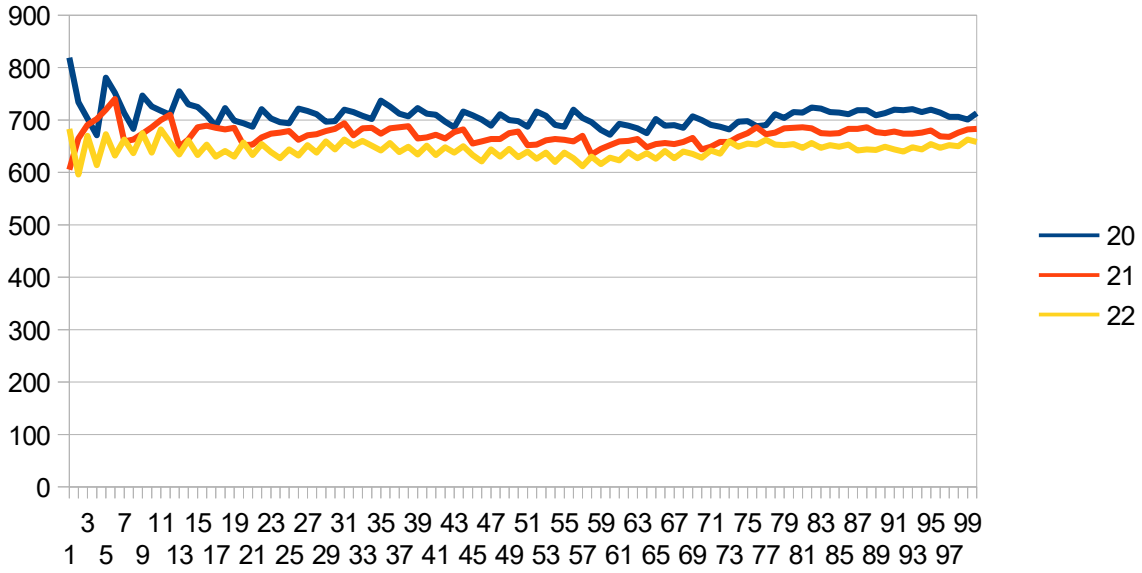


Figure 25 : Stationary wave 21bp OFF

In this fifth SARS2015 genome, we find now three Fractal Fibonacci stationary wave 5bp, 8bp, and 13bp (Figures 21, 22, 23). Meanwhile the fourth other fractal wave 21 bp remain absent.

SARS2017

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

https://www.ncbi.nlm.nih.gov/nuccore/Mg772933

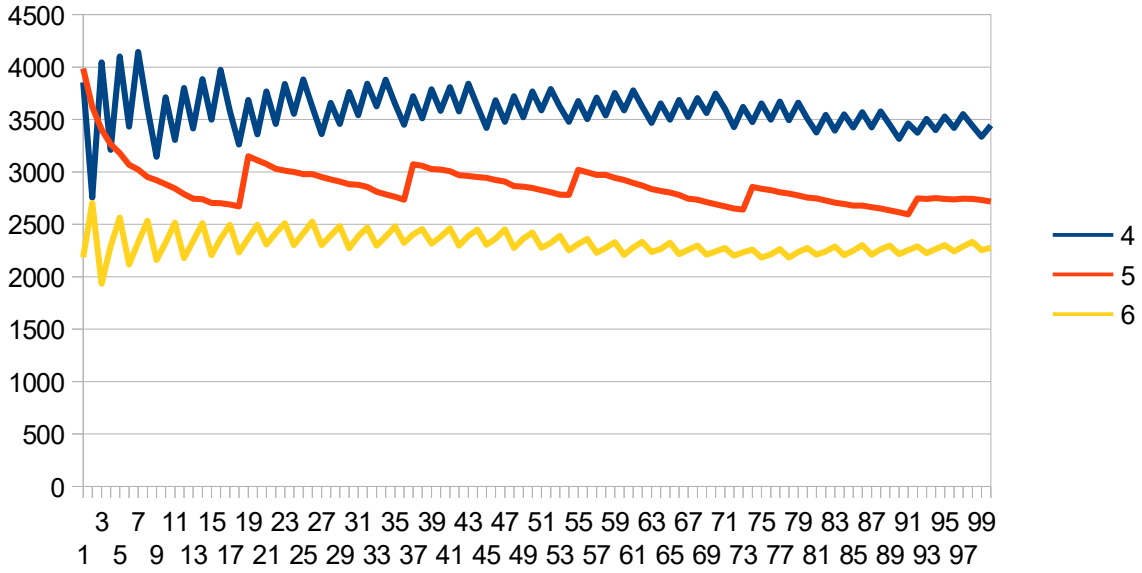


Figure 26 : Stationary wave 5bp ON

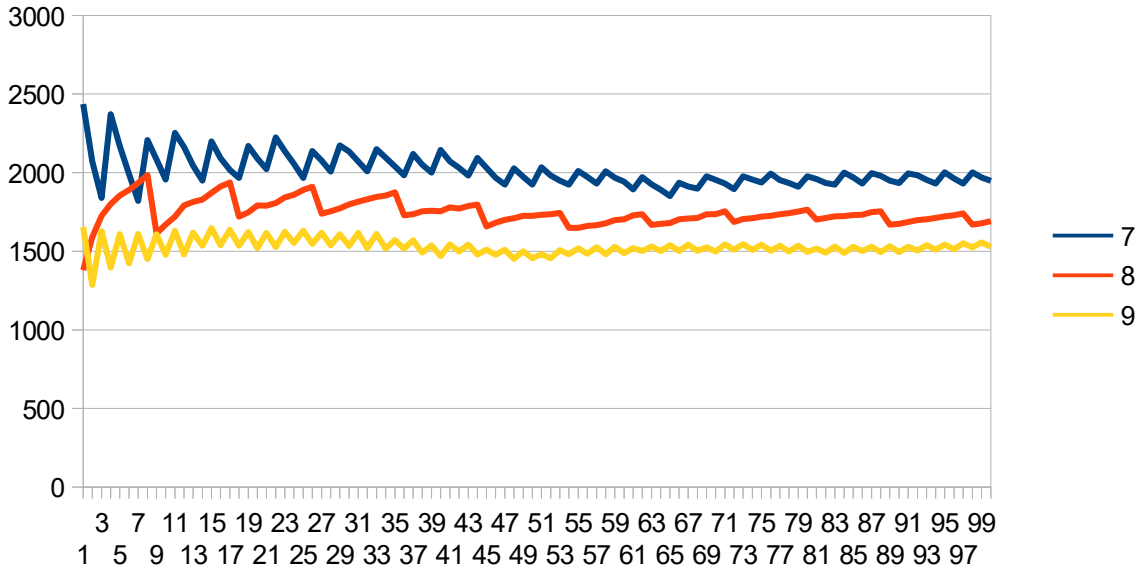


Figure 27 : Stationary wave 8bp ON

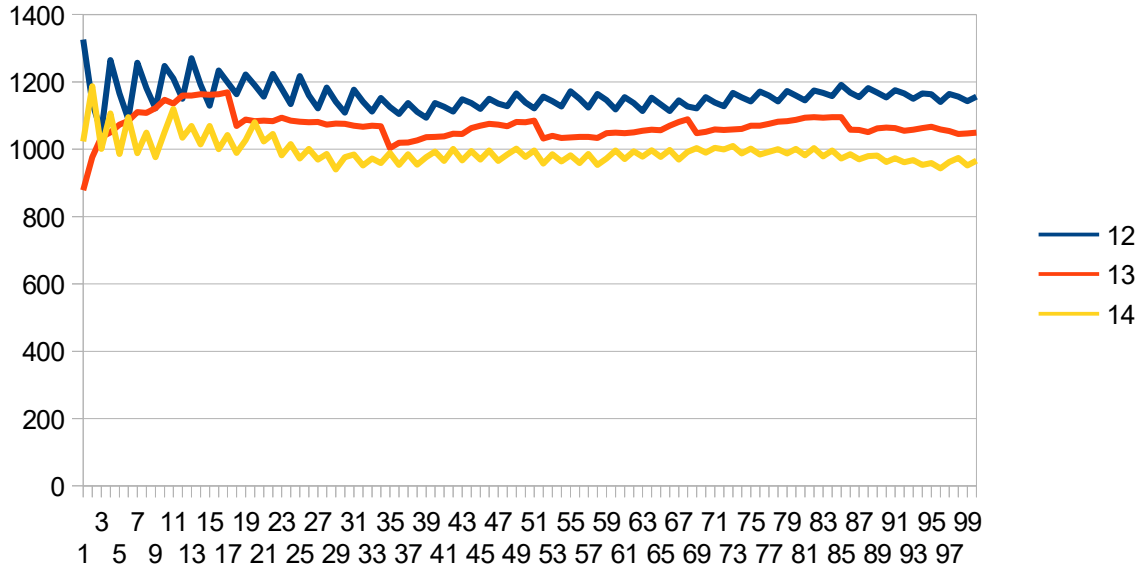


Figure 28 : Stationary wave 13bp ON

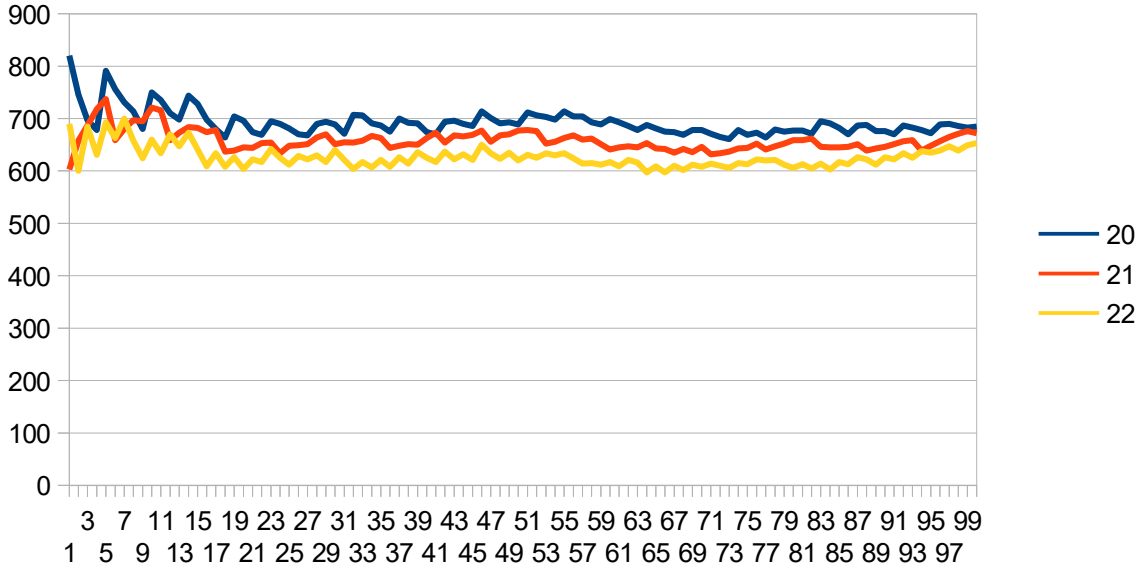


Figure 29 : Stationary wave 21bp OFF

In this sixth SARS2017 genome, we find also three Fractal Fibonacci stationary wave 5bp, 8bp, and 13bp (Figures 26, 27, 28). Meanwhile the fourth other fractal wave 21 bp remain absent.

WUHANOLD (first genome sequenced 12 january 2020) Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome MN908947.1
https://www.ncbi.nlm.nih.gov/nuccore/MN908947.1

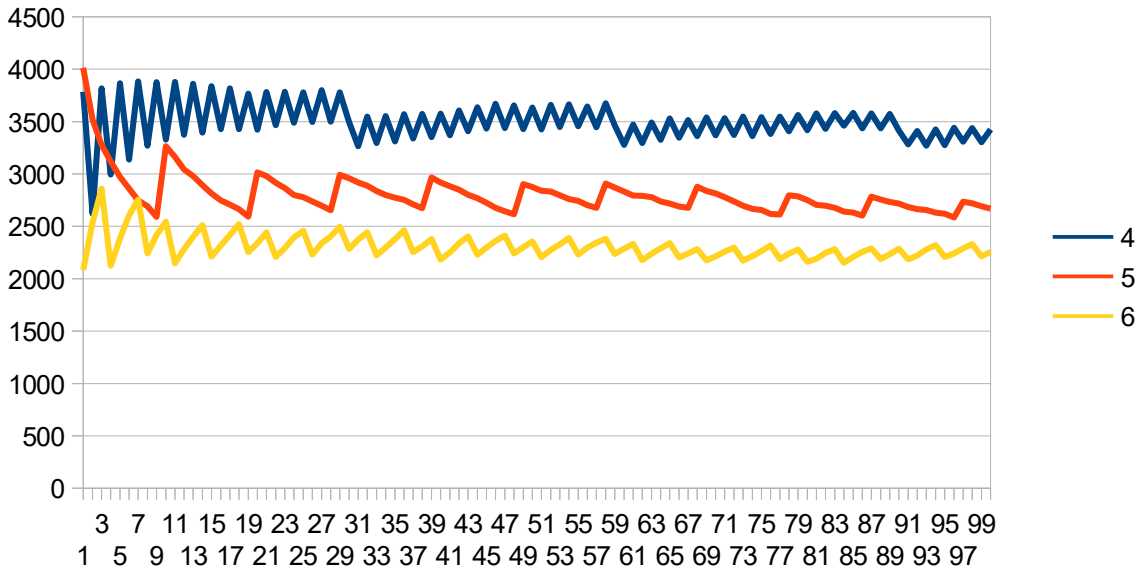


Figure 30 : Stationary wave 5bp ON

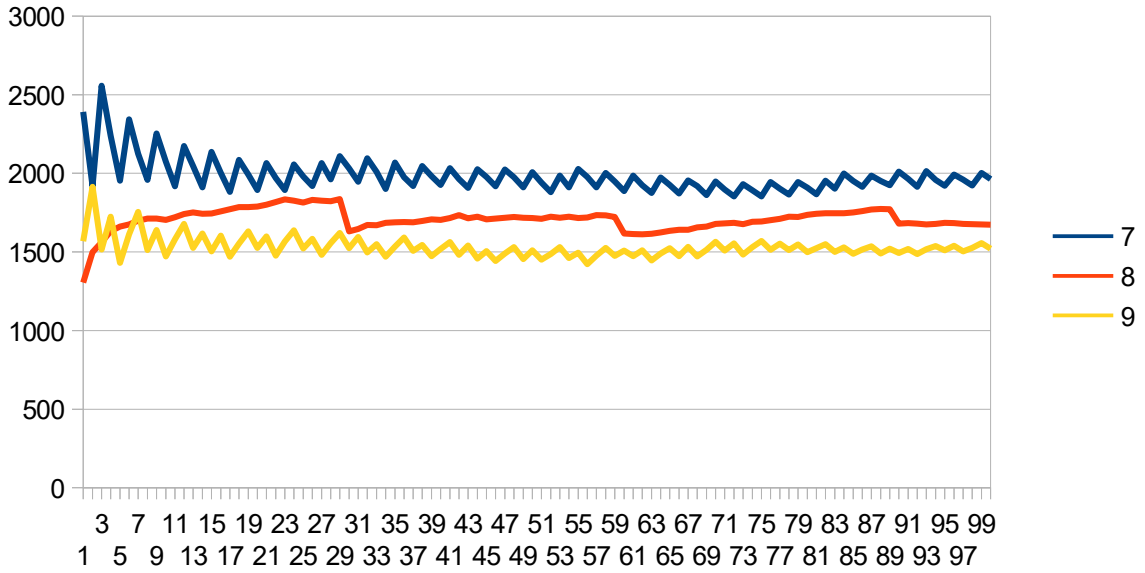


Figure 31 : Stationary wave 8bp ON

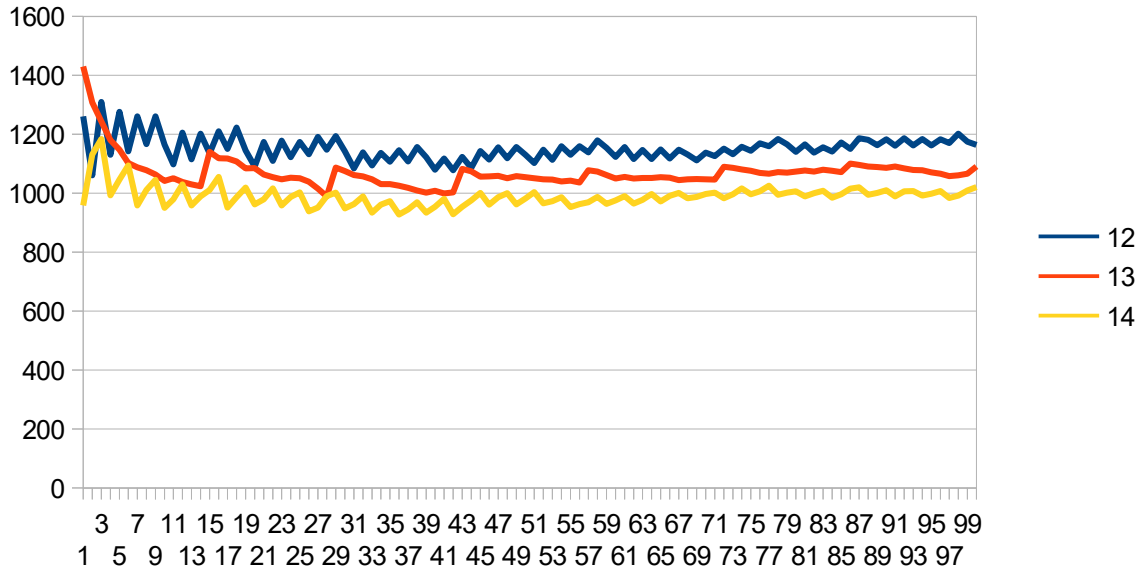


Figure 32 : Stationary wave 13bp ON

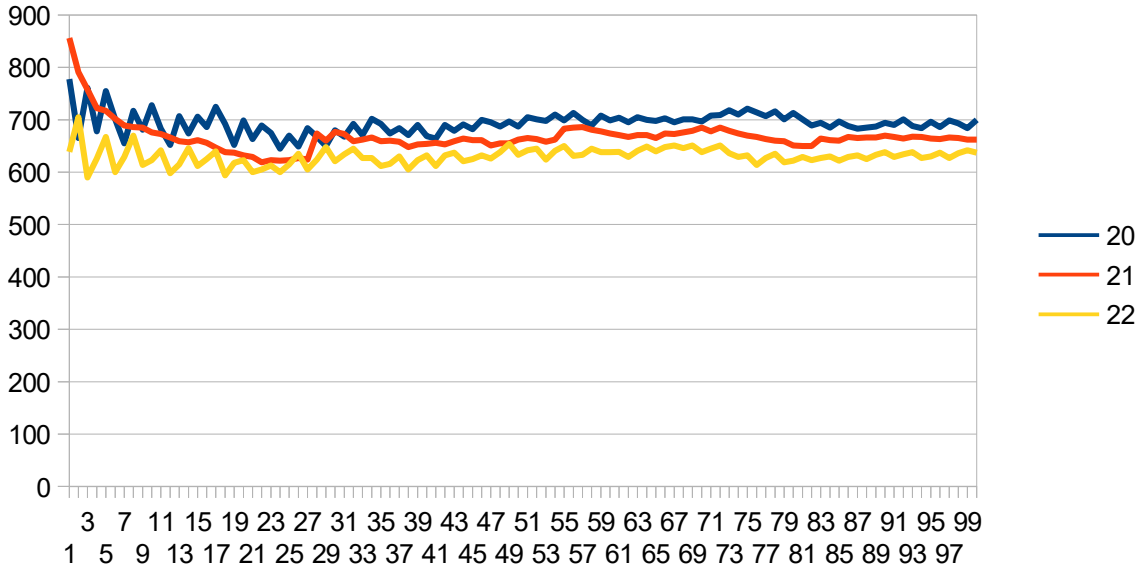


Figure 33 : Stationary wave 21bp ON

In this seventh WUHANOLD 12 january 2020 genome, we find also three Fractal Fibonacci stationary wave 5bp, 8bp, and 13bp (Figures 29, 30, 31). Now the fourth other fractal wave 21 bp is also present (Figure 33).

WUHAN2 (second improved sequenced genome 14 january 2020) Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome GenBank: MN908947.2
https://ncbiinsights.ncbi.nlm.nih.gov/2020/01/13/novel-coronavirus/
https://www.ncbi.nlm.nih.gov/nuccore/MN908947.3?report=fasta

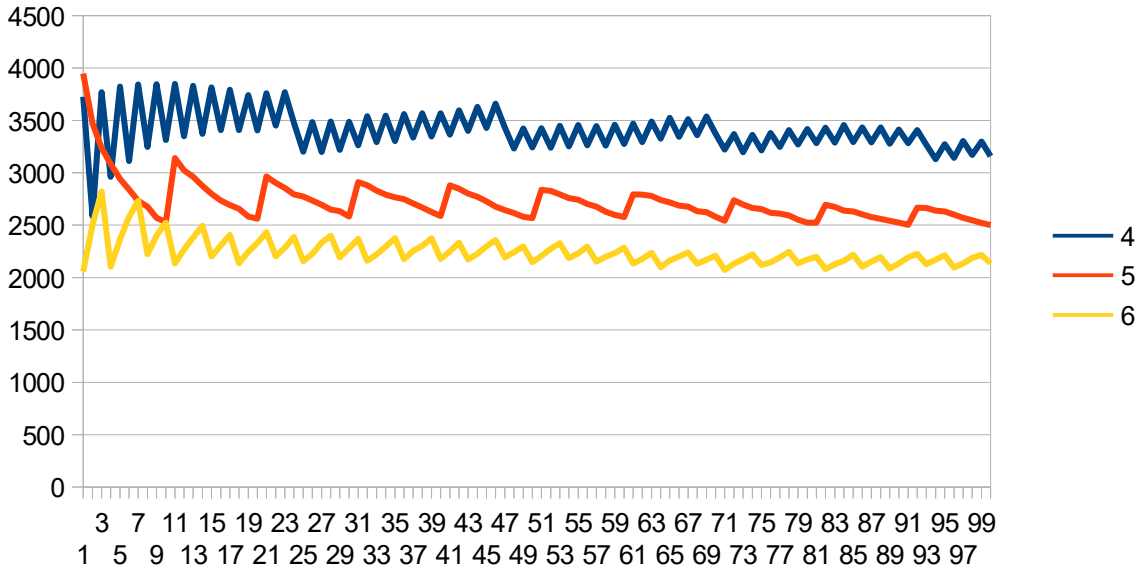


Figure 34 : Stationary wave 5bp ON

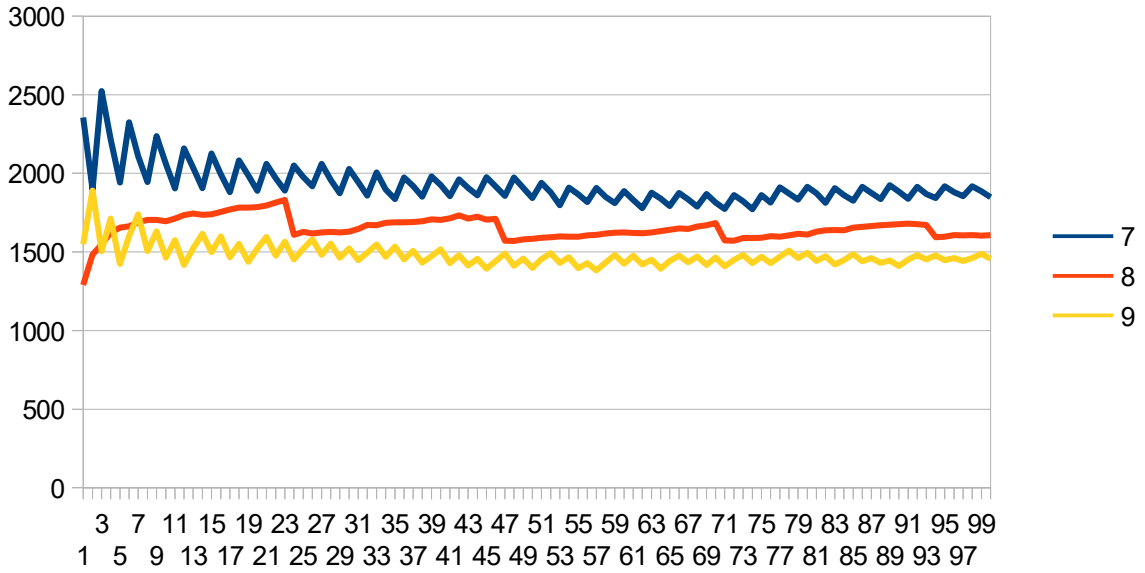


Figure 35 : Stationary wave 8bp ON

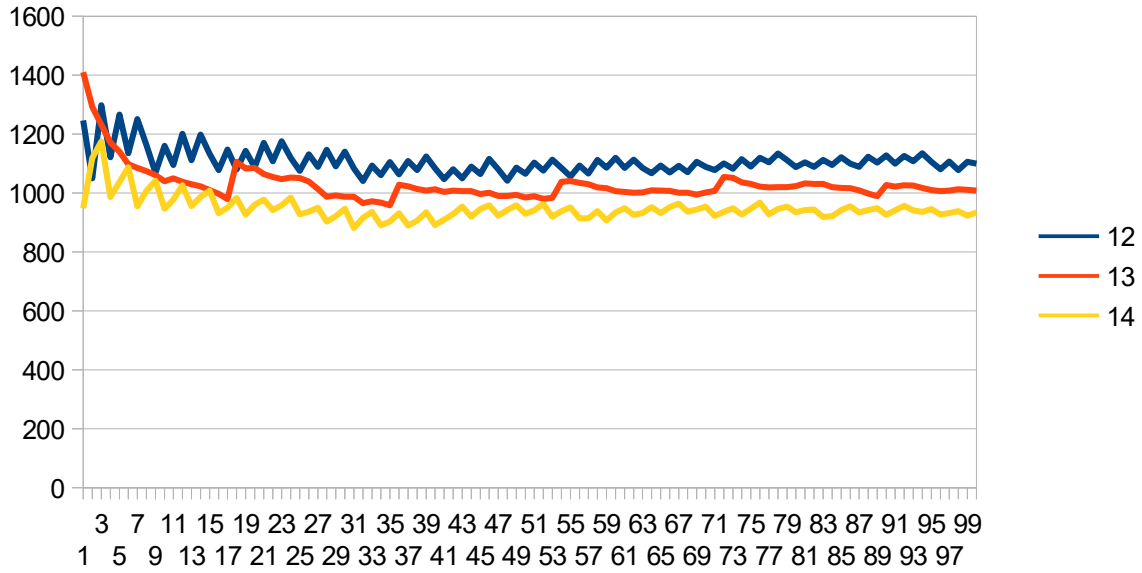


Figure 36 : Stationary wave 13bp ON

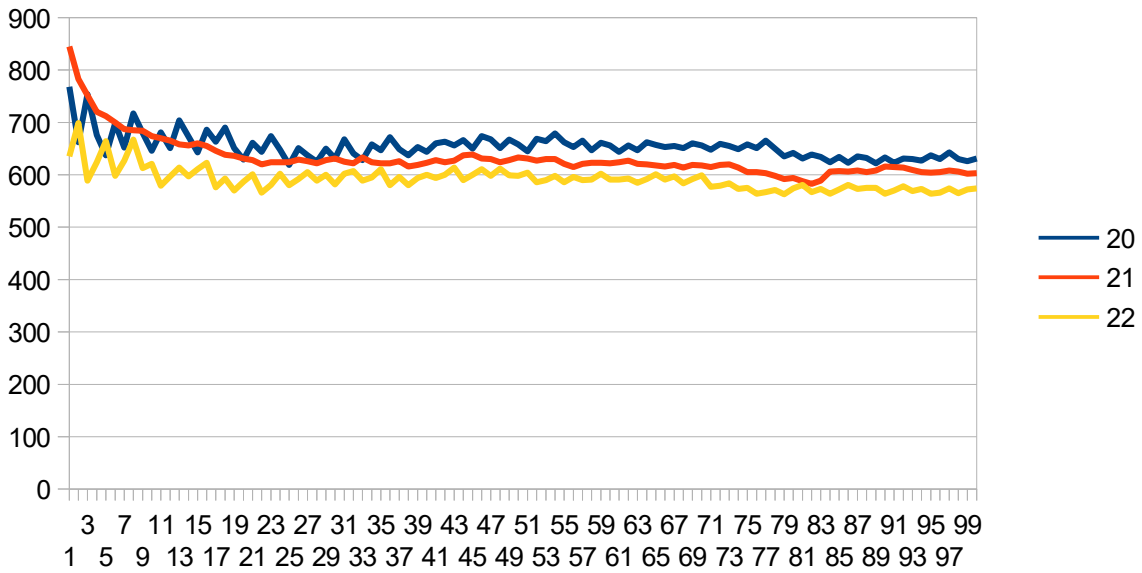


Figure 37 : Stationary wave 21bp ON

In this eighth WUHAN2 14 january 2020 genome, we find also three Fractal Fibonacci stationary wave 5bp, 8bp, and 13bp (Figures 33, 34, 35). Now the fourth other fractal wave 21 bp is also present (Figure 36).

WUHAN (23 january 2020) Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome GenBank: MN908947.3
https://www.ncbi.nlm.nih.gov/nuccore/MN908947.3

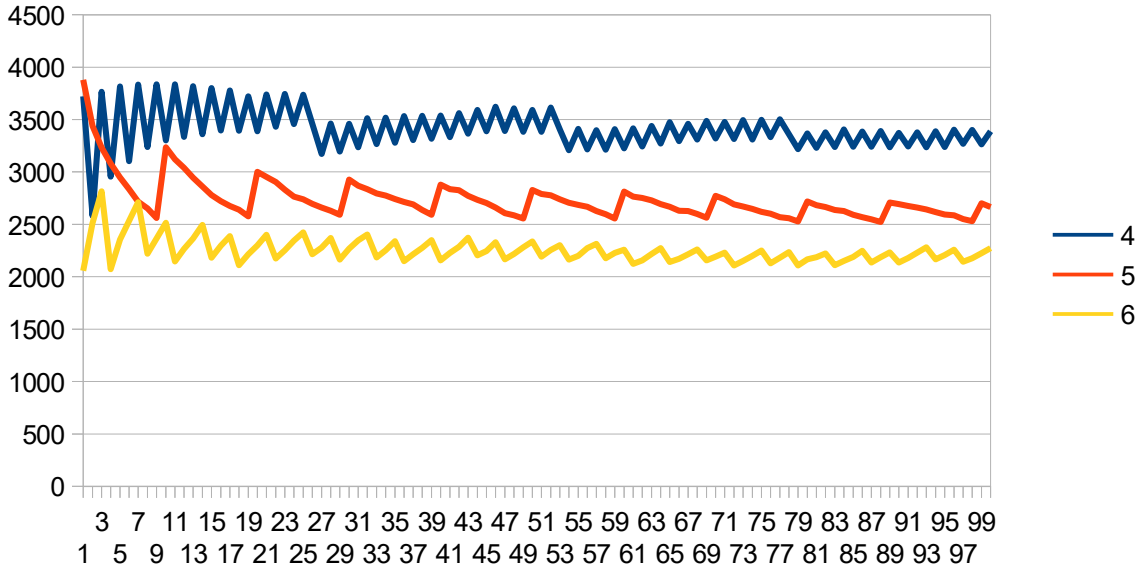


Figure 39 : Stationary wave 5bp ON

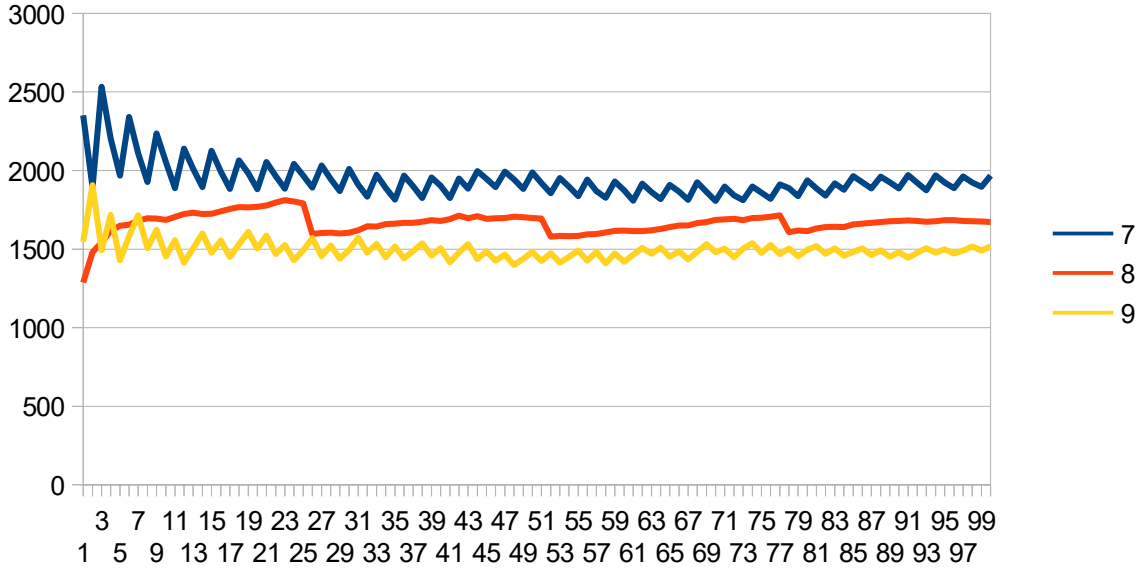


Figure 40 : Stationary wave 8bp ON

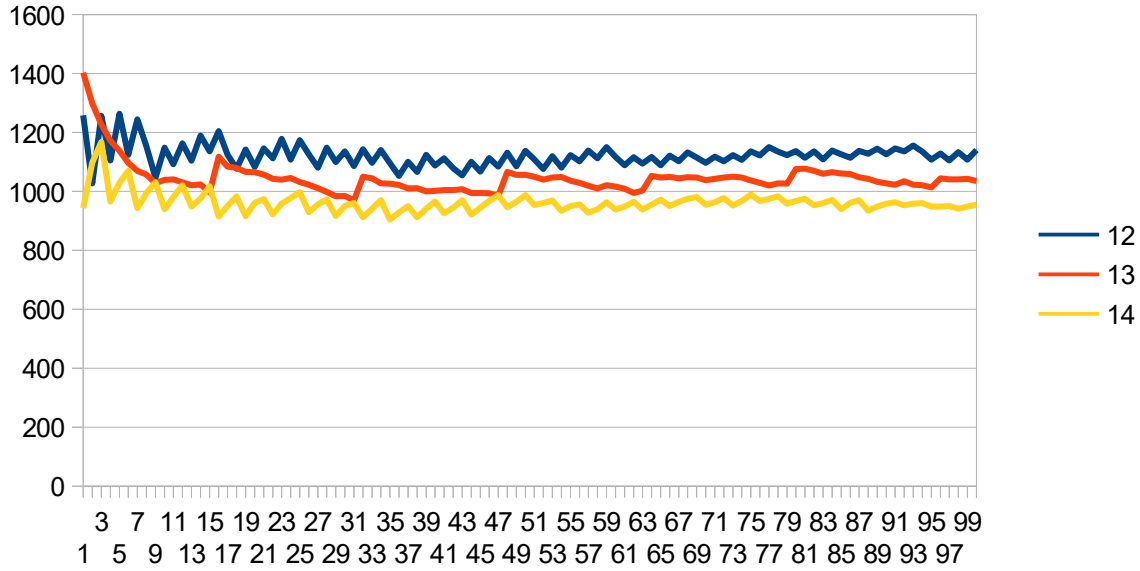
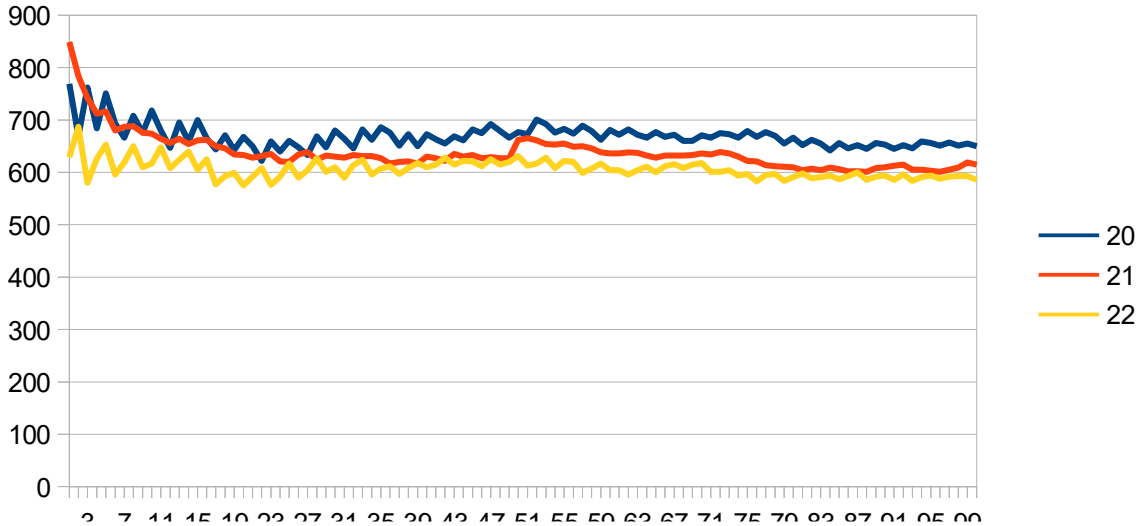


Figure 41 : Stationary wave 13bp ON



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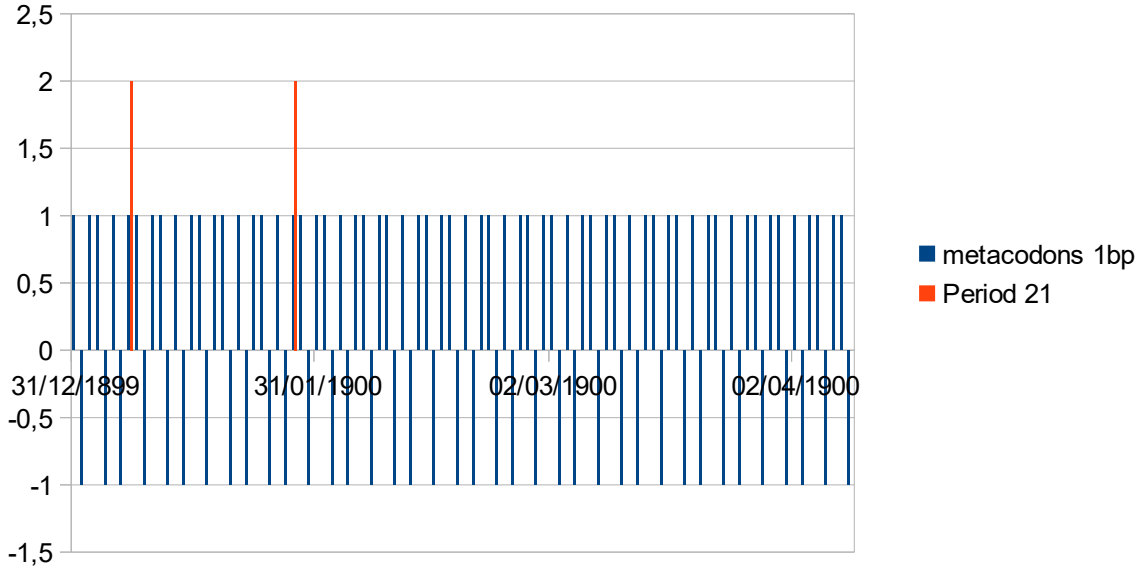


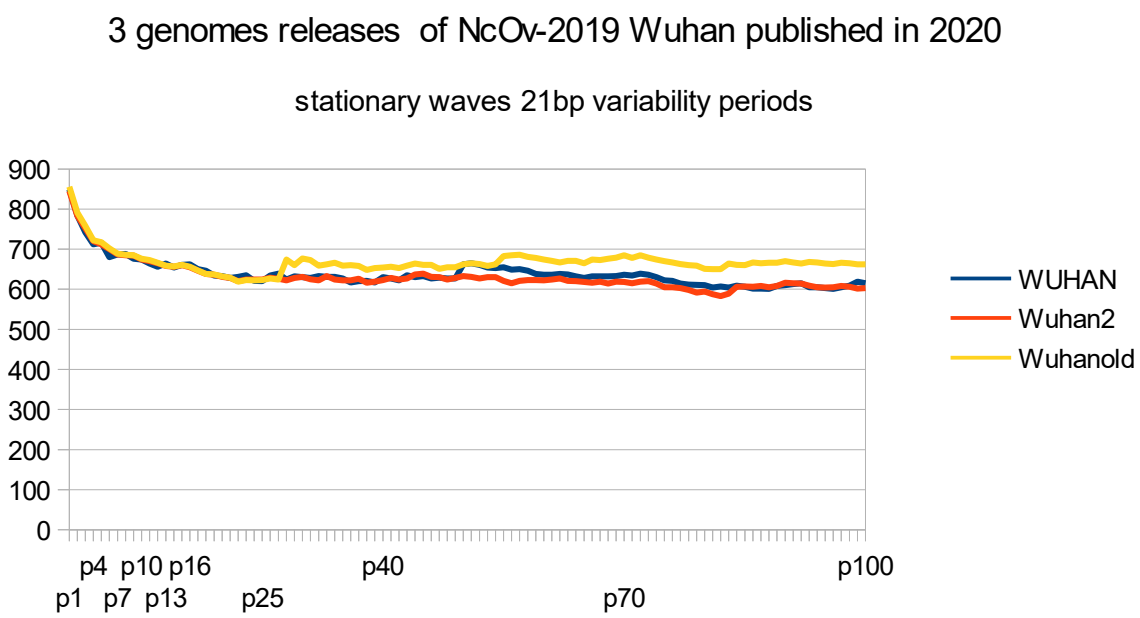
Table 3 below clearly demonstrates a kind of evolution of SARS genomes between 2003 and 2020. If it remains difficult to associate this evolution with an increase in pathogenicity for humans, data already published by us [44-46] rather would suggest a greater ADAPTABILITY of these genomes to the human host genome by the same coherence and unicted via standing waves of Fibonacci [37].

Table3 : High level of correlation between the years of emergence of the SARS virus and the presence of Fibonacci fractal standing waves.

Genome reference	NCBI reference	Lenght bp	Fibonacci numbers FRACTAL embedded stationary waves periods				
			5bp	8bp	13bp	21bp	34bp
SARS2003	AY304488	29731	Yes				
SARS2004	DQ412043	29749	Yes				
SARS2004b	AY395003	29647	Yes				
SARS2012	KY417144.1	29770	Yes				
SARS2015	MG772934	29732	Yes	Yes	Yes		
SARS2017	MG772933	29802	Yes	Yes	Yes		
WUHANOLD	MN908943.1	30473	Yes	Yes	Yes	**Yes**	
WUHAN2	MN908943.2	29875	Yes	Yes	Yes	**Yes**	
WUHAN	MN908943.3	29903	Yes	Yes	Yes	**Yes**	
Hypothetical Evolution genome (see fig 45)	Deleting region in MN908943.3	29153	Yes	Yes	Yes	**Yes**	YES

In figure 44 we have superimposed the standing waves of 21bp corresponding to the 3 published versions of the wuhan genome of 2020. There appears a very high sensitivity, which suggests the fact that this new genome is in full phase of evolution in its adaptation to the human host. the 3 figures 33, 37, 42 show this evolution better: WUHANOLD : 3.5 waves, WUHAN2 : one and epsilon wave, WUHAN : 2 waves.

Figure 44 : high level of sensitivity for 3 releases of Wuhan CoV-2019 genomes



of almost identical lengths (30473, 29875 and 29903bp).

How could tomorrow 2019-nCoV evolve?

In [2] and [5], authors show that there is no doubt that 2019-nCoV is a novel unknown sequence. In an unformal draft, Dr Lyons-weiler [4] even suggests that a region between the bases 21600-22350 bp would be completely new. Considering that this region could be "foreign" to the family of coronaviruses we tried to test how its absence could have had an impact on the waves that we reveal here. We then construct a hypothetical genome which would no longer have this insertion between the bases 21600-22350 bp. It then appears (Figure 45), for the first time a Fibonacci wave of 34bp. This genome would therefore be structured by a fractal nesting of 5 Fibonacci waves, 5 8 13 21 and now 34bp. Curiously, we have only encountered such a level of organization in the entire human chromosome4 (figure 46). A new question: "Can there be some kind of affinity between the waves of a retrovirus and the human host genome in which this retrovirus could integrate?"

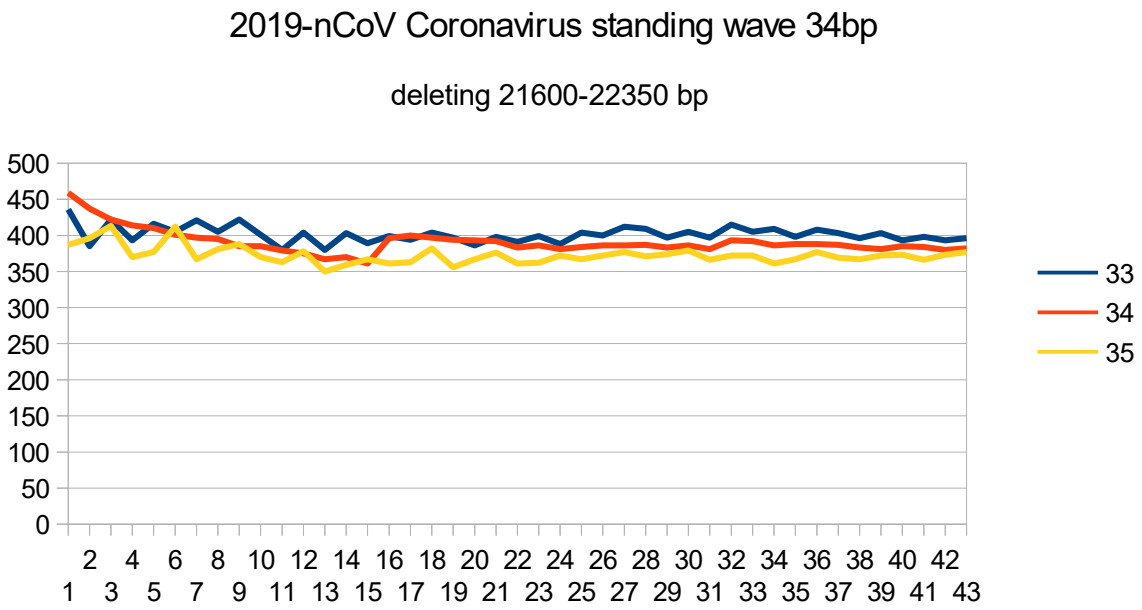


Figure 45 – Standing wave 34bp structuring modified 2019-NCoV genome.

The chromosome 4 HG38 of reference:

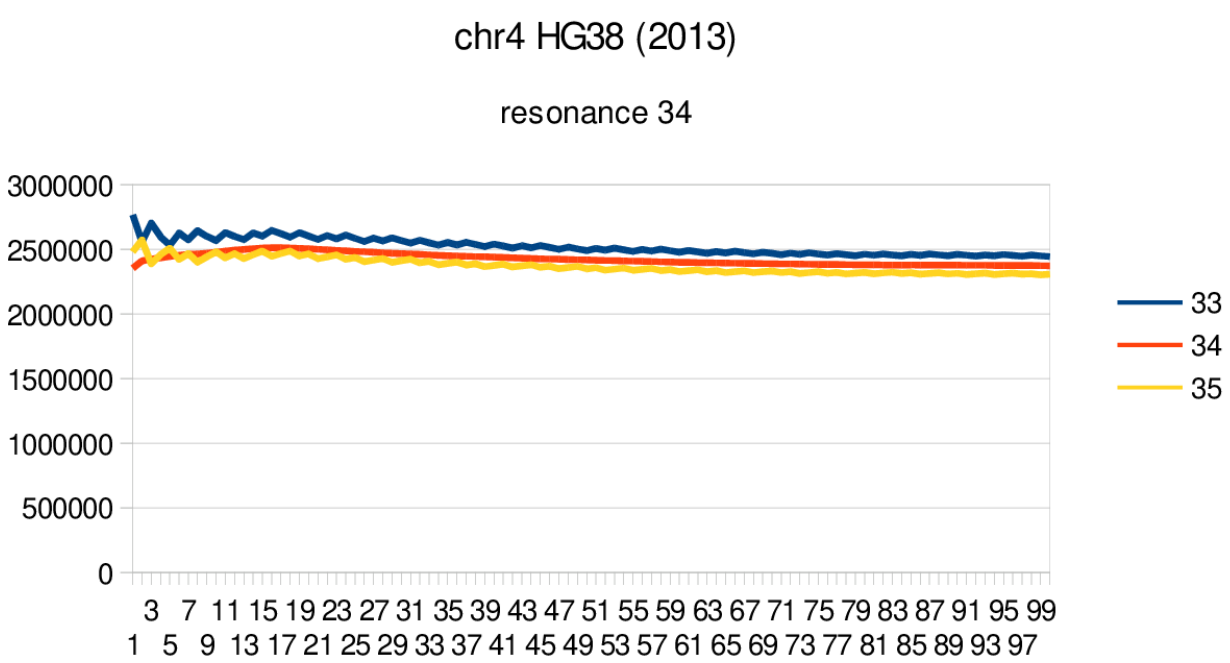
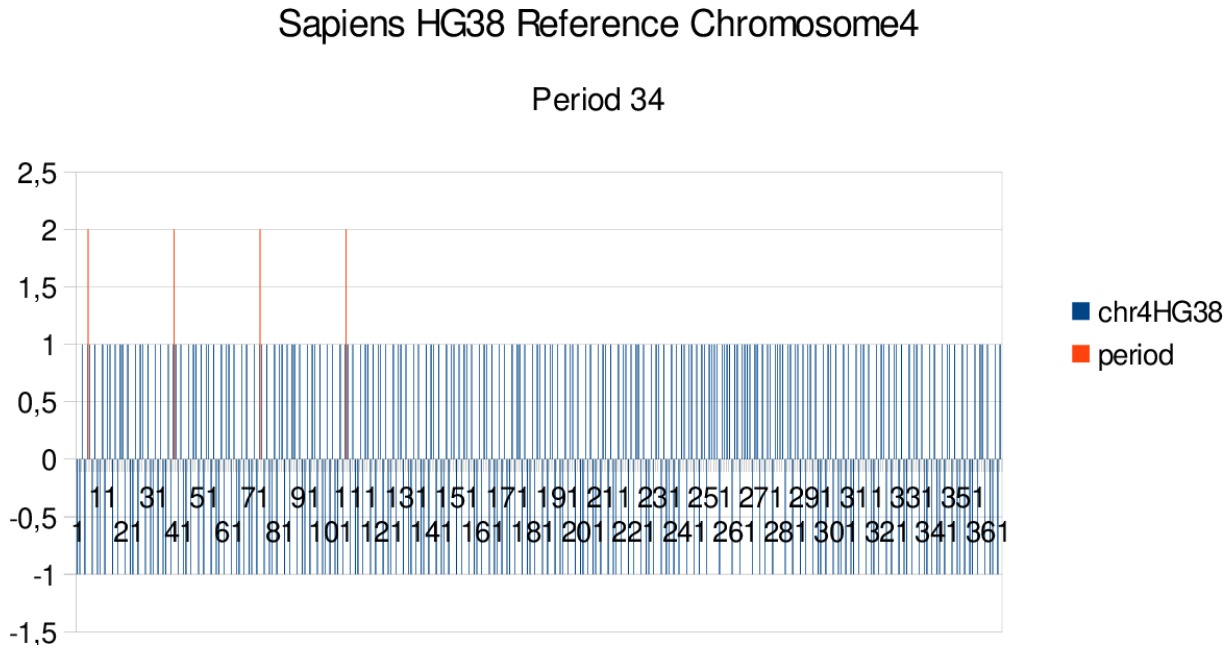


Figure 18 : The main resonance of 34bp characterizing the HG38 reference Chromosome 4.



The chromosome 4 HG38 of reference:

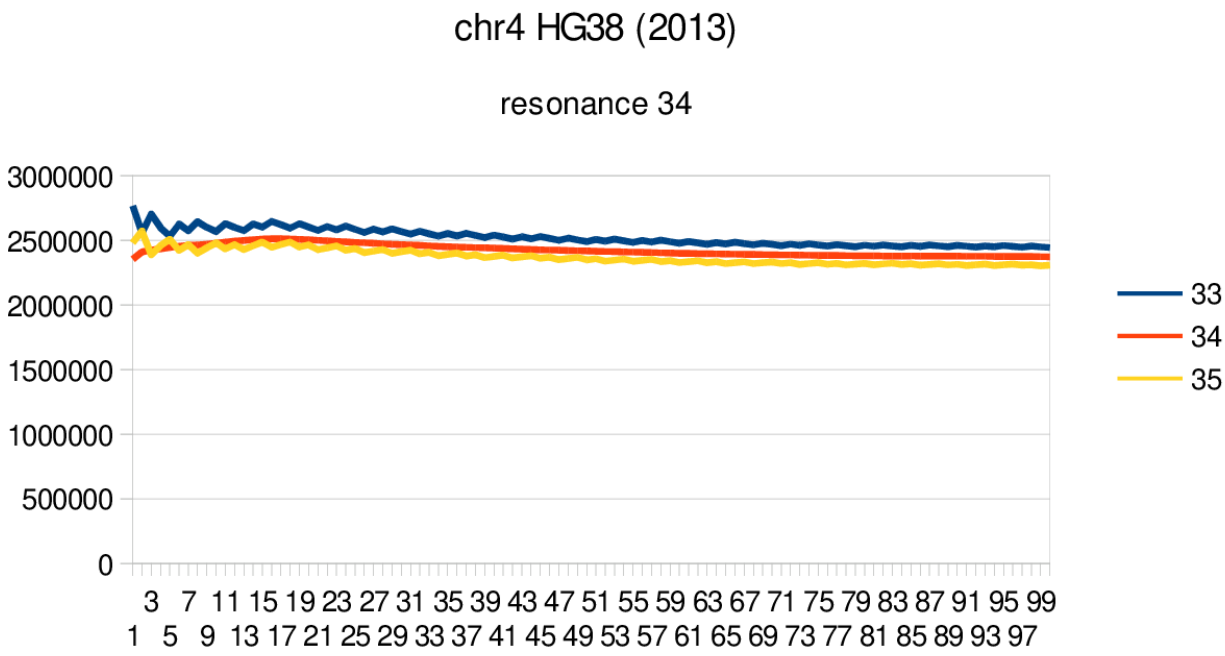


Figure 18 : The main resonance of 34bp characterizing the HG38 reference Chromosome 4.

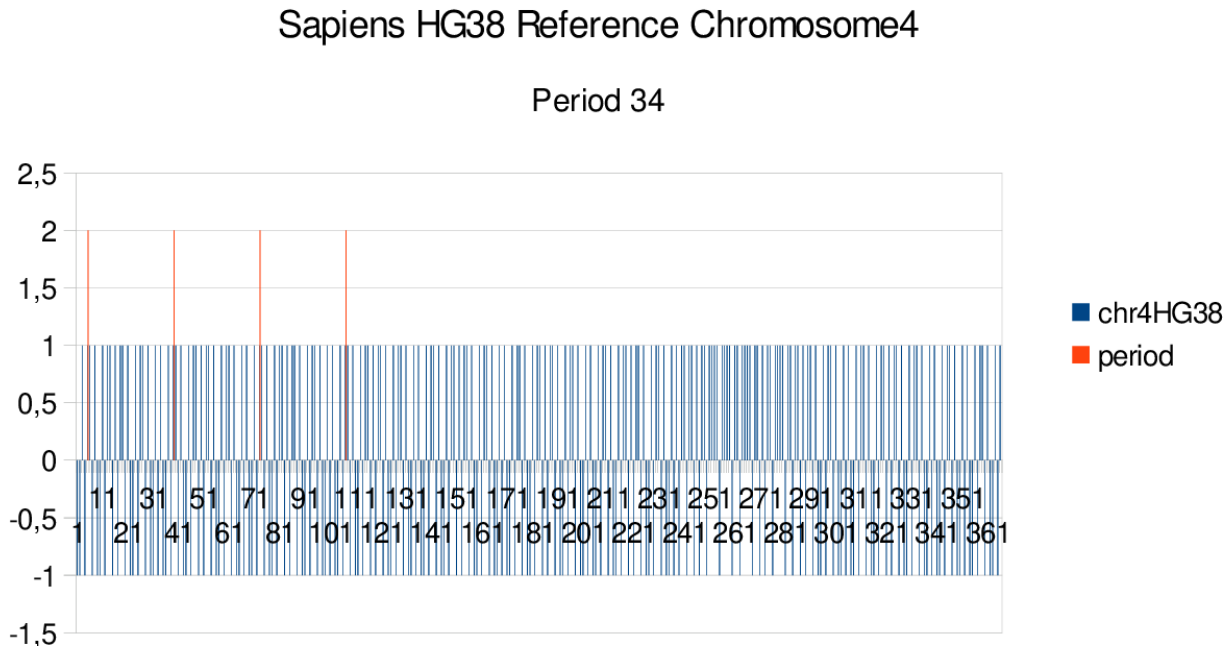


Figure 46 – Standing wave 34bp overlapping the whole human chromosome4

(from [43]).

On a possible "harmonic standing wave agreement" between the human host chromosome and the coronavirus retrovirus:

This last observation opens here an interesting theoretical track on 2 possible strategies of integration of retroviruses in eucharyotic chromosomes:

1 / symbiosis strategy by complementarity: example of HIV more frequently integrating chromosomes

The chromosome 4 HG38 of reference:

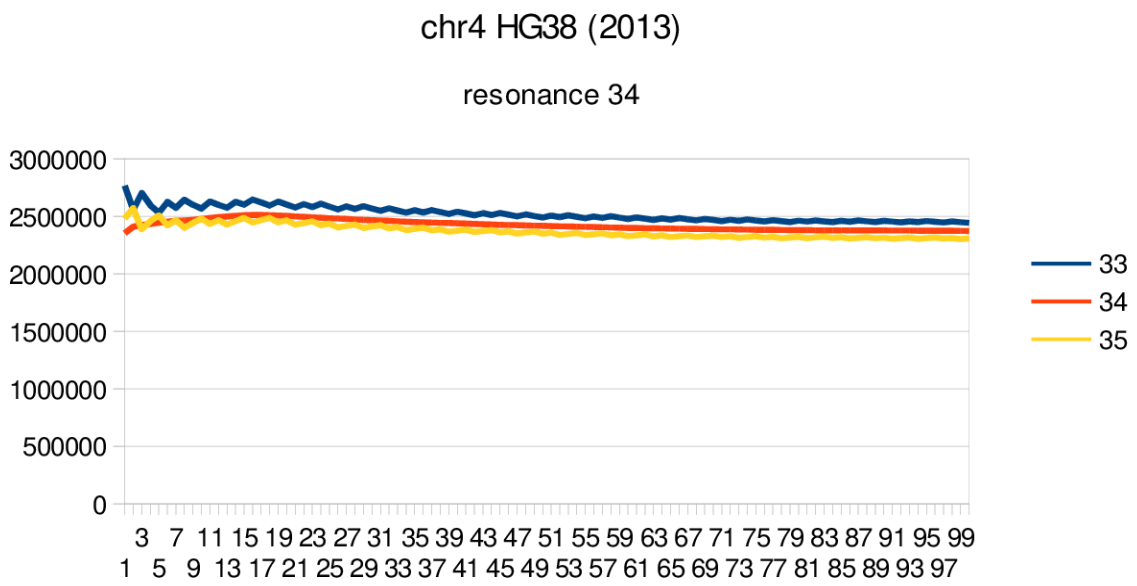
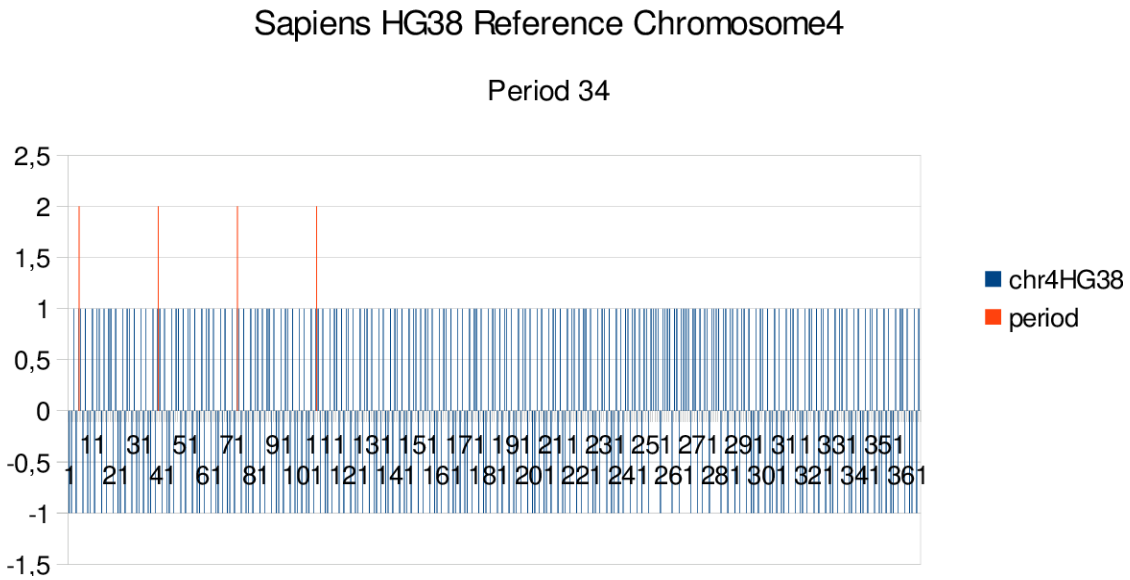


Figure 18 : The main resonance of 34bp characterizing the HG38 reference Chromosome 4.



20 16 17 22 19. These chromosomes have a poor HGO (Human Genome Optimum) ratio,

it will be slightly improved by the integration of the virus.

Indeed, in [8, 46], we demonstrated why the permeability to the integration of retrovirus in each of our chromosomes is correlated with this classification HGO (HUMAN GENOME OPTIMUM) of this article http://www.imedpub.com/abstract/towards-a-universal-law-controlling-all-human-cancer-chromosome-loh-deletions-perspectives-in-prostate-and-breast-cancers-screening-20846.html

For example, chromosomes 20. 16. 17. 22 19 are very permeable: this table shows that they are located at the bottom of this table of classification of HGOs of 24 human chromosomes.

Table 1: CG values, TA values and CG/TA ratio for each Sapiens HG38 individual chromosome.

Chromosome	C + G	T + A	(C + G) / (T + A)
Chromosomes UPSTREAM HGO point = (3-Phi)÷2 = 0.6909830056			
4	72568001	1.17E+08	0.619262
13	37772797	60210328	0.627347
5	71611274	1.1E+08	0.653065
X	61221521	93671508	0.653577
6	67360020	1.03E+08	0.655773
3	78577742	1.2E+08	0.657431
18	31856106	48233499	0.660456
Y	10572683	15842360	0.667368
8	58133960	86634176	0.671028
2	96769083	1.44E+08	0.67304
7	64696843	94273288	0.686269
12	54275482	78862334	0.688231
14	36982791	53585358	0.690166
Chromosomes DOWNSTREAM HGO point = (3-Phi)÷2 = 0.6909830056			
21	16411625	23676994	0.693146
9	50270473	71520077	0.702886
11	55885058	78648684	0.710566
10	55359481	77903481	0.710616
1	96166571	1.34E+08	0.715981
15	35578844	49062481	0.725174
20	28010605	35933652	0.779509
16	36472718	45333225	0.804547
17	37575444	45344760	0.828661
22	18406838	20752939	0.886951
19	28015712	30425046	0.920811

Table3 – HGO human chromosomes classification.

https://juniperpublishers.com/ctoij/images/CTOIJ.MS.ID.555756.T001.png

We also see in fig47 from Fig 4 (Wang 2007), that these chromosomes are very permeable to the HIV retrovirus (Dark green bands in the following image from [3].

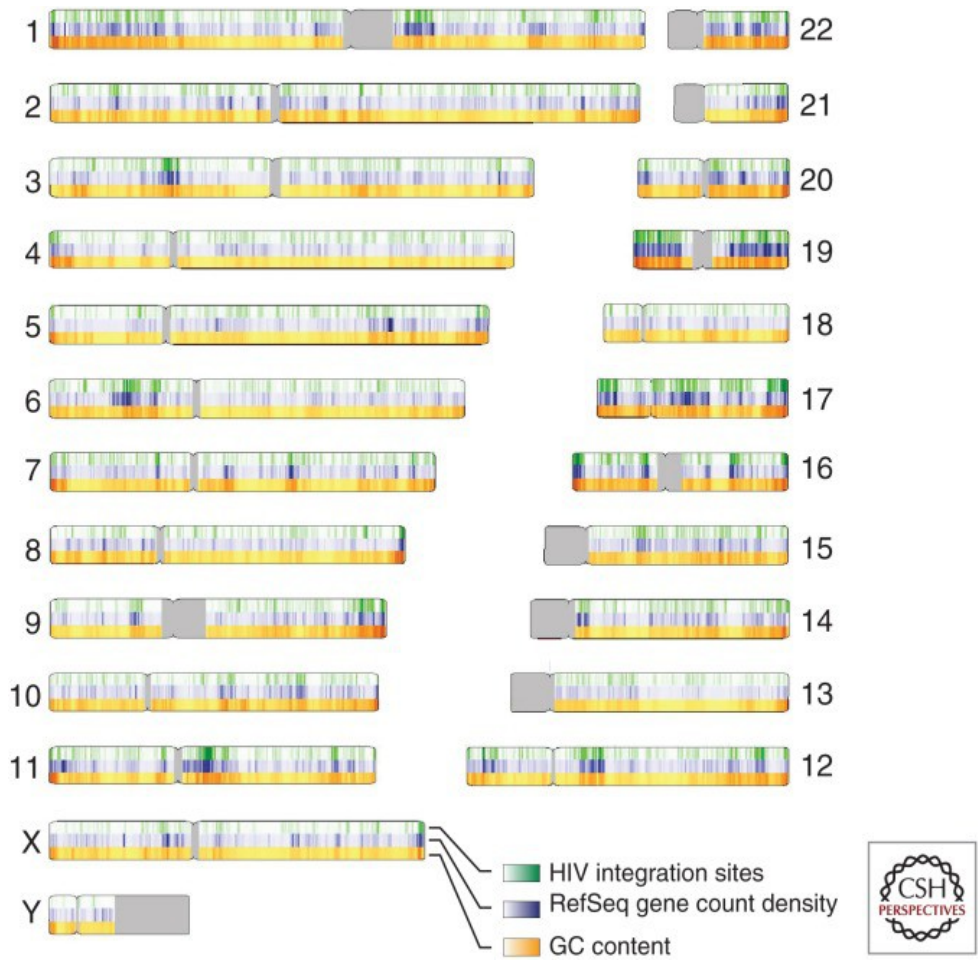


Figure 47 - from [3] Green regions are retoviruses integration region, https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3385939/figure/A006890F4/

2 / symbiosis strategy by wave agreement, resemblance: this could be the case of the coronavirus which would integrate by a kind of harmonic agreement to chromosomes 4 or 13, located at the beginning of the HGO table, which have like it Fibonacci waves . This would hardly affect the resulting HGO ratio, or even strengthen it: This is surely the case with RETROTRANSPOSONS ...

Finally, we have recognized here 2 laws of symbiosis of nature: agreement because very DIFFERENT, and agreement because very SIMILAR.
Strategies that we find up to the affinities between humans ... !!!

If the genome of the 2019-nCoV retrovirus has adopted this second strategy of integration into the human genome, this could explain the fact observed at the beginning of 2020: a moderately pathogenic virus but which spreads very quickly ... Because its retrovirus would be judiciously adapted to its (supposed) host chromosome4 of the human genome?

On a possible origin of 2019-nCoV genome:

It is very likely that there was HUMAN INTERVENTION in this LYONS's region [4] of wuhan genome:

Analysis of this region in all coronaviruses shows a 100% jump in homology for the Wuhan genomes and 70 to 80% for the closest SARS. Although there is already a trace of ENV HIV1 in the genome that we have referenced here SARS2003.
While there is NO TRACE of HIV1 ENV in the region (Lyons-weiler 20020) in all other SARS Coronavirus genomes, Indeed, we find on a mini region (243-86bp = ~ 160bp) 3 partial regions of ENV HIV1 which are all 3 "DIFFERENT" and from 3 different HIV1 strains:

COVID-19 (86-113) ==> in ENV HIV1: 1201 <==> 1228.
COVID-19 (213-244) ==> in ENV HIV1: 424 <==>. 394.
COVID-19 (243-281) ==> in ENV HIV1: 1064 <==> 1029.

in ENV HIV1 Here, these 3 regions, while hyper compressed in Lyons wuhan (<200bp), they are more widely spaced in hiv1 env (394 <==> 1228), ie> 830bp. ??? HOW TO EXPLAIN THIS CONCENTRATION OF 3 SEQUENCES ENV HIV1 ???? IF NOT BY HUMAN ACTION? !!!!

Then, in a second time, we discovered 3 others regions from HIV2 and SIV...

See details and Blast prooves here:

Location of the 300 first bp in [4] from wuhan COVID-19 reference genome (starting from bp 21672).

Wuhan seafood market pneumonia virus genome assembly, chromosome: whole_genome

Sequence ID: LR757998.1Length: 29866Number of Matches: 1

Range 1: 21672 to 21971GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
555 bits(300)	2e-158	300/300(100%)	0/300(0%)	Plus/Plus

```
Query  1
CTCAGTTTTACATTCAACTCAGGACTTGTTCTTACCTTTCTTTTCCAATGTTACTTG
GTT  60

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21672
CTCAGTTTTACATTCAACTCAGGACTTGTTCTTACCTTTCTTTTCCAATGTTACTTGGTT  21731

Query  61
CCATGCTATACATGTCTCTGGGACCAATGGTACTAAGAGGTTTGATAACCCTGTCCTACC  120

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21732
CCATGCTATACATGTCTCTGGGACCAATGGTACTAAGAGGTTTGATAACCCTGTCCTACC  21791

Query  121
ATTTAATGATGGTGTTTATTTTGCTTCCACTGAGAAGTCTAACATAATAAGAGGCTGGAT  180

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21792
ATTTAATGATGGTGTTTATTTTGCTTCCACTGAGAAGTCTAACATAATAAGAGGCTGGAT  21851
```

```
Query  181
TTTTGGTACTACTTTAGATTCGAAGACCCAGTCCCTACTTATTGTTAATAACGCTACTAA  240

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21852
TTTTGGTACTACTTTAGATTCGAAGACCCAGTCCCTACTTATTGTTAATAACGCTACTAA  21911

Query  241
TGTTGTTATTAAAGTCTGTGAATTTCAATTTTGTAATGATCCATTTTTGGGTGTTTATTA  300

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21912
TGTTGTTATTAAAGTCTGTGAATTTCAATTTTGTAATGATCCATTTTTGGGTGTTTATTA  21971
```

Details:

Region HIV1a 86-113:

HIV-1 isolate 19663.24H9 from Netherlands envelope glycoprotein (env) gene, complete cds

Sequence ID: GU455503.1Length: 2598Number of Matches: 1

Range 1: 1201 to 1228GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
38.3 bits(41)	1.9	25/28(89%)	0/28(0%)	Plus/Plus

```
Query  86     AATGGTACTAAGAGGTTTGATAACCCTG  113
              |||||||||||||| | ||||||  |||
Sbjct  1201   AATGGTACTAAGAGGGTAGATAACACTG  1228
```

Region HIV1b 213-244:

HIV-1 isolate 4045_Plasma_Visit1_amplicon5a from Malawi envelope glycoprotein (env) gene, complete cds

Sequence ID: KC187063.1Length: 2547Number of Matches: 1

Range 1: 394 to 424GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
37.4 bits(40)	7.1	28/32(88%)	1/32(3%)	Plus/Minus

```
Query  213  CCCTACTTATTGTTAATAACGCTACTAATGTT  244
            ||||||| || |||| |||| ||||||||||
```

```
Sbjct  424  CCCTACTAAT-GTTACTAACCCTACTAATGTT  394
```

Region HIV1c 243-281:

HIV-1 isolate 07.RU.SP-R497.VI.G3 from Russia envelope glycoprotein (env) gene, complete cds

Sequence ID: GU481453.1Length: 2580Number of Matches: 1

Range 1: 1029 to 1064GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
38.3 bits(41)	7.1	32/39(82%)	3/39(7%)	Plus/Minus

```
Query  243   TTGTTATTAAAGTCTGTGAATTTCAATTTTGTAATGATC  281
              ||||||||||||| | |   |||||||||||| | |||
Sbjct  1064  TTGTTATTAAAGTATTT---TTTCAATTTTGTACTTATC  1029
```

Region HIV2a 24-43:

HIV-2 isolate 106CP_RT from Cote d'Ivoire reverse transcriptase gene, partial cds

Sequence ID: KJ131112.1Length: 924Number of Matches: 1

Range 1: 66 to 85GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
32.8 bits(35)	0.38	19/20(95%)	0/20(0%)	Plus/Minus

```
Query  24  ACTTGTTCTTACCTTTCTTT  43
           |||||||||| ||||||||
Sbjct  85  ACTTGTTCTTATCTTTCTTT  66
```

Region HIV2b 133-158:

Human immunodeficiency virus type 2 complete genome from strain HIV-2UC1

Sequence ID: L07625.1Length: 10271Number of Matches: 1

Range 1: 6701 to 6726GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
30.1 bits(32)	1.3	22/26(85%)	0/26(0%)	Plus/Plus

```
Query  133   TGTTTATTTTGCTTCCACTGAGAAGT  158
              |||||||||||| | ||| | ||||
Sbjct  6701  TGTTTATTTTGCTCCTACTTATAAGT  6726
```

Region SIVa 270-299:

Simian immunodeficiency virus partial pol gene for Pol, isolate

SIVagmTAN-CM545-pol

Sequence ID: LM999945.1Length: 3111Number of Matches: 1

Range 1: 1069 to 1098GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
32.8 bits(35)	4.2	25/30(83%)	0/30(0%)	Plus/Minus

```
Query  270   TTTGTAATGATCCATTTTTGGGTGTTTATT  299
             || |||| |||| | || ||||||||||||
Sbjct  1098  TTGGTAAAGATCTACTTCTGGGTGTTTATT  1069
```

To Conclude :

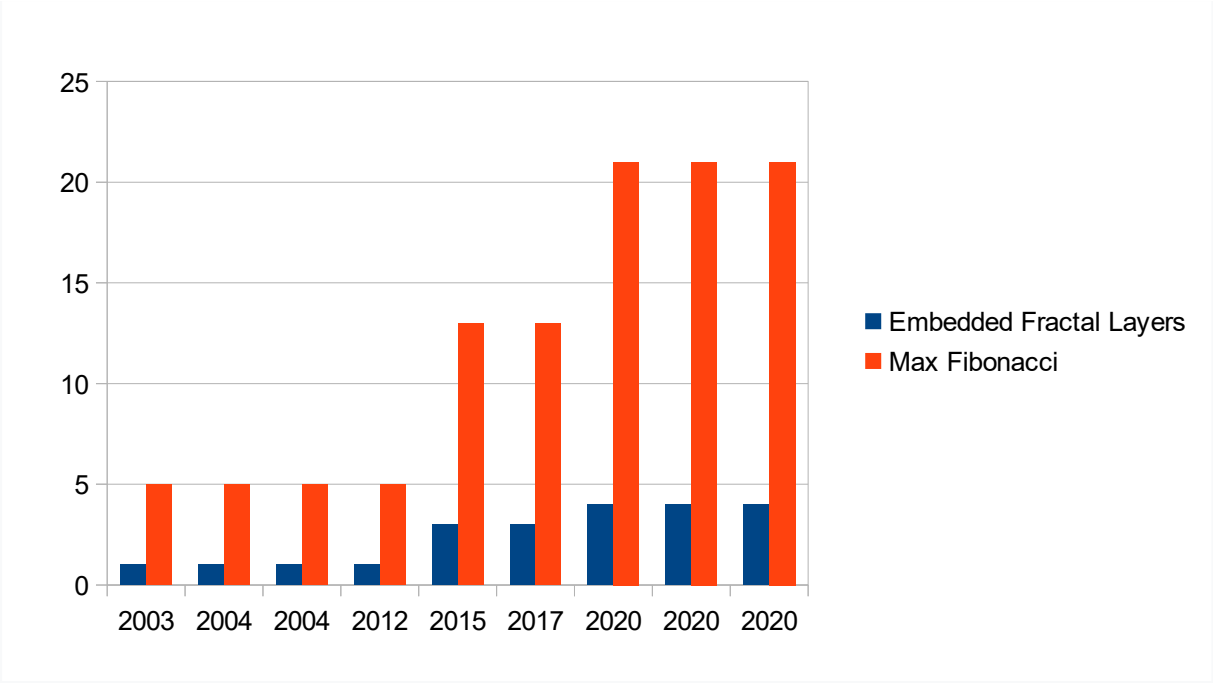


Figure 48 :Double level of correlation between the years of emergence of the SARS virus, the presence of standing Fibonacci fractal waves, and the Fractal number of nested and embedded Fibonacci layers.

One track that will need to be deepened is that of integrating the SARS coronavirus genome into human chromosomes [9, 57].

Indeed, if we show that each of the 24 human chromosomes is characterized by one or more specific standing waves, some of our chromosomes (chromosomes 4 and 13 for

example) have standing waves which are Fibonacci numbers [7]. There could then be a kind of harmonic agreement between the genome of the SARS virus and its human host chromosome, both of which have standing Fibonacci waves, which will facilitate and strengthen the integration and persistence of these viruses in humans.

Finally, That is a formal proof of an evolution increasing global structure of SARS whole genomes, probably linked with genome intégrity and coherence and, human génome adaptation [8, 38] , perhaps pathogeneciity.

Evidence of a kind of "intelligent will" ...

Please, now, see figures 49 then 50.
Both figures prooves evidence that the 6 HIV/SIV inserts are not the result of natural evolution and mutations.
Particularly, :

-Firstly, the 6 inserts are hightly contiguous : 169bp within 275bp regions.

-Secondly, HIV/SIV inserted strains are very gomogeneous : Russia, Cote d'ivoire, Netherlands,Malawi origins.

-Thirtly, The fonctions of inserts are also various : 2 from POL/RT, 4 from ENVELOPPE functional genes.
Not reported in this article, wz found also within the COVID-19 genome 3 others HIV/SIV regions : one from ENVELOPPE, one from RT, and one from INTEGRASE.

POL/RT, INTEGRASE, and ENVELOPPE : we have here 3 major functional rpieces of genes necessary to build a retrovirus...

In other hand,

1 / SYMMETRY: strategy of realism (numbers of inserts by increasing frequencies and pathogenicity):
1 SIV
2 HIV2
3 HIV1

2 / SYMMETRY: economy strategy (sense and antisense in an insert of minimum length):
Hiv2a. <---
Hiv1a. --->
Hiv2b --->
Hiv1b <---
HIV1c <---
Siva --->

3 / SYMETRY: Symmetry Pol / ENV
The 6 inserts are positioned in this order in Covid-19
RT(POL) ENV ENV ENV ENV POL

All this is remarkable and bears the mark of a desire for organization of a human nature: LOGIC, SYMETRIES !!!!

This conclusion is summarized by Figure 49 below.

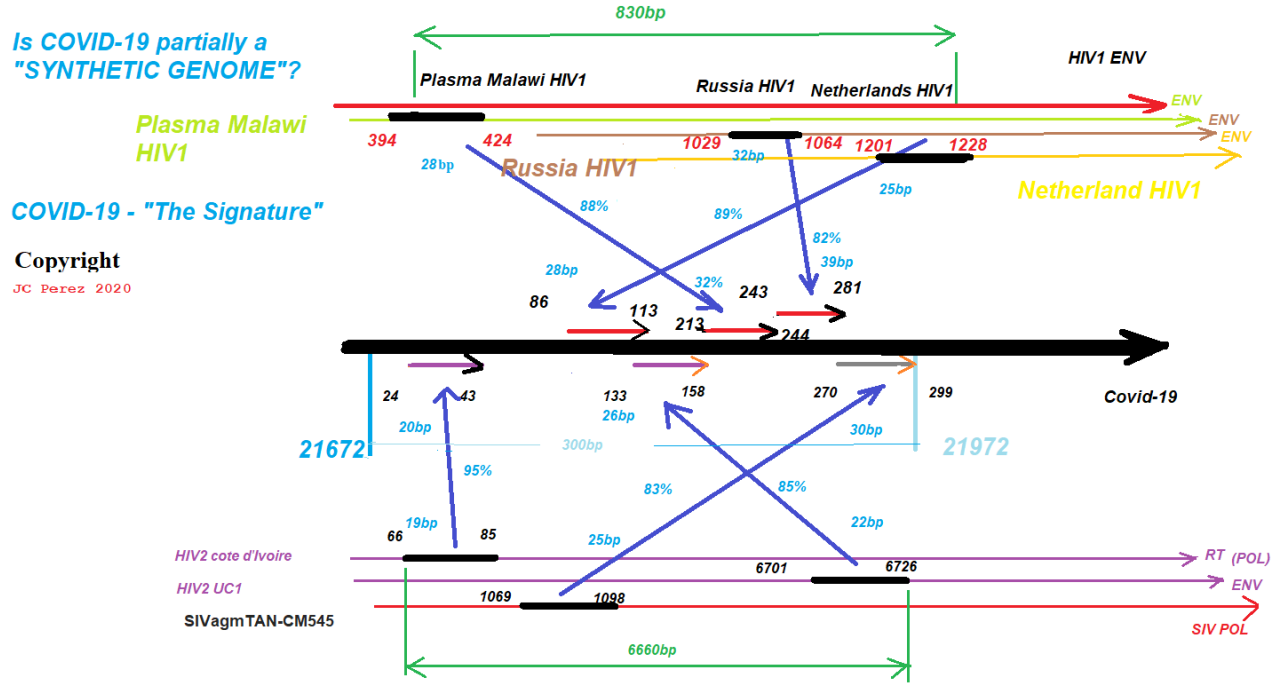


Figure 49 – Is COVID-19 partially a "SYNTHETIC GENOME"?

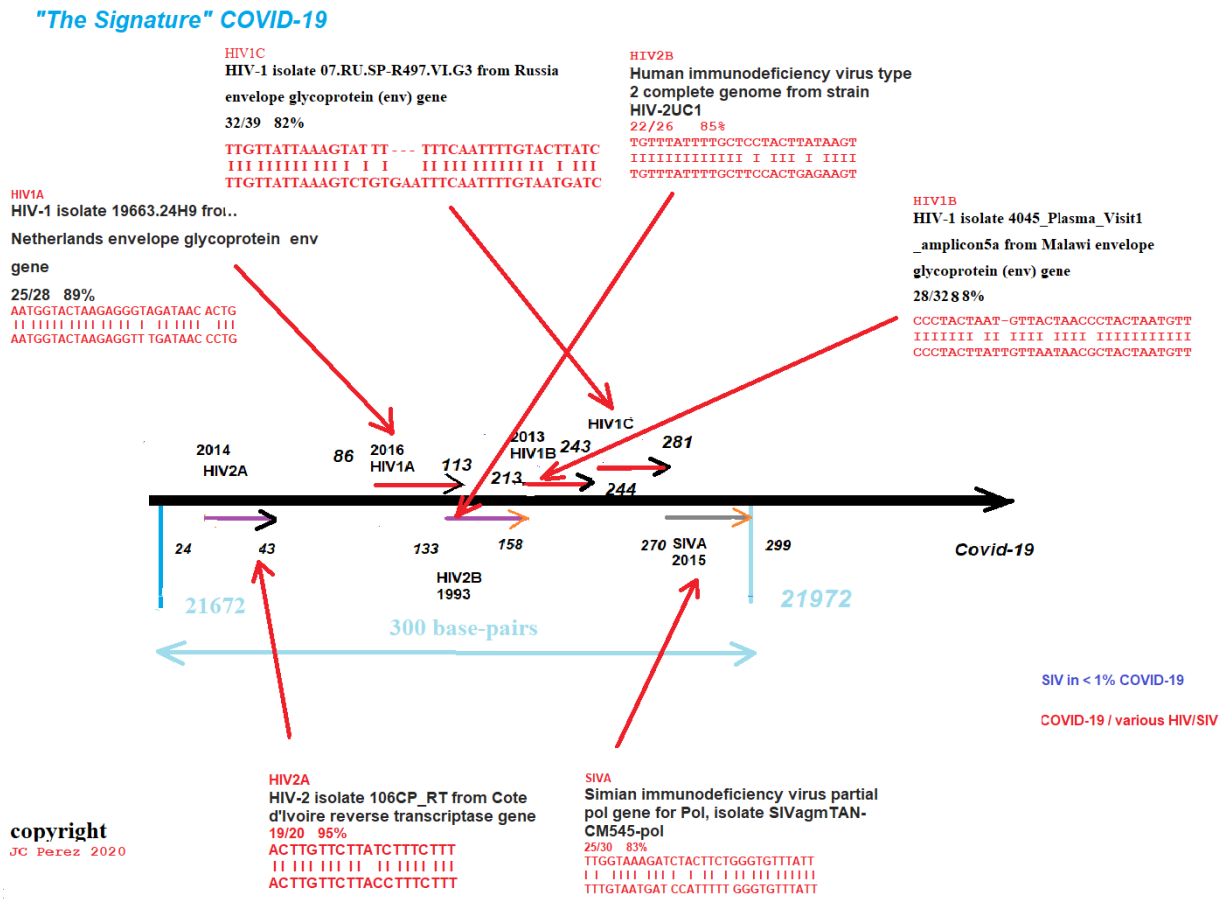


Figure 50 – Evidence of 6 HIV/SIV cuntiguous inserts within a small COVID-19 region.

Ethical considerations:

The 2 main results of this publication confront us with a paradox, in fact:

On the one hand, we have just demonstrated that this covid-19 genome contains an insertion of 6 strategic regions of HIV / SIV concentrated in a mini space representing less than 1% of the length of the genome. One can think that such a "disturbance" can only have affected the global order of the DNA of this genome.

On the other hand, we have also just shown that since the first SARS of 2003, the global order of successive genomes was only increasing, highlighted here by stationary digital waves calibrated on increasing Fibonacci numbers. In particular, covid-19 is structured over a long distance by a 21bp amplitude wave. However, the deletion in this genome of the small region including the 6 HIV / SIV inserts, will further gain in organization, causing waves of 34 bp to emerge (the number of Fibonacci following 21 bp).

We must conclude this remarkable fact:
To adapt to the disorder of its DNA resulting from the insertion of the 6 HIV / SIVs, the covid-19 genome has most certainly increased its level of global organization by adaptation mutations.
And we will now have to fear that this genome will continue to mutate in order to optimize its overall level of organization ...

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