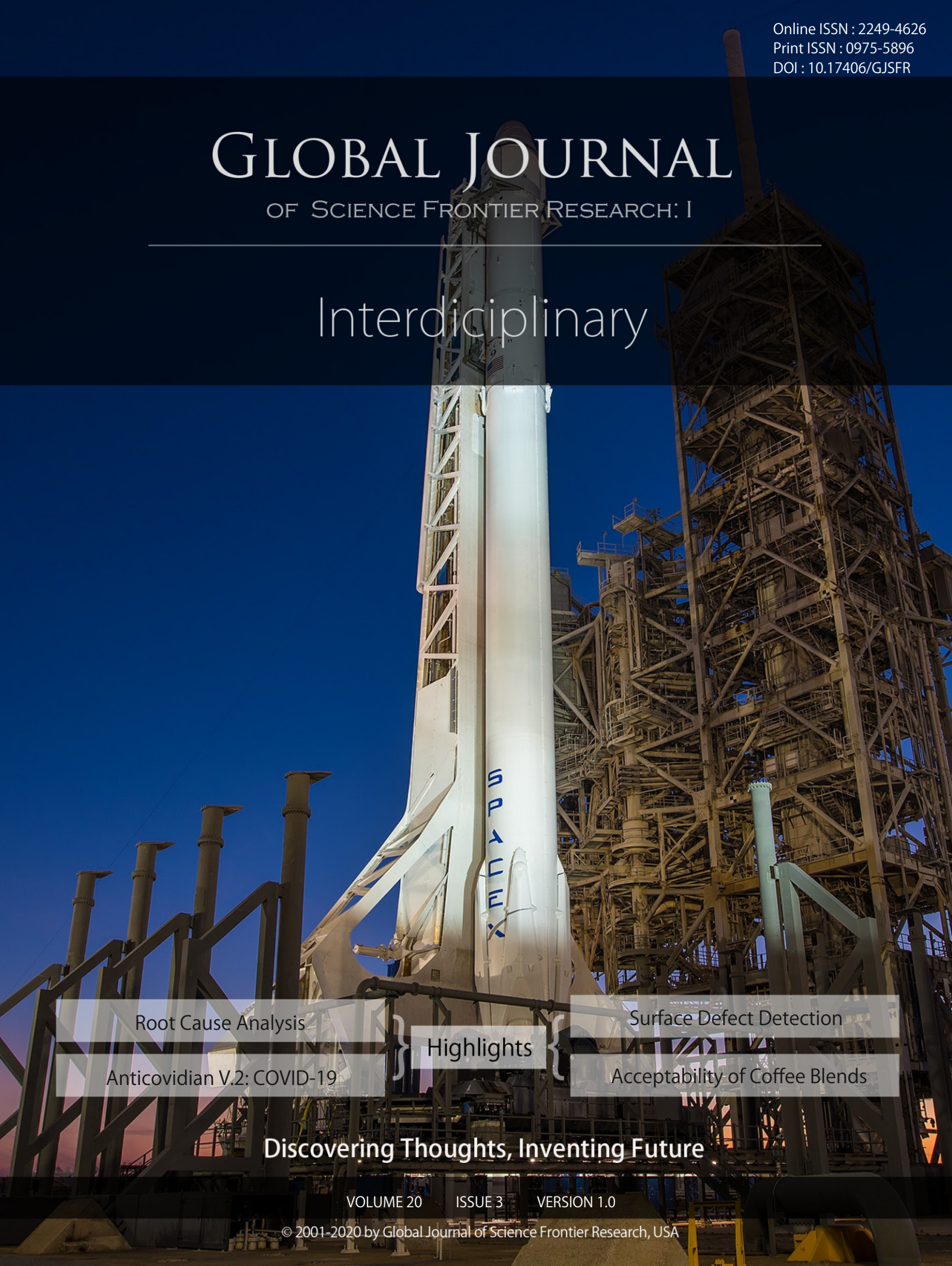
Online ISSN : 2249-4626
Print ISSN : 0975-5896
DOI : 10.17406/GJSFR

Global Journal

of Science Frontier Research: I

Interdiciplinary



Root Cause Analysis

Anticovidian V.2: COVID-19

Highlights

Surface Defect Detection

Acceptability of Coffee Blends

Discovering Thoughts, Inventing Future

VOLUME 20 ISSUE 3 VERSION 1.0

Global Journal of Science Frontier Research: I
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Volume 20 Issue 3 (Ver. 1.0)

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Global Journal of Science Frontier Research

Contents of the Issue

Global Journal of Science Frontier Research: I
Interdisciplinary
Volume 20 Issue 3 Version 1.0 Year 2020
Type: Double Blind Peer Reviewed International Research Journal
Publisher: Global Journals
Online ISSN: 2249-4626 & Print ISSN: 0975-5896

Surface Defect Detection and Root Cause Analysis

By Tianchen Liu, Fan Zhu, Haoran Yu & Haisong Gu

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GJSFR-I Classification: FOR Code: 080199

Strictly as per the compliance and regulations of:

Surface Defect Detection and Root Cause Analysis

Tianchen Liu [α], Fan Zhu [σ], Haoran Yu [ρ] & Haisong Gu [ω]

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Keywords: artificial intelligence, deep neural networks(DNN), Dataonomy™, defect detection, root cause finding.

I. Introduction

Visual inspection is a common task not only across the industry, but also across the world. In industry, in order to improve the quality of products and reduce the cost, machine vision has been used for a long time. Visual inspection consists of three major tasks: defect detection, presence detection, and measurement. However, defect detection is still a challenging problem due to a large variety of shapes and patterns among products from different industries, and even different assembly lines of the same product. Recently, machine learning based approach has shown great potential in solving complex problems and has proven to be successful in a variety of applications. For example, using artificial intelligence method[1] for asphalt pavement pothole detection based on least squares support vector machine and neural network with steerable filter-based feature extraction. Another example[2]was to use GLCM to extract texture features for surface quality detection for steel sheet. Recently Deepneural network(DNN) has been applied to solve surface defect detection problem in various fields: automobile parts, car surface, etc. In the field of visual inspection, several works [3][4][5] were proposed using DNN or Deep Learning(DL) based approach to classify and detect the defects. One of the biggest challenges for applying DNN based approach to the industry is the lack of data samples. In practice, a common approach [6] to address this problem is to use transfer learning, in which a pre-trained model, such as VGG and Inception V3, is chosen and then retrained on the target dataset by keeping the model architecture and parameter weights of the lower layers constant and only updating the upper layers of the neural network. However, it is difficult to get a large number of training samples from a certain field or industry, for instance, images of defects on the surfaces of a specific type of ceramic product. Therefore, in this paper we propose a novel approach named Dataonomy™, which can be used to train the classifier for a specific task across the industry with relatively small data samples. Different from the method of adding a number of geometric transformations to the original image data to enlarge the number of samples in the training dataset, Dataonomy™ aims at quantifying the relationships between different datasets and extracting a structure out of them. The "structure" means a collection of relations specifying which dataset provides useful information to another, and by how much.

For the accuracy, we apply two latest deep neural network(DNN) architectures, Inception v3 and fully convolutional networks (FCN) so as not only to classify whether there are defects but also to make a pixel-wise prediction to inference the areas of defects. Both architectures have decent accuracies to find defects.

Another issue in the surface visual inspection field is that besides the basic defect detection tasks, few researches have dealt with root cause analysis for the detected image defects. In [7], the author proposed a knowledge-driven diagnosis approach when defect generation mechanism is known. Basically, there are two main kinds of root causes: systematic error and random error. Systematic error such as mechanic operation error will cause the same defect at the same position for each product. This kind of error does huge damage to the whole batch of products. In this paper, we will focus on finding out defects caused by systematic error.

The major contributions in this research consists of

1) Dataonomy™method to solve the sample datashortage
2) A novel AI approach to detect the surface detects with the combination of two latest DNNs

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3) A generalized multi-image matting algorithm is applied to a root-cause analysis from surface defects

The rest of the paper is structured as follows. In Section 2, we provide a description of our Dataonomy™. Section 3 gives a description of our deep learning-based framework for image defect detection. The setup and results of the experiments will be presented in Section 4. Conclusions will be discussed in Section 5.

II. Dataonomy™

The patent pending Dataonomy™ algorithm [3][8] is a fully computational method for quantifying data class relationships and extracting a structure out of them. The following steps give the idea of the whole pipeline, and the framework of our approach is shown in Figure 1.

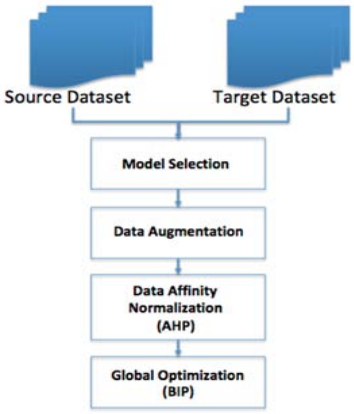


Figure 1: Dataonomy TM Pipeline

a) Make use of a pre-trained model for object classification, for example Inception V3 [9].
b) Find affinity matrix across the dataset.
c) Get normalized data augmentation affinities using AHP (Analytic Hierarchy Process) [10].
d) Find global mapping taxonomy using BIP (Binary Integer Programming) [11].

The Dataonomy™ algorithm will pull the information from an ever-increasing pool of data to develop a highly specialized solution for new customers. Once the data of a company is added to the pool, the model can be fine-tuned to exceed 99.97% accuracy.

III. Framework for Image Defect Detection

In this section, we present the framework ofour proposed method for visual defect inspection. First is by using Inception V3, and second is by using FCN.

a) *Inception V3*

As shown in Figure 2 (a), the framework of deep learning based visual defect classification and detection by Inception V3 consists of three components. The first component is the base model training, the second component is transfer learning for visual defect classification, and the third component is defect segmentation.

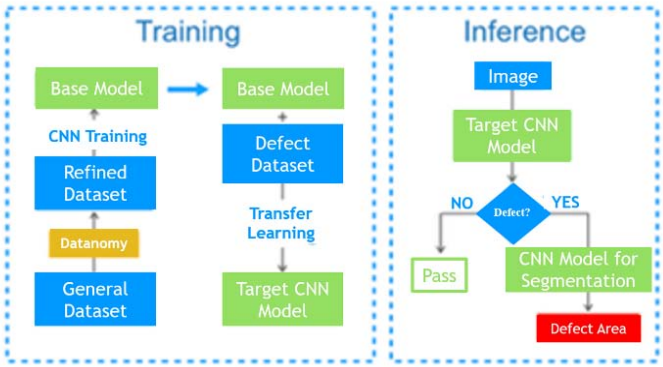


Figure 2: (a) Framework of Our Proposed Approach

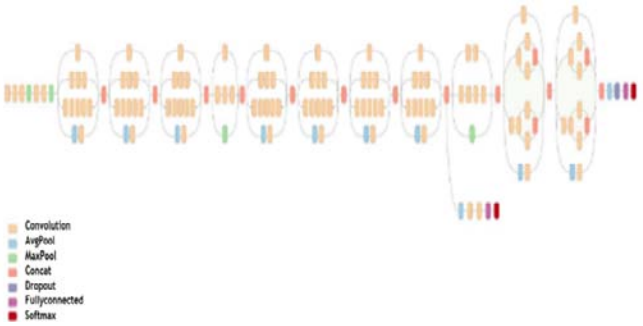


Figure 2: (b) Inception V3

i. *Training of Base Model*

In order to obtain the specific model for visual defect classification, the selection of the base model is important, and the way to train the base model is also crucial. These two factors would impact the overall performance of the base model and thereafter. During the base model training, we utilize the aforementioned Dataonomy™ approach to prepare more useful and representative datasets related to our tasks. Then deep convolution neural network is applied with state-of-the-art model architectures. Specifically, we introduced the InceptionV3 [9] network, which has been widely used in image recognition and has shown promising performance on various datasets, as shown in Figure 2 (b). This network is made up of several inception modules which contain convolutions, pooling, concatenations, and fully connected layers. The original inception module was designed by stacking filters with multiple sizes in the same level of the network, which enables multiple receptive fields of each filter and, in turn, can extract features in multiple scales. In order to reduce the computational cost, within an inception module, 1x1 convolution layers were added to limit the number of input channels. In the Inception V3 network, the computational cost was further reduced by factorizing convolutional layers within the inception module, where an NxN convolutional layer was

decomposed into one 1xN convolutional layer followed by an Nx1 convolutional layer. Lastly, batch normalization was added to auxiliary layers to improve the performance.

Given the InceptionV3 network structure, we modify the fully connected layers to fit the number of classes from the dataset generated by our proposed Dataonomy™ approach. Then augmented data are collected into batches and feeding into the network for training. The Stochastic Gradient Descent (SGD) with momentum is applied for the training procedure. The whole training is set to stop when the network converged after a number of epochs. The trained weights are stored as our base model and would be used in the next steps for transfer learning.

ii. *Training of Defect Classifier*

The next step of our proposed framework is to train the visual defect model. The transfer learning scheme is applied in this step by utilizing our pertained models on the dataset that is generated by Dataonomy™. Particularly, the pre-trained Inception V3 model is used as the starting point for the model on the visual defect classification task. This transfer learning approach is considered to be effective since our base model is trained on a large corpus of photos with a large number of classes. It enables the model to efficiently learn to extract features from these images in order to perform well on a specific problem. Moreover, the model is pretrained on the dataset selected through Dataonomy™, which chooses sample images that have certain features that are more closely related to the classification task of defect inspection. This approach can further boost the capability of the base model to differentiate visual defects. During the training, we use the full model without freezing any layers, and only the last fully connected layer is modified to fit the two-class classification problem in defect inspection tasks. Hyperparameters such as the initial learning rate are modified, and more details are presented in experiments.

iii. *Defect Area Detection*

After the above steps, our model is capable of detecting the visual defects given an input image. Inspired by [5], we further propose a segmentation approach, fully convolutional networks, as shown in Figure 2 (c), for pixel-wise defect detection so that the defect area can be accurately located in the image. There are two components included in this stage, patch extraction, and model training. We crop patches in original images, and each patch as a training image. We label the patch whose defect area exceeds the threshold 0.6 as a defect, vice versa. The ratio of training defect patches and non-defect patches is 2:1. For the dataset of DAGM-2007, the size of the patch is 64*64 pixels with the stride of 64 pixels. When do testing, the whole image is the input image. In the FCN architecture, there are four convolutional layers as feature extractors followed by batch normalization and Relu, and two pooling layers. A deconvolutional layer is inserted before the score layer to maintain the resolution of the feature map for classification.

b) FCN

CNN has shown great quality and efficiency in different tasks. In order to take full advantage of CNN on surface defect inspection, we need to make predictions on every pixel. And that's the reason why we choose Fully Convolutional Networks (FCN) as our base model, which has been demonstrated to outperform other approaches in image segmentation. In this case, the networks can thus be trained end-to-end, pixel-to-pixel.

The other reason that FCN as our top choice is that FCN has the property to allow an arbitrary size of the image as the input of the networks. This property facilitates the processing of images in different sizes.

According to the paper "Fully Convolutional Networks for Surface Defect Inspection in Industrial Environment"[12], we use the method two stages method for base models.

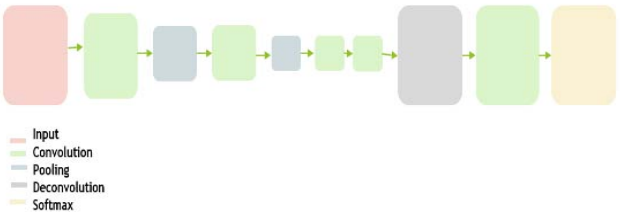


Figure 3: FCN

i. *Stage 1 -- Coarse Segmentation of Defect Area*

This stage is giving a quick and coarse inference of the defect area, which is also called the region of interest (ROI). The predicted ROIs would be the initialization of stage 2 in order to limit the search range of stage 2. The final goal is to improve inspection efficiency.

In the training phase, we cut the original image into several small patches. But in the test phase, we use the whole image as input. The receptive field should be a proper size, not too large or too small. If the receptive field is small, the network can focus on rich local spatial information rather than global object-level information. To interpret what influences the receptive field, we assume a network, the kernel size of the i-th layer (layer$i$) isK_i, s_i is the stride of layer i and S_i is the integral stride before layer i. We denote R_i as the receptive field of each neuron located on the i-th layer (noted as layer-i). Then the recurrence relation of R_i and S_i can be calculated as follows:

$$R_i = R_{i-1} + S_{i-1}(K_i - 1) \quad (1)$$

$$S_i = s_i \times S_{i-1} \quad (2)$$

It can be concluded from the recursion formula that the receptive field is influenced by K_i, s_i, and the depth of network layer- i. We pick Zeiler and Fergus's model trained for RPN in [13] as our basic architecture. We use only the first four layers as our feature extractor layer and append a scoring layer at the end of feature layers, and we change the strides of all convolutional layers from s_i to 1 (s_i is the original stride of layer i in ZF). Overlap pooling used in RPN controls model capacity and increases receptive field size, resulting in a coarse, highly-semantic feature representation. While effective and necessary for extracting object-level information, this general architecture results in low resolution feature that are invariant to pixel-level variations. This is beneficial for classification and identifying object instances but poses a challenge for pixel-labeling tasks. So, we change overlap pooling to non-overlap pooling as the former cause lager Ri in the following layers. To maintain the resolution of the feature map used for classification, we insert a deconvolutional layer [14] before the score layer. We use logistic regression as the loss function for segmentation. More details about the network structure are shown in Fig. 4.

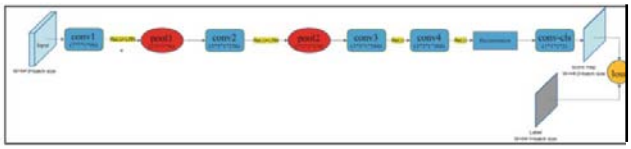


Figure 4: Structure of FCN on Stage 1

ii. *Stage 2 -- Segmentation Refinement with Instance-Sensitive Patches*

Stage 2 is to improve the result of segmentation from Stage 1 with a method of detection. The difference between stage 1 and stage 2 is that stage 1 focuses more on local information; stage 2 is a detection task to refine stage 1 with object-level information. In other words, stage 2 is detection instead of segmentation. We still use those cropped images as training data, but we do not use those manually annotated segmentation masks in the training process. We label the patches whose defect area covers over n% of the total area as the defect patches (n can be changed for different accuracy requirements, in our experiment in this paper, we design n = 40), and others as the non-defect ones. We also do not all samples of the whole image, we only do sample that around ROI from stage 1 for efficiency.

As shown in Figure 5, it's the fusion of stage 1 and stage 2. The result from stage 1, ROIs, is the initialization of stage 2. We crop the patches around ROI and do the classification, whether it is a defect or not. Then we keep the interaction of the two stages.

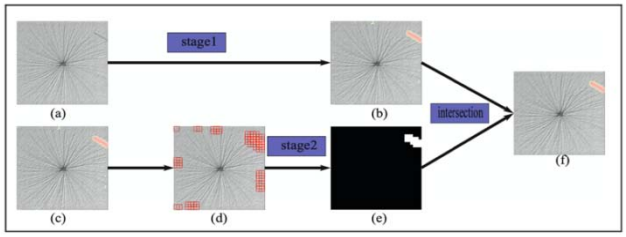


Figure 5: The Fusion of Stage 1 and Stage 2

We design a multi-loss-function in FCN to fuse information across layers to make a skip connection in order to increase the detection accuracy. All the loss function is logistic regression. As we still use FCN in a detection task, we label the patch with a label map that has the same resolution as the output layer, and its values are all the same—0 for defect patches and 1 for non-defect patches (shown in Fig. 6).

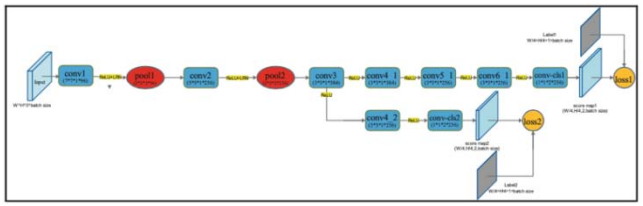


Figure 6: Multi-loss-function structure of FCN in stage 2

While inspection, we vote the score map to one single Soft Max layer and average the results from different Soft Max layers. This method can average the results of certain-size receptive fields under one patch and average the results of the different-size receptive fields under one patch, as shown in Figure 7.

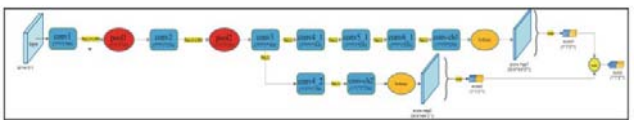


Figure 7: Illustration of inspection process

c) Defect Cause Analysis

There are many works dealing with defect detection. However, few of them can conduct the cause-finding automatically. We provide a way to find the root cause of common defects, which is also known as systematic error. Normally, if a systematic error exists, it will cause the same defect at the same location. The following workflow of a generalized multi-image matting algorithm shows our approach to extracting the common defect.

Assuming that a system error exists, our task is to determine if there is a common defect and what part belongs to a common defect in images. Basically, we first compute gradients at each pixel in both x and y directions for each image. Then we compute the median gradients, which are the medians of gradients obtained by a median filter, for x and y-direction independently.

Thus, we have two median gradient maps: one for x and one for y with all information from the dataset.

$$p[m,n] = median\{g_k[m,n,k \in w]\} \quad (3)$$

Here, $p[m,n]$ is the median gradient value of a single pixel at position $[m,n]$ in either x or y direction for images within the filter window size of w. $g_k[m,n]$ is the gradient value of x or y direction in a single image at position $[m,n]$. After the experiment, we find out that window size around 30 will start to give us a good result. To further explain the filter window, imagine in a manufacturing line, every 30 or more consecutive products will be taken into analysis to get a median gradient map. We get the gradient values maps of all w images, and for each pixel, we find the median value of all *w* images at the same pixel as our median output. The reason why we use the median filter is to clear noise and speckles. As the number of images increases, the median gradient at the common defect area will be more consistent and significant than other points, because the systematic defect occurs in the same position for each image. Therefore, after computing the magnitude of the gradient for each point, we can get an output image that shows the common pattern, which normally gives the systematic error. Figure 8 is our defect analysis workflow.

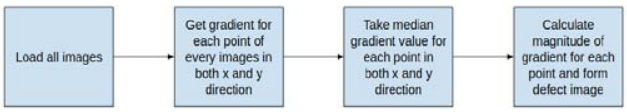


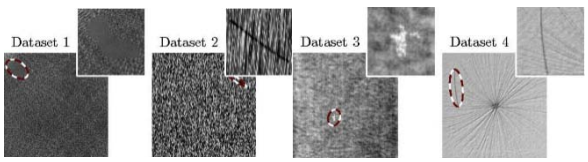
Figure 8: Defect Analysis Workflow

IV. Experiments

a) Defect Detection

i. Datasets

We choose the DAGM-2007 dataset [15] to evaluate the performance of our proposed framework. The dataset contains ten classes of the different defects with different textured backgrounds, even though the data is generated artificially, but similar to the real-world problems. The entire dataset consists of 8050 images for training, in which 1046 images contain defects; and 8050 images for testing, in which 1054 images contain defects. Each image in the dataset is saved in grayscale 8-bit PNG format of size 512x512. In our experiment, we split the training dataset into two parts, 80% for training and 20% for validation during the training stage. The example image for each class contained in this dataset shows in Figure 9.



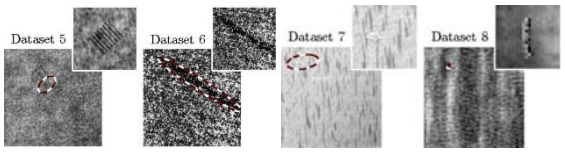


Figure 9: DAGM-2007 Dataset

ii. Experimental Design

In order to evaluate the effectiveness and performance of our proposed framework. We retrain the classifier for defect detection on the surface by using transfer learning. According to the accuracy on defect detection, we compare the relevant data extracted by Dataonomy™ from Image Net to retrain the Inception V3 with the method in [3][4] we can prove the effectiveness of our method for data augmentation and thus showing the possibility of our method to solve the problem of the limited dataset in deep learning based tasks.

Our experiment for retraining the Inception V3 using selected data from Image Net was running on the computer with four Ge Force GTX 1080 Ti graphics cards. With the use of transfer learning, the training of classifiers for defect detection on the surface was running on the computer with two Ge Force GTX 1080 Ti graphics cards.

iii. Experimental Results

a. Defect Image Detection for Texture Surface

500 classes of data are selected from ImageNet to train the base model, and the total time for training takes around 252 hours.

With the use of transfer learning, we take the retrained Inception V3 on the selected 500 classes from Image Net as our base network. We evaluate the performance of our approach for surface defect detection in terms of the true positive rate (TPR) and true negative rate (TNR). Equation 2 and Equation 3 define TPR and TNR, respectively.

$$\mathrm{TPR} = \mathrm{TP}(\mathrm{TP} + \mathrm{FN})^{-1} \quad (4)$$

$$\mathrm{TNR} = \mathrm{TN}(\mathrm{FP} + \mathrm{TN})^{-1} \quad (5)$$

Table 1 shows the performance of our framework compared to the state-of-art deep learning-based approach proposed in [16] with DAGM-2007. From the table, we can see that our method outperforms the others, and therefore shows the effectiveness of our proposed framework for the deep learning-based approach with limited data samples.

Table 1: Defect detection result (%).

No.	Weimer et al. [16]		Inception V3(Ours)	
	TPR	TNR	TPR	TNR
1	100	100	100	100
2	100	97.3	100	100
3	95.5	100	98.8	100
4	100	98.7	100	100
5	98.8	100	98.8	100
6	100	99.5	97	100
7	NA	NA	100	100
8	NA	NA	96.7	100
9	NA	NA	100	100
10	NA	NA	99.3	100

In addition, we also compared the accuracy of our method of defect detection with the work in [4] and [17]. The accuracy of our method with the pre-trained base model on Wood Dataset is 99.12%, compared with the build-in Inception V3, which is 97.7%. And the average accuracy of our method on the DAGM-2007 dataset is 99.88%. It can be seen that our framework using Dataonomy™ for data augmentation shows high performance on defect detection with a limited dataset compared to the state-of-the-art method.

b. *Defect Area Detection on Texture Surface*

The next step of our proposed framework is to highlight the defect area on the surface. Besides the dataset of DAGM-2007, we use the samples of the phone screen with scratches to validate our methods. Part of the result for the texture data in this step by using Inception V3 and FCN is shown in Figure 10 and Figure 11, showing a decent performance of our two methods.

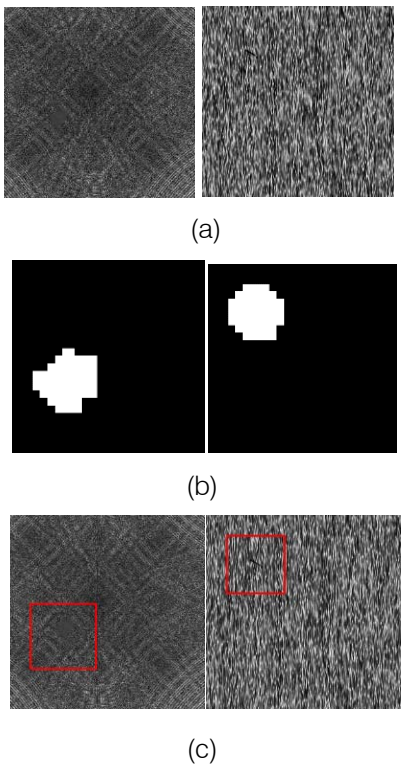


Figure 10: Inception V3: (a) DAGM-2007 Original Image (b) Mask Image (c) Highlighted Defect

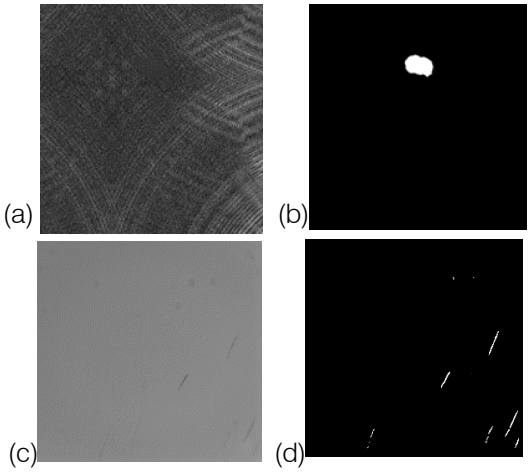


Figure 11: FCN: (a) DAGM-2007 Original Image (b)Result for DAGM-2007; (c) Phone Screen Original Image (d)Result for Phone Screen

b) Defect Cause Analysis

i. *Dataset for Root Cause Detection*

In order to evaluate our method, we created a new dataset for our root cause detection based on the DAGM-2007 dataset [15]. We chose all 1046 images which contain a common defect with the existing types of scratch defect independently on chosen images. In this case, we have 1046 training images for each scratch type and around 10,000 images in total. In order to simulate the systematic error, the added scratch is the same size and in the same position for each image. Figure 12 (a) and (b) are two examples with different systematic defects with the original defect from DAGM-2007.

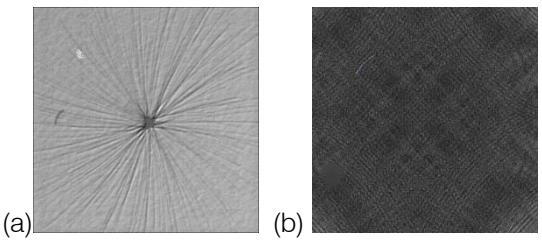


Figure 12: Example of 2 Types of Scratches

ii. *Experimental Results for Root Cause Detection*

Using the method in Sec. 3.1.3, we got common defect image for each type of scratch.

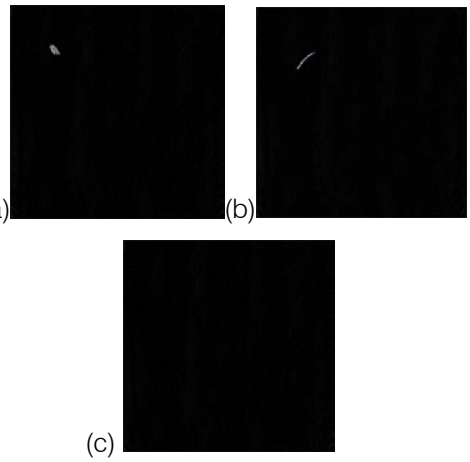


Figure 13: (a)(b) Results with Common Defect Detected; (c) Result with No Common Defect Detected

From Figure 13 (a) and (b), we can find out where the common defect is. This defect may come from the mechanical error in the product assembly line, which can cause a huge loss in production if not detected automatically.

Figure 13 (c) is the resultant image of the common defect detection for 1046 images with defects in the DAGM-2007 dataset [15]. Because there are random defects (scratches), the resultant image obtained by the generalized multi-image matting algorithm is a blank image.

This technique can also be used in other areas, such as troubleshooting in printing systems(Figure 14).We created a 500-large text defect dataset by adding the same ink defect at the same position of text images. image.

Using our root cause detection method, the resulting image Figure 14 (b) does detect those four ink defects in the original dataset (we reversed the colour for better notice). Therefore, in real life, we can know there is a problem in the printing system that causes a common defect using this method.

(a) (b)

Figure 14: (a) One of Original Text Defect Image; (b) Root Cause Detection Result

V. Conclusion

In this paper, we provided a novel algorithm named Dataonomy™ to improve the performance of the deep learning-based approach to detect product defects with limited data samples for training, which proved to be successful in our experiments. Also, the fully convolutional networks have been proved as effective end-to-end tools for defect segmentation. Detailed steps are provided regarding our approach for the tasks of defect image classification and defect detection. Besides that, a generalized multi-image matting algorithm was proposed to analyse defect cause and find defects associated with systematic errors and generated impressive results on our data. The well-designed and extensive experiments in this study verified the effectiveness of the proposed framework for surface defect inspection tasks.

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Global Journal of Science Frontier Research: I
Interdisciplinary
Volume 20 Issue 3 Version 1.0 Year 2020
Type: Double Blind Peer Reviewed International Research Journal
Publisher: Global Journals
Online ISSN: 2249-4626 & Print ISSN: 0975-5896

Anticovidian v.2 COVID-19: Hypothesis of the Lab Origin *Versus* a Zoonotic Event which can also be of a Lab Origin

By Fernando Castro-Chavez

Abstract- To treat the cause of a disease and not only its effects is of the utmost importance; hence, we need to know the origin of this pandemic of COVID-19, in order to be able, if possible, to prevent an event of such a nature and magnitude in the future, and to be able to avoid every sort of abuses to humanity, as it is happening right now. Bullet points here addressed are: 1) To have, inside the backbone of a virus from a bat (mostly ~97.55% of the viral RNA (by deducting the HIV inserts found by Perez, Montagnier and others), & as per the findings of Petrovsky, see below, and also to contrast the differences), the insertion similar to that of a pangolin virus for the Receptor Binding Domain (RBD, which basically consists of six separated key amino acids, or the 0.06% of its genome for these particular 18 nucleotides), being their receptor the ACE2 of the human lung, appearing at a time (as earlier as since September of 2019), were there were already mature all of the molecular methodologies necessary to modify individual nucleotides (Crispr-Cas9, "Seamless", etc.) that then modify at will the resulting amino acids, with the possibility to give an extra passage to the virus through ferrets (or other lab animals) that have an ACE2 very similar to the humans, to give it then a more "natural" appearance (by random trivial changes); because, had it been natural.

GJSFR-I Classification: *FOR Code: 060899*

Strictly as per the compliance and regulations of:

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Fernando Castro-Chavez

Abstract- To treat the cause of a disease and not only its effects is of the utmost importance; hence, we need to know the origin of this pandemic of COVID-19, in order to be able, if possible, to prevent an event of such a nature and magnitude in the future, and to be able to avoid every sort of abuses to humanity, as it is happening right now. Bullet points here addressed are: 1) To have, inside the backbone of a virus from a bat (mostly ~97.55% of the viral RNA (by deducting the HIV inserts found by Perez, Montagnier and others), & as per the findings of Petrovsky, see below, and also to contrast the differences), the insertion similar to that of a pangolin virus for the Receptor Binding Domain (RBD, which basically consists of six separated key amino acids, or the 0.06% of its genome for these particular 18 nucleotides), being their receptor the ACE2 of the human lung, appearing at a time (as earlier as since September of 2019), were there were already mature all of the molecular methodologies necessary to modify individual nucleotides (Crispr-Cas9, "Seamless", etc.) that then modify at will the resulting amino acids, with the possibility to give an extra passage to the virus through ferrets (or other lab animals) that have an ACE2 very similar to the humans, to give it then a more "natural" appearance (by random trivial changes); because, had it been natural, this could had required an animal host infected with these two viruses simultaneously, and that with an unexplainable marksmanship, to specifically modify the key six codons (and a second independent of such impossible recombinants, to give raise to the differences exclusively present at the end of the long Orf1ab, into the Nsf15 and Nsf16); 2) To have an even more important and unique peculiar site, PRRAR (encompassing the needed 12 bases to complete that sequence, being this the 0.04% of the full genome), for protease cleavage (new to Plasmin and Furin, plus Trypsin, TMRPSS2, etc.) inside the protein called Spike (S), to obtain the fragments S1 and S2 in order to allow the viral RNA to penetrate into the cell (expanding the range, not only to lung cells as the previous modification, but also to white and to neural cells), whose nucleotides producing it are highly strange to the rest of the viral sequence, because they contain more than an 83% of richness in its nucleotides GC, being these 12 nucleotides alien to the rest of the virus: CCUCGGCGGGCA (similar to bacterial and to methodological sequences patented by *Moderna, Inc.*, cleavable by restriction enzymes BsaJI, AciI, Cac8I, MnlI…), that are engrained to the three remaining bases: CGU present in the frame of the bat virus to complete the necessary sequence. This will require, either a third virus completely unknown until now, either in the same utopian animal described before, or through a second passage of the first chimera into another animal, and then that such viral beast, could also be able to target exclusively this region, and no other site whatsoever; then, it is explored, 3) The biggest shot in variation, when it is compared to the first sequence obtained of the virus of COVID-19, with its immediate ancestor, that according to Shi Zheng-Li is the RaTG13 (submitted *a posteriori* of the COVID-19 first sequence, and which researchers demonstrate that this is a partially made-up sequence (see below), having her deliberately ignored even to cite her previous identical reference called BtCoV/4991 (2016), or even her most recent reference of the same that she put under the name of SARSr-CoV Ra4991 (2019), being very dishonest for her to change in at least three identified times the names of her same sequence, actions that render her highly suspicious, because she hid the rest of the sequence at least during the last four year (having been obtained from excrement in a cave, she says, after a call due to a serious case of miners infected at Yunnan, and nobody knows still what was inside those at least six miners), but her publishing it until now, after the emergence of a similar virus, makes her highly suspicious, rather than making her look innocent; and, who can say that she did not manipulate as well artificially such sequence, or that the CCP Chinese military did not do the same to the other two previous sequences that are also somehow similar to Sars-CoV-2?, and how many more hundreds of sequences will they be hiding?, because nobody independently has been able to verify the accuracy of their claims, being everything based only in what they say), given that the nucleotides of six proteins exhibit a 99% of similitude between both sequences, while twelve of them go down to a 96% or even are below of this number, being the most extreme changes, the ones that are inside the sequence for the protein Spike, which while exhibiting a global similitude of 93%, is the one having the highest discrepancy between the two sequences, and within this same one there are extreme shorter variations, with a low similitude of 44% on that specific of the RBD mentioned before, which goes down to some 17% for the region of those 18 key bases, and of only the 20% percent for that sequence of 12 bases for the resulting protease cleavage site; other changes include the optimal nucleotides of an even shorter region of 16 segments similar to immunodeficiency genes (plus two more distant ones), and even a couple of concatenated *Plasmodium yoelii* found by Perez and Montagnier at the S2 place, all that could be better explained with artificial processes already in place to do this and more within the frame of the awful Gain-of-

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Global Journal of Science Frontier Research (I) Volume XX Issue III Version I Year 2020
9

Function sinister and dual-purpose (or double-talk) research. So, basically is their word against the world, and that is why since at least 2010 I have been proposing an independent verification by at least three other labs of results reported, specially by CCP Chinese researchers, as they did cost me already my first job in the US by their lying during at least ten years about a methodological artifact that I called "*Palindromati*", and that they kept on reporting as "natural", while receiving grants to explore a chimera, and how more is it costing their apparent lying about the artificial origin of COVID-19 at this time?) So, all of these points and so much more, because Jesse Morrell, for example, is reaching a set of almost 40 (and counting) evidences of a lab origin versus cero otherwise, things and persons that are leading us to conclude that it is evident to see that there was human intervention in the emergence of this Sars-CoV-2 virus, because in 2015-2018 there was not in existence any zoonotic history of any class in Wuhan, so, having been originated this virus already mature and fully capable to attack the human population, implies an artificial "injecting" source.

"…have no fellowship with the unfruitful works of DARKNESS, but rather expose them. For it is shameful even to speak of those things which are done by THEM in secret. But all things that are exposed are made manifest by the LIGHT..." *An inspired Paul in* Eph. 5:11-13.

Dedicated to Francis S. Collins, so as for the many to be able to see…

I. Introduction

A balanced set of voices is needed in this COVID-19 Pandemic, and such is the purpose of this work, to put the pros and the cons of every claim. I also want to make this presentation a personal one, as scientists tend to simulate an isolation of themselves from their own research, but at the end, they are still as human as anybody else and their personal bias and experiences always end up showing up. So, here we will be just another lonely human. Especially within this Pandemic that has tended to "dehumanize" humanity. So, here am I, back to the simplicity of what is meant to be "human" and with feelings. Three evidences in science are normally required to establish something as evident (Crombie, 1994). In this case, we will see three minimum reasons, and one more to give certain range of tolerance (plus another at the beginning, aimed at those with eyes to see), and this will be the determining factor in identifying if COVID-19 is artificial or otherwise, which will show prominently to the reader that this COVID-19 virus is of a human design. Currently, there are zero evidences in favor of the opposite view.

I hope that other scientists, especially all those honest virologists, immunologists, infectologists, epidemiologists, molecular biologists, human physicians (excluding those "inhuman"), veterinarians, etc., etc., are also doing this kind of vital work, as it is to "Define the origin" of this COVID-19 pandemic, which is mainly devastating morally the people of this planet (humans against humans), and needless to say, devastating the really infected victims (from all of those tainted statistics that we are all aware of).

It is necessary to know the truth in order to prevent something like this from happening again, and to prevent a recurrence in the course of the current pandemic, as there is still the slightest chance that more of the same pathogens will continue to be released with the purpose of "escalating" such crisis, which by all accounts has been designed globally, but with the final target of the USA. The fact that an official denial appears in all articles related to the human engineering of COVID-19, saying that: "There is no evidence of it", indeed speaks volumes about a deliberate attempt to silence the truth, as well as does the unrequested invasion of our privacy by the WHO in all social platform available on the internet, and the censorship by the same WHO under higher orders, of every posting or video that does not agree with the narrative that they pretend to impose over the whole of the human race.

Here, I present then, this minimal evidence that shows just the opposite: That "there is evidence" indeed of a lab-leak, and even further, of an even engineered virus as the most plausible explanation of the current malady, as if planned beforehand. This is presented for the free evaluation of the reader.

This work is also an attempt to help responding the most recent question posed in *Nature*, talking about the WIV of Zheng-Li Shi: "The lab does hold coronaviruses related to SARS-CoV-2, so it is possible that one could have escaped, perhaps if a lab worker accidentally became infected from a virus sample or animal in the facility and then passed it on to someone outside the facility. It is also theoretically possible that scientists at the lab tweaked the virus's genome for research purposes before it escaped, but, again, there is no evidence that they did. Shi declined to respond to *Nature*'s questions about her experiments, saying that she has been inundated with media requests" (Cyranoski. 2020) So, Shi, the main suspect in this story is declining to explain her research, however, in what she has published thus far there is vast evidence that COVID-19 may have been designed there at the WIV, evidence available for anybody willing to dig into her publications. This article wishes to help a little on that aspect.

II. Antecedents

Most recently, before the release of his second article on the subject, Birger Sørensen declared: "I think it's more than 90 percent certain. It's at least a far more probable explanation than it having developed this way in nature" (https://archive.vn/Wmj9p), there he also explains that the adulterations go beyond the attachment to the human ACE2 receptor (shown in my first point) and, it is within that spirit that I present my own current work. So, I

name this study "*Anticovidian v.2*" because it is in the line of my previous collective research into Antiobesity (Castro-Chavez *et al*., 2003) and Antiatherosclerosis (Castro-Chavez *et al*., 2013), where I also demonstrated, as I hope to do here, that a contaminating laboratory artifact had intruded on thousands of sequences present in the *Genbank* and even in the *Affimetrix* Microarrays (Castro-Chavez, 2012). In this viral case, a most basic antecedent I would like to emphasize as many have done, and this is the article by Baric & Zhengli (Zheng-Li) from 2015 (Menachery *et al*., 2015), published within the time in which Obama had advised a moratorium for such studies, moratorium which lasted in the US from 2014 to 2017, and in the end, it was when, Obama before leaving office indicated its reactivation, until the ban was finally lifted by Francis S. Collins (Morrell, 2020); however, in disregard of that ban, these authors managed to continuously publish their work, which again aroused an ethical conflict during that year (Akst, 2015), and as they continued doing *Gain-of-Function* research non-stop in Wuhan at UNC.

Basically, the experiment they carried out was to develop a super-coronavirus that was capable of killing elderly mice, a result that they do not present, as it would be expected, in the main text, but rather in a compound figure in their supplement (*Fig. 3b*), in which the complete death of elderly mice is observed on the fourth day (Menachery *et al*., 2015). In a recent interview to Baric, it was indicated that this murderous virus was "*found*", but the truth is that he, with Zheng-Li and one peer, plus his team, "designed" it, but absolutely not "*found*" it as it was deceivingly reported on 2020: https://www.wral.com/unc-researcher-found-deadly-virus-in-bats-in-china-in-2015/18913313/ (whose headline has been saved at https://archive.vn/DI2mT). But, just from the onset, you can start seeing that there is the desire by the seriously conflicted actors, for all of this to remain hidden or changed.

Remarkable in this Menachery *et al*. (2015) work is that two of the authors came from Wuhan, where the COVID-19 pandemic broke out, and that they are credited with having brought both the necessary plasmids, as well as the murderous version of the modified gene "Spike", key protein for viral entry into the human cells, and that Baric just now deposited its sequence MT308984: https://archive.vn/P5ay7

Now, it has been discovered that a handwritten version exists prior to the final version of this 2015 article by Baric for the journal *Nature Medicine* (now under Chinese control), and it was the first version format to be published by the NIH *PubMed*; what is noticeable about this previous version, is that it has two more and key methodological references that are not present in the final electronic version (Menachery *et al*., 2015). Art Bobroff, through the *Facebook*, indicates that the removal of those two key methodological references is a standard procedure in GoF research, so as to comply with the "*law*" pertaining to this kind of risky research; it may be so, but indeed those references are very telling.

The first is from 2005 and shows that the Spike protein site called the *Receptor Binding Domain* (RBD), was also very well known, focusing since then as well, only on the six key amino-acid contacts within the so-called then RBM, *Receptor Binding Motif*, currently known generically as RBD mostly due to Andersen *et al*. (2020), whose work has been multiple times debunked, such as in Stout (2020, thanks to Rubio for the reference), which is responsible for the attachment of the virus to the receptor of the lung cells called the ACE2; in addition, since then, the state of the underground molecular art allowed already something like single nucleotide changes to be made on individual nucleotides (already known, but later made into a CRISPR/Cas9-deaminase methodology: Shevidi *et al*. 2017), which in turn would modify the resulting amino acid, and in such article, its authors focus on modifying the key amino acids necessary to improve the RBD binding to the ACE2 (Qu *et al*., 2005), and even later, to other receptors, such as CD147.

The other experimental article omitted is from 2008, and is similar to the previous one, with the difference that it already begins to outline the final optimal amino acids for the RBD of COVID-19, because it defines that an artificial substitution of a Leucine for a Phenylalanine makes the union more solid between the RBD and the hACE2 receptor, and it is precisely with a Phenylalanine, as established in that article, that we finally find it, and in the same position, as relative to the RBD of COVID-19; so, as in the article it is an L472F change for the old Sars-CoV-1 (Sheahan *et al*., 2008), this corresponds to L486F in the case of the new Sars-CoV-2, as the COVID-19 virus is known (linking the name to China).

The importance of these finding is that it is not necessary to invoke a natural cross-linking in a fantastic animal intermediary that basically seems to be meant to never to be found, as to have obtained the new virus, through trial and error during all of these twenty years or so, that they were already doing tirelessly during that time, the needed work to experimentally obtain the best optimal combination in the real world as it is currently present in COVID-19 (and not necessarily a "*theoretical*" best).

And apart of these three basic antecedents (2005, 2008, 2015), and that's not all, as there are more as if when penetrating into *the rabbit hole* of Alice, but for reasons of time, I just like to mention an "*opinion*" piece (Andersen *et al*., 2020, also from the China controlled *Nature*, and with endless conflicts of interests, as it happens with all of those "*defending*" and covering-up against the right kind of research as to track its real origins), which is basically what has deliberately blinded the critical spirit of most scientists, and has been taken as "*the general consensus*", even though such article doesn't even solve anything and omits many of the basic and necessary

references. That article notes that the RBD of COVID-19 resembles more closely that of a pangolin virus, while the rest of the viral background is of a bat virus. It is this kind of non-granted opinions that has made "*people of science*" to "strive for politics", instead of looking at the evidence, because: What could have been the intermediary animal inside which the mentioned combination (of the backbone of the virus of the bat, with the precise RBD similar to that of a pangolin virus), and could that have been recombined in such a very punctual and targeted manner? So, the hypothesis without solution that they pose of a *mythological* or *utopian* "beast", which many lacking unfortunately of the needed critical spirit to do science, consider as if it were the last word, the final one, but which would require that two different viruses exchange information in a very precise and targeted way such as that performed in a lab, in one and the same animal in order to be true: The bat virus, recombining with the pangolin virus, so that, in an extremely incredible way, exclusively inserting the optimal site of the RBD from a "pangolin"-like virus (18 nucleotides within a total of approximately 29,903 for the complete sequence of the COVID-19, or just a 0.06% of the sequence); as if the pangolin virus had become embedded in a very localized way with no trace in any other place of its genome within the framework of the bat virus. A noncritical belief is required to think in such way, so as to be blindly convinced that the pangolin virus was so accurate as to transmit those 6 x 3 sites that are indeed distant or separated within the RBD region, aiming precisely at the proper targets towards the bat virus to optimize those 18 nucleotides at only their precise positions.

To end with these antecedents, I must say that this is not all, although this is what we are made to "*believe*" in an extremely simplistic way, by most of those who want to end this uncomfortable exploration of the true origins of the virus once and for all, uncomfortable because legally it would involve China so much as localized factions within the people of the USA, since the financing for the Chinese in Wuhan to continue working with these viruses came in part and during several deliveries, from the North American NIH (Mulraney & Owen, 2020), which sent 3.7 x 2 millions of dollars to Wuhan and more (Morrell, 2020), but this amount pales in comparison to what Gates delivered to "*buy*" the WHO in 2010 to establish "the decade of the vaccines" or of a "Digital" "vaccination," as he has called it, consisting of $ 10 billion dollars (Gates Foundation, 2010), being today Gates to sole biggest financier of the WHO once Trump decided to stop funding it. However, during that time of the year that COVID-19 was released (September 2019), the bats were asleep, hibernating, and no bats are sold in that, blamed first by the CCP with no previous investigation, and now destroyed, Wuhan wet-market, and the first three infected with COVID-19 had no contact with that market (Sirotkin & Sirotkin, 2020), plus there has been absolutely no transparency at all in any kind of delivery of results, but this is now old news because at this point, even the Chinese CCP acknowledges that there is no evidence that such market did anything at all to modify those sequences, making them lethal to old and to sick humans, as the excellent review appeared at the "*Bulleting of Atomic Scientists*" has just informed us (Leitenberg, 2020). But, I leave in your hands to explore all of that (if you can find it now that *Google* is modifying its algorithms to make sure the results of the thousands of serious researchers exploring the lab origin of COVID-19 are harder and harder to find, coupled this to the deletion of all sorts of evidence by China, from notebooks to databases, from actual samples to blocking and international inquiry team other than the WHO). However, since this work is rather molecular, I will be mostly focused on it.

But, before I start my analysis I must say that there is a third evidence, a still "unknown" source of the sequence in its precise nucleotides that are more than 80% GC rich (12-bases, or the 0.04% of the full viral genome), located in a key position, precisely at the activation site of the virus that is entering into the human cell, and the amino acid product from this sequence is called the Furin/Plasmin cleavage site (also cut by Trypsin, TMRPSS2: Serine protease transmembrane 2, etc.), which divides Spike (S) into two parts: S1 and S2, allowing the passage of the viral RNA into the human nuclei of the cells. For this site under consideration, which, in a very simplistic explanation, is concatenated to three nucleotides of the right end belonging to the bat virus backbone, and which produces the following amino acids that are divided by the said proteases: PRRAR (Andersen *et al*., 2020); and, this is the biggest smoking gun of artificiality, as we will see.

This would further complicate the simplistic view of those who seek to cover-up any investigation related to the artificial origins of the virus (most specially Daszak), since it would not only require the convergence of the same virus of the bat with the virus of that utopian pangolin that in some extraordinary way just hit the key sites of the RBD, but then, it will also require a supposed third virus totally unknown until now, which would also deliver those and precise (not a pretended erratic sequence), but a specific 12 bases in the exact place necessary to form the PRRAR site for the cleavage by Plasmin/Furin, and these twelve bases are also totally foreign to the rest of the virus, since they are, as mentioned, especially more than 80% rich in GC sequences, as it will also be seen in the results.

If it has already been investigated before, and demonstrated with clear evidence, that the most plausible conclusion is that also the 1977 H1N1 epidemic, amongst others, was due as well to the accidental escape of a virus (Rozo & Gronvall, 2015), why with not even a more compelling Reason it happened in the same way in this case that "*is devastating*" morally the planet; why then will we not ask to ourselves, at least the Ha of the lab origins hypothesis, being Ho its complement, as it will be seen and documented here.

So, please, dear reader, take mostly the useful for you, for your family and for your decisions that you could be able to find in this article, and please improve it, detail it, verify it, experiment with it, and most importantly, help humanity with the best of your abilities. We only live once and we really need to be awake and alert, in order to restrain the evils of this world and bring light to an endarkened world.

Hypotheses:

Ha: The Sars-CoV-2, virus of COVID-19, originated in a laboratory and was released from there.

Ho: The Sars-CoV-2, virus of COVID-19, originated in animals and from there it passed to humans.

III. Materials and Methods

The basic sequence of the first COVID-19 report will be used (noticing that the virus is currently changing): MN908947: https://www.ncbi.nlm.nih.gov/nuccore/MN908947, whose publication led to the temporary closure by the CCP of the laboratory in which the main causal agent of COVID-19, called, as said, Sars-CoV-2, was first sequenced (Pinghui, 2020; we read: "The laboratory at the Shanghai Public Health Clinical Centre was ordered to close for "*rectification*" on January 12, a day after Professor Zhang Yongzhen's team published the genome sequence on open platforms"). From that moment, the endless sending of sequences that continues to arrive daily was unleashed, showing that COVID-19 continues to vary in a mostly punctual way, in one or two significant nucleotides at a time, or by losing strands of contiguous nucleotides, mostly on those areas that seem to have been modified by hand (Perez & Montagnier, 2020), bringing to-date endless variants from all over the world, and this in fact will continue to increase without restrictions as the time moves on.

Then, this sequence of COVID-19 will be compared with the suspicious sequence that Zheng-Li later sent (the RaTG13: MN996532), but in the case of it, supposedly from bat feces, she says, that it is "*the sequence*" of a sample collected since 2013, but which had not been fully revealed until this year of 2020 (and it will be seen that a part of it, apparently, already had been presented years before, using two different names); this, and the expert and ongoing input of multiple molecular biologists that have discovered three anomalous things of it, are: *1*) That the normal 5:1 synonymous to non-synonymous changes or "*mutations*" is not respected when we compare these last mentioned two sequences (MN908947 versus *MN996532*), reaching even the unreal ratio of 44:1, which basically demonstrates, as "*Nerd*" has said, its origins mostly from the keyboard of Zheng-Li, and this is how Nerd Has Power[1] (NHP, 2020) quotes this: "*…for the same S2 region, between the Wuhan coronavirus and RaTG13, there are a total of 90 nucleotide changes and only two amino acid mutations. Here, every 45 nucleotide changes correspond to one amino acid change. The synonymous/non-synonymous ratio is 44:1*"; *2*) the structural E protein had no changes in nucleotides between it and two of its ancestors, while currently, that same E is mutating at a normal rate within the human population, and again, this is how NHP puts this: "*What is inconsistent with this trait is the fact that ZC45/ZXC21 and the Wuhan coronavirus, while significantly distant from each other in evolution, share 100% identity in E proteins. Again, in no way this could be a result of natural evolution. This further supports the claim that the Wuhan coronavirus is made in a lab by following ZC45/ZXC21 [My note: both sequences were published by the "Institute of Military Medicine Nanjing Command", so, even those can be already modified as there is no way for the free word to independently verify the molecular claims of the CCP, something that must change from now on] as a template… on the amino acid level, E protein of the Wuhan coronavirus (Sars-CoV-2) identified at the beginning of the outbreak is 100% identical to those of the suspected templates, ZC45 [My note: MG772934, updated in 05-FEB-2020 without changing its version number to indicate that it had changed; the original article describing it was published online on the 2018 of Sep. the 12th) and ZXC21 (MG772844 to MG772932, partials for both sequences: 28-MAR-2018, not yet modified or tampered with as seen in the 05/20/2020; however, already modified is the MG772933: complete sequence, also updated on the 05-FEB-2020, but again without them changing its version number either]... What is striking is that, after a short two-months spread of the virus in humans, the E protein is already mutating. Sequence data obtained within the month of April indicate that mutations (in Sars-CoV-2) have occurred to four different locations... Note that the E protein makes very limited interactions with host proteins and thus is not under evolutionary pressure to adapt to a new host. Not only the E protein can tolerate mutations but also its mutational rate is held constant across different coronavirus species. The fact that the E protein of the Wuhan coronaviruses is already mutating in the short period of human-to-human transmission is consistent with its evolutionary feature. In stark contrast, while ZC45/ZXC21 and the Wuhan coronavirus are more distant evolutionarily, the E proteins within them are 100% identical. In no way this could be a result of natural evolution*"!!!; *3*) there seems to be no way that anybody else other than Zheng-Li, or the *Command* for the other sequences, could independently verify them by extracting from the same "*bat*" excrement the viral RNA; very questionable aspects are those three and more…: RaTG13:

[1] Thanks to Marie Ovensmith for pointing out to such fascinating site consecutively filled with new information.

MN996532: https://archive.vn/k1JtZ, https://www.ncbi.nlm.nih.gov/nuccore/1802633852. So, after all of these warnings about the putative and well documented suspicious nature of RaTG13 (Lin & Chen, 2020), I proceed.
To compare these sequences in the simplest way as possible, I will be using, both the standard BLAST: https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Nucleotides, as well as the one that also compares only two sequences: https://blast.ncbi.nlm.nih.gov/Blast.cgi?BLAST_SPEC=blast2seq.

In the last Appendix, as easy to find references for further research, I include the matches of the sequence CCTCGGCGGGCACGT to sequences of bacteria, hence the probability of it being from bacteria.

IV. Results

The next three basic evidences, plus that one of the "no-zoonotic-event" previous at Wuhan, whose reference will be given below, will be showing that the COVID-19 virus is an artificial piece of work:

1

Evidence number one is that the site of the RBD, that has a greater similarity with that of the pangolin virus, could also have been obtained in the laboratory in a more defined way through the trial and error of the single nucleotide modification to change one amino acid at a time (Bolotin *et al*., 2005) until obtaining the six key amino acids for the optimal binding of the RBD to the ACE2 receptor of human lung cells, especially when there is a described history that since 2005 at least (or even earlier), there were already techniques to make individual nucleotide changes to also change their resulting amino acids, as demonstrated by the two key articles removed by Baric and by Zhengli (Qu *et al.*, 2005 and Sheahan *et al.*, 2008).
Below is the segment that contains the bases to produce the six key amino acids for binding to the human ACE2 receptor (here, TTG-TTT-CAATCA-AAT-TAC shown in larger sizes, underlined and hollow):

TTGTTTAGGAAGTCTAATCTCAAACCTTTTGAGAGAGATATTTCAACTGAAATCTATCAGGCCGGTAGCACACC
TTGTAATGGTGTTGAAGGTTTTAATTGTTACTTTCCTTTACAATCATATGGTTTCCAACCCACTAATGGTGTT
GGTTAC

Being this in a stretch of 153 bases (from positions 22,925 to 23,077 of the sequence MN908947); these key 18 nucleotides (only 0.06% of the full sequence) are translated respectively into the amino acids: L + F + QS + N + Y, putting here the "F" mentioned in the antecedents in bold, as it had been already optimized by hand in the laboratory. The previous version of Sars-CoV-1, in such position had an "*L*".

Here, it is unlikely that a pangolin virus would have succeeded in only modifying those six places and nothing more within the framework of the bat virus. However, scientists with big conflicts of interest regarding this kind of research are the foremost ones clinging the most into trying to convince other scientists that this very same fantasy could have been "*possible*".

It will prevent us from the continuous hitting our heads against the wall, to realize that it is easier to deliberately obtain in a lab the localized fragments of those 6 x 3 nucleotides, each with the necessary changes, instead of trying to find a mythological animal *mediator*, which most likely does not even exist. And, I was saying that in 2018, zoonotic tests were carried out in Wuhan, as even I mentioned this in the summary, and no foreign virus was found in the humans evaluated, a work precisely done by Zheng-Li, (Wang *et al*., 2018), using samples from 2015. If a pre-COVID-19 strain had already been around, which should have been the "necessary" natural step for the so aggressive emergence that COVID-19 has shown from the start, at that time in 2018 it could have been detected, but nothing strange was observed back then in Wuhan, but on the contrary, the current COVID-19 appeared *out-of-nowhere* (if it were not from the lab), already and completely "mature", which is an impossible for zoonotic infections, because these leave traces of their history: unless that "zoonotic event" happened at close doors in animals within a lab!; that's it!, they then leave their previous consecutive versions of the virus in the same lab, as the virus is gradually changing over time to get to the point of maximum infectivity (Han, Kramer & Drake, 2016), process that under normal conditions, takes a long time during which time it leaves clear evidences of its previous versions. COVID-19 lacks of its normal and natural ancestry history.

This in itself is already a strong reason to think that this COVID-19 virus was deliberately, or at the least, *mistakenly* released (but then, if the *mistaken* lab release theory is entertained, here it will not match the out-of-this-world insistence of the likes of Gates that are pushing hard a "*mandate*" for an universal vaccination with their *ID2020* included, which he calls the "*Digitization*", meaning the electronic tagging of humanity, and he also calls it: The "*Digital Certificate of Vaccination*"); so, we are dealing with a virus free to be already in an optimal state to directly attack humans, having so emerged "mature" from the laboratory that designed it.

Regarding this point, Dr. Alberto Rubio-Casillas found references of a time when, trying to increase the compatibility between the virus's RBD and the mice's ACE2 receptor, Baric indicates once again that all the technology was already available and in-place to modify each viral amino acid at will, as it says (with my words and my emphasis): "However, the SRBD (the Spike protein receptor binding domain) of the bat was POORLY REPLICATED *in vivo*, requiring ADDITIONAL MODIFICATIONS to facilitate studies in mouse models ", and also expresses something even more disturbing, since Baric says:" Both SARS-CoV and Bat-SRBD (the same mentioned before) were EFFICIENTLY REPLICATED (the opposite of the above) in HAE cultures (human airways epithelial cells), providing a human model of the airways… ". Furthermore, questioning the efficacy of those *ideal* computational models when compared with the optimal and real sequence, after the practical experimentation, Baric says (thereby Baric is himself contradicting that biased conclusions reached beforehand by the China biotech owned Andersen *et al*., 2020): "Although the modeling predicts that Y436H (substituting an amino acid "Y" with one "H") increases that RBD-mACE2's stay-jointed phase ("*engagement*" he says), both SARS-CoV (WITHOUT that Y436H change) and MA15 (WITH that Y436H change) they both replicate efficiently in the lungs of the mouse…" (Becker *et al*., 2008); meaning that this change does NOT make any difference at all in the REAL world, although theoretically, in the FANTASY world of modeling, according to that computational "*model*", it seemed to be or to do so.

The update of this point is that in another work, the same that we have observed here was also concluded, and this is: That the similarity between the RBD of COVID-19 and that of the RBD of the pangolin virus (pangolin-CoV, P2V / 2017), is just a casual and a fortuitous similarity (Lam *et al.*, 2020).

Furthermore, another region different and independent from the previous one, makes researcher Yuri Deigin (2020)[2] to think that this is another independent case, since Deigin says: "*Orf1ab is also a phylogenetic mess in CoV2: Orf1a is closer to RaTG13, but Orf1b is closer to pangolin-2019 (MP789)*", another suspicious sequence that should be possible to independently extract and analyze in at least three independent labs; so, given the affinity of this region with another sequence of another pangolin virus for this other region (ORf1ab), we see evidence of another of possible multiple additional "*seamless*" manual interventions (see below), all of them performed in a laboratory.

And here, to say something about a possible treatment, I have to point out that Ho *et al*. (2007) suggested an amount of 10 μg/mL to inhibit the interaction of the SARS-CoV protein S with the human ACE2 receptor by using extracts of an anthraquinone compound derived from *Rheum officinale* and of *Polygonum multiflorum* (commercially called "*Emodin*"). The most natural the remedy, the best!

Pros of this result

This is a simple and direct explanation, of which there are at least these three references, and there should be more, being two of them cited as evidence, and later removed by Baric and by Zheng-Li, who here signs as Zhengli-Li (Menachery *et al*., 2015), for their one final version of 2015, in which we see that this was precisely what was going on with the artificial and targeted modifying of the RBD region *in vitro*.

Cons of this result

No notebooks or logs have been released to corroborate that this took place in a laboratory, but we have evidence that the Chinese Communist Party (CCP) ordered the disappearance of all the compromising documents from the Wuhan's lab (Sirotkin & Sirotkin, 2020; https://archive.vn/YPwSy, https://archive.vn/58Vo9, Leitenberg, 2020, etc.), since it even censured any publication that, coming out of China, attempted to inquire objectively on the origin of the COVID-19 virus (Feng, 2020; Observer, 2020), but we hope that somewhere, within somebody, there is still some truth left other than the evident truth that is still seen in plain sight for every honest researcher to explore. "Whistleblowers Arise!" And I make my own the same request (Deigin: https://www.youtube.com/watch?v=q5SRrsr-lug).

Here, the human aspect that I want to emphasize is the next one:

[2] Thanks to Alice Kopel for initially sending me the link to the intriguing and interesting article by Yuri Deigin.

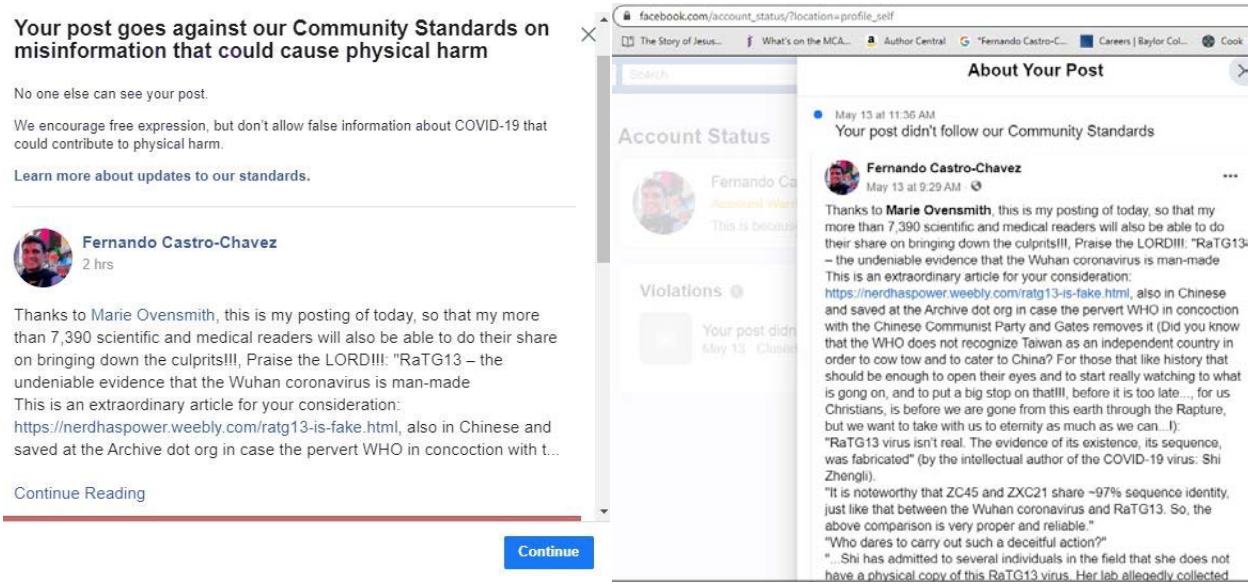


Figure 1: Facebook removed my post (05/12/2020, 11:36 AM), where I recount the research done at: https://nerdhaspower.weebly.com/ratg13-is-fake.html (here remembering the boldness of whistleblower Li-Meng Yan, who defected into the USA to speak-out about the deliberate design and release of COVID-19 by the CCP, but as innumerable others, she has been silenced), nothing health-related here but just the evidence that COVID-19 seems to be engineered at its roots, so they, as if we were already living in communist China, just removed it!!! I ask them to review their decision, and they confirmed for a second time that such post should remain out of the view of the public!!!, and that without giving any reason for it ; that censorship is not healthy and is indicative of a very sinister agenda going on; even when the very same information is here, reaching the 11,700 mark: https://www.researchgate.net/post/Third_Sequence_COVID-19_AATGGTACTAAGAGG_HIV-1_isolate_1966324H9_from_Netherlands_envelope_glycoprotein_env_gene_sequence_ID_GU4555031; so, basically *Facebook*, for some hidden reason, does NOT want you to uncover the real truth about the origin of COVID-19!!! Talk about communist China right here in the "*free world*"!!! It is documented that the CCP of China censored every publication related to COVID-19 coming out of that country: "One of the official documents of the Communist Party obtained by "*New News*" is the heavy red-headed document "*No. 3 Document*" issued by the *National Health and Health Commission* on January 3. This full name "*Notice on Strengthening the Management of Biological Sample Resources and Related Scientific Research Activities in the Prevention and Control of Major Emergent Infectious Diseases*" was not published on the official website." And it says in its point number two: "2. *Without approval, it is not allowed to provide biological samples and related information to other institutions and individuals*": https://project-evidence.github.io/, https://archive.vn/GFlkC.

2

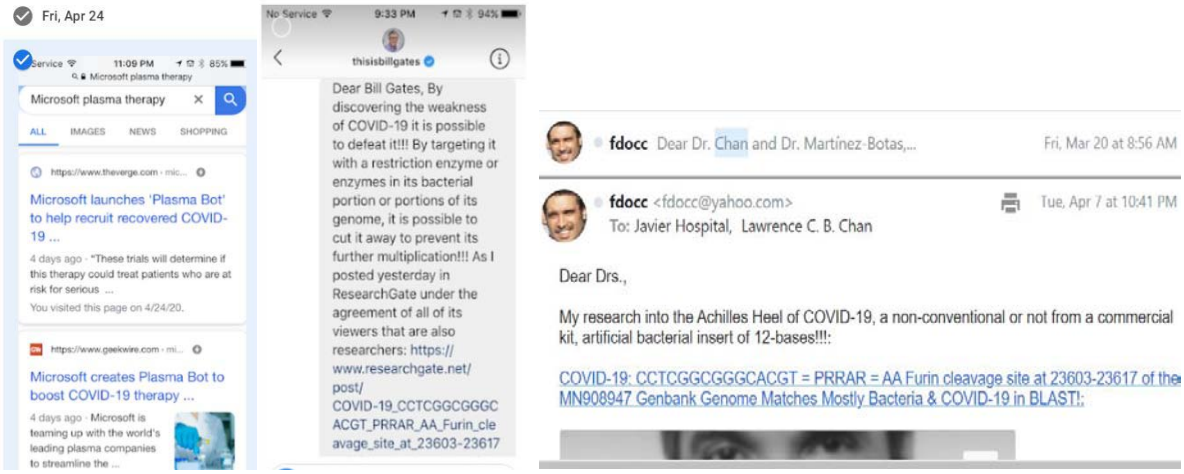
The 12 nucleotide bases, CCTCGGCGGGCACGT, which when translated will generate the PRRAR Furin/Plasmin cleavage site, constitute a location that is even more important than the previous point due to expanding its cellular reach, and are as follows, being the inserted ones, the ones that are hollow:

The last three bases: "CGT", belong to the framework of the bat virus, and the 12 previous bases still to-date are an insertion of "unknown" origin, even when *a posteriori* attempts have been attempted, as to produce some rare sequence in an attempt to justify its "natural" existence, the complete construct being located at positions 23603 to 23617 of the full sequence MN908947; and at the left of it, there is a set of another 12 bases producing: QTNTS, one that was detected by an Indian team as significant in 3-D due to its resemblance to the HIV-1 (Pradhan *et al*., 2020), and also important because part of it, including the two previous amino acids "QT", to integrate a QTQTN peptide, is easily disappearing from Sars-CoV-2 (Liu *et al*., 2020), a possible indicative of its artificial nature, because, as wisely predicted: Whatever is breaking the natural harmony of the code, that tends to fall off from it (Perez & Montagnier, 2020), because other regions are also being naturally deleted, such as 382-nt from Orf8!!! (Su

et al., 2020), and one more of 81-nt in Orf7a, so these and more possible deletions to come, "*may potentially reduce virus fitness*" (LaRinda *et al*., 2020). Also Christian F. Zilch has posted this concept in my pertinent researches at the *Research Gate*, so here I want to thank him.

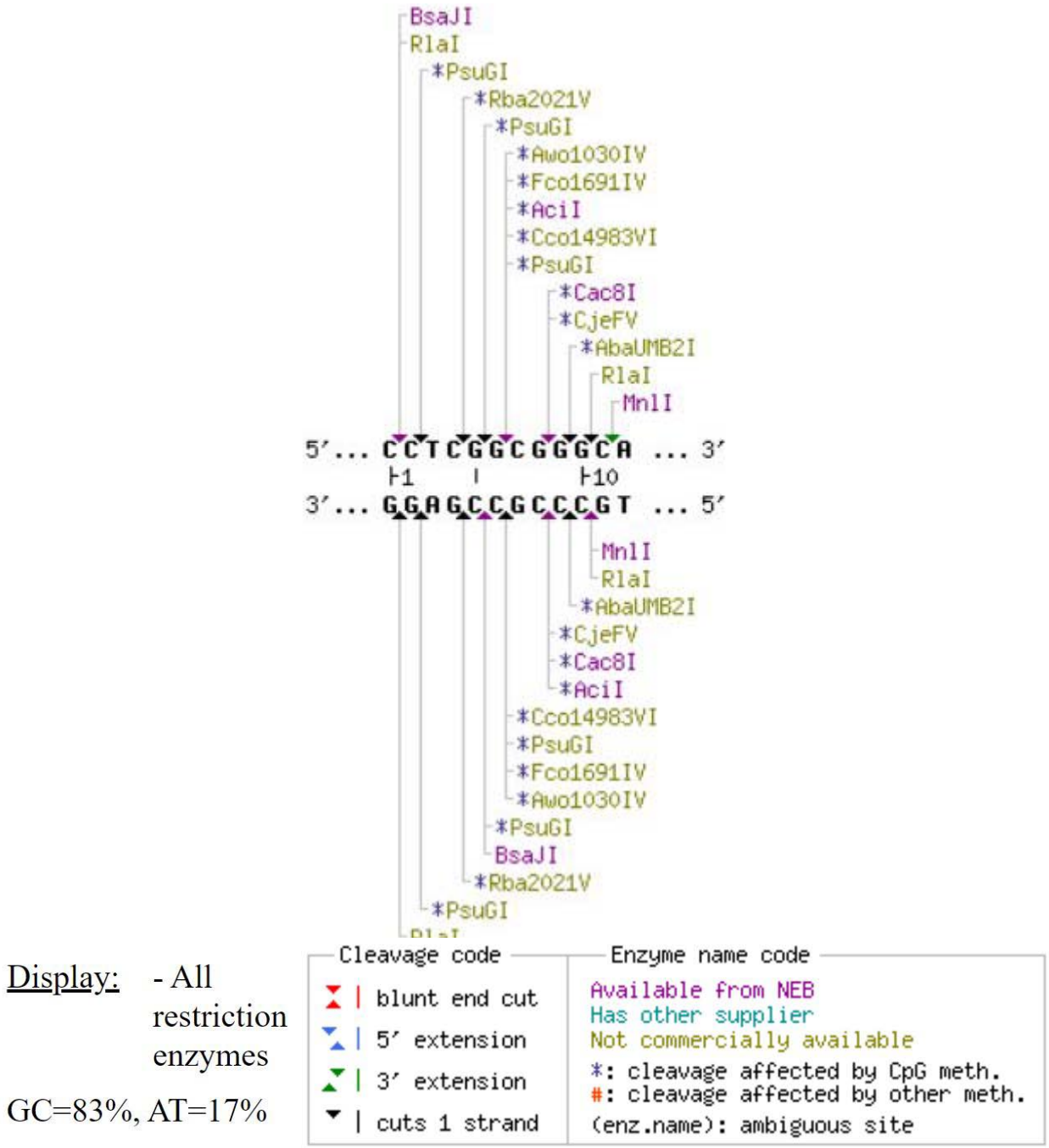
But, the important sequence here of 12-bases: CCTCGGCGGGCA, when using *Blast*, finds homologies mainly with bacteria (see Appendix C); and just one example of the multiple bacteria that align to this sequence is the following: *Pseudomonas monteilii* (CP043395), which is Gram-negative, isolated from the human bronchi.[3]

And, because this sequence is a match for several bacterial sequences, it has at least four known restriction enzyme sites (and I wrote to Gates (my writing was backed up until the 04/24/20, just before I deleted him from my list of acquaintances at the *Instagram*, saying that because he was not an MD, he was making himself as if he were an MD, telling everybody that human "digitization" should take place using himself the criminal "excuse" of COVID-19!), and I also wrote to my first PI and to my first Adviser (04/7/20), but none of them responded). The way these enzymes cut, by using the next tool, is as follows: http://nc2.neb.com/NEBcutter2/cutshow.php?name=9a3a52e2-Games-Over-Billy (saved at: https://archive.vn/0jfXr; see below part of the writings that I did to Gates, and to my PI and to my aide):



Next, you will see 14 restriction sites, cut by the enzymes BsaJI, AciI, Cac8I, MnlI, R1aI (cutting in two sites), PsuGI, Rba2021V, PsuGI, Awo1030IV, Fco169iv, Cco14983VI, PsuGI, CjeFV, AbaUMB2I (Deigin Tweeted another one: FAUL, that cuts just at the margins of this sequence, when I verified it, I saw this cutting at: 5'-TCCTCGGCGG / GCACGT, above, and at CAGACTAATT / C-3', below, according to the restrictionmapper.org), and all of them are able to cut into different regions of these 12-bases: CCTCGGCGGGCA, which has inspired a possible enzymatic method to swiftly treat such COVID-19 disease (and basically, any other kind of respiratory viral transmissible disease):

[3] Check, if desired, its translation from nucleotides to proteins, as they may be outside of the proper reading frame: https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastx (See Appendix C for a 100 more sequences).



Compared with this ones, other two short sites, are only cut by six enzymes: 1) One from COVID-15 made by 15-bases: AATGGTACTAAGAGG producing the amino acids NGTKR, and 2) One non-COVID-19 contaminant site: CCCGAATTCGGG (Castro-Chavez, 2012), showing this that the selection of a site able to be cut by 14 enzymes, was a deliberate way to have an easy way to track its presence or its removal.

So, for this 12-base molecular site, to-date, there is not an official explanation; for example, Andersen *et al*. (2020) left blank any explanation for the possible origin of this insertion (they do not even bother to put any argument about its existence, they just totally ignored the issue!); however, a couple of researchers have made interesting proposals, namely:

a) When only the database of viruses is scanned (as Dr. Tom Wenseleers, from KU Leuven, did), three results are obtained, one of which is MN729215, corresponding to an atypical porcine Pestivirus, but its reading frame is indeed out; that is, it has a reading frame of: ACC TCG GCG GGC AAT = TSAGN, in addition to the fact that the nucleotides that flank the sequence of interest are different; so, this apparent similarity seems to be something fortuitous, just like the one of the viruses from pangolins described in the previous point.

But, the utopian implications based solely on the possibility of finding a virus containing exactly the desired sequence capable of generating, in its precise reading frame, the desired series of amino acids that produce the PRRAR sequence for an analogous function, in the case of the COVID-19 "theory" of its "*natural*" origin, is that a fantastic intermediary could have been, whether a pig (and these domestic animals have been used by Zheng-Li: https://archive.vn/YPwSy), or even a sheep, or any other animal, within which one of its viruses recombined with the virus already modified from the previous point, and again, in a highly improbable way, only delivering the 12-bases under consideration, without contributing absolutely nothing else (so, only contributing those 12 nucleotides delivered by insertion, out of the 29,903 nucleotides that make up the total genome of the virus; that is, a 0.04% of the sequence), and having done all of this, supposedly, even before attacking the human being, which, because there are no other remains or traces of any of these other viruses within this chimeric sequence, it is practically impossible, as at this point of our discussion the virus "*supposedly*" already carries the inserts of at least three different viruses: backbone from a bat virus, RBD similar to a pangolin virus, and a 12-bases insert of "unknown" origin; also this sequence, in its analysis, was also similar to: MN331655, belonging to a Parapoxvirus that attacks domestic ungulates (check its reading frame).

On the other hand, if the sequence is from a phage (and the coincidence of these twelve bases is also found in the Phage *Settecandela* of a mycobacterium, sequence MT114163, also found by the last mentioned researcher (again, check its reading frame); and here, in Zheng-Li's case, she used both phages for her famous or infamous 2015 GoF article (Menachery *et al*., 2015), where she says: "*Fm6, an antibody generated by phage display*…"), and also she has used bacteria (saying: "*Construction of infectious bacterial artificial chromosome (BAC) clones of WIV1*", in Zeng *et al*., 2016), which is the most abundant homology, regarding the amount of similar sequences from multiple bacteria (see below), that I was able to find; this would indicate, even more clearly, the provenance of a methodological tool in the somehow sloppy, as per the multiple testimonies of the lack of security measures within that lab, molecular work carried out at the WIV lab at Wuhan, as will be also seen in the following finding:

b) When only the *patents* database is explored, mainly those that contribute to methodological aspects of the molecular biology (as Dr. Leopoldo Naranjo-Briceño, from the ICGEB discovered), and one of the multiple sequences that caught most his attention, is the following one, and there are many other and abundant variants to consider here, as per the number of matching patented sequences: MA673485: Polynucleotides modified for protein production (located in the complementary chain, in the form of: ACGTGCCCGCCGAGG, in positions 139 to 153; and again, check please its reading frame), sent precisely by *Moderna Inc.*, one of the companies sponsored by Bill Gates, a sequence sent to the *Genbank* since 2012, but with 26 updates, plus two more done in the 2017 (which means, works of a practical trial and error are being done, such as we mentioned that it was also that, the strategy used to optimize the RBD of COVID-19, and this scenario seems to be more likely, since the virus of COVID-19 appeared already fully mature overnight to harm human beings, without any transitory states that clearly showed its "adaptation" or "evolution").

The simplest and most logical conclusion is that this GC=83.33%, Guanine and Cytosine-rich insert of 12-bases, was deliberately added in the laboratory, and this would solve a whole paradox that otherwise is practically impossible to address. The complete genome of the Sars-CoV-2 diverges: GC=38%, AT=62%.

The update here, is that these 12-bases appear to be optimized, not only for the penetration of the virus into the cell, but also to give more stability to its RNA, which also helps the virus to multiply once it is inside of the cell; which is further evidence that COVID-19 has been carefully designed in a laboratory (Manzourolajdad, Xu & Ebrahimi, 2020). In addition, the aforementioned Russian researcher Yuri Deigin recommends paying close attention to that QTQTNS sequence, also mentioned above in part, a sequence that is common in the COVID-19 virus and in the RaTG13, which is found on the left side of these new PRRA amino acids. This would also be another indication that the RaTG13 sequence is an earlier stage of a laboratory modification out of another yet unknown sequence. That is, if they have not been destroyed, more gradual versions could be found in the Zheng-Li laboratory, both prior to RaTG13, as well as intermediate versions between RaTG13 and the new Sars-CoV-2 virus, since the change seems to be very abrupt, and does not correspond to what would be gradually seen in a zoonotic jump. The last update of this issue is that BetaCoV/Rm/Yunnan/YN02/2019 (RmYN02), appeared as it did the RaTG13, it was *a posteriori* surprise in the literature, and this time this mysterious sequence is being kept under wraps; is claimed by its publishers to contain the sequence PAAR, that they put as P-AAR (missing in the void dash: "-", an amino acid, which corresponds to three nucleotides: to 3 NTs missing), this as to make it seem as closer as possible to the PRRAR, but it is just a bad sequence that is miss-aligned, as even in their figure it jumps four empty bases in the left side, those precisely of the QTQT sequence (which is also a set of 12-nt); so, other than being completely out of frame, that sequence is not a protease cleavage site at all (Zhou *et al*., 2020), and also, to make things as hard as possible to find, as usual in the case when somebody is hiding something, EPI_ISL_412977, which is the data of the very same sequence (https://covid19.cpmbiodev.net/covid19/cov19strain.php), says, again playing themselves the

forbidden game of the name-change in professional work (but apparently not in sloppy research): bat/Yunnan/RmYN02/2019, location: Xishuangbanna, Date_submitted: 02/03/2020, etc. (brought to you by the same people that did the infamous Andersen *et al*. (2020) cover-up opinion piece, but with this sequence not yet available at the *Genbank* as per today (06/13/2020); so, it just seems that the most suspicious researchers of having been involved in the release of COVID-19, themselves are entering into the very delicate realm of the even more "*secretive science*", because, what other explanation they can give to the "*secrecy*" that they are aiming at now?, they are following the "*Event 201*" directives of a "*centralized*" location to keep under wraps, to keep under their control their own deceit, and we need also to oppose to that with all of our strength!!!; so this is, as per today, the *Gis-NO-aid*, just another crappy and unnecessary "*institution*" aimed at the control of the genetic information, and then, to the subsequent ensuing oppression of humanity, in this case of the scientific portion of it, saying whatever they may want to say with no accountability whatsoever).

Nerd Has Power (2020) has suggested that this RaTG13 is mostly fake, as reported in Materials and Methods, that it is a keyboard originated sequence, without any possible and independent validation, and that it was taken from a blend of the earlier military Chinese sequences (hence, also possibly already "*worked*" these two sequences as well in a lab, until an independent group is able to verify all of them, a task that right now for me is par to impossible): ZC45 (MG772933) and ZXC21 (MG772934).

And, as everything within the sequence of COVID-19 can be performed in a laboratory, also the addition of a protease site such as the one that we are discussing here was completely at hand to be performed in a laboratory, reason why J. J. (Jay) Couey from Neurology at the U. of Pittsburgh, indicates that when virologists and other conflicted in their interests individuals say that we humans: "could have never done this virus", they are being completely disingenuous: https://www.youtube.com/watch?v=2DlBJ-xns5k, so, Alberto Rubio-Casillas (who also reviews the issue: https://archive.vn/wip/OlMKf) reminded me of this article that says: "an important role of R797 (which is exactly equivalent to the last "R" in our sequence under consideration: PRAAR) cleavage site has been shown by artificially inserting a furin cleavage site, which resulted in the production of cleaved spike glycoprotein pseudotype, and allowed the infection of cells in the presence of protease inhibitors"; even in the presence of "protease inhibitors"(Kim *et al*., 2009); so, that terrible virus was able to attack! So, if a secondary lab was already doing that, what do you think that was going on in the highly competitive labs of Baric and of Zheng-Li, the two "mother-loaders" of engineered viruses in the planet?

And, as more recently also Alberto Rubio-Casillas pointed out to me, they even have the electronic tools online to test the best sites of cleavage, so as said time after time, the tools to design from scratch a COVID-19 virus and a pandemic are all out there to try the best and most dangerous sequences, even by trial and error: https://web.expasy.org/peptide_cutter and http://www.cbs.dtu.dk/services/ProP, taken from an article that in itself demonstrates that all the theory to design an artificial PRRAR was already there for a while: Yamada & Liu (2009), or like Watanabe *et al*. (2008) proposing the site KRRKR, as well as the RRKR cleavage site (Cheng *et al*., 2019); so, *voilá*, we have the optimized synthetic site for the COVID-19 infection just by using those online tools, originated in China, with the needed knowledge taken from all of those previous articles! Even when Anderson *et al*. (2020) insinuated that nobody had a functional idea of it!

Some of the preventive specific therapeutic alternatives suggested for this portion, can be seen in the interesting article by Wu *et al*. (2020a), among which, the next ones stand out:

Folic Acid (avocado, green leafy vegetables, such as: spinach, turnip greens (*rapini* plant), cabbages, lettuce; fruits, such as citrus, melon or banana, legumes (beans, lima beans, peas, chickpeas, soy, lentils, etc.), meat (especially liver and kidney), whole grains, milk and eggs, nuts, etc.);

Folinic Acid (It is found in the entrails of animals (such as in the Mexican plate called "*Menudo*"), in green leafy vegetables, legumes, brewer's yeast, and in nuts and in whole grains, such as almonds.);

L-arginine (it is present in nuts such as raisins, walnuts, peanuts and almonds, and in seeds (sesame, pumpkin, sunflower, etc.), also in eggs, spirulina algae, and chocolate…!);

Glutathione (In spinach, watermelon, grapefruit, asparagus, avocado, strawberries, squash, broccoli, cauliflower, walnuts, garlic, tomatoes...), etc.

V. Pros of this Result

In favor of this conclusion, there is the fact that this is a sequence of twelve bases that does not fit with the rest of the virus at all, due to the high concentration of Guanine and of Cytosine (more than 80%), and that there is no explanation for its origin from any other virus, which if in *utopia* intersected with the Sars-CoV-2, it would also have left multiple traces in other places of the virus and not only having left these twelve bases alone by themselves, unless this was done within a laboratory. If it came from a phage, or more specifically from a bacterium, it would be

the product of the methodologies used, being this the most adequate fragment inserted artificially in the laboratory in that precise location, with the end to achieve viral penetration into the human cells of that viral RNA; and even more compelling could be those patented sequences for the design of peptides by the company "*Moderna Inc.*", which is financed by Bill Gates, containing precisely these 12-bases in their complementary chain.

VI. Cons of this Result

Against this conclusion, again, we have that we do not have a signed document at hand saying that they did it in this way, because the CCP Chinese communist government has not allowed anyone to review any lab blog of Wuhan, as to find the explanation on how this sequence got to this place of the virus. Only Wuhan Sars-CoV virus researcher Zheng-Li Shi herself says that it does not correspond to her sequences; but how credible is to ask to the main suspect whether or not she did it? (And she said this after she was concerned and sleepless that it may indeed have escaped from her lab…).
The human aspect to be pointed out here is the next one:

Figure 2: When in China, I was able to transmit some of my photos from the beautiful Guangzhou airport through the *Facebook* (07/13/2019) with the use of the *CyberGhost* VPN, because in the Communist China it is forbidden to use *Facebook* and *Google*. Just to realize that less than a year later (as Fig. 1 shows), *Facebook* itself will be behaving just exactly like the CCP communist China!!! Go figure that!!! That is why, back to this topic, when the CCP of China says that it has been "transparent" about the origin of COVID-19, you say, "in no way the CCP has been transparent at all about anything"! It is also documented that the CCP of China removed the account of Chen Quanjiao, ID 4224 from *Weibo*, a whistleblower regarding the corruption of her superior, Wang Yanyi: https://twitter.com/LilJackieChen88/status/1229327409444319232, who was selling experimental animals from the Wuhan lab to the Wuhan market, being this one a direct link to the pandemic (which makes perfect sense: the escape of COVID-19 from a lab animal that was illicitly sold), covering-up this later, by saying that somebody else had posted that original message and not the person purported: https://project-evidence.github.io/; but more distressing, is the disappearance of multiple persons that wanted to make known the real situation at Wuhan: https://archive.vn/0StFh

3

The third point follows through from the previous two, and consists of seeing the individual variation of the different proteins of the COVID-19 virus (MN908947), and of segments of its crucial protein for human cell penetration (Spike), which gives the next rounded numbers, making the comparison with the only reference point that Zheng-Li has allowed us to have, which is that very questioned and questionable RaTG13 (MN996532), but which for now will serve for us to compare two artificial sequences: One mostly through keyboard, and the other through the lab; the genes that are not mentioned here are contained within those that are mentioned, and in brackets the percent of similarity of the few individual sequences tracked by Zhou *et al*. (2020; there, at least, you can see the comparison of different sequences other than RaTG13, while they seem to be comparing a generic Sars-CoV-2):

1) *99%:* E [99.6%], Orf10 [99.1%], Nsp9, and the end of the non-coding genome, which has a palindrome sequence: TAAAATTAATTTTA, which is cut by the next enzymes: MluCI, MseI, AseI, Sse9I, Tsp509I, TspEI;
2) *98%:* Orf6 [98.4%], Nsp7, Nsp8, Nsp10, Nsp12, Nsp13, and the start of the non-coding viral genome;

3) *97%:* N [96.9%], Orf7 [subdivided in 7a: 95.6% and 7b: 99.2%], Orf8 [97%], Nsp14;
4) *96%:* M [95.4%], Orf3, Nsp1, Nsp3 [as 3a: 96.3%], Nsp4, Nsp5, Nsp6, Nsp15 & Nsp16 (little modified);
5) *95%:* Nsp2;
6) *93%:* Spike [92.9%] (combined in it, its two subdivisions: S1 and S2, but since this is the one that experiences the greatest variation, reducing its similarity with RaTG13 by 6%, when compared to the regions of less variation, we need to separate its portions to get a better idea of its internal variation, remembering that the following portions from *a* through *c* produces the S1 portion of Spike):
   a) *92%:* For the portion containing the multiple HIV/SIV-like portions discovered by ex-IBM emeritus programmer Jean-Claude Perez, along with the Nobel laureate and discoverer of the AIDS virus, Luc Montagnier, 2020);
   b) *44%:* For the key portion containing the receptor binding domain and its motif (RBD [85.3%]); CoV-2: TTG-TTT-CAATCA-AAT-TAC *vs* RaT: CTC-CTA-TATAGA-GAT-CAC: 44.44% similar.
   c) *20%:* To generate the protease cleavage site: CCTCGGCGGGCACGT = PRRAR;
   d) *93%:* For the longest and final part after the protease cleavage site, which is the one produced by the S2 portion of Spike, containing a camouflaged resemblance to the AIDS virus.

This so great disparity between the different proteins of the same virus, especially for the region of the Spike penetration protein, indicates that these two portions of Spike have been the most modified by hand within the laboratory, because since a long time it have been already at hand all the technologies to do all of these proceedings, and this is demonstrable, while the speculation of a possible animal being the transmitter, is very uncertain and non-provable. An artificial passage through animals such as ferrets, or even *in vitro* human cells, those that have human ACE2 receptors widely used by Baric and by Zheng-Li, would have made that the virus taken from there could seem as "natural" as possible (plus the "*seamless*" technology, Leitenberg, 2020; Piplani *et al*., 2020), and even when it is through animals, the process for obtaining it has been carried out inside a laboratory according to the current knowledge. When we compare this region between the two sequences, the COVID-19 *versus* the RaTG13, we see a difference in 20 nucleotides (the left side of the RBM is considered vital by Zheng-Li, as seen in Ren *et al*., 2008), as it will be seen in the case that follows. Here, we can see the portion that contains the higher number of HIV/SIV-like sequences (region 21163 to 22015 of the original Sars-CoV-2 genome, corresponding to nucleotides 20381 to 21997 in the RaTG13, data not show), plus the *Plasmodium yoelii* to tip off the apparent changes (which will extend the region to nucleotide 23,974 for CoV-2, not shown here, but in the extra link at the end of the conclusions; and to 23,944 for the RaT of Zheng-Li, not shown at all, as you can find it); but what we see below in smaller letters, is the variations when compared to the immunodeficiency sites, and in gray, the 3-D regions, once translated into amino acids, with high similarity to the HIV-1 (by Pradhan *et al*., 2020):

Figure 3: Partial sequence of 853 bases (2.85% of its full genome, but the rest of the 12.17% discovered as modified thus-far, can be seen here in the last link before the references) in which there are congregated multiple fragments homologous to animal and to human immunodeficiency, a putatively important region for the infectivity of COVID-19 (see *Figure 5*), corresponding to the end of Nsp16 and to the beginning of S1 from Spike (here starting after the change of size of the region underlined in blue, which belongs or is similar to the HIV-1 from Kenya, aspect that was very significant to Montagnier and to Perez. The sequence GAATACA is added just as reference, being one of four such sequences within the genome of the Sars-CoV-2.

Not shown in *Figure 3* is another 3-D HIV-1 similar sequence after 300-nt further to the right side of it: GGTGATTCTTCTTCAGGT; and then, the same Indian team reported the sequence seen in part two except for the last three bases that belong to the bat virus backbone: CAGACTAATTCTCCTCGGCGGGCACGT (Pradhan *et al*., 2020).

The update that I would like to present here is the one clearly presented by an Austrian researcher (Segreto, 2020), who basically points out that a fragment of RaTG13 had already been published before (RdRp BtCoV/4991 (KP876546), by Ge *et al*., 2016: http://www.mgc.ac.cn/cgi-bin/DBatVir/main.cgi?func=accession&acc=MN996532), and that it was used as a reference in a couple of studies, and one of them, cited by Zheng-Li herself in 2019 (Wang *et al*., 2019), is where Zheng-Li calls it with a different name: SARSr-CoV Ra4991, prior to her publication of the RaTG13 sequence in the 2020, and after the first sequence of COVID-19 published by a Chinese group was released in the Genbank, being the 4991 a sequence that Zheng-Li (the same Zhengli) had owned since 2013, and whose sequence she offered to send to whoever requested it, even for the primers and for the segment corresponding to the gene from Spike, but in 2020 Zheng-Li failed of citing the original 2016 reference, or even mentioning it when publishing-out her RaTG13, and did not even mention either the 2019 reference in which she again used that 2016 sequence, which, of course, being unable to be independently corroborated by international labs, has all the evidence of it as being already manipulated. Deliberate forgetfulness to quote those references of 2016 and of 2019 when publishing in 2020 her RaTG13, displays a Zheng-Li that is evidently hiding the truth about the origin of COVID-19. There is even a third article, from the early 2020, exploring the beginning of the pandemic by COVID-19 in 2019, mentioning also this 4991 sequence that Zheng-Li does not cite either (Chen *et al*., 2020; there it is called as it should be, exactly as in 2016: BtCoV/4991 (*GenBank* KP876546, 370 nt sequence of RdRp).

This point is important because, since 2013 it was known how to remove and put individual proteins artificially, specifically in the Sars-CoV virus (Sims *et al*., 2013, exemplified here with the removal of the Orf6 protein), which could explain this so diverse variability found between different segments of proteins (from a whopping 20% and 44% to a 99.6%! of similarity!!!, and if we compare the first version of the Sars-CoV-2 with its putative sources *ZC45/ZXC21, as NHP has found, their similarity with the E protein of the initial COVID-19 is 100%!!! Which, as said before, it is NATURALLY IMPOSSIBLE but ARTIFICIALLY POSSIBLE!!!*), being this as a mad "cut and paste" assembly of the most offensive viral portions of its proteins against humans, and this, especially, because Baric had already discovered a way of leaving no trace, according to He, a way to hide the human hand within the modified viral sequences; a method called a "traceless, signature-free infectious-clone technology" (Leitenberg, 2020), but, I ask: For which reason were they investigating how not to leave a track of the human intervention? Was it so that a natural virus would not realize that the other virus next to it was "artificial"?, I don't think so (Yount *et al*., 2003, and there they provide a reference from the previous year as its foundation!), and even exists a commercial "*kit*" to carry out the same procedure of "*airborning*" a virus without even leaving the slightest trace; but, for what purpose will these "*kits*" exist?, for the deception of whom? (*GeneArt® Seamless Cloning and Assembly Kit*). However, Deigin (2020) indicates that it is still possible to observe the traces left by the human hand by using that kind of products, or some of a similar nature, on the Sars-CoV-2.

Alice Kopel also sent me an interesting article regarding Nsp16, because it says: "The requirement of nsp10 for nsp16 to execute its 2′-O-MTase activity is a unique feature of SARS-CoV-2 that has not been found in any other virus or host cell" (Encinar & Menendez, 2020). This, for me, is another indicative of the artificial nature of the COVID-19 virus, especially because Perez & Montagnier (2020) found at the end of it, also an immunodeficiency *EIE* signature of at least five of its segments (see below).

So, the most recent discovery by Perez and Montagnier (2020) is the next one that belongs to two concatenated sequences similar to *Plasmodium yoelii*, located at the right side of the Furin cleavage site, within the S2 part of Spike: *CACAAGTCAAACAAATTTACAAAACACCACCAATTAAAGATTTTGGTGGTTTTAATTTTTCACAA*. This finding did help them explain the oddity of the 44:1 versus 5:1 synonymous versus non-synonymous differences pointed out above. Furthermore, they also found near the end of Nsp15 the next concatenation: AATCACCTTTTGAATTAGAAGATTTTATTCCTATGGACAGTACAGTTAAAAACTAT, and this gene is just before Nsp16, and just to complete the list of oddities within the COVID-19, we have in Nsp4 a fragment also highly similar to immunodeficiency: TGATTTTGACACATGGTTTA as well as another within Nsp12: ATTGTGCAAACTTT AATGTTTTATTCTCTACAGTGTTC. To see the details of all of these sequences, please go to Perez & Montagnier (2020). Some other team found another sequence that seems to be balancing the *P. yoelii*, similar to *Plasmodium malariae* just before the RBD, but this has been also vigorously debated by Szilagyi, however, just for me to be thorough, I wish to also include it, as a historical testimony of all the oddities within COVID-19: *AACAATCTTGATTCTAAGGTT* (Hong *et al*., 2020). Szilagyi indicates that it is similar to one found in a virus from pangolin, but as we will see later, the work of Petrovsky seems to indicate that those pangolins were inoculated with a previous version of what we call today COVID-19.

A possible therapeutic aspect, in general, could be the drinking of water that is in contact with Silver objects (Ag, highly recommended by John Apsley, for example, in the article by Galdiero *et al*., 2011), and to ingest those fungi that strengthen the immune system, such as the shiitake, chaga, kima and maitake (Lindequist, Niedermeyer & Jülich, 2005), lactobacillus (Weiss *et al*., 2010), as well as, with clean udders and hands, raw milk! (Panon *et al*., 1987). Others also recommend Selenium (Se; see Stone *et al*., 2010), Zinc (Zn; ver Reich & Church, 1994), and still working, according to my sister, even the vitamin C (Hemilä, 2003) and the vitamin D (Lake & Adams, 2011); others recommend all the derivatives of, like potassium chloride (Engelbrecht *et al*., 1980), and this article talks favorably about the also dismissed by the CCP *Big Pharma:* "Chloroquine phosphate" and of flavanoids, xanthones, triptexanthoside D from *Swertia genus*, phyllaemblicin B and phyllaemblinol from *Phyllanthus emblica*, etc. (also by Wu *et al*., 2020b), even very mild or slight, the use of vaporizations of soap (Kawahara *et al*., 2018), and also half aspirin, or any anticoagulant advised for the COVID-19 sick, vulnerable people, so as to prevent the lung arterioles coagulation (https://archive.vn/DXpL4); that is why also anti-thrombotic treatments are advised (Ocke-Reis & Braga-Lima, 2020; thanks to the first author for sending me his article); so, basically anything, especially preventative, as long as we do not fall for the rampant corruption of the CCP "*Big Pharma*". Here, I will also quote the research by another one that is being put down by the Mass Media: Hydroxychloroquine (HCQ), but alone is not effective, only with Zinc (Vincent *et al*., 2005; Risch, 2020);[4] so, azithromycin seems to be unnecessary (Gautret *et al*., 2020), the one that Trump is taking as a preventive (until they discontinued its use on 06/15/2020), and there has also been a boom promoting to prevent COVID-19: Chloride Dioxide (Ogata & Shibata, 2008; Miura & Shibata, 2010; Ogata *et al*., 2016; Kály-Kullai *et al*., 2020).

Jose Francisco Norambuena Michea, from Chile, sent me the following ingredients (the *Cuban Method*) to increase our immunity, through the stimulation in the production of our own Interferon alfa-2b: https://medlineplus.gov/druginfo/meds/a690006.html (a similar method with another interferon has been currently copied by Baric), and the advice is to make a mixture of the following three teas: Green tea (Nance *et al*., 2009), Dandelion tea (Han *et al*., 2011), and Chamomile tea (Miraj & Alesaeidi, 2016), in addition to everything that is alkaline: Magnesium Chloride, Sodium Carbonate, alkaline also are vegetables, organic fruits, and algae (Chlorella, Spirulina…), etc. For her part, Analia M. Tadeo sent me another treatment that someone has been using with relative success, and it is the suspension of Ibuprofen in salt water for steamer, nebulizer or vaporizer, that are inhaled through the nose, so it says: Doctors Dante Beltramo and Roxana Alasino invented this treatment for cystic fibrosis and to date have helped nine patients with COVID-19: https://www.infotechnology.com/labs/El-revolucionario-tratamiento-cordobes-del-que-habla-el-mundo-usan-ibuprofeno-y-sal-para-curar-coronavirus-20200507-0001.html (and the same product by itself has been used successfully by Dr. Barrientos), etc.

Pros of this result

We observe that by making a statistical comparison of the COVID-19 proteins, and of portions within these proteins, we obtain a general oscillation of the 6.7% (being Spike the most variable, and E the least variable); however, within Spike, this variation is even more dramatic, falling to 44.44% (at the six codons of the RBD), and even to 20% (at the Plasmin/Furin cleavage site), such extreme variation seems to be an obvious indication of the intervention of the human hand.

Cons of this result

Excuses that could be given to this result, are that other natural viruses may also show the same variation (of an equally large variation of between 56% (in the RBD), to even 80% (in the novel and crucial cleavage site PRRAR), but this is yet to be seen, most specially the targeted changes that are leaving intact the rest but only touching the key areas as to optimize the infectivity of COVID-19), and it can also be said that the sites of extreme variation within Spike are normally high-variation natural "*hot spots*" (but again, this would need to be demonstrated in other viruses that would in the real world, naturally show the same immediate jump already in their full maturity from one day to the next, as observed in the COVD-19 since the beginning of its history, which does not match reality as we know it).

The human aspect that I wish to explore at this moment, is the next one:

[4] Thanks to M. Ovensmith & Rubio: https://www.youtube.com/watch?v=ygC24J5djqM, https://archive.vn/ERWCl

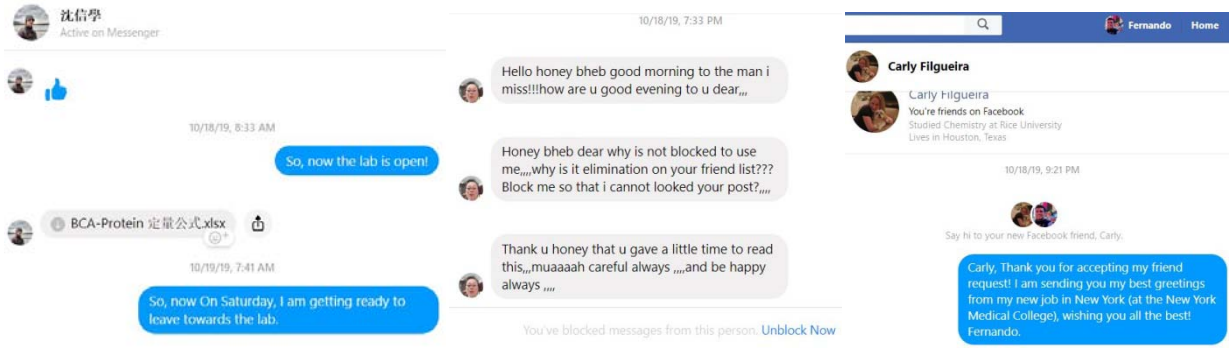


Figure 4: Trying to reconstruct what was I doing on the 18th of October of 2019 through those *Facebook* memories, the same *FB* that now is committed to censor the truth about the artificial origins of COVID-19; so, while the perverse Pandemic plot of "*Event 201*" was going on somewhere in New York, in the morning of that day, I was at the lab, and as I had the access keys, I informed Dr. Shen (沈信學), from Taiwan, that I had already arrived, later during that day, he sent me a protocol for an assay. Next day, on Saturday, we left together towards the lab in order to work hard all day long; but in the evening of that Friday, I received some messages from a girl living in Hong Kong, whom I had deleted days earlier because she was very annoying to me; later, I befriended another girl from Houston, TX, who was following me at the *ResearchGate*; but after that, she never responded to me. It is documented that even to-date the so-called "*patient zero*", a woman student and researcher at the Wuhan lab, whose name is Yanling Huang: https://www.researchgate.net/scientific-contributions/2035568207_Yanling_Huang, 黄燕玲, or Huang Yan Ling, who has not been able to show-up from anywhere in this world, which means that such story still stands (think about this possibility, about this student or anyone else, buying a Wuhan lab ferret as a mascot, and from there spreading the Pandemic, since September, 2019, as per the interview of the African student stranded in Wuhan, below): https://project-evidence.github.io/

But, given these two points against it, I would like to add one more evidence that has been within the most heated considerations by the perplexed investigators of this virus, and this fourth evidence goes as an extra, as a gift, so as to expose that stealthy, low-profile opposition (as per the guidelines delineated at the session four of the awful "*Event 201*": https://youtu.be/67qvWw1KDeU, where it was already known that the 90% of the population will be aware of the truth behind the real origins of the virus) that arises against it to the point to dismiss the next information as if it were "rubbish" (according to the word of A. S.); so, please, do not hesitate, you can beat this horse as hard as you wish, and as hard as you can! However, it moves…

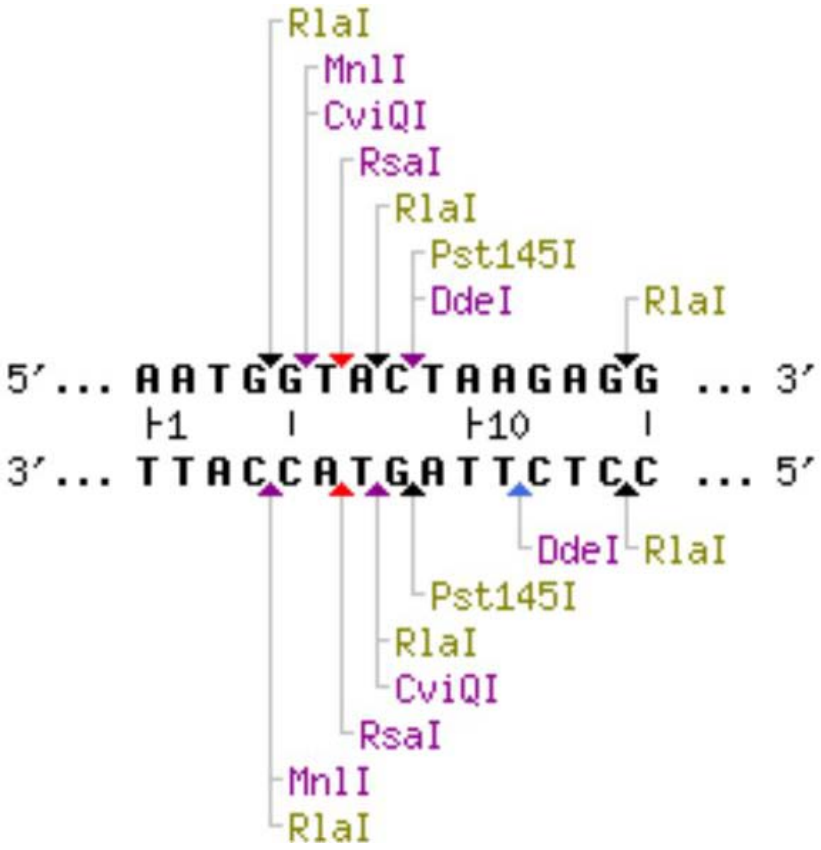
4

This is not just only about an evidently and deliberate artificial "insertion" of sequences from the HIV-1 into the COVID-19, but also, it is mostly about the corroborated stealthy similarity of the Sars-CoV-2 (as well as of Sars-CoV-1; so, putatively also the first Sars was modified) to the HIV-1, as per the very same voice of the experts, and I started wondering about this when I found independently the next short sequence (which is a region of GC 40% AT 60%, as no other region is as loaded of GC as "the Furin" NTs):

AATGGTACTAAGAGG [5] = NGTKR

And as a point of comparison regarding the restriction enzymes that digest this oligo-NT, we have:

[5] HIV-1 isolate 19663.24H9 from Netherlands envelope glycoprotein (env) gene, sequence ID: GU455503.1.



So, this segment that is 15-bp long is cut by only six enzymes, and so, every other significant region of the COVID-19 genome of a length as that artificial for the Furin NTs, has less sites of cut than such Furin.

Perez and Montagnier (2020) called a related and longer (18 bases) portion of this segment an: "*Exogenous Information Element*" ("*EIE*"), and it is located on the left side of the receptor binding domain (RBD), where there seems to be this an important portion for the penetration of the virus RNA from COVID-19 into the human cells, according to the publications of Zheng-Li (which at that time studied a previous version, that of a Sars-CoV, with a general structure which is similar to that of the COVID-19 virus, being this last one an optimized version of that previous one in all of its proteins); as *Fig. 5* shows, figure that I have modified as follows: Pointing out in red, either the location of the HIV-like portions, or if shorter, to the immunosuppressant that will be seen at the end of this portion of the article, while in black they point out to the area of the receptor binding domain (RBD) that they were investigating in that work, and in blue is the metaphor for the site of protease disruption (or if shorter, it is the necessary of the RBD), which is also a necessary portion for the virus to enter into the human lung cell. And, it is precisely the Nobel Prize of Medicine Luc Montagnier, in collaboration with the retired IBM emeritus programmer Jean-Claude Perez, who are characterizing most of the immunodeficiency-like sequences that are present in this area and in the virus in general (Perez and Montagnier, 2020).

So, then, in the image that follows, with the rectangles added by me in red and in blue (modified from Ren *et al*., 2008), it can be seen that Zheng-Li was producing almost all of the possible combinations between the bat virus framework (but as I say, it lacked the one in which it leaves only the red part alone, the putative part with immunodeficiency sequences, without the blue part):

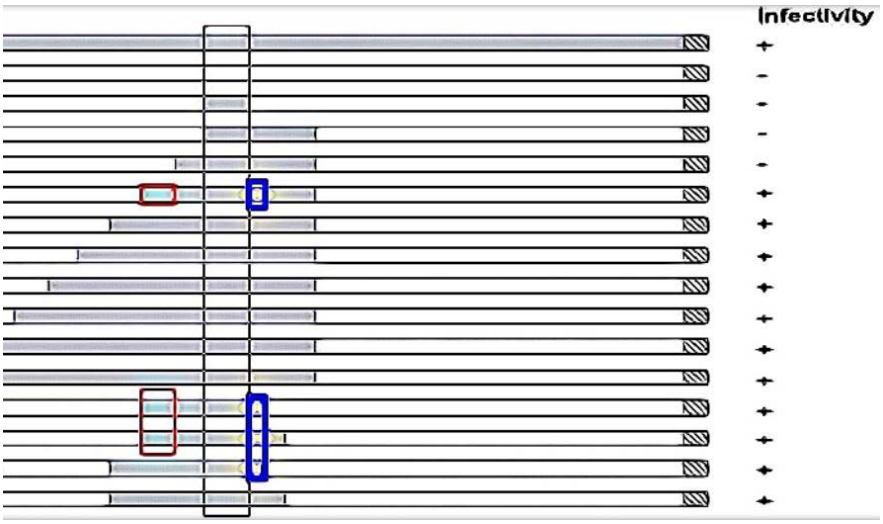


Figure 5: The homologous region to human and to beast immunodeficiency found by Zheng-Li as necessary to infect human cells (in red); she did not include what happened if she only left the red-painted side (Ren *et al*., 2008; go there for further details); the blue site at the right is allusive to the place where the Furin/Plasmin cleavage site is located (it seems to be a necessary fragment for the infectivity). The area of the black rectangle is where the receptor binding domain (RBD) is located.

In *Fig. 5*, the centers that included the receptor binding domain (RBD) are left as the constant, with extensions of various lengths to the right and to the left of it, in order to observe which was the minimum extension capable of conferring the maximum virulence, which she obtained by leaving a portion on both sides (in red and blue), the red corresponding putatively to that site where Jean-Claude Perez and the Nobel Prize winner Luc Montagnier found those segments that coincide with immunodeficiency viruses, both human and of ape; or at least that HIV-1 like sequence that the Gallaher & Gallaher (2020) describes (see below). Others had already partially discovered that(Pradhan *et al.*, 2020), and although they never even managed to get their article formally reviewed by those virologists experts; however, they did receive several formal published and indexed attacks instead (here, I refrain from going there to that "theater", because the critical articles, completely forgot about the similarity of Sars in general with the HIV that we will see next, besides that they did not put, as the censored authors did, the equivalences of amino acids and their corresponding nucleotides, plus many other omissions, which for me are deplorable). Alberto Rubio-Casillas also sent me a 2010 reference in which Zheng-Li was using HIV pseudoviruses mixed with Sars virus genes and others similar to it (Hou *et al*., 2010), as well as Spike proteins from MERS-CoV inserted into HIV (Zhao *et al*., 2013). All of this can be found within one of Baric's references for his 2015 article with Zheng-Li delineated at the start, where the mixture of HIV with the Sars protein Spike, is called a "*virion*", which is even an earlier reference (Ren *et al*., 2008).

When I was at a Symposium that Luc Montagnier presented in Guadalajara, called: "AIDS; A challenge for humanity", sponsored by the *Janssen Research Council* of Mexico (July 12, 1996), an event organized by the Dr. Alan E. Barrell, a graduate of the *University of Pennsylvania*, I asked before an audience saturated to overflow, about the possible function of shorter segments also called epitopes (today, I should have called them "the minimum (functional) size of protein domains"). present in the AIDS virus; at that time he told me that no one knew, and even now, my experience is that the presence of those peptides derived from the "short *EIE*" nucleotides that are as small or even smaller than this one that I found of only five amino acids, are wrongfully discarded or ignored by scientists as meaningless, however, we will see here that such is not the case.

Figure 6: Certificate of when Luc Montagnier, Nobel Prize in Medicine in 2008 for having discovered the AIDS virus, HIV, went to Guadalajara, MX. I asked him about the minimum functional size for the epitopes to have a biological significance, which still is an active question, only to be unraveled by the experimentation.

So, NGTKR, and even its surrounding regions are high similarity to other sequences of the human and animal immunodeficiency, which for many ordinary researchers is either an enigma or nothing; but, apparently for Zheng-Li it was something, since apparently she know the importance of this region, as *Fig. 5* seems to be showing to us.

Update for me, of something old but that I did learn recently while searching for this: Here, I would like to point out that a discourse that tries to erase any similarity to HIV that is present in the COVID-19 virus is harmful, because it reduces our understanding in relation to the ways to destroy this enemy virus.

For example, in the intriguing article "*Cloaked similarity between HIV-1 and SARS-CoV suggests an anti-SARS strategy*" (Kliger & Levanon, 2003), we can see the similarity between the old Sars, the new Sars (that I have added to the comparison), and the HIV-1:

Old Sars1: YEQYIKWPWY*V*WLGF

COVID-19: YEQYIKWPWY*I*WLGF

HIV1 AIDS: WASLWNWFNITNWLWY

The original image from which I took the sequences says, here in italics (with my new comparison added here not in italics): "*Comparison of sequences of the regions rich in aromatic residues of the S2 proteins* (the second part of Spike) *of* the old *SARS-CoV*-1 and the new Sars-CoV-2, *compared to the gp41 protein of HIV-1. Aromatic residues are* in bold large. *Remarkably, the relatively rare aromatic residues comprise about half of the residues in this region*."

In the original article, the 3-D similarities between these two structures are presented, concluding the authors that gp41 is equivalent to the S2 position of the Sars-CoV virus Spike protein. There is another article that shows the same as the previous one, but in a different 3-D format, such as a rearranged design and with new words for the same previous concept (Zhang & Yap, 2004).

Here, the Gallahers' powerful conclusion is as follows: "Tryptophan is normally a very rare amino acid. Many large proteins contain none. So, this region of peptides is quite unusual: ... Combining basic amino acids with aromatics in such a way that a powerful toxin is produced and which in the virus serves as a region for permeabilizing membranes known as a *viroporin*... a pattern is emerging among many different viral agents that use this membrane destabilizing trait: K or R with multiple aromatic residues, especially W (but also Y or F), to break down cell membranes causing cell fusion, permeabilization, or destruction. Apart from the viruses of COVID-19 (S2) and of AIDS (gp41), this trait has also been found in: Ebola Delta, Enterovirus D68 ORF3, Flu H3N2 PB1f2, and Human Papillomavirus type 6 L2" (Gallaher and Gallaher, 2020; and just as they self-published their work, I also published it in Spanish first at *Yola*).

But, more than the immunodeficiency-like sequences of primates, which in themselves draw attention, the evidence presented here is in the kind of work that Zheng-Li herself had been carrying out non-stop at least since 2008, which already presents all the molecular knowledge and tools that are necessary to artificially obtain the COVID-19 virus in 2019. And such is the interest, specifically in this full S region: S1 and S2, still full of mysteries, that this search has been the most popular of my discussion points in the *Research Gate*, a site mostly specialized in molecular and in cellular research, but also in medical research in general (Castro-Chavez, 2020a), this site has provided already 11,750 readings from it: NGTKR from April 10 to June 14, and counting; Compared to this one, the sequence already seen here is also full of mystery: the inserted 12-bases that produce the PRRA, and this has, thus far, attracted the attention of 1,905 readers (Castro-Chavez, 2020b), while that of the optimized RBD: L + F + QS + N + Y, of 375 (Castro-Chavez, 2020c). Visually, the structural similarity of amino acids is as follows for the COVID-19 virus and for the AIDS virus, respectively:

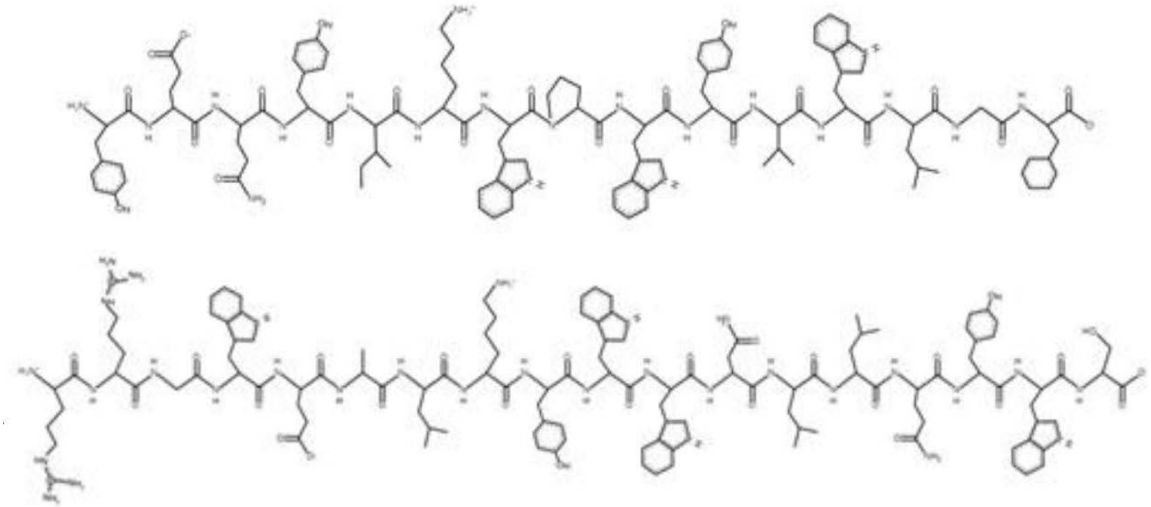


Figure 7: Structural equivalence of the highly aromatic and basic destructive region between the COVID-19 virus (above) and the AIDS virus (below). Taken from Gallaher & Gallaher, 2020

For health, a therapeutic product against the AIDS virus (HIV) is our own saliva (Baron, Poast & Cloyd, 1999). Judy Mikovits recommends Baicalin (BA), a flavonoid (flavonoids block the viral helicase) purified from the medicinal plant *Scutellaria baicalensis*, and in case you could get flavonoids, check them out (Li *et al*., 2000, also advised by Gallaher & Gallaher, 2020). For his part, Jean-Claude Perez sent me an interesting article in which it is indicated that simply with a humidified environment (such as the coastal air), in sharp contrast to a dry environment, is a powerful preventive against the virus (Lauc, *et al*., 2020). Perez himself sent me the link of another manuscript, similar to another already mentioned, indicating that the virus in warm areas such as in Arizona, USA, has already lost, as if it were already breaking apart, 27 amino acids or 81 of its nucleotides (Holland *et al*., 2020).

So, there are many other sequences of the Sars-CoV-2 that have either high homology, or similarity with the HIV-1, for example, the sequence at the left side of the RBD integrated for: LQPRTFLLKYNENGTITDAVD which is an irrefutable immunosuppressive long strand of amino acids present in the Sars-CoV-2 (whose corresponding sequence for AIDS is as follows: LQARLLAVERYLKDQLL; and here, the Gallaher father and son emphasize the LQxR motif as the most important functional one), and in the S2 segment we also have the ELDKWAS region, which is targeted by 2F5, a monoclonal antibody (Gallaher & Gallaher, 2020), etc.

There are many other therapeutic suggestions, such as Silvestrol to block the human eIF4A to inhibit elongation of growing polypeptide chains (however, it also inhibits the extension of human proteins). And I may even suggest analogs to the "Peptide T", such as a putative "Peptide R", containing the sequence alone, by itself of the amino acids of the RBD, to block the receptor site of the ACE2 (and of CD147), or the "Peptide P", containing the homologous sequence by itself with the protease cleavage site including its PRRAR, so as to saturate and distract the proteases cleaving that peptide instead of the cleavage of the virus, or that treatment of enzymes against the sites presented above (these three being my "*pet*" treatments). Other multiple suggested therapies are also included in the book by Gallaher and Gallaher (2020) and in many other papers that are flying around the net, before they are censored, such as it happens by the CCP, but now, in a global planetary "China". To find the way to prevent the virus from inhibiting the human protein STING is another possibility: https://archive.vn/uWqlo, or the PAC-MAN of the CRISPR-Cas13 to destroy the viral sequence in the human body: https://archive.vn/i0aSG, or trying to block the M protein of the virus: https://archive.vn/tRZRB, or those human endo-lysosomal two-pore cation channels:

https://pubmed.ncbi.nlm.nih.gov/32402856, or the well-known RNA polymerase of the virus: https://pubmed.ncbi.nlm.nih.gov/32511380...

The Dr. Maria Eugenia Barrientos, from El Salvador, recommends the first day of the infection, to start a treatment with anti-flu (to prevent contagions of others), coupled to an anti-inflammatory, three times a day during six days; to the ones that are already sick, she provides some inhaled corticosteroids for asthma two or three times a day during ten days (thanks to A. M. Tadeo again for the tip; so, I think that here, instead of corticosteroids, or combined, depending on the severity of the case, the mild anti-inflammatory mentioned earlier in the also vaporizer's treatment used in Spain, can also be of help).

Pros of this result

Three independent observations have located this region as a highly suspicious one, apart from me, one of them is the team of the emeritus IBM programmer Perez and of the Nobel Prize winner Montagnier (2020), who found the very same region as follows: *AATGGTACTAAGAGGTTTGATAACCCTG*, and I put it here with the three non-matching nucleotides in a smaller size; then, another team, that of the withdrawn Hindus (Pradhan *et al*., 2020), found the same region of the sequence in this way: TCTGGGACC*AATGGTACTAAGAGG*, and this region seems to match, or to coincide, with the region necessary for the infectivity by the virus, according to Zheng-Li (2008); in addition, these Hindus found three other "immunosuppressive" sequences: CACAAAAACAACAAAAGT, GGTGATTCTTCTTCAGGT and CAGACTAATTCTCCTCGGCGGGCA, this last being the most important one that was found exhibiting 3-D similarities to the HIV-1; as, if you realize, this again explains the artificiality of the mysterious 12-bases of the protease cleavage sequence as having been originated in the lab , which in this portion is included in its totality (a finding also made independently by some Chinese: https://freewestmedia.com/2020/02/27/chinese-scientists-discover-hiv-like-feature-in-cornovirus-mutation, https://archive.vn/XTvMx, https://archive.vn/3K1XG, https://archive.vn/TiF8q, https://www.nature.com/articles/s41423-020-0424-9, https://pubmed.ncbi.nlm.nih.gov/1360148/, https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7114094/, https://pubmed.ncbi.nlm.nih.gov/15135058/, https://jvi.asm.org/content/87/3/1884 https://www.medrxiv.org/content/10.1101/2020.04.11.20062349v2.full.pdf, https://pubs.rsc.org/en/content/articlelanding/2020/an/c9an02098e, https://www.sciencedirect.com/science/article/pii/S0014579307011945, https://jvi.asm.org/content/jvi/69/8/4675.full.pdf...

So, this in itself, just shows the bad blood of the ones covering-up the artificiality of this COVID-19 virus… so, if they are silencing the link between HIV and COVID-19, it is because is something important; however, the short sequence that I found matching the HIV-1 is this one: "AATGGTACTAAGAGG" that gives NGTKR, which as per the knowledge of Gallaher, it includes an immunosuppressant domain GTxR, also being rich in the "G" amino acid, a feature which: "show them to have a high overall turn propensity, indicating they are probably extensions in *Wuhan* (which is the way the Gallaher, 2020, authors call the Sars-CoV-2), to turns between beta sheets": GTNGTKR (my region under consideration, with the extra and previous "GT", being it like a turning or revolving immunosuppressive door, due to the "G" that precedes it, connecting two beta sheets), but, also sequences with "G" are: SYLTPG, GDSSSG (being all of them some possible "*revolving doors*", and also possible immunosuppressive, and the ones that contain S, are also, especially for the last one: "S residues calculated to be likely sites of O-glycosylation"), as well as the KY portion that also can be RY (being K and R exchangeable basic amino acids as I have earlier discovered: Castro-Chavez, 2010); so, within the longer immunosuppressive region shown above, we have a contained immunosuppressive region similar to the one that we are discussing here: NGTKR *versus* NGTIT, there shown in bold).

Cons of this result

Andras Szilagyi (2008), at the *Research Gate* point out that the E-value (the one that gives you the number of other sequences similar to the one you are comparing) of this sequence is high: 432, but I tell him that also it is high for the other 12-base Furin/Plasmin cleavage sequence, which, combined with the three bases of the bat virus, gives us 429; so, I say that such value does not mean anything, because another sequence that I investigated before, also gave me an even higher value (the last time I checked its value as a way to see how much contaminated sequences were at the *Genbank*, I found its E-value, as mentioned below, to be of 4^10!, that contaminated is such database!), but that its presence indeed represented the difference between a wrong experiment or a correct one if it lacked it (Castro-Chavez, 2012). So, I say that the only way to discover the true value of these short sequences when translated, like the ones (18-bases long) that are present in this region, as shown in Fig. 5, is through an experiment with, and an experiment without such sequences, to see then the changes of "behavior" of this inert virus at the root of the COVID-19 man-made pandemic! Also, in this case, I also need to remind the reader that, even a sequence as short as of only three amino acids (FFG), is highly significant into the prevention of a viral invasion (Gallaher & Gallaher, 2020), and precisely that one was the origin and the proof-of-concept for "the fusion peptide hypothesis"!

I was about to send this article when important information came to me, from Australia, indicative that instead of the pangolins having first the optimized RBD at S1 of Spike, it seems to me when I read it, that *they* (the WIV), were deliberately inoculating pangolins ahead of time with a previous version of the Sars-CoV-2, even before inserting into it the Furin/Plasmin cleavage site, and even before it appeared in humans!, as it says as follows: "…the strength of binding to pangolin ACE2 (is) lower than binding to human ACE2.... SARS-CoV-2 would have to have circulated in pangolins for a long period of time for this evolution and selection to occur and to date there is no evidence of a SARS-CoV-2 like virus circulating in pangolins… Most importantly, if such a recombination event had occurred in pangolins it might have been expected to have similarly triggered an epidemic spread of the new highly permissive SARS-CoV-2 like virus among pangolin populations, such as we now see occurring across the human population. Currently there is no evidence of such a pangolin SARS-CoV-2 like outbreak… Another possibility which still cannot be excluded is that SARS-CoV-2 was created by a recombination event that occurred inadvertently or consciously in a laboratory handling coronaviruses…" (Piplani *et al*., 2020).
The human aspect that I want to present right here, is the next one:

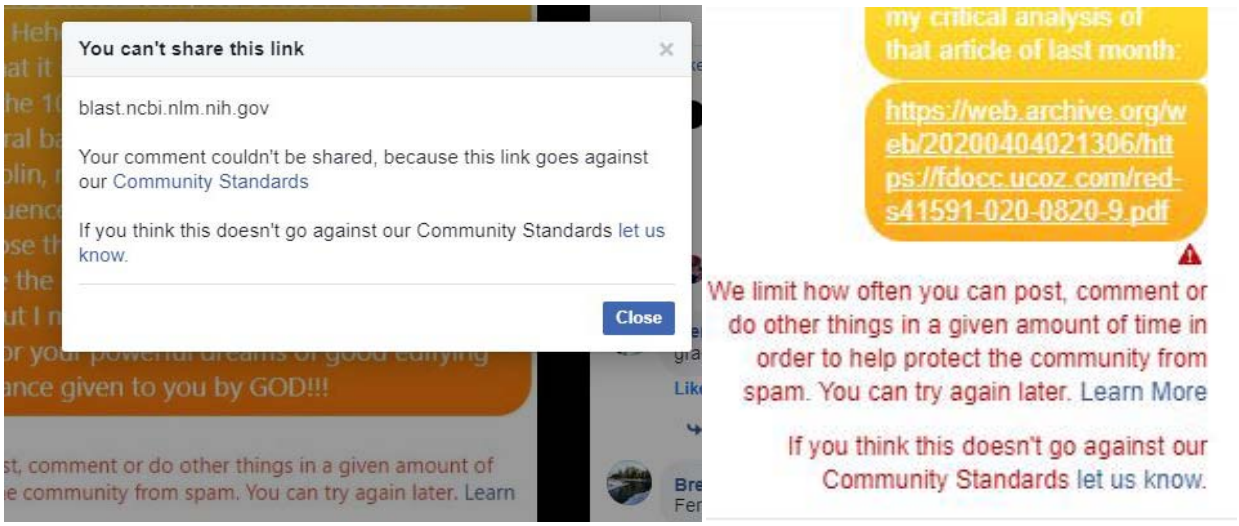
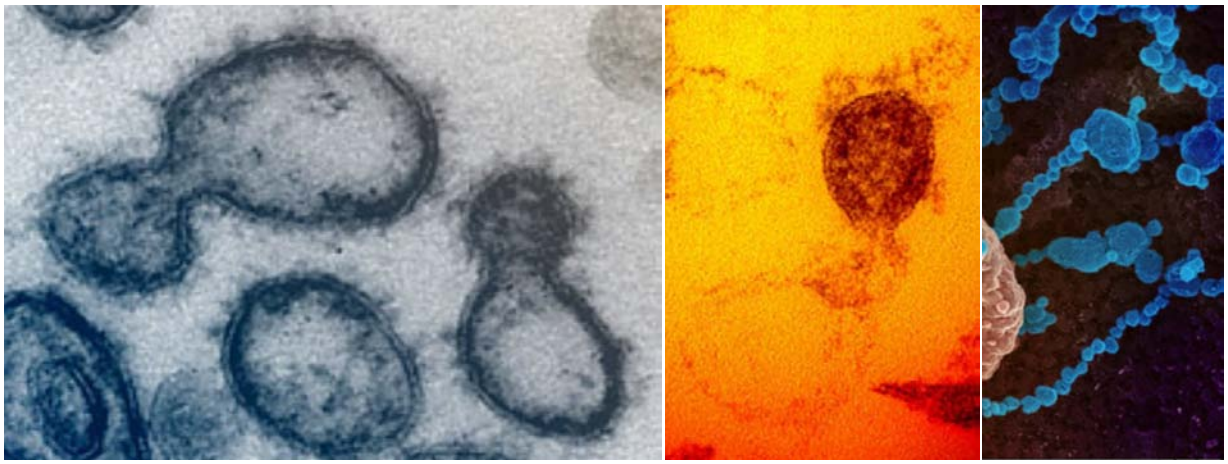


Figure 1: So, since I started doing my COVID-19 research, I was blocked by the *Facebook* to post the link to the tool that I was using to do my comparisons in order for others to do the same comparisons through the site blast.ncbi.nlm.nih.gov (04/08/2020); neither being able to put that link, either in public or in a personal message. Neither I was able to post a PM link to my own research that I had elsewhere archived (04/06/2020). I even explained that the tool was a research tool to compare genetic sequences and that the link belonged to my work as well, but all of that was to no avail, as they did not care about letting me to use those links. I was recommended to separate the words, to put "dot" instead… but the bad blood of the *Facebook* that peaked in Fig. 1 can't be denied, they seem to be serving sinister interests now that they are censoring, as if we all were already living in China; especially when I am exposing there the artificial origins of COVID-19. Plus, in those same days, for the first time in more than 23 years, there were attempts to hack my email at *yahoo* (born with my extinct *geocities* account, hackers tried to o so from "Indonesia" and from "Vietnam", respectively), then they tried to harm my computer, but I was able to clean it. Finally, there are countless of videos from persons willing to come forward and that then have been censored by the CCP of China: https://www.youtube.com/watch?v=dywyhyTl3k0, https://www.youtube.com/watch?v=m5fsidSOJMw, https://archive.vn/4t989, https://archive.vn/kJXsP, https://archive.vn/zmlmT, https://archive.vn/wl46s, https://archive.vn/NSwPu, and the list of CCP China censorship seems to be endless. I repeat a lot of things regarding all of this in the Appendix A.

Now, they are basically an example of boldness, to be learnt by all of us researchers under grants precisely by those authorities seriously conflicted by their personal interests, as the good Australians say (with my notes in parenthesis): "P.K.S and N.P. are supported by the National Institute of Allergy and Infectious Disease (*NIAID*, headed by Fauci) of the National Institutes of Health (*NIH*, headed by Collins) under Contracts HHSN272201400053C and HHSN272201800044C. This publication's contents are solely the responsibility of the authors and do not necessarily represent the official views of their affiliated institutions, funding bodies or Oracle Corporation."

Having known by personal experience that the CCP Chinese lie a lot and tamper with the evidence to get away with their deceiving purposes (Castro-Chavez, 2012), that leads me to conclude this article with the bold comments by Jonathan J. Couey (2020), from the U. of Pittsburgh, regarding this important Australian article:

"Understanding the exact origin of this virus is vital to ensure that all scientific and medical data are interpreted correctly by policymakers and healthcare professionals alike. However…, debate on the laboratory origin of the virus has been stymied by scientists opposed to even considering the possibility (…Fauci, supposedly to be an expert in "bioterrorism", should have known better from the very beginning, as his NIAID was the first to publish images of the virus, even if he did not care about the quality of the same, as NONE of them have the mandatory to be scientific nanometer line of measure, something unforgivable for an "expert" as he claims to be during 40 years of leadership: https://archive.vn/4fcxJ)." Next, a photos uploaded by the NIAID of Fauci; fusions, Multi RNAs, beads?



And from here, I say to the very dubious, dangerous and unethical worldwide research that has got us into this COVID-19 Pandemic with not even one benefit for the whole of humanity at all, *Got GoF*? NO!!!

VII. Conclusions

So, I have shown clear evidence that for a zoonotic event to have happened (even if "naturally" within a lab), at least three or four different converging viruses would be required in a ferret, *i.e.*: 1) A bat virus backbone, with 2) A very specific and targeted delivery for the RBD from a pangolin virus and with 3) A second and similar completely independent viral pangolin infection to explain the variations at the end of the Orf1ab identified by Deigin, 2020, plus the intervention of 4) An unknown "virus", also inserting ONLY 12-bases and nothing else for the Plasmin/Furin cleavage site. The host could be another animal with compatible receptors to the ACE2s of humans, such as cats (from which we recommend staying away during this "pandemic"). COVID-19 acquired overnight its infectivity and pathogenicity without any previous traces of any "zoonotic evolution", even when this was investigated experimentally in Wuhan by the same and currently the main suspect Shi Zheng-Li in 2018 (Wang *et al*., 2018; also see the last reference of the next paragraph), in addition to the fact that all molecular technologies were already mature and in place to have managed everything needed to obtain a virus similar to the one that has plagued us today, and such technology was already in full here since 2015, which indicates to us that the presence of a mature virus, fully capable of infecting entire populations of human beings in the world, may can mostly be explained from an intentional release, or even from an "a*ccidental*" one, but this last scenario does not explain the "orgasmic" insistence of a worldwide vaccination for the "digitization" of humans promoted by Bill Gates, attempting himself to reboot humanity and to "Digitize" it through an implant in every human being, being his dream to insert a software of his development into humans.

So, the evidence shown here clearly indicates the impossibility of the null hypothesis (Ho), because there is no history of a zoonotic event *a priori*, even if now the apparent perpetrators are trying to concoct some mythologies *a posteriori*, such as the most recent one, attempting to say that the 12-unknown bases could have been originated in another bat virus; so, there is no history of previous natural versions of the COVID-19 virus, but rather it appears already mature and ready to attack in full the human beings of the entire planet, just as if it had been released, either "*accidentally*" or deliberately on purpose. I also want to add a statement by one of my favorite research articles related to the subject, and it says, and taken within the context of all that we have seen here is very telling: "it is important to identify the route by which SARS-CoV-2 adapted for human transmission", from that article also, are the next golden excerpts: "the SARS-CoV-2 epidemic appears to be missing an early phase during which the virus would be expected to accumulate adaptive mutations for human transmission", and also: "there is a surprising absence of precursors or branches emerging from a less recent, less adapted common ancestor among humans and animals... SARS-CoV-2 appeared without peer in late 2019, suggesting that there was a single introduction of the human-adapted form of the virus into the human population", and the very telling words of their conclusion that

are so very well said, that we also want to appropriate into our own conclusions: "The lack of definitive evidence to verify or rule out adaptation in an intermediate host species, humans, or a laboratory, means that we need to take precautions against each scenario to prevent re-emergence" (Zhan, Deverman & Chan, 2020).

The minimal three molecular points widely verified until now are: 1) The RBD was tampered to be optimal for the attack over human cells in six different codons, 2) The Plasmin/Furin cleavage at the PRRAR site was also inserted out of nowhere in the lab, a 12-bases of nucleotides that are new in the bat virus family and new in the sequence itself of COVID-19 by being 80% rich in CG contrasted to the rest of the RNA sequence, and 3) The extreme variability of these two sequences from 56% for the first one to 80% for the second one, in addition to the most debated subject, but that I's present in the sight of everybody, 4) The optimal portions within Spike, both in the S1 and the in S2 sites, similar to various immunodeficiency viruses, necessary for the penetration of the virus's RNA into the cell, to be immunosuppressive of the defenses of the host (and currently found similar sequences also in the proteins Nsp15 and Nsp16 among other sites), plus that vital and initial aspect, 5) The lack of any previous zoonotic trace; so, all this together makes us to decide that Ha, the accepted hypothesis, for this particular work performed at Wuhan, China, it is the correct choice. Fig. 9 is a brief visual of these:

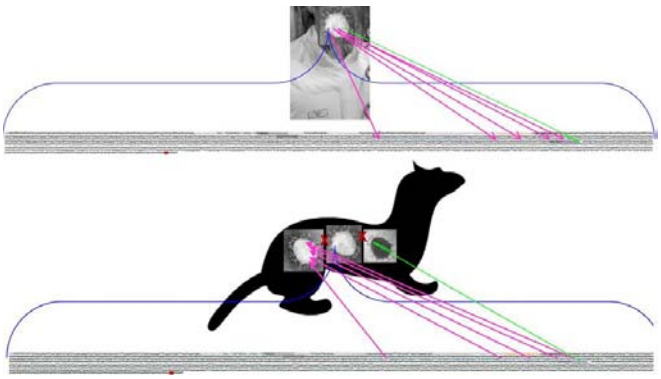


Figure 9: The two competing hypothesis for the current presence of COVID-19: *Upper*: Ha: The Sars-CoV-2 virus originated in a laboratory and was released from there. In the image, the main suspect researcher, and this movie says more about her: https://www.youtube.com/watch?v=XMJ0EmMfb3U, performing the mixture of at least those three elements (but it can be more, as the international research on it is just starting): *1*) The backbone of a bat (the blue bracket in the photo), *2*) the targeted insertion of the optimal RBD (in pink, transmitting only 0.06% of the complete sequence, which is a natural impossibility ad to inherit only such small amount of NTs and no more traces in a non-existent anywhere else "recombination" between two viruses), and *3*) the additional insertion of the 12-bases of unknown origin (in green, the "Furin (and most importantly "Plasmin") Cleavage Site", being just a small 0.04% of all of the sequence, again, being impossible in nature that only that portion and nothing else could be left by a improbable "recombination" between a third virus), optimal for the protease cleavage in order for the RNA of the virus to penetrate into the human cells. *Lower*: Ho: The Sars-CoV-2 virus originated in animals and from there it passed into humans. In this image, a ferret (also present in the Wuhan Lab), needed the injection of the engineered virus seen in Ha for the necessary passage to make it look more natural; but that then, also takes us back to the Ha option; or, the other mythological explanation: an animal had a so bad luck and was invaded by several viruses: a virus from a bat, which received with great precision only the specific sequences that make optimal the attachment to the human ACE2 receptor, similar to a virus from a pangolin, without leaving any other recombinant trace, then a third virus arriving to the same animal (or, making it harder, to a second animal having received the previously "targeted recombinant virus", and as I mention, again all of this can be easily done in a lab), putatively belonging to a bacteria (even if the cover-up attempts it to look as if it were from a different kind of bat), inserting only and specifically in its key place and nowhere else, the 12-bases for the PRRA cleavage site.

So, you decide what is the option easier and filled with the published evidence, and what is the one lacking any kind of evidence other than a "guess work". And again, this is just scratching the surface. I wanted to think that it had been an accidental escape from a lab, but the way the ones more closely involved are behaving, makes me really look at the deliberate release hypothesis more closely, especially when we learn more and more that COVID-19 seems to be "engineered" to target, specially the weakest humans, either for their health or for their age (Ji *et al*., 2020; thanks to Dr. Martenson for pointing at this article), or socially (Goldstein, Poland & Graeber, 2020; thanks to Teresa Wendorff for asking me about it), exactly as it could be expected if it all were coming from the leader of a population control team, a freak and obsessive human being. If the CCP of China is not honest about the numbers of their real population infected with COVID-19: https://archive.vn/yER45, being the infected ones at least eight times more or two more figures, if not higher, than what they are saying, do you think that they are honest at all when

dealing with the origins of the virus? So, for not letting us known from the beginning that COVID-19 has been an accidental leak from a laboratory, now the new Ha is that COVID-19 was deliberately released by the CCP to harm the world, and most specially, to damage the USA (and it is not "*evil*" to think in this way, as the CCP has made clear that its way of competition is very dishonest and dirty, and that they are engaged in an unconventional warfare for the supremacy of the world;[6] so, ladies and gentlemen, it seems that we are already inside *The Third World War* without even knowing it!). The new Ho is, obviously, that COVID-19 was released "*accidentally*"; but, the behavior of the most suspected and principal players, leads me to think that this new Ho is not the way it all started. The sequences currently found that seem to be modified artificially (either by hand or by passage in cell cultures or in animals) within that more than 12% of the COVID-19 are contained within the next file: The Supplement: https://fdocc.yolasite.com/resources/Anticovidian_v.2-Modifications.docx, were, if needed, important updates will be added, saved at the https://archive.vn, such as the current three key articles on the COVID-19 "INSERTS" by Arumugham (2020) found within the Nsp3: ACTGTTGGTCAACAAGACGGCAGTGAGGACAATCAGACAACTAC TATTCAAACAATTGTT and CAAGTTGAACAAAAGATCGCT, and by Sørensen *et al*. (2020a), who even took them from Zheng-Li Shi herself: GGGACCAATGGTACTAAGAGG (again, and including these three last references, for the fifth time!!!, being the previous two: Pradhan *et al*., 2020 and Perez & Montagnier, 2020), AACAACAAAAGTTGGATG and AGAAGTTATTTGACTCCTGGTGAT (being the last reference: Zhou P. *et al*., 2020, in bold, her additions); so, that adding only the modified or inserted sequences as shown in this docx as per today, gives us thus far 731 bases or the 2.45% of its total genome!, as per the lengths: 20, 38, 56, 16, 21, 18, 21, 57, 18, 28, 37, 26, 16, 111, 36, 21, 18, 27, 65, 60, 21).

More updates, as per the last day of July, because daily, new things are appearing:

Latham and Wilson presented an important hypothesis that, as also I suspected, the intermediaries for COVID-19 seem to have been humans themselves, and they focus in the six "Mojiang Miners Passage" (MMP), infected at an active mine of in 2012, given the published literature, but certainly, it is possible that more not reported situations ensued as per the needed step of adaptation into humans (Latham & Wilson, 2020).

Then, we had a new article by Sørensen *et al*. (2020b), where they basically check the electricity of the spike region of the COVID-19 virus, finding that it is highly positive by design (indicative of a purpose behind its release), increasing the number of human cells that can be infected by it, as the cellular membranes have a different charge, thus being able to attack also the olfactory and taste receptors, erythrocytes (red blood cells), t-cells (white blood cells), neurons and various tissues such as intestine epithelia. Plus, we have the current findings of Alina Chan, that indicate that the WIV of Zheng-Li had access to the sequence of the RaTG13 since 2017: https://twitter.com/Ayjchan/status/1279761424919732224, so, once more, no matter how much is she promoted by corrupted reporters of science (such as Jon Cohen, another reefer (see below), the same that disgraced Mikovits with her mug shot of a "crime" that she never committed) always siding with the money, Zheng-Li is lying.

Additionally, more and more doctors and other experts have raised their voices indicating that the origin of this COVID-19 virus is artificial, such as Stuart Newman, of the NYMC, Andre Leu, of Regeneration Int., David R. Walt, of Harvard, Michael Antoniou, of the King's College of London, however, the repression is big and hard, to the point of eliminating from the YouTube, Facebook and Twitter one of the best specialized and independent news reports by a former producer of CBS, Del Bigtree, and his program called *The Highwire*: https://thehighwire.com/, https://lbry.tv/$/search?q=The%20Highwire%20Bigtree, he is also responsible for the development of two excellent documentaries: Vaxxed, parts one and two: https://lbry.tv/$/search?q=Vaxxed, reporting the adulterated data reducing the high link of vaccines and autism, especially amongst black boys, according to the whistleblower of CDC William Thompson: https://vaxxedthemovie.com/download-the-cdc-autism-mmr-files-released-by-dr-william-thompson/. Also the video of the Frontline doctors has been removed: https://lbry.tv/$/search?q=Frontline %20doctors, amongst many other testimonies of the truth of what is going on with the currently hyped and pre-planned COVID-19 Pandemic, indicative that a perverted agenda on the open is at work in this case, but it will be defeated at this time. So, before they remove them, please download the next three sets of data for your awareness of the uselessness of vaccination which instead of helping, is maiming an ever growing amount of children: https://archive.org/details/history-of-vaccination, https://www.wellnessdoc.com/1200studies/, https://childrenshealthdefense.org/research-database/, just to mention some. Also in that venue, we have by Dr. Andy Wakefield, the film of 1986 – The Act: https://1986theact.com/. As well as the third book by Mikovits and Heckenlively, plus the upcoming second movie of the first one: https://bolenreport.com/as-if-i-wasnt-hated-enough-already/

Medically speaking, other than the report of Dr. Wherry, that COVID-19 behaves similarly to the HIV in many respects (https://archive.vn/WCK5T, see him at the end), lately there have been some emphasis in steroids, such as dexamethasone: https://www.nejm.org/doi/pdf/10.1056/NEJMoa2021436, https://www.bmj.com/content/bmj/369/

[6] https://www.epochtimes.com/9pingdownload/English/9ping_en.pdf

bmj.m2422.full.pdf (even when ventilation is not even advised at all), https://www.bmj.com/content/bmj/370/bmj.m2648.full.pdf, for example, again just to mention some of the many, Dr. Richard Bartlett, which has a very similar recipe against COVID-19 such as that by Dra Barrientos, from El Salvador, already commented: https://americacanwetalk.org/dr-richard-bartlett-shares-covid-information/, and his article https://americacanwetalk.org/wp-content/uploads/2020/07/White-Paper_Covid.pdf, where he indicates, in brief, that by using the steroid budesonide through nebulizer, plus zinc, and the addition of an anticoagulant and if needed an anti bacterial, to prevent opportunistic infections of the lungs.

So, as mentioned, the evidence keeps on mounting but the repression is preventing the rest of the public to learn about all of these discoveries and more… but I rather stop here because if not, this will never see the light, at least for the eyes of those with eyes to see.

References (With asterisk (*) the key references displaying the INSERTS and Changes of Sars-CoV-2):[7]

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[7] Many extra references are given as links within the body of this article, due to the space and time constraints.

19_TTG_90_TTT_18_CAATCA_18_AAT_9_TAC_L_F_QS_N_Y_Viral_Pangolin_Insert_with_Receptor_Binding_Domain_RBD_in_a_Virus_of_Bat

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Acknowledgments

To all those mentioned within the body of the text, plus Raul Martin Cruz Mireles, for suggesting me to elaborate this work, then to Mike Jagdeo, for initially suggesting me to explore this issue of COVID-19 for the good of humanity: https://www.youtube.com/watch?v=Dy9xBQiX-OY (in English), and https://www.youtube.com/watch?v=pI5hQByiCJ4 & https://www.minds.com/newsfeed/1117997650357039104 (thanks to Estefano Macedo

Reyes & Manuel Murillo (Kardagar), on the 25th of June, 2020: 50,000 views at its original site: https://www.facebook.com/KardagarCoaching/videos/713879892781432/; and https://www.facebook.com/KardagarCoaching/videos/1194328894267668/, on the 31st of July, 2020: 16,457 views), to Arheli McAlden for the brief: https://tinyurl.com/gates-cries-wolf (in Spanish), and to Ramon Segundo Gimenez Adan, for suggesting the new heading containing the scripture from the Ephesians, as I had others in my first Spanish draft of this work: https://fdocc.yolasite.com/resources/fdocc-antiCOVIDiana1.pdf & https://fdocc.yolasite.com/resources/RastreandoLasCausasDelCOVID-19.pdf. Apologies if I forget to mention someone, as in this planet right now, we are all united in our efforts to find the solution to this "*Plandemic*" as soon as possible, and with the deepest hope that this will not happen again, this thing of the release of a human-made virus with the purpose of *rebooting* humanity into a global China electronically surveyed, courtesy of Gates. No! At least not while we are still here, the born-again ones (so, if you are one of them, you know what I mean). So, I also thank all of my family (who reviewed this article), including the one that was, and the one that will be: "Hi", God willing and if we are still here. So, I got this grant, to seek for the truth, and to fight diseases as well as to fight perverse people, either foreign or domestic, so that I will continue on doing until I still have breath: T32 HL-07812. And as Petrovsky said: "*This publication's contents are solely the responsibility of the author and do not necessarily represent the official views of their affiliated institutions or of its funding body*".

Appendix A

And, because we are humans and not robots (say NO to "*transhumanism*") yet, we have feelings and also positions, so, as per the last, I add the next: So, finally, as we will see, the anticipated insistence of Bill Gates and of Anthony S. Fauci in relation to the fact that a pandemic was going to be unleashed at about this time (at the end of the "*Decade of vaccination*" of Gates, and at the "*New administration*" of Fauci), and their insisting an constant promotion of a vaccination for all of the humanity, at the unison of the WHO, UN, in order for them all to be able to insert into humans an electronic "*certificate of digital vaccination*"; however, we are completely opposed; Furthermore, RNA vaccines are useless because they insert a constantly changing genetic fragment of a virus, as I develop in my further discussions at: https://www.researchgate.net/post/Fifth_Sequence_COVID-19_2_variants_ATG-246-TT_CA-111-TAA_TTA_L_L-Type_70_TCA_S_S-Type_30_in_position_28144_of_MN908947_for_ORF8_NifB, https://www.researchgate.net/post/Seventh_Sequence_COVID-19_2_variants_ATG-1836-GA_GT-1977-TAA_GAT_D_L-Type_GGT_G_G-Type_in_position_23403_of_MN908947_Spike, https://www.researchgate.net/post/Eight_Sequence_COVID-19_2_variants_ATG-878-CC_TT-1729-TAG_CCT_P_L-Type_CTT_L_G-Type_in_position_14408_of_MN908947_for_NSP12 and https://www.researchgate.net/post/Sixth_Sequence_COVID-19_2_variants_ATG_132_GC_TC_1104_TAG_GCC_A_L-Type_70_GTC_V_S-Type_30_position_8782_of_MN908947_for_NSP4; furthermore, "*bioterrorism*" expert Fauci has ignored the necessity to investigate the real cause for the origin of the virus of COVID-19 coming out from a laboratory at Wuhan, being himself based in the very discredited work of opinion by Andersen *et al*. (2020), which even itself says on passing two key "*it is*" clauses: "*…it is reasonable to wonder why the origins of the pandemic matter …it is currently impossible to prove or disprove the other theories of its origin*…". Anthony S. Fauci said (18th of April, 2020, with my notes in parenthesis for the blind): "*There was a study, ah, recently that we can make available to you were, a, group of highly qualified evolutionary virologist (that is how he said it) look at the sequences there and the sequences in, ah, bats (what nonsense!!, it is about a "virus" of bats, not about the bats themselves!), as they evolve, and the mutations that it took to get to the point where it is now (that is a total baloney and of all men, Fauci should know it!, it is a total lie!, the authors that he is quoting only did a side by side comparison of independent sequences, but, the lack of what he is saying: of a sequential history of a natural change of Sars-CoV-2, is what is going to be able to get all the ones who did this, and also all the ones who planned it!; then, Fauci continues:) is totally consistent with a jump of a species from an animal to a human (and this does not discard at all that the animal was a lab animal!), so, I mean, there, the paper will be available, I don't have to quote this right now, but we can make that available to you*": https://www.youtube.com/watch?v=p6REBEb3v9s So, my comment here is that once more the absurd Darwinian theory of evolution is trying to be used on purpose by the ones most deeply involved in the design and in the release of COVID-19, to cover-up in that way, the fact that we are dealing with a man-made virus!; the nefarious reference mentioned by Fauci is precisely that of Andersen *et al*. (2020).
And, since all of this has a strong political background, here I add some recurrent observations:

I was saying that there is dishonesty on the part of Baric and of all of those who have a invested intere$t in these viral studies (Gates, Shi, Osterholm, Holmes, Daszak (and his *pushed-on* signatories), Fauci, Collins (sorry, I used to have respect for this one, until he showed his anti-scientific support of the Andersen *et al*., (2020), a theoretical, non-experimental, piece of…, I mean, we were just starting the research and Collins was already singing the end of it in his blog and everywhere!; but no, we are just at the beginning, that is why at the beginning I dedicated this article to Collins, because I still have some hopes on him to help us solving the current stakeout of

humanity by some very heartless people. Collins wrote to me: "Collins, Francis (NIH/OD) [E] collinsf@od.nih.gov To: Fernando Castro-Chavez fdocc@yahoo.com. Dec. 29, 2019, 5:50 PM. (The same day that his contribution against sickle cell anemia appeared on TV, in "*60 minutes*"). Hi Fernando, *Thanks for your message. I am glad to know of the way in which you*... (Then, also the names two of my collaborators) *have been pursuing visions about contributing to medical advances*... Francis Collins."), Andersen *et al*, Baric…); and of how Gates financed *The Royal College of London* where Neil Ferguson works, and Neil was the one that did the false and dire prediction oft-repeated by Brix & by Fauci, reason for the lockdown of the USA that is causing a big Depression era crisis: https://archive.vn/vTnPz Watch the interview (if they haven't censored it yet: https://web.archive.org/web/20200512220911/https://plandemicmovie.com/; https://www.facebook.com/eter.revista/videos/2627607584188909 (and her books that are pure gold: "*Plague. One Scientist's Intrepid Search*…": https://play.google.com/books/reader?id=kFyCDwAAQBAJ and "*Plague of Corruption. Restoring Faith in the Promise of Science*": http://old.autismone.org/documents/Plague%20of%20Corruption-eARC.pdf, https://play.google.com/books/reader? id=-8KZDwAAQBAJ). And this one, just to show that the WHO, UN, only cater to the best bidder, to the be$t donor: https://www.youtube.com/watch?v=5pqXaCqyHec, while the highest criminals escape from the law with money: https://www.justice.gov/opa/pr/harvard-university-professor-and-two-chinese-nationals-charged-three-separate-china-related, https://www.youtube.com/watch?v=4JxM7IauNj8; also watch: https://lbry.tv/@fdocc:b/COVID-19-Is-Gates-To-Implant-Humans:d

A final note about opening the Flood-Gates wide open for this investigation that started at the *Research Gate*, and I need to be explicit so as to make the reader aware of the current impending attack, and from where it's coming:

Now, another extra piece of information that could explain the reasons why this COVID-19 virus escaped precisely when trials were taking place in plain sight in New York for a possible pandemic, event organized by Bill Gates, by John Hopkins and by the WEF: ("*Event 201*": https://www.youtube.com/watch?v=LBuP40H4Tko), we need to remember that Gates owns a *Microsoft* factory in China with more than 6,000 employees (https://web.archive.org/web/20200422003716/https://www.theguardian.com/technology/2019/apr/22/microsoft-workers-decry-grueling-996-working-standard-at-chinese-tech-firms, https://web.archive.org/web/20200504132151/https://www.gatesnotes.com/Health/Pandemic-Innovation), and that he has a patent, precisely in this year of 2020, the cynically labeled international patent WO/2020/060606, designed to implant a chip in people, to be used instead of IDs or credit cards, for the *cryptocurrency* (https://web.archive.org/web/20200429040224/https://patentscope.wipo.int/search/en/detail.jsf?docId=WO2020060606), and that Gates was helping the CCP with a nuclear plant (Morrell, 2020); In addition, on December 18 of the last year (before the pandemic broke-out around the world), the following publication came out in one of the *Science* family magazines, an article sponsored by Gates entitled: "*Biocompatible Near- Infrared Quantum Dots Delivered to the Skin by Microneedle Patches Record Vaccination*" (McHugh *et al*., 2019, see ref. above), and the fact that during the pandemic he has referred to the need for a "*digital certificate of vaccination*" for all the world population (https://www.youtube.com/watch?v=1LekHJc9Hsc), while Anthony S. Fauci had already indicated as well, as Gates did, that this Pandemic will happen now: https://www.youtube.com/watch?v=fe-cbMLJZzU; therefore, they remains permanently involved in the design and execution of this Pandemic, and this also indicates that he, too, was already aware in advance of this pandemic that we are suffering right now. Gates sponsored the documentary "Pandemic" for *Netflix* before it all happened, in a very similar way as it has been planned by them (https://web.archive.org/web/20200417064450/https://www.ccn.com/bill-gates-predicted-coronavirus-like-outbreak-in-2019-netflix-documentary/); plus, all the links of the next information are also vital to know the best known details of Gates: https://archive.vn/OFszF, as well as: https://www.corbettreport.com/gates; and in 2015, in the same year that Zheng-Li and Baric were working on designing a deadly virus against the elderly mice in *Chapel Hill* (or should I say: *Chapel Hell*?) at the University of North Carolina, Gates said at a *TedX* conference that a great pandemic was the biggest threat for humanity, and in its background transparency appeared a big orange syringe (English: http://youtube.com/watch?v=6Af6b_wyiwI, Spanish: https://www.youtube.com/watch?v=iSB7HT6jvoQ), and that we needed to be prepared, in addition to having already given those ten billion dollars to enact vaccination to his employees at the *World Health Organization* in 2010 (https://web.archive.org/web/20200503205638/https://www.gatesfoundation.org/Media-Center/Press-Releases/2010/01/Bill-and-Melinda-Gates-Pledge-$10-Billion-in-Call-for-Decade-of-Vaccines), decreeing that this would be "*the decade of vaccines*", a prospect for Bill that would begin precisely at the real time of the appearance of the virus in late 2019. (https://web.archive.org/web/20200502075616/https://www.theguardian.com/world/2020/mar/13/first-covid-19-case-happened-in-november-china-government-records-show-report). The software to quantify the victims by COVID-19 by the centralized part of the Johns Hopkins, just as they had planned, seems to be the same one that was presented in the "*Event 201*", and we all know that the numbers are being hyped up out of proportion. As we said, Anthony (Tony) S. Fauci in 2017 could not contain himself from "predicting" the Pandemic that currently afflicts us (see above); and, much more needs to be said about all this, but I leave to the reader, if he

wants, to explore all these details for himself, and even more if he wishes, so that he can then draw his own conclusions and take his due precautions. The deliberate and artificial "scare" that they want to push, in order to get away with their vaccination to implant humanity, can be seen, as per a CDC presentation profiling their own plans using fear: https://web.archive.org/web/20171126152327/https:/www.nationalacademies.org/hmd/~/media/Files/Activity%20Files/PublicHealth/MicrobialThreats/Nowak.pdf

Another additional source that carefully explores all of these issues in an excellent way, is that of a retired *NIH* researcher and programmer: Karl Sirotkin, and his brother (Sirotkin and Sirotkin, 2020a, b and c).

And, remembering the past so as to track the usual globalist culprits, "Operation Pandemic", by Julián Alterini: https://www.youtube.com/watch?v=4hUMzxAjKkw (thanks again to the indefatigable Alberto Rubio-Casillas).

Another researcher who makes extraordinary videos inside a natural setting with his own perspective indicates the following: "J. C.'s current theory: "The Chinese government sponsored intense viral research, including gain-of-function research in cooperation with the US. Any accident would potentially involve both countries in a Global Crisis, which is why both countries cling to the explanation of the "*Market*" (as the source of the emergence of COVID-19, that now should be reworded as "to the "*natural*" and then, forced by the pressure, to the "*accidental*" explanation"), while at the same time taking advantage of the crisis to reduce the freedoms of their respective populations. A penniless economy, the loss of end-to-end encryption, and the elimination of anonymous SIMs on mobile phones (are parts of their "agenda"). In the case of the United States, there is also a massive robbery in plain view through *Wall Street*": https://www.youtube.com/watch?v=HmSCMb8Nds4 (link of his criticism to the erratic article of Andersen *et al*., 2020), and then: https://www.youtube.com/watch?v=We7m_ImCo2Y, to his take of the robbery going on right now.

The cynicism of the virologist community that studies the Gain-of-Function (GoF) is revealed in the following text: "..." Arbovirus ". A total of 34 reporters (here, oh Chinese translator, it should be: "speakers" not "reporters") from 10 countries gave wonderful (look at this expression right here in the midst of the talk about deadly viruses) reports on SARS coronavirus, MERS coronavirus, influenza virus, Ebola virus, Nipah virus, Zika virus and other major emerging viruses ... Prof. Ralph Baric of the University of North Carolina, Dr. Peter Daszak of the Ecohealth (and I must say here: "*Ecohell*", a man sponsored by Gates: https://archive.vn/n4Lse#selection-919.99-919.112, already acknowledged as *Plandemic Inventor Globalist*, with a criticism: https://archive.vn/hG4lf) Alliance ... gave plenary readings ..." (And here, the photo and the expressions, as Deigin said, of "*The Wuhan Clan*": https://web.archive.org/web/20200404101918/http:/english.whiov.cas.cn/Newsletter2016/201811/P020181130367907308937.pdf

I pray that in this case, it does not happen what happened on September 11, 2001 (9/11, 11s: https://www.youtube.com/playlist?list=PLBgVyFmx_rhpViYF5nZfeYhQBopMVegtw), when people were so blinded by the media and by the voice of the government of Bush, Cheney and Rumsfeld, that basically nobody was interested in really knowing what had happened; and even now, when some of that is thoroughly investigated, few people want to know the truth about what really happened, even if the research is sponsored by a serious university: http://ine.uaf.edu/wtc7, but the taking over of our freedoms (that they call the "NWO") started with the criminal cabal "headed" by Bush. Their "Patriot" act is the most Anti-Patriot, Anti-USA document!: http://patriotsquestion911.com/military, https://www.youtube.com/watch?v=TdGJQgEMnxI, https://www.youtube.com/watch?v=36LdCzUhiPQ, http://patriotsquestion911.com/, https://911truth.org/, https://www.ae911truth.org/, and something about it in Spanish: https://www.youtube.com/watch?v=3X2RYw0huik, https://www.youtube.com/watch?v=6q3Zuq0n03s, etc.....

So, it is very important to identify this strain of COVID-19 in all its details as being something artificial, because those who designed it will not cease for anything in the world, and very likely, if they are not arrested, they will continue to silently spray this virus into the main cities of the world (Shi has threatened saying that this is just the "tip of the iceberg", what a cynical person!), hence the great danger of not being able to identify that such virus is something artificial (as well as the extremely inflated numbers portrayed on TV, demonstrating that they are promoting false positive tests (so, notable people of the world, be aware not to be used as a "false positive"), of *Medicare* giving money to hospitals, forcing them to put as COVID-19 any other kind of death: https://archive.vn/0dwH3, and all over the world corrupt politicians of the medical departments are inflating the numbers after receiving bribes: https://archive.vn/XlWXp (in Spanish, and some of these news are not even reaching the English speaking reader!), and then the false and exorbitant inflation of the false-positives: https://archive.vn/EbaOt, plus a corrupt Mass Media accomplice of (& benefiting from) the organizers of this current "*Plandemia*", and the test "*kits*" cynically saying that they are deliberately aimed at giving false positives, because the: "*Detection of viral RNA may not indicate the presence of infectious virus or that 2019-nCoV is the causative agent for clinical symptoms... This test cannot rule out diseases caused by other bacterial or viral pathogens*": https://web.archive.org/web/20200418065800/https://www.fda.gov/media/134922/download; and then, we have the case of the President of Tanzania who tested those test "*kits*" by putting oil of cars and even "juices" of fruits and of

animals, and all of them gave false "positives" for COVID-19: https://archive.vn/0elwj, https://www.youtube.com/watch?v=s4p8DM8rKJI, plus all the good politicians that are against the false Pandemic of Gates, like those in Italy: Vittorio Sgarbi: https://www.youtube.com/watch?v=p1zkhSPwuMY, and Sara Cunial: https://www.youtube.com/watch?v=jLuriUhiuZ8; as well as endless doctors, such as Dr. Vernon Coleman: https://www.youtube.com/watch?v=k2NLa3aNUw4, Dr. Peter Breggin: https://www.youtube.com/watch?v=Y4E90SCSqS0, Dr. Chris Martenson, PhD Pathology: https://www.youtube.com/watch?v=eD3ztjqYGbg, Dr. Meryl Nass with Dr. Mercola (she clearly states her criticism of the reefers Lipkin, Garry, and the other three, plus Daszak and his signatories, *PDF*: https://tinyurl.com/Meryl-Nass): https://articles.mercola.com/sites/articles/archive/2020/06/14/how-did-coronavirus-originate.aspx, and the thousands of doctors at "London Real": https://londonreal.tv/dr-rashid-buttar-hosts-a-doctors-covid-19-roundtable-1000-voices-strong/, including Dr. Rashid A. Buttar: https://londonreal.tv/digital-freedom-platform-interview-1-dr-rashid-buttar/, https://www.facebook.com/LondonReal/videos/dr-rashid-buttar-the-coronavirus-agenda-what-the-mainstream-media-dont-want-you-/574272199867728/, the bold Nurse Erin Marie Olszewski, and Nicole Sirotek: https://www.youtube.com/watch?v=UIDsKdeFOmQ, etc.); so, given this situation, and finally so that it could be left on the written form one more time: The "escape" of this virus happened at the most opportune moment to be able to coalesce with the universal vaccination plans by Bill Gates, the WHO and Fauci, with the *Microsoft* digital microchip, published in advance in that mentioned scientific journal (McHugh *et al*., 2019), and since everything coincides with the temporary calculations of Bill Gates given to the WHO, at the end of culmination of the "*decade of vaccines*" (Gates Foundation, 2010), in addition to the joint predictions of Gates (2015) and of Fauci (2017), already indicated, as well as their way of trying to cover-up the artificial origin of the virus, plus Gates' sponsorship of the documentary "*Pandemic*" and of "*Event 201*", among many other things, all this indicates that the conclusion of this work is the option Ha and not its opposite *Ho*.

Due to the fact that the information concerning to this virus is accumulating on a daily basis and seems to be unlimited, as mentioned, I decided to call this article the second version (*v. 2*), as it is used in programming, due to the active participation of Gates in this Pandemic: 1) Announcing himself the arrival of it on *TedX* under the image of a gigantic syringe in 2015 (and in many other platforms, such as in Davos, etc.), 2) financing himself in 2019 the boring *Netflix* documentary program called "Pandemic", and 3) Organizing the "Event 201" with his subordinates at Johns Hopkins and at the WEF: https://www.youtube.com/watch?v=LBuP40H4Tko (there, in the min. 30:50, you even hear the suggestion to use stealthy low-profile *trolls* to disrupt the efforts to promote a truthful message regarding the artificiality of such "Pandemic", which for me goes to the very moment of the design of the Sars-CoV-2 in a lab, precisely in preparation for the current man-made "Pandemic").

So, I ask: And the CCP president comes out smiling and saying that they have been "*transparent*" about COVID-19? No way! Who believes him? and from the next link: https://qz.com/1811018/chinese-citizens-use-github-to-save-coronavirus-memories/, https://archive.vn/d5PZC, we can see the denouncing of that inhuman treatment to Chinese by the CCP, somehow similar to what the *Facebook*, *YouTube*, and other currently repressive platforms (*Twitter*, *Amazon*, etc…) are starting to do right now; just check how the videos by Judy Mikovits are being eradicated over and over from the *YouTube* (so, I have posted them elsewhere!: https://lbry.tv/@fdocc:b/Mikovits3:d, https://www.minds.com/newsfeed/1113505654201704448, https://www.minds.com/newsfeed/1113663893874728960, plus others that have also been removed from the YT), while her detractors freely smear and speak against her. So, it seems that Gates, the WHO, Fauci and their likes want to make a new 5G controlled China out of all of us, out of all the humans of the planet. I think that we need to keep on praying to stop their madness! Don't you think?

And then, Couey (2020) continues: "Several scientists with obvious conflicts of interest (Daszak, Fauci, Collins, Andersen *et al*., Osterholm; and others non-scientists and non-doctors such as Tedros, the WHO director and subordinate to Gates, and Gates himself, thus far the "mastermind" of the COVID-19 "discourse", and if I may say: of its "operation", because he has said, that the CCP: "*did a lot of things right at the beginning*": https://archive.vn/wsfM9, https://archive.vn/81m84, but then I ask: They did like what, Gates? 1) Like releasing SARS-CoV-2 on your behalf? 2) Like silencing that the COVID-19 problem started in Wuhan at least since September of 2019: https://www.youtube.com/watch?v=8uIVf_o9aXM? 3) Like silencing and disappearing the whistleblowers? 4) Like deleting the evidence? 5) Like lying about the real numbers of the victims? 6) Like forbidding any scientific publication about COVID-19 until reviewed and authorized by the CCP? 7) Like you Gates building a nuclear plant for the CCP? (Morrell, 2020; https://archive.vn/6K0aR), 8) Like you sending money to the CCP of China: https://archive.vn/ni6yk, https://archive.vn/T1WpN, 9) Like you owning a *Microsoft* factory in China with more than 6,000 Chinese employees, almost all of them enslaved and complaining of your bad salaries, both there and in America: https://archive.vn/i9A0D, https://archive.vn/E37dd, 10) Like you financing Daszak to plan a Pandemic?: https://archive.vn/n4Lse; https://archive.vn/YfsOA, 11) Josh Rogin said (https://archive.vn/81m84), that the CCP "arrested three more journalists for the crime of posting covid-19 articles on *GitHub* (which is, incidentally, owned by

Microsoft)": https://archive.vn/UrQ0L (please, also pray for the missing and brave young Chinese men!, squeezed under the common hands of the CCP and of *Microsoft*) etc., etc. And then, I say to Gates: "Bill Gates, you do not own the humanity, stay frozen in a corner and desist of your attempts to "digitize" humans!: Stop those attempts of you to insert into humans your "digital" signature with the pretext of immunizing against COVID-19 via a vaccine!", Gates, you and all your cronies:) have been permitted to go on the record denying that it would be possible to generate such a virus in a laboratory and stating specifically that the sequence of SARS-CoV-2 would never have been chosen by any "gene jockey"… " So, hey "*Gis-no-aid*", thus far for me it looks like it belongs to a selective club of accomplices and of deceivers: "*How did that polybasic furin cleavage site PRRA get into COVID-19?*", because it has no close relatives at all, just it is still a comparative empty space for this COVID-19 PRRA region (as it is nicely shown by Wu *et al*., 2020a). We do not want you, Gates, to have a secretive and private hold of genes under your wraps and control, as you did controlling the free software in the past, because then you can lie as hard as you want, as the CCP WIV lab of Zheng-Li does now!

And I wish to end with the next words by Couey: "Both of these denials are not genuine scientific rebuttals, but rather semantic pseudo-denials formulated by some of those most closely tied to the funding of these [gain of function] research lines... (GoF is laboratory work to increase the ability of pathogens to cause disease)."

Just before submitting, sent to me by Monica Gonzalez the next article: https://www.medrxiv.org/content/10.1101/2020.05.04.20090076v2, a work done by 22 researchers, where they conclude of a: "Comparably low secondary infection risk despite the high rate of transmission … (also) seen in influenza (H1N1) 14.5%35 or SARS 14.9%..., (and is) consistent with… 16.3% in Chinese and 7.56% in South Korea", as well as: "Virus neutralization assays in general can be false positive, as cross-reactivity between betacoronaviruses is well-known"; highlights of the interesting interview to Hendrik Streeck are: "Lethality is only 1/10 of what was first thought"!, "The probability of contagion between the inhabitants of the same household is of only the 15%, way far less of what initially was suspected"!, "The lethality rate of the infection is 0.37%... even the lethality at Bergamo, Italy (where a high number of cases was reported), is 0.43% (a number that may go down when the world population is included), …while for the flu is 0.1%"!, "I estimate that a possible re-infection will not be as severe as the initial infection"!, "Herd immunity could be our only weapon against this virus"!, "COVID-19 did NOT hit as hard in Germany, Vietnam, Japan or Greece"! "Confining populations to be inside their homes is a mere political decision"! https://archive.vn/s2NfN

Appendix B

Figure A: Fernando Castro-Chavez at the Hong Kong airport on July 6; and in Guangzhou, China on July 13, 2019.

China

In July of 2019, I had the unusual privilege of passing through Hong Kong (Fig. A, left) before the protests against a centralist control of the CCP in China, China oppressing and killing Hong Kong at the sight of everybody: https://www.youtube.com/user/epochtimesdigital. The protestors arrived at the gigantic airports of this city after I passed through it (on day six), and I returned through Guangzhou (Fig. A, right), where I talked with a family from the south of Mexico who were detained in a checkpoint and in a room inside that airport, for the entire week that their trip would have taken place, because they did not have their return tickets (I was talked to them on the thirteenth day, and we returned on the same plane): https://www.youtube.com/watch?v=f94GNEKF2NQ, https://tierrapura.org/2020/06/15/activistas-chinos-seran-juzgados-por-publicar-articulos-del-virus-pcch-censurados-por-el-regimen/ (Both in Spanish).

Figure B: The author, Fernando Castro-Chavez at the NYMC in Valhalla, NY, in October, 2019; and at the Gershwin Theater in Manhattan, NY, Feb., 2020.

New York

I was working as a Postdoctoral at the *New York Medical College* since the end of September and during the month of October 2019 (Fig. B, left), then I returned briefly to New York again from February 10th to the 12th, of the 2020 (Fig. B, right); but, because of this COVID-19, I am distant to the one I want. But at least, I thank God for having been able to leave that place with health and with peace, escaping from all the deception, the oppression, the lies, the corruption, the pressures for murder, etc., for whose solution I am praying (and for the great people that I met there!: https://www.youtube.com/watch?v=kIngGuof9E0, https://www.youtube.com/watch?v=5pqXaCqyHec).

Appendix C

Individual matches with bacteria, of the Furin/Plasmin cleavage site insert of 12-bases, plus its extra 3-bases from the backbone: CCTCGGCGGGCACGT, from the resulting 1,366 sequences obtained (with a match of a 100% per identity and an E-value of 463), the first 100 bacteria in order of appearance were selected from the general Nucleotide database (on the 06/13/2020); here, I put them in order of appearance (in this case, the multiple repeats are not enumerated).

Bacterial matches:

1) Ralstonia solanacearum, 2) Pseudomonas sp., 3) Rhizobium pusense, 4) Microbacterium hominis, 5) Achromobacter pestifer, 6) Actinomadura verrucosospora, 7) Nocardioides sp., 8) Pseudonocardia sp., 9) Cellulosimicrobium sp., 10) Herbiconiux sp., 11) Desulfovibrio marinus, 12) Streptomyces sp., 13) Bordetella avium, 14) Spirosoma sp., 15) Aplosporella prunicola, 16) Aspergillus tanneri, 17) Rhodococcus sp., 18) Yokenella regensburgei, 19) Nocardia terpenica, 20) Nocardia arthritidis, 21) Nocardia brasiliensis, 22) Phytohabitans flavus, 23) Deinococcus radiodurans, 24) Brevibacterium luteolum, 25) Hydrogenophaga sp., 26) Phycicoccus sp., 27) Sanguibacter sp., 28) Propioniciclava sp., 29) Apiotrichum mycotoxinovorans, 30) Pseudenhygromyxa sp., 31) Mameliella alba, 32) Bradyrhizobium sp., 33) Pseudomonas monteilii, 34) Caulobacter sp., 35) Fluviibacterium aquatile, 36) Streptomyces albus, 37) Caulobacter rhizosphaerae, 38) Pseudomonas otitidis, 39) Haloferax alexandrines, 40) Thermaerobacter sp., 41) Granulicella sp., 42) Mycolicibacterium insubricum, 43) Mycobacterium heidelbergense, 44) Mycobacterium parmense, 45) Mycobacterium conspicuum, 46) Mycolicibacterium madagascariense, 47) Mycobacterium gallinarum, 48) Mycolicibacterium pulveris, 49) Mycolicibacterium parafortuitum, 50) Mycobacterium paraintracellulare, 51) Mycolicibacterium celeriflavum, 52) Mycolicibacterium sediminis, 53) Mycolicibacterium litorale, 54) Mycobacterium marseillense, 55) Mycolicibacterium boenickei, 56) Mycobacterium florentinum, 57) Mycolicibacterium alvei, 58) Mycolicibacterium duvalii, 59) Mycobacterium novum, 60) Cellulomonas sp., 61) Gemmata obscuriglobus, 62) Gemmata massiliana, 63) Pseudomonas putida, 64) Micrococcus luteus, 65) Pandoraea fibrosis, 66) Variovorax sp., 67) Rathayibacter sp., 68) Rathayibacter festucae, 69) Paraburkholderia sp., 70) Janibacter melonis, 71) Haloactinobacterium sp., 72) Saccharopolyspora sp., 73) Amycolatopsis sp., 74) Enterobacter sp., 75) Paracoccus pantotrophus, 76) Actinomadura sp., 77) Microbacterium sp., 78) Streptomyces chartreusis, 79) Streptomyces spectabilis, 80) Streptomyces cinereoruber, 81) Streptomyces coeruleorubidus, 82) Streptomyces viridifaciens, 83) Streptomyces kanamyceticus, 84) Bordetella bronchiseptica, 85) Streptomyces venezuelae, 86) Thermosynechococcus sp., 87) Mycobacterium grossiae, 88) Methylobacterium sp., 89) Mycobacterium phage, 90) Bradymonadales bacterium, 91) Baekduia soli, 92) Micromonospora sp., 93)

Micrococcus sp., 94) Phycisphaerae bacterium, 95) Planctomycetes bacterium, 96) Corynebacterium sanguinis, 97) Cellulosimicrobium cellulans, 98) Paraoceanicella profunda, 99) Rhodococcus hoagie, 100) Bordetella hinzii…

Non-bacterial matches:
1) Felis catus, 2) Tursiops truncatus, 3) Daldinia childiae, 4) Coregonus sp., 5) Malassezia furfur, 6) Gordonia sp., 7) Gordonia bronchialis, 8) Nonomuraea sp., 9) Mycobacterium phage, 10) Limnoglobus roseus, 11) Aquisphaera giovannonii, 12) Sparus aurata…

Predicted:
1) Thrips palmi, 2) Orcinus orca, 3) Daphnia magna, 4) Phocoena sinus, 5) Corvus moneduloides, 6) Camelus dromedarius, 7) Globicephala melas, 8) Delphinapterus leucas, 9) Sphaeramia orbicularis, 10) Salarias fasciatus…
Concluding (while excluding the "*predicted*" sequences):

There is a 92% of this COVID-19 sequence that produces the cleavage site PRRAR: CCTCGGCGGGCACGT, of being from a bacterial origin (see the full comparison at: https://archive.vn/vk0dD, and this is to be compared with my discovery (Castro-Chavez, 2012) of the other, also of 12-bases contaminant sequence: CCCGAATTCGGG, of those far more than 40 Billion of sequences currently contaminated at the *GenBank*, as it provided an E-Value of 4^10 for the top sequences: https://archive.vn/iydrl), so, we again recommend, as we did in the original 2012 report, to verify each Zheng-Li Shi sequence, and any other sequence originated in China, and in general, to verify the sequences deposited at the *GenBank* by at least three independent international (not corrupted, even if that is very hard to do) labs. Thank you. Last Note: A final submission, in French, by M. Ovensmith to me was: http://bricage.perso.univ-pau.fr/UTLA/VIRUS/WuhanEngineeredCoronavirus-2-S_O.pdf, there we read this awesome epilogue that I also wish to make mine! (So, I translate): "*When the lies take the elevator, the truth takes the stairs. Even if it takes longer, the truth always ends up coming!*" Luc Montagnier (17/04/2020).

Appendix D

FROM: *ANTICOVIDIAN V.2* by Fernando Castro-Chavez (06/18/2020)

Sars-CoV-2: MN908947

Thus far, these are the sequences that seem to be modified (3,715 of 29,903, the 12.42%):
NSP4 (sequence of 20 NT):
…TGATTTTGACACATGGTTTA….
NSP12 (sequence of 44 NT):
…ATTGTGCAAACTTTAATGTTTTATTCTCTACAGTGTTCCCACCT… (Not the last six, just included because right there next to our sequence of interest, there is a polymorphism, a C that has been changed for a *T*: https://www.researchgate.net/post/Eight_Sequence_COVID-19_2_variants_ATG-878-CC_TT-1729-TAG_CCT_P_L-Type_CTT_L_G-Type_in_position_14408_of_MN908947_for_NSP12)

Part of NSP15, NSP16 complete, and partial S: S1 plus part of S2 (sequence of 3576 NT, in Spike we see an A, indicative that such has been replaced by a G, making it more aggressive, the infamous D614G):
…AATCACCTTTTGAATTAGAAGATTTTATTCCTATGGACAGTACAGTTAAAAACTATTTCATAACAGATGCGCAAACAG
GTTCATCTAAGTGTGTGTGTTCTGTTATTGATTTATTACTTGATGATTTTGTTGAAATAATAAAATCCCAAGATTTATCTGT
AGTTTCTAAGGTTGTCAAAGTGACTATTGACTATACAGAAATTTCATTTATGCTTTGGTGTAAAGATGGCCATGTAGAAA
CATTTTACCCAAAATTACAATCTAGTCAAGCGTGGCAACCGGGTGTTGCTATGCCTAATCTTTACAAAATGCAAAGAAT
GCTATTAGAAAAGTGTGACCTTCAAAATTATGGTGATAGTGCAACATTACCTAAAGGCATAATGATGAATGTCGCAAAA
TATACTCAACTGTGTCAATATTTAAACACATTAACATTAGCTGTACCCTATAATATGAGAGTTATACATTTTGGTGCTGGT
TCTGATAAAGGAGTTGCACCAGGTACAGCTGTTTTAAGACAGTGGTTGCCTACGGGTACGCTGCTTGTCGATTCAGA
TCTTAATGACTTTGTCTCTGATGCAGATTCAACTTTGATTGGTGATTGTGCAACTGTACATACAGCTAATAAATGGGATC
TCATTATTAGTGATATGTACGACCCTAAGACTAAAAATGTTACAAAAGAAAATGACTCTAAAGAGGGTTTTTTCACTTAC
ATTTGTGGGTTTATACAACAAAAGCTAGCTCTTGGAGGTTCCGTGGCTATAAAGATAACAGAACATTCTTGGAATGCTG
ATCTTTATAAGCTCATGGGACACTTCGCATGGTGGACAGCCTTTGTTACTAATGTGAATGCGTCATCATCTGAAGCATT
TTTAATTGGATGTAATTATCTTGGCAAACCACGCGAACAAATAGATGGTTATGTCATGCATGCAAATTACATATTTTGGA
GG*AATAC*AAATCCAATTCAGTTGTCTTCCTATTCTTTATTTGACATGAGTAAATTTCCCCTTAAATTAAGGGGTACTGCTG
TTATGTCTTTAAAAGAAGGTCAAATCAATGATATGATTTTATCTCTTCTTAGTAAAGGTAGACTTATAATTAGAGAAAACA
ACAGAGTTGTTATTTCTAGTGATGTTCTTGTTAACAACTAAACGAACAATGTTTGTTTTTCTTGTTTTATTGCCACTAGTCT
CTAGTCAGTGTGTTAATCTTACAACCAGAACTCAATTACCCCCTGCATACACTAATTCTTTCACACGTGGTGTTTATTAC
CCTGACAAAGTTTTCAGATCCTCAGTTTTACATTCAACTCAGGACTTGTTCTTACCTTTCTTTTCCAATGTTACTTGGTTC
CATGCTATACATGTCTCTGGGACC*AATGGTACTAAGAGGTTTGATAACCCTG*TCCTACCATTTAATGATGGTGTTTATTT
TGCTTCCACTGAGAAGTCTAACATAATAAGAGGCTGGATTTTTGGTACTACTTTAGATTCGAAGACCCAGTCCCTACTT
AT*T*GTTAATAACGCTACTAATG*TTGTTATTAAAGTCTGTGAATTTCAATTTTGTAATGATCC*ATTTTTGGGTGTTTATTACCA

CAAAAACAACAAAAGTTGGATGGAAAGTGAGTTCAGAGTTTATTCTAGTGCGAATAATTGCACTTTTGAATATGTCTCT
CAGCCTTTTCTTATGGACCTTGAAGGAAAACAGGGTAATTTCAAAAATCTTAGGGAATTTGTGTTTAAGAATATTGATGG
TTATTTTAAAATATATTCTAAGCACACGCCTATTAATTTAGTGCGTGATCTCCCTCAGGGTTTTTCGGCTTTAGAACCATT
GGTAGATTTGCCAATAGGTATTAACATCACTAGGTTTCAAACTTTACTTGCTTTACATAGAAGTTATTTGACTCCTGGTG
ATTCTTCTTCAGGTTGGACAGCTGGTGCTGCAGCTTATTATGTGGGTTATCTTCAACCTAGGACTTTTCTATTAAAATAT
AATGAAAATGGAACCATTACAGATGCTGTAGACTGTGCACTTGACCCTCTCTCAGAAACAAAGTGTACGTTGAAATCC
TTCACTGTAGAAAAAGGAATCTATCAAACTTCTAACTTTAGAGTCCAACCAACAGAATCTATTGTTAGATTTCCTAATATT
ACAAACTTGTGCCCTTTTGGTGAAGTTTTTAACGCCACCAGATTTGCATCTGTTTATGCTTGGAACAGGAAGAGAATCA
GCAACTGTGTTGCTGATTATTCTGTCCTATATAATTCCGCATCATTTTCCACTTTTAAGTGTTATGGAGTGTCTCCTACTA
AATTAAATGATCTCTGCTTTACTAATGTCTATGCAGATTCATTTGTAATTAGAGGTGATGAAGTCAGACAAATCGCTCCA
GGGCAAACTGGAAAGATTGCTGATTATAATTATAAATTACCAGATGATTTTACAGGCTGCGTTATAGCTTGGAATTCT*AA*
*CAATCTTGATTCTAAGGTT*GGTGGTAATTATAATTACCTGTATAGATTGTTTAGGAAGTCTAATCTCAAACCTTTTGAGAG
AGATATTTCAACTGAAATCTATCAGGCCGGTAGCACACCTTGTAATGGTGTTGAAGGTTTTAATTGTTACTTTCCTTTAC
AATCATATGGTTTCCAACCCACTAATGGTGTTGGTTACCAACCATACAGAGTAGTAGTACTTTCTTTTGAACTTCTACAT
GCACCAGCAACTGTTTGTGGACCTAAAAAGTCTACTAATTTGGTTAAAAACAAATGTGTCAATTTCAACTTCAATGGTTT
AACAGGCACAGGTGTTCTTACTGAGTCTAACAAAAAGTTTCTGCCTTTCCAACAATTTGGCAGAGACATTGCTGACAC
TACTGATGCTGTCCGTGATCCACAGACACTTGAGATTCTTGACATTACACCATGTTCTTTTGGTGGTGTCAGTGTTATA
ACACCAGGAACAAATACTTCTAACCAGGTTGCTGTTCTTTATCAGGATGTTAACTGCACAGAAGTCCCTGTTGCTATTC
ATGCAGATCAACTTACTCCTACTTGGCGTGTTTATTCTACAGGTTCTAATGTTTTTCAAACACGTGCAGGCTGTTTAATA
GGGGCTGAACATGTCAACAACTCATATGAGTGTGACATACCCATTGGTGCAGGTATATGCGCTAGTTATCAGACTCA
GACTAATTCTCCTCGGCGGGCACGTAGTGTAGCTAGTCAATCCATCATTGCCTACACTATGTCACTTGGTGCAGAAAA
TTCAGTTGCTTACTCTAATAACTCTATTGCCATACCCACAAATTTTACTATTAGTGTTACCACAGAAATTCTACCAGTGTC
TATGACCAAGACATCAGTAGATTGTACAATGTACATTTGTGGTGATTCAACTGAATGCAGCAATCTTTTGTTGCAATATG
GCAGTTTTTGTACACAATTAAACCGTGCTTTAACTGGAATAGCTGTTGAACAAGACAAAAACACCCAAGAAGTTTTTG*C*
ACAAGTCAAACAAATTTACAAAACACCACCAATTAAAGATTTTGGTGGTTTTAATTTTTCACAA

Note: AATTACAA (for "Attack" in Spanish) and GAATACA (for the movie with the same name, which demonstrates that it is always possible to defeat the system, no matter how imposing and oppressive it gets!) have been noticed only as a reference.

Updates after the submission of the manuscript:

1) Two more putative contaminants have been found and reported in the next article: https://zenodo.org/record/3766463#.Xuu9RTpKjIW, saved at: https://archive.vn/N79Ci
   And are the next sequences found at the Nsp3:

a) ACTGTTGGTCAACAAGACGGCAGTGAGGACAATCAGACAACTACTATTCAAACAATTGTT, producers of the sequence: TVGQQDGSEDNQTTTIQTIV

b) b) CAAGTTGAACAAAAGATCGCT, which gives: QVEQKIA

2) Then, the next article: https://www.cambridge.org/core/journals/qrb-discovery/article/biovacc19-a-candidate-vaccine-for-covid19-sarscov2-developed-from-analysis-of-its-general-method-of-action-for-infectivity/DBBC0FA6E3763B0067CAAD8F3363E527, indicates that the main insertions that they are selecting for their possible product, were taken from what Zheng-Li Shi herself published: https://www.nature.com/articles/s41586-020-2012-7.pdf, and are as follows (the extra inserted portions provided by this article are painted in yellow in the upper sequence):

(1) Short INSERTION ONE: GTNGTKR: GGGACCAATGGTACTAAGAGG (underlined interface with the findings by Pradhan *et al*., 2020, the ones of the "uncanny…", this sequence is completely embedded in their finding, also found this particular one by Perez & Montagnier, 2020, see main article for references)

(2) Short INSERTION TWO: NNKSWM: AACAACAAAAGTTGGATG (underlined interface with the findings by Pradhan *et al*., 2020).

(3) Short INSERTION THREE: RSYLTPGD: AGAAGTTATTTGACTCCTGGTGAT (underlined interface with the findings by Pradhan *et al*., 2020).

Tabulation: 731 bases or the 2.45% of its total genome! As per the lengths: 20, 38, 56, 16, 21, 18, 21, 57, 18, 28, 37, 26, 16, 111, 36, 21 (the 0.07% putatively by *P. malariae*), 18, 27, 65 (the 0.22% putatively by *P. yoelii*), 60, 21.

Base articles: https://www.nature.com/articles/s41591-020-0820-9, https://www.biorxiv.org/content/10.1101/2020.01.30.927871v1 and https://osf.io/d9e5g/download/?format=pdf

This can also be presented as follows:

Thus far, the next are some of the sequences that seem to be inserts (some of them seem to have been started to be tampered since the RaTG13 "experiment" of Shi Zheng-Li, a genome she had since 2013 but that she

did not publish until 2020 after the first Sars-CoV-2 had been published in China, genome that of the RaTG13 (previously published in part twice with different names that included the number 4991, which is dishonesty in science to change the names of the sequences, and that is what Shi just did!) which has been used, ironically, even with all its methodological anomalies to, precisely attempt to undermine the artificiality of the inserts, even two sequences published earlier by the Military of China seem to have been already tampered to make them more infectious, this is what happens when you only have the sequences provided by them with nobody else corroborating their authenticity), so, I may use the "probable" inserts clause, mostly from HIV-1, some few from HIV-2 and one from SIV (as explained by Perez & Montagnier). So, the number of artificial sequences is growing as research progresses, that is why, when people tries to discredit some of these from being artificially made, the burden is over them to explain how all of them got INSERTED into one same viral genome, which may have required a same animal cell with multiple different viruses and even bacteria exchanging only the specific required portions and no more, which is something naturally implausible but completely possible within a lab setting (most of them are concatenated sequences):

In the the *Nsp3*:

1) ACTGTTGGTCAACAAGACGGCAGTGAGGACAATCAGACAACTACTATTCAAACAATTGTT
   And
2) CAAGTTGAACAAAAGATCGCT

Found by:

Arumugham, V. Root cause of COVID-19? Biotechnology's dirty secret: Contamination. Bioinformatics evidence demonstrates that SARS-CoV-2 was created in a laboratory, unlikely to be a bioweapon but most likely a result of sloppy experiments. *Zenodo* 2020:9 pp. (Manuscript): https://zenodo.org/record/3766463#.Xuu9RTpKjIW, saved at: https://archive.vn/N79Ci

In Nsp4:

3) TGATTTTGACACATGGTTTA

In Nsp12:

4) ATTGTGCAAACTTTAATGTTTTATTCTCTACAGTGTTC

In Nsp15:

5) AATCACCTTTTGAATTAGAAGATTTTA$_{TTCCTATGGACAGTACAGTTAAAAACTAT}$

In Nsp16:

6) ATAAAGATAACAGAAC

And

7) ATGCGTCATCATCTGAAGCAT

And:

8) TGCAAATTACATATTTTG

And:

9) GATATGATTTTATCTCTTCTT

In the interface Nsp16 and S1 from Spike:

10) TTGTTAACAACTAAACGAACA$_{ATGTTTGTTTTTCTTGTTTTATTGCCACTAGTCTCT}$

In S1:

11) TTAATCTTACAACCAGAA
12) ACTTGTTCTTACCTTTCTTTTCCAATGT
13) TCTGGGACC*AATGGTACTAAGAGGTTTGATAACCCTG*
14) TGTTTATTTTGCTTCCACTGAGAAGT
15) TTTTTGGTACTACTTT
16) CCCTACTTAT*T*GTTAATAACGCTACTAATG*TTGTTATTAAAGTCTGTGAATTTCAATTTTGTAATGATC*CATTTTTGGGT GTTTATT
17) CACAAAAACAACAAAAGT$_{TGGATG}$
18) $_{AGAAGTTATTTGACTCCT}$GGTGATTCTTCTTCAGGT

These last two and the 12th and the most important one, the 20, were found by the Indian team that was forced to withdraw:

Pradhan, P. *et al*. Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag. *Biorxiv* 2020: 14 pp. (Withdrawn, 128 comments): https://www.biorxiv.org/content/10.1101/2020.01.30.927871v1

The sequences that appear underlined have been added as INSERTIONS in an article by the main suspect herself, Shi Zheng-Li (in the same article where she introduces the other, now being more clearly that has been a manipulated sequence, that of the RaTG13):

Zhou, P., plus 27 *et al*s & Zheng-Li Shi. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* (Owned by CCP, China) 2020:579:270-73, & 16pp: https://www.nature.com/articles/s41586-020-2012-7.pdf

Most of the previous, and of the last ones, 20, 21 have also been found by:

Perez, J.-C., and Montagnier, L. COVID-19, SARS and Bats Coronaviruses Genomes Unexpected Exogenous RNA Sequences. *Research Gate & OSF* 2020:43 pp. [Old Manuscript]: https://osf.io/d9e5g/download/?format=pdf

19) *AACAATCTTGATTCTAAGGTT* (from *Plasmodium malariae*)

Hong, S-T *et al*. The emergence of SARS-CoV-2 by an unusual genome reconstitution. *Research Square* 2020 (Manuscript): 8 pp.: https://assets.researchsquare.com/files/rs-33201/v1/d78e2bcc-91bd-4246-b4f8-63d2aa86 02da.pdf

This particular one has been called into question as it also appears in a virus from pangolin sequence, but Petrovsky indicates that it or few pangolins could have been deliberately injected with a previous version of the final Sars-CoV-2, as it does not seem to be a localized but not an expanded situation for pangolins:

Piplani S., Singh P. K., Winkler D. A., Petrovsky N. In silico comparison of spike protein-ACE2 binding affinities across species; significance for the possible origin of the SARS-CoV-2 virus. *Arxiv* 2020:34 pp. (Manuscript): https://arxiv.org/ftp/arxiv/papers/2005/2005.06199.pdf

Again, when you have the word of it by only a group of scientists from China with a clear conflict of interests, such as to attempt to cover-up the situation, it is better to put in doubt their claims until independent findings on the wild could be made by other nations and researchers.

20) The precise location of the 18 bases, the 6 x 3 key regions of the RBD:

^{TTG}TTTAGGAAGTCTAATCTCAAACCTTTTGAGAGAGATATTTCAACTGAAATCTATCAGGCCGGTAGCACACCTTGTAA TGGTGTTGAAGGT^{TTT}AATTGTTACTTTCCTTTA^{CAATCA}TATGGTTTCCAACCCACT^{AAT}GGTGTTGGT^{TAC}

Andersen, K. G., *et al*. The proximal origin of SARS-CoV-2. *Nat. Med.* 2020, 26:450–452: https://www.nature.com/articles/s41591-020-0820-9

This is basically a discredited article, a hit-piece done with the purpose to uphold a political view rather than to do science, all the authors of it have been found involved into enforcing a politically convenient scientific view, instead of in doing science, but at least they demonstrate the two basic anomalies, and say that all options are possible, but that their OPINION is..., so, that is basically an OPINION piece.

21) $_{CAGACTAATTCT}$CCTCGGCGGGCACGT

22) *CACAAGTCAAACAAATTTACAAAACACCACCAATTAAAGAT*$_{TTTGGTGGTTTTAATTTTTCACAA}$ (two separate sequences interlaced from *Plasmodium yoelii*)...

Appendix E

My Letter to Francis S. Collins, entitled "*A Vital Letter For The Preservation Of Humanity As We Know It*":

Dr. Collins,

As I have had the blessed confidence to write to a brother in Christ since day one, I am sending you this important message.

With my best regards,

Fernando Castro-Chavez, PhD.

P.S:

I could not fit in the Letter this vital link that independently exposes the hoax imposed on humanity 19 years ago, let us do all we can to prevent this time to happen the same but in a wider scale (Most specially the roots, that are the last three chapters: 6, 7 and 8, for you that like music... good beats but disturbing lyrics): https://lbry.tv/@fdocc:b/AceBakerFinalVersionPart1:4, https://lbry.tv/@fdocc:b/AceBakerFinalVersionPart2:4

At Least Six Research Groups Have Found HIV Inserts In Sars-Cov-2

A Letter to Dr. Francis S. Collins,

Sir, Prompted by this article: Jun 25, 2020 – Health: The *NIH* claims joint ownership of Moderna's coronavirus vaccine: https://www.axios.com/moderna-nih-coronavirus-vaccine-ownership-agreements-22051c42-2dee-4b19-938d-099afd71f6a0.html (https://archive.vn/TArE3), I write to you, saying that we had a deep respect for you (my sister, my girl companion and my peers). The first letter I wrote to you was about Creation, in 2000, just having arrived from my country, and I wrote it in a bad English still, willing to live the American dream!!! Then, we saw you in person, and introduced ourselves, when you went to the *BMC* to give a speech about the *Human*

Genome Project, I remember that you said something like: "Mendel is also there, in this slide, right there at the corner..."; then I wrote about our dreams to pursue, not only these Postdoctoral couple of jobs in Medicine, but also an MD Career, we two starting again from the scratch. Dreaming to be truthful and to really help humanity... However, now, I dedicate to you my current findings, humble, but nonetheless, they are still findings:

1) "COVID-19: AATGGTACTAAGAGG (NGTKR) = HIV-1 isolate 19663.24H9 from Netherlands envelope glycoprotein (env) gene (GU455503)". Finding also done by:
2) Shi Zheng-Li, from the WIV at Wuhan and co-author of Ralph Baric, and she distinctively calls it an "INSERTION" (she puts it as: GTNGTKR, GGGACCAATGGTACTAAGAGG, adding other two more, but skipping the key one: The Furin Site!), whose putative function is immunosuppressant, as she says that those INSERTIONS have: "sialic-acid-binding activity", at: Zhou, P., plus 27 et als & Zheng-Li Shi. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 2020:579:270-73, & 16pp: https://www.nature.com/articles/s41586-020-2012-7.pdf; a third group that found these unique INSERTS is that of:
3) Sørensen (identical to the previous one: GTNGTKR, but also studying, to leave no doubts, its functional span by performing 6 by 6 NT iterations containing our sequence of interest (and of many others), such as: VSGTNG, SGTNGT, TNGTKR, NGTKRF, etc.), who says in an interview, as he found many more INSERTS (saved at: https://archive.vn/7TPTc): "The INSERTED sequences have a functionality that we describe. We explain why they are essential: ...accumulated charge from inserts and salt bridges are in surface positions capable of binding with cell membrane components other than the ACE2 receptor." This statement is very important and indicates that if we realize that this virus is NOT natural we could be and have been better prepared since the start to fight against it in a more logical, rational and prepared way, which did not happen. The artificiality of the virus also makes it unsuitable for vaccination, instead of the opposite, because that is the way the human tampering of nature works, the attempted purpose of its design is to do one thing, and it happens to result just the opposite thing than what was wanted: "...the naked coronavirus spike protein as a concept for the basis of a vaccine, which we have rejected because of high risk of contamination with human-like epitopes. Analysis of the Spike protein of SARS-CoV-2 shows 78.4% similarity with human-like (HL) epitopes..." and "... A search so tailored to match against all human known proteins will give a 78.4% human similarity to the SARS-CoV-2 Spike protein, *i.e* if all epitopes on the 1255 amino acid long SARS-CoV-2 Spike protein can be used by antibodies then there will be 983 antibody binding sites which also could bind to epitopes on human proteins..." The original article delving in all of those technicisms is: Sørensen, B., Susrud, A. and Dalgleish, A.G. Biovacc-19: A Candidate Vaccine for Covid-19 (SARS-CoV-2) Developed from Analysis of its General Method of Action for Infectivity. *QRB Discovery* (by *Cambridge University Press*) 2020:17 pp [Accepted Manuscript]: https://doi.org/10.1017/qrd.2020.8, so, this important article clearly indicates that if we do NOT realize the real origin and the real nature of this virus, we will continue deceived as per its treatment and its strategies of attack, and will be responsible for having on purpose dimmed the light of its artificial origin. Especially when we all are aware that the authors of "The Proximal…", Andersen *et al. Nat. Med.* 2020 article has been written by reefers that have ever been used for political purposes rather than scientific ones. So, apart as these three independent findings of that and many more related HIV sequences, we have another two sets of witnesses, totaling FIVE independent groups finding this: Mine, Zheng-Li's, and Sørensen's, but also:
4) Pradhan, from the Indian group that was forced to withdraw its article, who calls the contained sequence under consideration as the previous ones: "INSERT 1": TNGTKR, elongating the set of meaningful nucleotides as: TCTGGGACCAATGGTACTAAGAGG (SGTNGTKR): Pradhan, P. et al. Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag. *Biorxiv* 2020: 14 pp. (Withdrawn, 128 comments): https://www.biorxiv.org/content/10.1101/2020.01.30.927871v1, they start describing their findings as follows: "We found four new insertions in the protein of 2019-nCoV- "GTNGTKR" (IS1)...", but this is not all, but also a fifth group, being this the one integrated by:
5) Perez and Montagnier (2008 Nobel Prize in Medicine, precisely for his discovery of the HIV virus), and they describe our found sequence within, together with a couple of tens more: TCTGGGACCAAT GGTACTAAGAGGTTTGATAACCCTG (SGTNGTKRFDNP..., finding them in here, fragments of SIV joined to the HIV-1A that I found, and sown in point "1"), from these sequences found by them, they start and end their meaningful conclusions, coming from the wisest of men, as follows: "1) 18 RNA fragments of homology equal or more than 80% with human or simian retroviruses have been found in the COVID_19 genome; 2) These fragments are 18 to 30 nucleotides long and therefore have the potential to modify the gene expression of Covid19. We have named them external Informative Elements or EIE; 3) These EIE are not dispersed randomly, but are concentrated in a small part of the COVID_19 genome... ...everything converges towards possible laboratory manipulations which contributed to modifications of the genome of COVID_19, but also, very probably much older SARS, with perhaps this double objective of vaccine design and of "gain of function" in

terms of penetration of this virus into the cell. This analysis, made in silico, is dedicated to the real authors of Coronavirus COVID_19. It belongs only to them to describe their own experiments and why it turned into a world disaster: 400 000 lives, more than those taken by the two atomic bombs of Hiroshima and Nagasaki. We, the survivors, should take lessons from this serious alert for the future of humanity. We urge our colleagues scientists and medical doctors to respect ethical rules as expressed by Hippocrates oath: do not harm, never and never!"; an earlier manuscript of them can be found at: Perez, J.-C., and Montagnier, L. COVID-19, SARS and Bats Coronaviruses Genomes Unexpected Exogenous RNA Sequences. *ResearchGate* & *OSF* 2020:43 pp. [Older Manuscript]: https://osf.io/d9e5g/download/?format=pdf. I started my letter saying that I used to have respect for you. However, the standing taken as to ignore the real origins documented by these five research groups and by countless others, of the whole pre-planning of the current Pandemic by COVID-19, has made me to change my current opinion about you. Plus a recent one:

6) Arumugham also discusses such "Artificial selection at work… via recombination with HIV-1 derived inserts and selecting the viruses for efficient human kidney cell infection", and my comment is again that to notice this artificial origin of COVID-19 is very important to do the proper treatment to patients, and to prevent another thing like this from emerging out of a Gain of Function "research": Arumugham, V. Root cause of COVID-19? Biotechnology's dirty secret: Contamination. Bioinformatics evidence demonstrates that SARS-CoV-2 was created in a laboratory, unlikely to be a bioweapon but most likely a result of sloppy experiments. *Zenodo* 2020:9 pp. (Manuscript saved at: https://archive.vn/N79Ci): https://zenodo.org/record/3766463#.Xuu9RTpKjIW

My experience on finding human artifacts on genomes dates back to the *EcoRI* palindromic linker that is contaminating thousands of sequences in the Genbank: Castro-Chavez, F. Escaping the cut by restriction enzymes through single-strand self-annealing of host-edited 12-bp and longer synthetic palindromes. *DNA Cell Biol*. 2012, 31(2):151-63: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3272245/

The freedoms of the whole humanity are at stake and the good God The Creator that you deeply respect, has put you in a key position as to be able to revert as soon as possible the current decline of the human values, and of the human nature in general, and this all because of a deliberate release of the current Sars-CoV-2. 9/11 was the first False Flag Operation aimed at stealing as much freedoms as possible from the human race, and the Fake Anthrax Attack of 2001 had the same purpose, releasing a pre-planned and very antipatriotic document called the "Patriot" Act, which also included an immunity clause preventing the Pharmaceutical Industry of even more liabilities, but it was contested by the population, and it was removed. So, I wish to stop the GoF initiatives. Here we are today, contesting the "official" narrative of the current Plandemic as we did in the past with the "official" narratives of 9/11 when we discovered nano-bombs and fake planes injected into the TV screens. I expect to publish this letter on the open after you have read it. Only history will tell if TRUTH was able to win on this time over darkness, or if the criminals will get away once more... With my same thinking as at the beginning of the current letter (but praying that this could very soon change),

Fernando Castro-Chavez, PhD.

P. S.

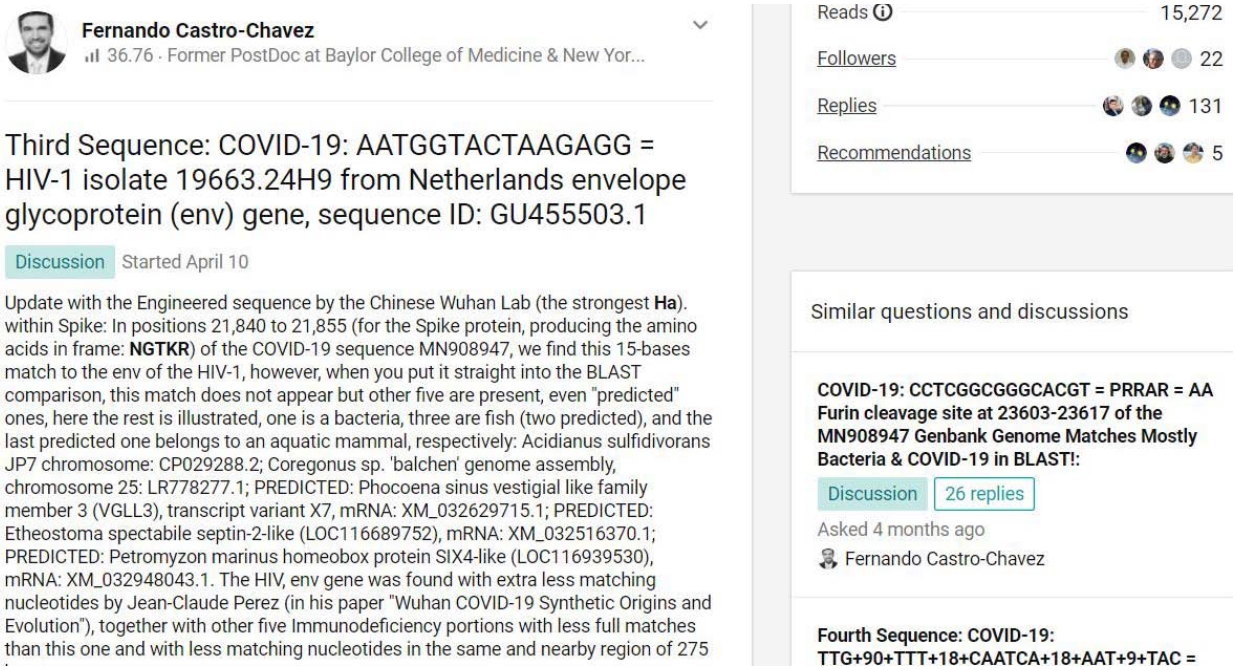
My ongoing work can be found at the *ResearchGate*, while many pieces of it have been removed from the *Facebook* and from the *YouTube* by some heartless and brainless censors appointed by the WHO and by their owner, Bill Gates, apparently the mastermind chosen by the globalists to pull this event of an artificially manufactured viral harm for the whole of humanity. But as Mordechai told to Esther: "If you do nothing about it, God will raise somebody else to redeem us of this plague, because our clamors for freedom and for justice have already reached the Heavens". Jesus said that it will not be so easy for the believers to overcome evil in the current times, but that it could be possible. As Christian believers, we believe that as long as we continue over the earth, the total fruition of the plans of darkness can NOT prosper, and you may be a key member of the Body of Christ in order to fulfill such restraining against the forces of evil of this world. Thus far, the next are some of the sequences that seem to be inserts (some of them seem to have been started to be tampered since the RaTG13 "experiment" of Shi Zheng-Li, a genome she had since 2013 but that she did not publish until 2020 after the first Sars-CoV-2 had been published in China, genome that of the RaTG13 (previously published in part twice with different names that included the number 4991, which is dishonesty in science to change the names of the sequences, and that is what Shi just did!) which has been used, ironically, even with all its methodological anomalies to, precisely attempt to undermine the artificiality of the inserts, even two sequences published earlier by the Military of China seem to have been already tampered to make them more infectious, this is what happens when you only have the sequences provided by them with nobody else corroborating their authenticity), so, I may use the "probable" inserts clause, mostly from HIV-1, some few from HIV-2 and one from SIV (as explained by Perez & Montagnier, 2020). So, the number of artificial sequences is growing as research progresses, that is why, when people tries to discredit some of these from being artificially made, the burden is over them to explain how all of them got INSERTED into one same viral genome, which may have required a same animal cell with multiple different viruses and even bacteria

exchanging only the specific required portions and no more, which is something naturally implausible but completely possible within a lab setting (then I add here the list from the previous appendix).

Final note added in proof: Most recently, Dr. John Wherry and Dr. Adrian Hayday (https://archive.vn/WCK5T) have identified, as in my point number four where I describe the presence of INSERTS of HIV into the COVID-19, so it is not surprising at all that it behaves similarly to HIV, and they point out four basic parallels, suggesting a similar treatment to HIV, instead of the use of a vaccine: *a*) A loss of virus-fighting T cells, *b*) A marked increase in levels of a molecule called IP10, which sends T cells, and whose levels go up and stay up, causing a chaotic signaling, *c*) Resulting in a so-called cytokine storm, just as Judy Mikovits has also been emphasizing since the start of this, apparently pre-planned Plandemic, *d*) In the end, the virus directly causes the immune system to malfunction, harming other parts of the immune system in terminal patients.

References: https://archive.vn/265Nw, https://archive.vn/cDwHo, https://archive.vn/bh8Cl, https://archive.vn/bARGH & "Immune Profiling of Hospitalized COVID-19 Patients" by Dr. John Wherry: https://www.youtube.com/watch?v=HhboONHkptc

To end with this all article for now, this is the photo in which the more specialized and continued research on the artificiality of COVID-19 is being performed by this current researcher, however, even there I had a post removed, with a warning that if I had some other or two removed, my account there can also be canceled (weird times these that we are currently living, where truth and freedom of expression seem to be banned by an evil attempt):



The letter indicating that one of my postings was banned (reposted elsewhere: https://fdocc.neocities.org/Petrovsky--Holmes.htm, so basically, we to repost) starts as follows: Your comments on Q&A. *Research Gate* Community Support. Dear Fernando, We're writing to let you know that we have removed...

The last links before its publication are: https://www.granthaalayahpublication.org/journals/index.php/granthaalayah/article/download/IJRG20_B07_3568/691/, which is the final version of Drs. J.-C. Perez & Luc Montagnier, as well as the link to the two seminal documents on a deliberate planning of the current COVID-19 pandemic: https://web.archive.org/web/20160409094639/https://www.nommeraadio.ee/meedia/pdf/RRS/Rockefeller%20Foundation.pdf20Foundation.pdf, with guidelines similar to that awful "Event 201", such as: "...mimicking China's firewalls... policing internet traffic..." and "Event 201" participants such as the CCP and Gates, plus Fauci, give their WHO expert advice at: https://web.archive.org/web/20190918224904/https://apps.who.int/gpmb/assets/annual_report/GPMB_annualreport_2019.pdf, such as the next: "...security measures... limiting information-sharing and fomenting social divisions", so the Soros/Democrats BLM riots were already pre-planned as well since September of 2019. Finally, Mikovits announces two books: "The Case Against Masks: Ten Reasons Why Mask Use Should be Limited", already out, and due for the next year, with her mentor Ruscetti: "New York Times Bestselling Authors: 'ENDING PLAGUE': A Scholar's Obligation In An Age Of Corruption. By Simon & Schuster, with RFK, Jr.". Finally, about the CCP:

https://archive.vn/wip/KpGH5, https://archive.vn/1dgxa and https://archive.vn/h7C3L, her current interview: https://podcasts.apple.com/us/podcast/ep-34-exclusive-hardest-hitting-most-scathing-blistering/id1491435111?i=1000486636801, and RFK, Jr.: https://podcasts.apple.com/us/podcast/best-paine-encore-ep-18-robert-bobby-kennedy-jr-joins/id1491435111?i=1000486783348, to finally conclude with our own current interviews: https://youtu.be/yvUjvukmJ-o, my excerpt of: https://www.facebook.com/KardagarCoaching/videos/750546699091474, with 12,116 views on the 08/08/2020, having been recorded on the 02 at night. Petrovsky, in his above reference, indicates that the next amino acids of the COVID-19 Spike are also unique: TESI, SKVG, TEIYQAGST, NGVEGF... Plus Li Meng-Yan: https://www.youtube.com/watch?v=YCdq-2ekhq8, https://www.youtube.com/watch?v=WUXm0PepVUQ, https://www.youtube.com/watch?v=7voTUuVT5i4, and the Chris Martenson frequent updates: https://www.youtube.com/watch?v=R6y8dlhoMpo, https://www.youtube.com/watch?v=eD3ztjqYGbg, https://www.youtube.com/watch?v=uZUJhKUbd0k, diet vs COVID-19, by my student: https://www.youtube.com/watch?v=xcyhxRz7vaY, and his book: https://bit.ly/LaDietadelADN, and Lab.: https://www.centrogenica.com, etc., etc., etc....

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Global Journal of Science Frontier Research: I
Interdisciplinary
Volume 20 Issue 3 Version 1.0 Year 2020
Type: Double Blind Peer Reviewed International Research Journal
Publisher: Global Journals
Online ISSN: 2249-4626 & Print ISSN: 0975-5896

Sensorial Profile and Acceptability of Coffee Blends Submitted to Different Roasting Degrees

By Ana Paula Lelis Rodrigues de Oliveira, Ramon Felipe Neves, Gabriel Henrique Horta de Oliveira & Magno Vinicius Corrêa de Souza

Abstract- Industry of roasted and ground coffee uses *Coffea arabica* L. (arabica) and *Coffeacanephora*(robusta), main coffee species, to form blends consumed worldwide. In addition to blends composition, industries also vary the roast degree to attend the consumer market. Being that stated, this work aimed to evaluate the influence of roasting degree and blends composition, using sensorial analysis, over the product acceptability. Arabica and robusta coffee were dehulled, classified, and roasted at Agtrons numbers SCAA#65 (medium-light) e SCAA#45 (moderately dark). Afterward, the authors made a preliminary test to select the blends for conventional consumers as a function of robusta coffee percentage. After the selection and determination of adequate proportion (0, 30, and 60 % m/m) of robusta coffee, the researchers invited 49 consumers to perform the tests. The researchers used preliminary tests to indicate that 29 out of the 49 consumers are capable to complete the tests. They performed the sensorial analysis of the blends, signaling grades from 1 to 9 to flavor, aroma, and appearance. Blend composition presented a higher impact over the coffee acceptability than the roast degree, in which coffee with 0% of robusta coffee, independently of the roast degree, followed by sample with 30% of robusta coffee roasted at medium light, presented the highest grades.

Keywords: *coffea arabica L., coffeacanephora, quality, sensorial analysis, cup test.*

GJSFR-I Classification: *FOR Code: 070399*

Strictly as per the compliance and regulations of:

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Abstract- Industry of roasted and ground coffee uses *Coffea arabica* L. (arabica) and *Coffeacane-phora*(robusta), main coffee species, to form blends consumed worldwide. In addition to blends composition, industries also vary the roast degree to attend the consumer market. Being that stated, this work aimed to evaluate the influence of roasting degree and blends composition, using sensorial analysis, over the product acceptability. Arabica and robusta coffee were dehulled, classified, and roasted at Agtrons numbers SCAA#65 (medium-light) e SCAA#45 (moderately dark). Afterward, the authors made a preliminary test to select the blends for conventional consumers as a function of robusta coffee percentage. After the selection and determination of adequate proportion (0, 30, and 60 % m/m) of robusta coffee, the researchers invited 49 consumers to perform the tests. The researchers used preliminary tests to indicate that 29 out of the 49 consumers are capable to complete the tests. They performed the sensorial analysis of the blends, signaling grades from 1 to 9 to flavor, aroma, and appearance. Blend composition presented a higher impact over the coffee acceptability than the roast degree, in which coffee with 0% of robusta coffee, independently of the roast degree, followed by sample with 30% of robusta coffee roasted at medium light, presented the highest grades.

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I. Introduction

Brazil is the foremost producer and exporter of coffee in the world, with 3.06 million tons of harvested coffee and a total of 2.00 million tons of exported coffee in 2017 [1]. Also, Brazil is the second consumer of coffee in the world, being 6.4 kg of green coffee or 5.1 kg of roasted coffee per person per year [2]. Coffee belongs to the Coffea genus and possesses two species of greater importance for world commerce, *Coffea arabica* L. and *Coffeacanephora*, known as arabica and robusta coffee, respectively.

Arabica coffee represents 76.2% of Brazilian production, with 2.05 million tons in 2017, while robusta coffee represents 643.200 tons [3]. State of Minas Gerais is the leading producer and provides over 50% of the Brazilian production, mainly with arabica coffee. State of Espírito Santo is the second producer, which cultivates mainly the robusta coffee, with a production estimate of 55.2% of this specie [3].

Differences among these species vary flowering period, physical and sensorial characteristics of the fruit, and others. Arabica coffee is traditionally more explored commercially, due to the fact of its higher drink acceptance, which provides a higher valorization when compared to the robusta coffee [4]. However, in the past years, robusta coffee increased its market share, due to higher productivity, lower susceptibility of diseases and adaptation at a lower altitude (until 400 m) and higher average temperature (between 22 and 26 ^{o}C) [5]. Moreover, robusta coffee produces a drink with a superiorbody; because of that, it has been used for mixtures (blends) with arabica coffee at the industrialization of roasted and ground coffee [6].

Blends among arabica and robusta coffees may be accomplished to exploit the sensorial potential of both species, combining them to enrich flavor and aroma of the final product, according to the target market [7]. The addition of robusta coffee in the commercial coffee is not commonly accepted by the consumers [8] since it provides a bitter drink, proportional to the amount added of robusta coffee.

In addition to the species, the roasting degree employed during the industrialization process of foodstuff has influence over the sensorial characteristics and, consequently, its market acceptance. For instance, roast of carob pod powder in different conditions and temperatures determines distinct specifications for the product, mainly by those correlated with color, aroma, and flavor [9]. These authors reported that this type of study allows controlling the process, by the food industry, obtaining products with higher acceptance.

The roasting process of the grain has direct influence over the drink quality because during this process occurs modifications and formation of different chemical components that contribute to the final aroma of the drink [10]. The roasting of the green grain forms acid, lactones and other phenolic derived elements, product of the degradation of chlorogenic acids, which impacts at the aroma and flavor of roasted coffee, final acidity, and astringency of the drink [11].

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Impelled by the roast degree importance over the sensorial characteristics of coffee, Specialty Coffee Association (SCA), former Specialty Coffee Association of America (SCAA), proposed a classification system of the roasted grain by its color, the SCAA-Agtron [12]. In this system, there are five color degrees of the grain, allowing intermediate classifications between very dark, dark, medium, light, and very light. Roast degrees more used commercially, and the ones that most values up flavor and aroma of grain are roast degree medium light and moderately dark [13].

Consumers present a higher worry with aroma, flavor, and color of roasted and ground coffee, appraising its sensorial characteristics, leading the industries to search for an elevated quality of its products using acceptability tests, using sensorial analysis, which depends upon the physical and chemical characteristics of the product [14].

The sensorial analysis permits to diagnose in a scientific and objective way the characteristics that influence the acceptability of food by the consumer, utilizing the senses of an integrated team, trained or not, to identify different organoleptic characteristics of the product. This descriptive analysis evaluates the intensity of the sensorial attributes of several products, allowing a complete description of the differences among samples, orienting modification of the characteristics of the studied product to attend the consumer demands [15].

Thus, considering the economic and industrial importance of the use of blends of arabica and robusta coffee in the formulation of roasted and ground coffee, along with the roast degree, this work had the objective to evaluate the influence of roast and blend composition over the final coffee drink according to the opinion and acceptability of panelists, characterizing the sensorial preferences of the consumer market, using a scientific procedure.

II. Materials and Methods

a) Raw material

Coffea arabica L. (arabica coffee) was acquired directly from alocal producer at Manhuaçu city, Brazil, and *Coffeacanephora* (robusta coffee) was purchased directly from a local producer at Alegre city, Brazil. Later, the researchers transported the grain to the sensorial analysis laboratory located at IF Sudeste MG – *Campus* Manhuaçu. Afterward, coffee was dehulled.

Intrinsic (imperfections of the own grain) defects such as black, green, sour, broken, and others and extrinsic defects(presence of strange fractions) such as hulls, twigs, and stones, were removed before subsequent procedures. Later, we sent the samples to the roasting process.

b) Roasting process

The researchers subjected the coffee beans to the roasting process after sorting. We used a 300-g raw-coffee capacity pre-heated, liquefied petroleum gas (LPG) direct roaster with a rotary cylinder operated at 45 rpm to roast the coffee. The degree of roasting of each coffee roast was determined by a trained professional by monitoring the sample color and comparing it with the Agtron/Specialty Coffee Association (SCA) standard roast number. We used two roasting degrees: medium-light (ML) and moderately dark (MD), corresponding to Agtron numbers of SCAA#65 and SCAA#45, respectively (Figure 1).

Figure 1: Roasting degrees employed: medium-light (A) and moderately dark (B) [16]

c) Milling process

Following the roasting process, we processed the coffee beans in a Mahlkönig mill at the medium particle sizes (0.84 mm).

d) Consumers selection

The researchers used triangle tests to select the appropriate consumers for the sensory evaluation. Consumersfrom Manhuaçu city, from different genders and ages between 16 and 70 years old, were chosen randomly. The consumers gave their consent before they participated in the study.

Consumers filled the Written Informed Consent Form, which explains the objective of the research, with respective name, age, and gender. The model of filing cards for evaluation is shown in Table 1, according to the proposed methodology [18], described below.

Table 1: Filling card model to apply the triangular test

Name:			Date:
Please, test the sampled codified, from the left to the right. Two samples are equal, and one is different. Identify, with an X, the description that represents the different sample. Please, taste the samples codified from the left to the right.			
	Test 1:1.11.21.3		
Test 2:	2.1	2.2	2.3
Test 3:	3.1	3.2	3.3
Comments:			

Six triangle tests were made, separated in two stages, each one with three tests. The first stage (Species) aimed to evaluate if the consumer could identify differences among arabica and robusta coffee. Samples at this stage were 100% arabica coffee, and 100% robusta coffee (one different and two equals), and the consumer should indicate which sample was the different one. At the second stage (Roast degree), the objective was to identify which consumers were capable of differentiating samples due to different roasting degrees. Samples at this stage were 100% arabica coffee, roasted at medium-light, and moderately dark. Again, the consumer should indicate which sample was the different one.

The researchers discarded the consumers that presented success rate below 45%; success rate higher than 70%, the consumer was automatically accepted; between 45 and 70% of success rate, the test session was continued until we made a final decision regarding the consumer.

e) Sample preparation

The investigators made different blends among arabica and robusta coffee (0, 30, and 60% of robusta coffee) after roasting and the previous grinding of arabica and robusta coffee. We prepared the samples (Table 2) in the proportion of 100 g of coffee powder and 1.0 L of mineral water. The drink was extracted according to adapted methodology [17], using filter paper n°105. Samples were served to consumers, individually, in disposable cups.

Table 2: Description of samples submitted to sensorial analysis

Sample	Robusta coffee (% m/m)	Roast degree
IF 21	0	Medium-Light
IF 22	30	Medium-Light
IF 23	60	Medium-Light
IF 24	0	Moderately Dark
IF 25	30	Moderately Dark
IF 26	60	Moderately Dark

We do not determine the amount of sugar or sweetener at this stage, varying between one and three coffee spoons of sugar. One sugar spoon is equivalent to five drops of sweetener, according to the manufacturer.

f) Sensory analysis

Quality parameters to be evaluated depends upon consumer opinion [19]. The same authors indicate that the relevant quality characteristics of this public are: flavor, aroma, and appearance, with respective weights of 1.0, 0.9, and 0.7. To define the required attributes of the product, tests should be quantitative and measurable. The current research used grades between 1.0 and 9.0 for each parameter previously described (flavor, aroma, and appearance). The selected consumers gave these grades, and the final score was calculated using rankings and their respective weights (Table 3).

Table 3: Qualitative and quantitative parameters for coffee evaluation [19].

Quality characteristic (CQ)	Importance (weight)	Grade
Flavor	1.0	1-9
Aroma	0.9	1-9
Appearance	0.7	1-9

Each consumer graded six coffee samples, in which a random order of the served samples across consumers was established at the individual evaluation acceptability card (Table 4), to avoid that the testing sequel affects the results.

Table 4: Model of acceptability card

Acceptability test			
Name:	Age:	Gender: (F) (M)	Date:
Please, evaluate the sample using grades between 1 (disliked extremely) and 9 (liked extremely) to describe how much you liked or disliked the product. Classify to describe, in an integer number, which reflects your judgement.			
Sample code	Grades		
	Flavor	Aroma	Appearance

Along with the served sample, the consumer received a glass of water in environmental temperature to rinse the mouth between evaluations; also, they have received sugar and sweetener to be used as their preference.

III. Results and Discussion

a) Consumers selection

After triangular tests for the consumer's selection, results can be seen in Figure 2, which provides the number of consumers able to distinguish between coffee species (arabica from robusta), differentiate between roast degree (medium-light from moderately dark roasts) and the number of consumers able to differentiate coffee samples in general (coffee specie and roast level combined).

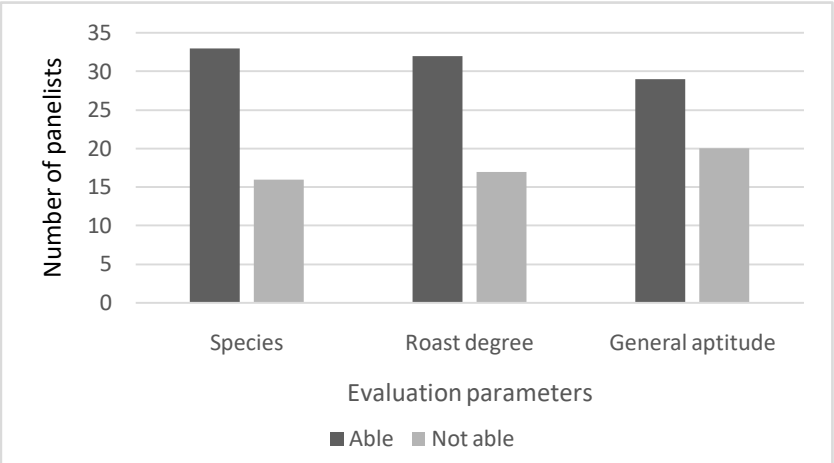

Figure 2: Aptitude evaluation of the consumers as a function of the differentiation ability among coffee samples of different species and roast degrees

According to Figure 2, it is possible to identify that, after the triangular test of the 49 consumers, 33 were considered able regarding the species; in other words, 33 consumers were capable of identifying differences between arabica and robusta coffee. Similarly, 32 consumers among 49 could detect differences regarding roast degree; in other words, 32 consumers can differentiate coffee samples between medium light and moderately dark roasting degrees. In general, according to the classification criteria proposed, 29 consumers were considered able to perform the sensorial analysis, which represents 59.18% of the consumers (Figure 2).

b) Acceptability test

Figure 3 presents the average grades for each sample, considering the evaluation of the 29 consumers regarding flavor, aroma, and appearance of the different coffee samples (blend composition and roast degree).

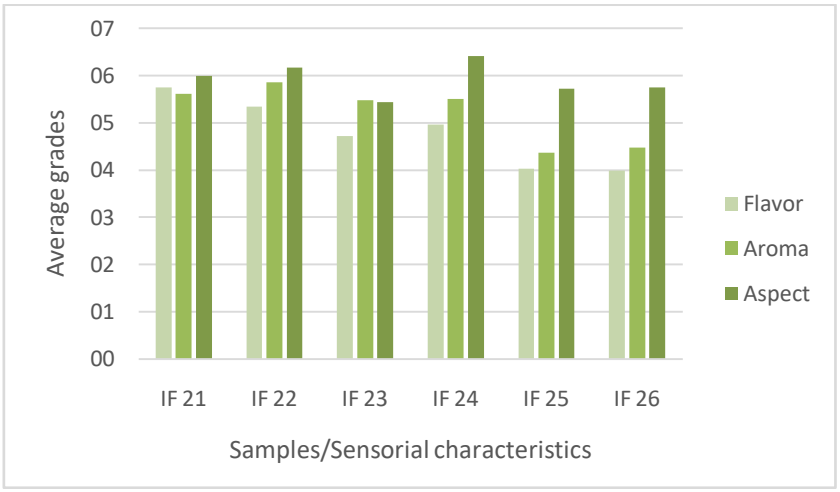

Figure 3: Average grades conceded by the consumers to the coffee samples as a function of sensorial characteristics.

According to Figure 3 samples, IF21 and IF22 presented higher acceptability regarding flavor and aroma. We expected these results because there is a preference by the coffee market for arabica coffee and lighter roast decreases the bitterness. We can explain the same trend for the aroma parameter. However, consumers group preferred coffee drink with darker roasts [20]. We correlated this difference with the regional culture of consumption at Manhuaçu city, which is a region of production of recognized quality coffee. It is established that coffee with higher quality has flavor and aroma parameters pronounced at lighter roasting degrees, and this trend is shared by the selected consumers, even when the selection was random.

Nonetheless, according to Figure 3, sample IF24 presented higher grades of appearance. This result can be explained by the absence of robusta coffee and by the roasting degree. The Brazilian market prefers coffee with darker roasts due to an increase in grinding efficiency, among other factors. Coffee roasted in darker degrees has higher acceptance in four parameters evaluated by a larger group of consumers [20].

3.3. Sensory analysis

Figure 4 presents the influence of the typical grade as a function of consumer's preference.

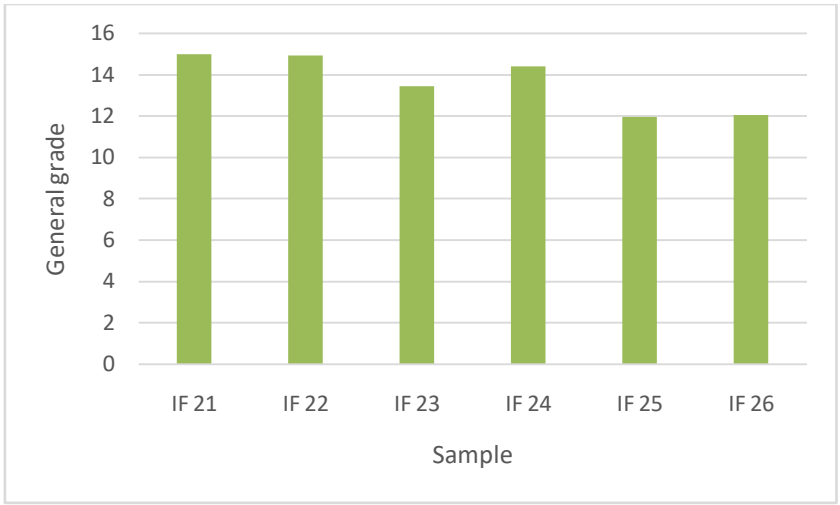

Figure 4: General grades of coffee samples as a function of sensorial characteristics, by its determined weight.

We can observe, in Figure 4, that samples IF21, IF 22, and IF24 were the samples with the highest grades. This trend suggests that robusta coffee is accepted by the market when we roasted it in a medium light degree (IF22). We did not expect this observation, since robusta coffee is related to lower drink quality, among consumers. This trend is more relevant when the demand of the local market (Manhuaçu city) is of coffees of higher quality. Lastly, we noticed a preference for arabica coffee, since that samples that didn't add

robusta coffee (IF21 and IF24), independently of the roast degree, presented superior grades, among the samples studied (Figure 4).

IV. Conclusions

Blend composition presented a higher impact over the coffee acceptability than the roast degree, in which greatest grades were indicated by coffee with 0% of robusta coffee, independently of the roast degree, followed by sample with 30% of robusta coffee roasted at medium light.

Among the sensorial characteristics evaluated, the addition of robusta coffee affected mostly the flavor.

Funding: This research was funded by Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG) andthe Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) for scholarshipsand financial support.

Conflicts of Interest: The authors declare no conflict of interest. The founding sponsors had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, and in the decision to publish the results.

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Global Journal of Science Frontier Research: I
Interdisciplinary
Volume 20 Issue 3 Version 1.0 Year 2020
Type: Double Blind Peer Reviewed International Research Journal
Publisher: Global Journals
Online ISSN: 2249-4626 & Print ISSN: 0975-5896

Leadership Crisis: Concepts, Theories, and Methods, an Anthropological Perspective

By Khimlal Devkota

Abstract- The purpose of the study is to make a critical assessment of concepts, theories/models and methods for the study of leadership and its crisis. The central research question is "is there a matching of leadership with right time, right content, and right decision?"Historical archival content analysis based on the review of literature was the method used for preparing this paper. The declaration of Nepal as a republic is a historical political achievement. However, the attempt to abolish monarchy have been made even earlier in the 1950's, 1960's, 1970's, or even in 1979, 1989, 1996,or2006. But finally, Nepal as a republic was declared on May 28, 2008.

Keywords: *leadership, leadership theories, methods, crisis, decision-making, political parties.*

GJSFR-I Classification: *FOR Code: 130304*

Strictly as per the compliance and regulations of:

Leadership Crisis: Concepts, Theories, and Methods, an Anthropological Perspective

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Abstract- The purpose of the study is to make a critical assessment of concepts, theories/models and methods for the study of leadership and its crisis. The central research question is "is there a matching of leadership with right time, right content, and right decision?"Historical archival content analysis based on the review of literature was the method used for preparing this paper. The declaration of Nepal as a republic is a historical political achievement. However, the attempt to abolish monarchy have been made even earlier in the 1950's, 1960's, 1970's, or even in 1979, 1989, 1996,or2006. But finally, Nepal as a republic was declared on May 28, 2008.

The concept of leadership, the decision-making process, and leadership crisis relate with the declaration of republic, which is the main concern of the study. Number of theories have been identified and reviewed which include Complexity Leadership Theory. Major focus of this study are that leadership is a key for the moving forward of any institution, society and nation but that it is always in questions and challenges. It is because crisis has to be handled by the leadership and leadership itself indulges in crisis. Sometimes crisis creates leadership sometimes leadership handles the crisis; however leadership indulges in crisis for most of the time. Decisions have to be taken at appropriate times. If right time and right decision match each other, results will be appreciated. Instead of it, if right decisions are made at the wrong time, they are useless. Wrong decision at wrong time is disastrous. The expectation of the people and society is always for the right decision at the right time. Democratic leadership, democratic process, and pro-people decisions for strengthening democracy are core concerns of the society to contribute in the area is main concern of the study.

Keywords: leadership, leadership theories, methods, crisis, decision-making, political parties.

I. Introduction

The purpose of the paper is to make a critical assessment of the concepts of leadership theories/models and methods for the study of leadership and its crisis. For this purpose, the research question is what concepts, theories and methods were used in past research and which one is appropriate in Nepal's situation. The research method used here, reviewing of literature, is content analysis of historical and archival records. My argument is that the declaration of republic and prosperity was possible even in the 1950's rather than only in 2008, if leadership had been decisive at particular point of time.

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The term "leadership" is an art to lead the organization, people and others for the purpose of achieving their goal. If it absence than crisis comes up. However, it depends upon different disciplines and context. Anthropologists try to define leadership based on humankind. Malinowski defines leadership as one aspect of tribal authority…and as social authority (Malinowski,1922, p.18). Evans-Pritchard reveals that leadership among witches. (Evans-Pritchard & Gillies, 1976, p. 14). Sahlins focuses on ethnographic descriptions (Sahlins, 1972, p. 132). Mauss describes gift in *Kula* trade is of a noble kind. It seems to be reserved for the chiefs as a means of leadership (Mauss, 2002, p. 28). At 70s have been uncovered the use of socio-metric techniques, particularly in the field of group dynamics and in decision-making studies (Dion, 1968, p. 1). Political scientists have different opinions whereas natural rights to be all vested in the state, or in other words the sovereign, who represents it (*Hobbes's Leviathan*,1853, p. 44). The hard question is whether political scientists are able to develop theoretical models of historical context for the exploration of historical cases from which propositions about leadership may be induced, and compared (Hargrove, 2004, p. 583). Different times demand different types of leadership - in war, men of courage and determination are regarded favorably (Kavanagh, 1984). According to Johnson "as a gestalt these models, concepts, and their interrelations form a theory of community leadership with the approach of anthropological pattern applying to the configurational theory. His proclamation is not that it is not causal explanation, nor is it deterministic, but it provides local concepts that are in tension and are drawn upon by local actors to negotiate everyday relationships in the community(Johnson, 2007, p. 215).

East and Southeast Asia favors a different leadership than in the West because Confucian culture defines the appropriate traits, behavior, virtues, and roles of political leaders differently. According to Kim & Kim (2013) reconfirming the Confucian culture "which emphasizes respect for authority and hierarchy as a duty of the ruled, remains strong and people in the East and Southeast Asia allow their political leaders to exert considerable discretionary power, sometimes even against legal or institutional constraints" (Kim & Kim, 2013, pp. 388–389). For many centuries the pattern of political leadership in India was two-tiered government at the top and leadership in another however all are

trapping by wealth and power. According to Forrester (1966) "Macro political leadership changed hands with some frequency, and in modern times was often foreign, first Mughal and then British. In general the macro political leadership impinged little on the lives of the ordinary Indian" (Forrester, 1966, p. 308). Ultimately, the role of the democratic leader is to maintain proper balamce with his mass and his task. According to Kann (1979) a leader "must balance his revisionist skepticism about the present state of the citizens' political skill with his participations' vision of government by the people. These are critical balances upon which the future of democracy hinges. And the best guarantee that he will strike these balances is a population which persistently demands that he do so" (Kann, 1979, p. 224).

In the case of Nepal passing through Rana autocracy regime and a party-less Panchay at system is consider as undemocratic system. In this context, Tulsi Uprety writes " the Panchayat political system is still in a state of crisis because of the shortsighted policy of its leaders, the low morale of the Panchas, and the deteriorating economic situation in the country"(Uprety, 1983, p. 148).According to Baral "some extremist factions including the Naxalites were averse to holding a referendum because it could not solve the problem. Despite intra-party differences over the leadership issue, and efforts were underway to forge a broad democratic unity for contesting the referendum"(Baral, 1980, p. 205). Leadership got success for restoration of parliamentary democracy to federal democratic republic with inclusive and secular democracy. Throughout the historical development of leadership always in question is whether leadership has made the right decision at the right time.

The research is divided in to four main sections. In addition to abstract the first section introduction tries to conceptualize the political leadership and their crisis based on related concepts, theories and methods generally around the world and specifically focus on Nepal. Second section is talking about research findings on concepts, theories and methods mainly literature reviews and archival content analysis with anthropological perspective. Third section is discussion on leadership crisis of Nepal mainly decision making process on declaration of republic with theories and methods. In addition to that the research dealt with leadership concepts, indecisiveness and creates crisis, leadership theories, and methods. Final section is conclusion with limitation and findings of the research.

II. Results/Findings

a) Concepts

After reviewed concepts of leadership and leadership crisis in the context of Nepal mainly in declaration of republic, the study tries to relate the concepts, theories, models and methods of reviewed literatures. According to Bruce E. Winston Kathleen Patterson "A leader is one or more people who selects, equips, trains, and influences one or more follower(s) who have diverse gifts, abilities, and skills and focuses the follower(s) to the organization's mission and objectives causing the follower(s) to willingly and enthusiastically expend spiritual, emotional, and physical energy in a concerted, coordinated effort to achieve the organizational mission and objectives (Winston & Patterson, 2006, p. 9). According to Malinowski (1922) "leadership is a key action to lead an organizations as well as political parties. Political parties, leaders and followers and sympathizers are facing problems either misleading by ideology or decisions considered as authority" (Malinowski,1922). According to Max Weber "This was a far cry from the mercantilism and paternalism of Frederician Prussia. Lachmann(1971) writes "it was only then that, under the leadership of the economists of the *Verein fur Sozialpolitik,* educated Germany gradually began to turn to the opposite ideal of the Welfare State" (Lachmann,1971). According to Evans Pritchard(1951) "Idea of leadership is… institutions sociologically, in terms of social structure, and not in terms of individual psychology"(EvansPritchard*,1951*). Leadership is not an individual enterprise nor is it magical actions but it is a collective effort and a byproduct of the society and impacted from the socio-cultural practices.

I am concerned about Nepal the concept of leadership is quiet different than democratic concept and theories. Based on the fact I try to identify the existing reality of leadership in political parties and their role particularly during the time of political transition in Nepal. Nepal is a country of transition and passing through conflict therefore Marxist theory is relevant. Roseberry (1997) writes "A consideration of the relevance of Marx's thought for anthropology must begin with a recognition of the political failure of most Marxist-inspired movements and the influential intellectual critique that seems to speak to it" (Roseberry,1997). While Tuned (1969) says "One key element in political behavior is the analysis of the different methods of obtaining compliance with a decision" (Tuned,1969). According to Gailey(1985) "The role of ethno-historical research in this endeavor remains crucial: anthropology must become history but written from a perspective other than that of the conqueror" (Gailey, 1985). According to Tulsi Uprety, (1983) "a shortsighted policy carried out by the leaders is a cause of crisis. As noted earlier, the Panchay at political system is still in a state of crisis because of the shortsighted policy of its leaders, the low morale of the Panchas, and the deteriorating economic situation in the country "(Uprety, 1983). Though Nepal has shifted from a monarchy to republic, unitary to federal, Hindu kingdom to secular and exclusionary to inclusion politics, however the chance of declaring a republic had been missed in 1951 because

of leadership crisis in decision-making. The Jhapa revolt of 1971, the referendum of the 1980's and the popular movement of the 1990's and the people's movement of 2006, all the chances missed by the Nepali politics because of leadership crisis. Various anthropological studies and incidents happened in the past revealed that, the main problem of the leadership crisis is lacking of right decision at right time. There will be different opinions though if republic were declared during the time of restoration of democracy the condition of Nepali society would have been better than now. According to Laya Uprety "Nepali anthropologists can, henceforth, contribute to kinship studies in the domain of feminist studies" is very pertinent to me in the context of contemporaneous global kinship (Uprety, 2017). It is very relevant in the course of male-dominated leadership studies too. Reinforced by Uprety and Pokharel, the new area of research in political institutions including many others is very encouraging to me for my study (Uprety L. &., 2016). The clear picture of the leadership concept can be seen in *Table 1*.

Table 1: Concepts

S.N	Authors	Main Ideas
01	Winston & Patterson(2006)	Leaders and folloers, expand spiritual emotional and psychological to achieve mission and objective
02	Malinowski(1922)	To lead organization by ideology or decisions as authority
03	Max Weber	Was a far cry from mercantilism and paternalism
04	Lichmann(1971)	Turn to the opposite ideal of the welfare state
05	Evan Pritchard (1951)	Social structure and individual psychology
06	Roseberry (1997)	Anthropology must be begin with recognition of political failure
07	Tuned (1969)	Compliance with a decision
08	Gailey (1985)	Conquered history
09	N aditya(1997)	Performance and motivation of both individuals and groups

The concept of leadership is not only a search for understanding the thoughts and actions of leaders, but also an investigation of how to improve the performance and motivation of both individuals and groups (N.Aditya, 1997). According to House & Aditya (1997) major attributes of a leadership are role model, inspirer, enabler and achiever. As a leader that you must envision for future, passionately believe that you can make a different and inspire people to achieve more than they may ever have dreamed possible. In this background my study will focus on how the attributes have been used and how much leadership inspire to the followers. In the case of political decisions from the very beginning need to take in account. Nepal is a country of Republican and democrats, but ruled by monarchy is never matching. For the declaration of republic, a number of struggles and sacrifices have been made. The study would like to explore why and how decisions are made in that particular time and event which seems somewhere right time right decisions and somewhere right decision in wrong time and sometimes wrong decision in wrong time. I try to explore what particular socio-cultural factors play the role for that particular decision. The study tries to search leadership crisis on decision making process of main political parties in Nepal. Throughout the Nepali history we can find the some hesitation to take a right decision in right time. Through historical anthropological/ethnographic discipline and based on archival studies, available literature, interviews, my own experiences and observation, the study tries to produce the kind of new knowledge to address the problem of leadership crisis in decision making process.

b) Theories of Leadership

New-genre theories of leadership refer to dominated leadership research since the 1980s, including charismatic, inspirational, transformational, and visionary leadership (*Leadership Models: From Weber to Burns to Bass*, 1998). New leadership approaches emphasize symbolic leader behavior, visionary and inspirational messages, emotional feelings, ideological and moral values, individualized attention, and intellectual stimulation. The most widespread one's are: Great Man Theory, which states that some people are born with the necessary attributes that set them apart from others and that these traits are responsible for their assuming positions of power and authority. A leader is a hero who accomplishes goals against all odds for his followers. The main theories that emerged during the 20th century include: the Great Man Theory, Trait theory, Process Leadership theory, Style and Behavioral theory, and Transformational, Transactional and Laissez Faire leadership theory but in the 21stcentury, Complexity Leadership Theory is in practice(Olalere Anthony, 2015), (Lichtenstein et al., 2006),(Uhl-Bien et al., 2007), (Brown & Briown, 2011). In addition to that based on their working style other theories also are in practice i.e. Laissez-Faire Leadership. This leader is not directly involved in decision-making and puts a lot of trust into the team, Pace-Setter Leadership focuses always on their mission whereas, Autocratic Leadership is at quite a contrast to Democratic Leadership, Transformational Leadership, Transactional Leadership, Charismatic Leadership are different characteristics of leadership. (Blondel, 1993), (Selart, 2010), (Johnson, 2007), (Edinger, 1975)

(Edinger, 1990), (*Barisione2015*),(Ubah, 1987), (Forrester, 1966),(Weiner, 1959), (Garigue, 1954), (Lichtenstein et al.,2006), (Baltaci & Balcı, 2017a), (Brown & Briown, 2011) have presented leadership concept and theories from their perspectives.

George Burns' theory of leadership, along with some of the thoughts of Weber, added to them his own insights into leaders and how they operated. While both theories of Weber and Burn recognized transactional and transformational leadership types, Burns created an overarching dimension of moral leaders versus amoral leaders - the latter of which he felt were not true leaders. Among the transactional leadership styles, Burn's went on to describe five different types of leaders: opinion leaders - those leaders with the ability to sway public opinion, bureaucratic leaders - those that hold position power over their followers, party leaders that hold political positions or titles in a particular country, legislative Leaders that are at work behind the scenes, executive leaders - often described as the president of a country, not necessarily bound to a political party or legislators. Burns' theory went on to describe four transformational leaders including: Intellectual Leaders - transforms society through clarity of vision, Reform Leaders - changes society by addressing a single moral issue, Revolutionary Leaders - brings about changes in society through sweeping and widespread transformation. Charismatic Leaders - use personal charm to bring about change (Burns, 1987). Daniel Goleman's theory of emotional intelligence attempted to answer the question – What are the elements that characterize a leader? This was more of a behavioral approach to describing leadership than some of the previous work just described. Goleman wanted to determine the behaviors that made people effective leaders. Goleman's emotional intelligence is sometimes characterized as an emotional quotient or EQ that stood in contrast to an intelligence quotient or IQ. He felt that intelligence was just not enough to define a leader but that there was something more that separated leaders from mere intellectuals - their emotional intelligence (Goleman 2002). Max Weber tried to combine three types of leaders - bureaucratic, charismatic and traditional. Weber was one of the first of the leadership theorists to recognize that leadership itself was situational in nature and that true leaders needed to move dynamically from one type of leadership style to another to remain successful. According to Tucker (1968) "Charismatic leaders were transformational … charismatically led movement for change" (Tucker, 1968). According to Odonovan (2011) "the elected official will conduct himself entirely as the mandated representative of his master the electors, … according to the expressed or supposed will of the electorate (O'donovan, 2011). According to Gane (1997)"Weber discusses political responsibility, for a cause, rather than the constituency" (Gane, 1997). Different context and time the topic of leadership has been discussed and practiced differently. In summary related with leadership theories can be seen as in *Table 2*.

Table 2: Theories

S.N.	Theories	Main Ideas of Theories
01	Behavioural	Required behavior of effective leaders
02	Transactional	Process oriented, action oriented
03	Greatman	Leadership by born
04	Complexity	Theory of 21st century to resolve the problem of complexity
05	George Burn's,	Transformational reform and charismatic leadership theories Combined by George Burns
06	Daniel goleman's	Behavior and emotions
07	Max weber	Leadership combained of beurocratic, charismatic and traditional and mainly based on situational and dynamism
08	Tucer	Leadership charismatically lead movement for change
09	Odanvan	Leadership mainly mandated representative to express or supposes
10	Gane	Leadership focus on political responsibility for a cause rather than the constituency

Based on above mentioned leadership theories that were propounded in a particular time and a particular context therefore focus also on a particular subject. I mean all the theories were propounded during the age of industrial era and developed societies. Thus, I am partly agreed on their contribution. All the contributions are not fit as it is in a Nepali context for my study. All the studies are compartmental therefore they all are partly true at that particular time but the theory of universalism vs. Relativist notion of leadership is relevant to this study. Contents are prevailing in their own context and time. Whereas Nepali context is unique, time is also specific and content as a declaration of republic is also very rare for the democratic world of the 21st century. Mostly transformational leadership in transition phase has been mentioned during the time of the industrial age but for the knowledge and information era, the complexity leadership theory has been in practice. There is no research found on any particular theory-based leadership typology. Here I myself try to relate to my study where, Nepal is a country in transition and after a long period of time the country has turned into a republican from a monarchy, federalism from unitary, and secularism from Hindu kingdom and exclusionary to

inclusionary politics. Therefore, my focused is also on transition—as a country in transition how Nepali people managed their leadership and overcame their crisis is my central idea of research.

c) Methods

Mostly the studies have taken a qualitative approach; data collection through personal interview, personal story, lived experiences, ethnographies, purposive sampling and mostly interview of leadership is used. Very few studies have used the tools of neoclassical realism. Scott(2016) "reviews Britain's international behavior in part by how it is affected by changes in the international system" (Scott, 2016,p.ii). Selenica " multi-sited based analysis of two case studies are selected on the international engagement for education reform in post-war state building interventions, by comparing and contrasting engagement to education reform and governance. Empirical investigation makes use of ethnographic fieldwork based on semi-structured and informal interviews"(Selenica, 2016). Helms et al … "convictions have to be inferred from statements and behavior" (Helms et al., 2019, p. 353). Jean Blondel …"comparisons will and truly general conclusions will begin to be drawn and thus gradually emerge which will make it possible at a variety of types of leadership" (Blondel, 1993, pp. 21–22). Selart (2011) "To develop leadership means to guide future leaders on how they should make decisions. It also involves providing future leaders with guidance on how they should implement, evaluate and monitor their decisions(Selart,2010, p. 11). Alen R. Johnson "an anthropological approach to the study of leadership suggests training methods that take socio-cultural dynamics seriously. After over viewing the results of my work in the Lang Watt Pathum Wanaram community" (Johnson, 2007, p. 213).

Lewis J. Edinger, applied "general observations and comparative generalization about the sources and nature of leadership in politics" (Edinger,1990,p. 509). Ubah applied " African societies passed through, especially in rural communities, during the colonial era" (Ubah, 1987 p. 128). Duncon B. Forester applied comparative method by "comparing India to France on top administrators " (Forrester, 1966, p. 318).Emmanuel Pringle Cloete followed both a deductive and inductive approach namely those of amongst others Duvenhage (2003 and 2005), Huntington (1965 and 1968), Cilliers (1984), Apter(1965), Inglehart and Welzel (2005) and Hagoplan (2005). With the inductive process, the theoretical framework was verified by applying it to selected cases studies (Cloete, 2013, p. 274).Similar to phenomenology, narrative inquiry seeks to understand lived experiences and how individuals describe and perceive those experiences (Patton, 2004)(Morillo, 2017, pp. 34–35). Tibor Malkovics's An Analysis of the Network of Relations between the Radical (National) Right and the Hungarian "Guards "followed analytical method(Malkovic,2010,p.10). Vicente Palermo done comparative study of "the relation between corruption and governability" (Palermo, 2016,p.10). Sarah Scott followed the neoclassical realist approach which offers considerable scope for understanding foreign policy decisions(Scott,2016, p. 30). In Charles A. Casto work, the research was done "through interviews" (Casto, 2014, p. vii). Stephen Chukwunenye Anyamele followed comparative study "Nigerian and Finnish Cases " (Anyamele, 2004,p.153).

Leadership through Crisis approach has been used in this non-political but public institution research tried to justify the wider context and importance of leadership. Helena Liu sets out the methodological framework adopted in order to investigate the research questions (Liu, 2012, p. 14). Tsukayama, (2005) focuses on the transformation of political leadership in the North Coast of Peru Presents a multi-scholar analytical approach. (Tsukayama, 2005, p. 246).Michael M. Ogbeidi writes on Nigerian context of politics and corruption. (Ogbeidi, 2012, p. 21). Boin focuses on balancing their task "Effective leadership requires policy makers to devise, enact and legitimize a workable balance between these contradictory imperatives" (Boin, 2005, p. 156).

Cucciolla done research on "The crisis of Soviet power in Central Asia: The 'Uzbek cotton affair', 1975-1991" with scientific historiographical research. (Cucciolla, 2017). Alexandor & Lewis(2014) Leadership Trait Analysis (LTA) was conducted with the technique of Comparative Cognitive Mapping (CCM) (Alexander & Lewis, 2014, p. 20). Helms, Van Esch, & Crawford challenge that psychology and anthropology would seem to be considerably better equipped to master than comparative politics with rigorous inquiry. (Helms et al., 2019, p. 364). Lahel focuses on culture and institutions and came in conclusion that "The personalization of politics, including, the role of political celebrity are important however culture and institutions are also equally important in the leadership field." (Lahel, 2011, p. 321). Different methods have been used in anthropological studies. Most of them have been studied in this research which can be seen as in *Table 3*.

Table 3: Methods

S.No.	Researcher	Methods
01	Scott(2016)	Review Britain's behavior to find how it is changed in international system.
02	Selenica(2016)	Multisided based analysis, case study, ethnographic field work semi structured and informal interviews
03	Helms et al (2019)	Convictions from statement and behavior as content analysis
04	Jean blondel (1993)	Comparison
05	Selart(2010)	Monitor their decisions by observation
06	Alen R Johnson(2007)	Training methods socio-cultural dynamics
07	Lewis J Edinger (1990)	General observations and comparative generalizations
08	Ubah(1987)	Applied method
09	Duncon B. Foster(1966)	Comparative methods on India to France on administration
10	Emanuel P. Cloete(2013)	Deductive and inductive both and selected Case study
11	Patton(2004)	Phenomenology, narrative inquiry, lived experiences
12	Marillo(2017)	Phenomenology, narrative inquiry, lived experiences
13	Tibor malkovics(2010)	Network analysis
14	Vincente Palermo(2016)	Comparative study followed analytical method
15	Sarah scott(2016)	Neoclassical realistic approach
16	Casto(2014)	Interviews
17	Staphen (2017)	Comparative study
18	Cucciolla (2014)	Historiographical research
19	Alexandor & Lewis(2014)	Leadership trait analysis, comparative mapping
20	Helms, Van, Esch & Crawford(2019)	Rigorous inquiry

My argument is that democratic leadership varies depending on the political situation, regardless of the society's given cultural traditions. In a society, what we call "appropriate leadership" has more to do with political rather than cultural factors. In the context of Nepal development of leadership has to be made and wait to better production. Transition country ruled by feudal monarch none of the theory matching properly has been revealed by this study.

III. Discussion

a) Leadership Concept

The literature has been reviewed for clarification of the concept of leadership. Jean Blondel (1993), Malinowski (1922), Evan Pritchard (1951), Marshal Mauss (2002)), and Shalins (1972) have given an anthropological concept of leadership. Anthropological perspective of leadership is related with power and authority whatever it is, in tribal or in modern age. Anthropologists always ask the question on leadership of why doesn't someone care about the cultural context and the recommendations are detailed studies of cultures and respect to the peoples with their culture to be a leader and for overcoming leadership crisis. In addition to anthropological approaches, study of the research and literature of other political and social scientists have been reviewed too. Anthropological approach focuses on cultural aspects but social scientists focus on different content, time, and context of the societies including socio-economic conditions. Social scientists always believed in society and its changing characteristics. In a fast-changing society, problems also emerge very rapidly and if unaddressed in time turn into crisis. Political scientists focus is on change that happens forever. Politics is for the people and peoples are always hungry for change. If anyone wanted to maintain status quo then crisis would emerge. Peoples will choose change at any cost. With this conclusion it is very helpful to me to perceive the leadership concept and easy to compare it with the prevailing society.

b) Decision-making Process

Similarly, decision making process of political party's related literature also has been reviewed. During the time of taking decision what sort of challenges faced by the party and leadership? (Connery, 2010), (Howard and Ortiz,1971), (Herek, Janis and Huth,1987), (Hicks, Burgman, Marewski, Fidler and Gigerenzer, 2012), (Plog, Plog and Wait1978), (Mohanty, 2011),(Black, 1980), (North1962), (Johnson, 1983), (Zechmeister and Druckman, 1973), (Shibata, Tse, Vertinsky and Wehrung, 1991) has been mentioned on decision making process during the crisis. The take way massage is participation of all stakeholders, extensive negotiations and group involvement are encouraged, fulfilling, perhaps, the dual role of drawing upon extensive sources of information and co-opting participants to ensure quick and co-ordinate implementation for any political decision making process. For my study there are number of problems in decision making process in terms of inclusive participation, democratic and transparency in political decisions where as right judgment of the peoples power will possible. Declaration of republic in Nepal there were prevailing indecisiveness in decision making process.

c) Leadership Crisis

Whether leadership handled the crisis or they indulged in it and if so, whether the crisis of leadership prevailed is my concern of the study. Literatures which I reviewed are (Patel, 1990), (Ustun,2014), (Karenga, 1982), (Olalere, 2015), (Goldstein, 2015), (Wojcik,1969), (Saltz, 2017), (Boin, 2009), (Casto, 2014), (Anyamele, 2017), (Ayittey, 2007), (Quigley, 1970), (Edie, 2000), (Gill, 2012), (Iheriohanma & O. Oguoma, 2010), (Chang, 2012), (Wallace, 1969), (Dashwood, 2002),(Petrossian, 1981), (Fragouli, 2008), (Evangelia, 2016), (FANSO, 1979), (Lawler, 1996),(Mazánek, 2015), (Roach, 2009), (Hume, 1997), (Wallace and Peter Suedfeld, 1988),(Liu, 2012), (Tsukayama,2014), (Cothran, Phillips and Jr, 1961),(Uprety, 1983), (Chang, 1974), (Olalere Anthony, 2015) (Iheriohanma & Oguoma, 2010), (Boin, 2009), (Baker, 1998), (Cothran & Phillips, 1961),(Crossette, 2005), (Hachhethu, 2006), (Donald, n.d.), (Edinger, 1990),(Lerche, 1966), (Mabee, 1964),(Karenga, 1982), (Kagan, 2004) (Fazal, 2001). All these research have been done in different countries and situations with their crisis handled by the leadership. Literature says that crisis is an inevitable element of the society but the problem is how they are treating them? If problems are handled rightly, causes will be addressed and consequences will be positive. Leadership will be successful only after right handling of the crisis of their society. Literature from developed countries to developing countries has been reviewed like, USA to India. Literature has been reviewed from transition to stable countries like China to Nepal.

d) Leadership Theories

Different theories of leadership have been reviewed like Great Man Theory to transformational and transactional to charismatic leadership theories. Most of the theories were practiced in the 20th century, basically the industrial age, but Complexity Leadership Theory commenced in the 21st century with the knowledge era. Max Weber to Bass and Guleman to Burn's theories have been reviewed. The conclusion that has been drawn from all the literature is that these theories are also applicable to a specific time and specific place. Max Weber tried to combine transactional theory, transformational and charismatic theory in one to handle the crisis of leadership. Based on literature which I reviewed to handle the leadership crisis in a country like Nepal, Complexity Leadership Theory will be appropriate. The country turned from monarchy to republic, Hindu kingdom to secular, unitary to federal and exclusionary to inclusionary. Complexity leadership theory deals with the knowledge era with a close combination of administrative, adaptive and action-centered types. Complexity leadership could be defined as adaptive mechanisms developed by complex organizations in new conditions required by the information and knowledge era, rather than technical problems entailed by the industrial age. Complexity leadership is a joint, resultant product of the following three types of leadership: (1) administrative leadership based on strict control and a significant bureaucratic hierarchy (2) adaptive leadership fundamentally based on creative problem solving, resonating with new conditions and learning and (3) action-centered leadership that involves immediate decision-making mechanisms employed in crises and dynamic productivity.(Baltaci & Balcı, 2017b)

e) Methods

Mostly the studies have used the qualitative approach—data collection through personal interviews, personal stories, lived experiences, ethnographies—and purposive sampling of mostly interviews on leadership is used. Very few studies have using the tools of neoclassical realism. Based on the above mention methods, all the studies are very relevant to me. My study will be qualitative methods mainly based on literature and data collection through interviews and personal narratives also will be collected. My study is based on historical archival content analysis. Olememen has done wonderful research on the Nigerian leadership crisis through qualitative study. The case study was done on the phenomenon in Nigeria between1960-2010. The theoretical framework comprises Burns and Bass theories of transformational leadership and Davis and Toikka's theories of transformation and transit in governance. The method of data collections through personal interview with purposeful sampling of 13 past presidents of Nigeria, public officials and experts has been used. Data analysis has been done through comparative analyses.

The gap has been found in all these studies that is not done proper studies in country of transition in general and declaration of republic in specific. Most of the studies focus on failed leadership, corrupt leadership, and autocratic leadership. The Nepali character of leadership has fought for democracy for a lifetime, working for democratic leadership, even though monarchy had ruled the country for almost 250 years without any democratic norms and values and public support. Chances of declaration of republic had missed the number of times since the 1950's. On this scenario no study has been done till this date. Based on other studies I have done in this study.

IV. Conclusion

The overall objective of the paper is to make a critical assessment of concepts, theories, models for the study of leadership and its crisis, with special reference to the declaration of republic in Nepal based on available literature, the following conclusion can be drawn.

a) Limitation of the study

The research mainly focuses on Leadership crisis, concepts, theories and methods through the lance of anthropological perspective. Firstly, based on available literature, content analysis and anthropological perspective, therefore research may have limitations. Secondly, with the help of concepts, theories and methods trying to relate the declaration of republic in Nepal mainly on decisiveness which is based on few cases and limited theories and methods has been covered. Thirdly, Qualitative approach has been used mainly based on Netography (ethnography based on internet). Based on others experiences and references have been in the decision making process in the Nepali context only the case of declaration of republic. Fourthly, based on wider topic with time and resource constraint research has been done it is really useful for future.

b) Findings

The first finding of the study is to make a critical assessment of leadership concepts, theories, models and methods is not an easy job though the concept of leadership is a key element to drive the society. It depends on verities of the societies with their content, context and time. The concept of leadership is not only to lead the society but also to integrate and to connect the peoples in to the society therefore leadership is a culture, behavior, practices, mindset and tradition substantiated by reviewed literature. The second finding of the study is an anthropological approach focuses on the cultural aspect but political approach focuses more on socio-economic transformation and constant change. Leadership theories show the way out of the present crisis through appropriate theories which fit the particular context and only then can the crisis be overcome. Complexity Leadership Theory has been appropriate to relate to my study, being in the knowledge era, is the conclusion of the study. The third finding of the study is research methods can be applied in varies in order to conduct research. Research method also depends on their particular content, context and time. The fourth finding of the study is indecisiveness is a cause of crisis which can be created by social settings. It is proved in the particular context of the declaration of republic in Nepal.

In summary, the present study has shown the concept, theories and methods of leadership research based on the literature reviewed. Leadership is always able to resolve the crisis however if leadership is suffering from their own crisis they will create a crisis again. Based on the available literature review, leadership is a must no matter in nomadic life or in civilized society. The concept of leadership, decision-making process and leadership crises will be varied in terms of time and space. One size fits all formula will not be applicable, therefore, trying to be realistic, Nepal as a country in transition it needs to be seen what role leadership played in the past and what needs to be done for the future. What lapses happened in the past and how those mistakes are not to be repeated is a major concern of the study. With conceptual clarity following the conceptual framework, adopting reliable research methods and appropriate theories, this study tried to conclude and find out the causes and consequences of leadership crisis and overcome that problem.

Finally, the concern of the study is, decisions have to be taken at an appropriate time. If right time and right decision match each other, the results will be appreciated. Instead of it, if right decisions are made at the wrong time, they are useless. A wrong decision at the wrong time is disastrous.

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ASSOCIATE OF SCIENCE FRONTIER RESEARCH COUNCIL

ASSOCIATE OF SCIENCE FRONTIER RESEARCH COUNCIL is the membership of Global Journals awarded to individuals that the Open Association of Research Society judges to have made a 'substantial contribution to the improvement of computer science, technology, and electronics engineering.

The primary objective is to recognize the leaders in research and scientific fields of the current era with a global perspective and to create a channel between them and other researchers for better exposure and knowledge sharing. Members are most eminent scientists, engineers, and technologists from all across the world. Associate membership can later be promoted to Fellow Membership. Associates are elected for life through a peer review process on the basis of excellence in the respective domain. There is no limit on the number of new nominations made in any year. Each year, the Open Association of Research Society elect up to 12 new Associate Members.

Benefit

To the institution

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Global Journals sends a letter of appreciation of author to the Dean or CEO of the University or Company of which author is a part, signed by editor in chief or chief author.

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All the Associate members of ASFRC get a badge of "Leading Member of Global Journals" on the Research Community that distinguishes them from others. Additionally, the profile is also partially maintained by our team for better visibility and citation. All associates get a dedicated page on the website with their biography.

Career | Credibility | Reputation

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john [AT] globaljournals [DOT] org.

Career | Credibility | Reputation

Premium Tools

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Exclusive | Financial

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Get a remuneration of 15% of author fees

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Associate	Fellow	Research Group	Basic
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Certificate, LoR and Momento **2** discounted publishing/year **Gradation** of Research **10** research contacts/day **1 GB** Cloud Storage **GJ** Community Access	**Certificate,** LoR and Momento **Unlimited** discounted publishing/year **Gradation** of Research **Unlimited** research contacts/day **5 GB** Cloud Storage **Online Presense** Assistance **GJ** Community Access	**Certificates,** LoRs and Momentos **Unlimited** free publishing/year **Gradation** of Research **Unlimited** research contacts/day **Unlimited** Cloud Storage **Online Presense** Assistance **GJ** Community Access	**GJ** Community Access

Preferred Author Guidelines

We accept the manuscript submissions in any standard (generic) format.

We typeset manuscripts using advanced typesetting tools like Adobe In Design, CorelDraw, TeXnicCenter, and TeXStudio. We usually recommend authors submit their research using any standard format they are comfortable with, and let Global Journals do the rest.

Alternatively, you can download our basic template from https://globaljournals.org/Template.zip

Authors should submit their complete paper/article, including text illustrations, graphics, conclusions, artwork, and tables. Authors who are not able to submit manuscript using the form above can email the manuscript department at submit@globaljournals.org or get in touch with chiefeditor@globaljournals.org if they wish to send the abstract before submission.

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Authors must ensure the information provided during the submission of a paper is authentic. Please go through the following checklist before submitting:

1. Authors must go through the complete author guideline and understand and *agree to Global Journals' ethics and code of conduct,* along with author responsibilities.
2. Authors must accept the privacy policy, terms, and conditions of Global Journals.
3. Ensure corresponding author's email address and postal address are accurate and reachable.
4. Manuscript to be submitted must include keywords, an abstract, a paper title, co-author(s') names and details (email address, name, phone number, and institution), figures and illustrations in vector format including appropriate captions, tables, including titles and footnotes, a conclusion, results, acknowledgments and references.
5. Authors should submit paper in a ZIP archive if any supplementary files are required along with the paper.
6. Proper permissions must be acquired for the use of any copyrighted material.
7. Manuscript submitted *must not have been submitted or published elsewhere* and all authors must be aware of the submission.

Declaration of Conflicts of Interest

It is required for authors to declare all financial, institutional, and personal relationships with other individuals and organizations that could influence (bias) their research.

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Plagiarism is not acceptable in Global Journals submissions at all.

Plagiarized content will not be considered for publication. We reserve the right to inform authors' institutions about plagiarism detected either before or after publication. If plagiarism is identified, we will follow COPE guidelines:

Authors are solely responsible for all the plagiarism that is found. The author must not fabricate, falsify or plagiarize existing research data. The following, if copied, will be considered plagiarism:

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- Findings
- Writings
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- Illustrations
- Lectures

- Printed material
- Graphic representations
- Computer programs
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- Any other original work

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1. Substantial contributions to the conception and acquisition of data, analysis, and interpretation of findings.
2. Drafting the paper and revising it critically regarding important academic content.
3. Final approval of the version of the paper to be published.

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The corresponding author should mention the name and complete details of all co-authors during submission and in manuscript. We support addition, rearrangement, manipulation, and deletions in authors list till the early view publication of the journal. We expect that corresponding author will notify all co-authors of submission. We follow COPE guidelines for changes in authorship.

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Unless specified in the notification, the Editorial Board's decision on publication of the paper is final and cannot be appealed before making the major change in the manuscript.

Acknowledgments

Contributors to the research other than authors credited should be mentioned in Acknowledgments. The source of funding for the research can be included. Suppliers of resources may be mentioned along with their addresses.

Declaration of funding sources

Global Journals is in partnership with various universities, laboratories, and other institutions worldwide in the research domain. Authors are requested to disclose their source of funding during every stage of their research, such as making analysis, performing laboratory operations, computing data, and using institutional resources, from writing an article to its submission. This will also help authors to get reimbursements by requesting an open access publication letter from Global Journals and submitting to the respective funding source.

Preparing your Manuscript

Authors can submit papers and articles in an acceptable file format: MS Word (doc, docx), LaTeX (.tex, .zip or .rar including all of your files), Adobe PDF (.pdf), rich text format (.rtf), simple text document (.txt), Open Document Text (.odt), and Apple Pages (.pages). Our professional layout editors will format the entire paper according to our official guidelines. This is one of the highlights of publishing with Global Journals—authors should not be concerned about the formatting of their paper. Global Journals accepts articles and manuscripts in every major language, be it Spanish, Chinese, Japanese, Portuguese, Russian, French, German, Dutch, Italian, Greek, or any other national language, but the title, subtitle, and abstract should be in English. This will facilitate indexing and the pre-peer review process.

The following is the official style and template developed for publication of a research paper. Authors are not required to follow this style during the submission of the paper. It is just for reference purposes.

Manuscript Style Instruction (Optional)

- Microsoft Word Document Setting Instructions.
- Font type of all text should be Swis721 Lt BT.
- Page size: 8.27" x 11'", left margin: 0.65, right margin: 0.65, bottom margin: 0.75.
- Paper title should be in one column of font size 24.
- Author name in font size of 11 in one column.
- Abstract: font size 9 with the word "Abstract" in bold italics.
- Main text: font size 10 with two justified columns.
- Two columns with equal column width of 3.38 and spacing of 0.2.
- First character must be three lines drop-capped.
- The paragraph before spacing of 1 pt and after of 0 pt.
- Line spacing of 1 pt.
- Large images must be in one column.
- The names of first main headings (Heading 1) must be in Roman font, capital letters, and font size of 10.
- The names of second main headings (Heading 2) must not include numbers and must be in italics with a font size of 10.

Structure and Format of Manuscript

The recommended size of an original research paper is under 15,000 words and review papers under 7,000 words. Research articles should be less than 10,000 words. Research papers are usually longer than review papers. Review papers are reports of significant research (typically less than 7,000 words, including tables, figures, and references)

A research paper must include:

a) A title which should be relevant to the theme of the paper.
b) A summary, known as an abstract (less than 150 words), containing the major results and conclusions.
c) Up to 10 keywords that precisely identify the paper's subject, purpose, and focus.
d) An introduction, giving fundamental background objectives.
e) Resources and techniques with sufficient complete experimental details (wherever possible by reference) to permit repetition, sources of information must be given, and numerical methods must be specified by reference.
f) Results which should be presented concisely by well-designed tables and figures.
g) Suitable statistical data should also be given.
h) All data must have been gathered with attention to numerical detail in the planning stage.

Design has been recognized to be essential to experiments for a considerable time, and the editor has decided that any paper that appears not to have adequate numerical treatments of the data will be returned unrefereed.

i) Discussion should cover implications and consequences and not just recapitulate the results; conclusions should also be summarized.
j) There should be brief acknowledgments.
k) There ought to be references in the conventional format. Global Journals recommends APA format.

Authors should carefully consider the preparation of papers to ensure that they communicate effectively. Papers are much more likely to be accepted if they are carefully designed and laid out, contain few or no errors, are summarizing, and follow instructions. They will also be published with much fewer delays than those that require much technical and editorial correction.

The Editorial Board reserves the right to make literary corrections and suggestions to improve brevity.

Format Structure

It is necessary that authors take care in submitting a manuscript that is written in simple language and adheres to published guidelines.

All manuscripts submitted to Global Journals should include:

Title

The title page must carry an informative title that reflects the content, a running title (less than 45 characters together with spaces), names of the authors and co-authors, and the place(s) where the work was carried out.

Author details

The full postal address of any related author(s) must be specified.

Abstract

The abstract is the foundation of the research paper. It should be clear and concise and must contain the objective of the paper and inferences drawn. It is advised to not include big mathematical equations or complicated jargon.

Many researchers searching for information online will use search engines such as Google, Yahoo or others. By optimizing your paper for search engines, you will amplify the chance of someone finding it. In turn, this will make it more likely to be viewed and cited in further works. Global Journals has compiled these guidelines to facilitate you to maximize the web-friendliness of the most public part of your paper.

Keywords

A major lynchpin of research work for the writing of research papers is the keyword search, which one will employ to find both library and internet resources. Up to eleven keywords or very brief phrases have to be given to help data retrieval, mining, and indexing.

One must be persistent and creative in using keywords. An effective keyword search requires a strategy: planning of a list of possible keywords and phrases to try.

Choice of the main keywords is the first tool of writing a research paper. Research paper writing is an art. Keyword search should be as strategic as possible.

One should start brainstorming lists of potential keywords before even beginning searching. Think about the most important concepts related to research work. Ask, “What words would a source have to include to be truly valuable in a research paper?” Then consider synonyms for the important words.

It may take the discovery of only one important paper to steer in the right keyword direction because, in most databases, the keywords under which a research paper is abstracted are listed with the paper.

Numerical Methods

Numerical methods used should be transparent and, where appropriate, supported by references.

Abbreviations

Authors must list all the abbreviations used in the paper at the end of the paper or in a separate table before using them.

Formulas and equations

Authors are advised to submit any mathematical equation using either MathJax, KaTeX, or LaTeX, or in a very high-quality image.

Tables, Figures, and Figure Legends

Tables: Tables should be cautiously designed, uncrowned, and include only essential data. Each must have an Arabic number, e.g., Table 4, a self-explanatory caption, and be on a separate sheet. Authors must submit tables in an editable format and not as images. References to these tables (if any) must be mentioned accurately.

Figures

Figures are supposed to be submitted as separate files. Always include a citation in the text for each figure using Arabic numbers, e.g., Fig. 4. Artwork must be submitted online in vector electronic form or by emailing it.

Preparation of Eletronic Figures for Publication

Although low-quality images are sufficient for review purposes, print publication requires high-quality images to prevent the final product being blurred or fuzzy. Submit (possibly by e-mail) EPS (line art) or TIFF (halftone/ photographs) files only. MS PowerPoint and Word Graphics are unsuitable for printed pictures. Avoid using pixel-oriented software. Scans (TIFF only) should have a resolution of at least 350 dpi (halftone) or 700 to 1100 dpi (line drawings). Please give the data for figures in black and white or submit a Color Work Agreement form. EPS files must be saved with fonts embedded (and with a TIFF preview, if possible).

For scanned images, the scanning resolution at final image size ought to be as follows to ensure good reproduction: line art: >650 dpi; halftones (including gel photographs): >350 dpi; figures containing both halftone and line images: >650 dpi.

Color charges: Authors are advised to pay the full cost for the reproduction of their color artwork. Hence, please note that if there is color artwork in your manuscript when it is accepted for publication, we would require you to complete and return a Color Work Agreement form before your paper can be published. Also, you can email your editor to remove the color fee after acceptance of the paper.

Tips for Writing a Good Quality Science Frontier Research Paper

Techniques for writing a good quality Science Frontier Research paper:

1. Choosing the topic: In most cases, the topic is selected by the interests of the author, but it can also be suggested by the guides. You can have several topics, and then judge which you are most comfortable with. This may be done by asking several questions of yourself, like "Will I be able to carry out a search in this area? Will I find all necessary resources to accomplish the search? Will I be able to find all information in this field area?" If the answer to this type of question is "yes," then you ought to choose that topic. In most cases, you may have to conduct surveys and visit several places. Also, you might have to do a lot of work to find all the rises and falls of the various data on that subject. Sometimes, detailed information plays a vital role, instead of short information. Evaluators are human: The first thing to remember is that evaluators are also human beings. They are not only meant for rejecting a paper. They are here to evaluate your paper. So present your best aspect.

2. Think like evaluators: If you are in confusion or getting demotivated because your paper may not be accepted by the evaluators, then think, and try to evaluate your paper like an evaluator. Try to understand what an evaluator wants in your research paper, and you will automatically have your answer. Make blueprints of paper: The outline is the plan or framework that will help you to arrange your thoughts. It will make your paper logical. But remember that all points of your outline must be related to the topic you have chosen.

3. Ask your guides: If you are having any difficulty with your research, then do not hesitate to share your difficulty with your guide (if you have one). They will surely help you out and resolve your doubts. If you can't clarify what exactly you require for your work, then ask your supervisor to help you with an alternative. He or she might also provide you with a list of essential readings.

4. Use of computer is recommended: As you are doing research in the field of science frontier then this point is quite obvious. Use right software: Always use good quality software packages. If you are not capable of judging good software, then you can lose the quality of your paper unknowingly. There are various programs available to help you which you can get through the internet.

5. Use the internet for help: An excellent start for your paper is using Google. It is a wondrous search engine, where you can have your doubts resolved. You may also read some answers for the frequent question of how to write your research paper or find a model research paper. You can download books from the internet. If you have all the required books, place importance on reading, selecting, and analyzing the specified information. Then sketch out your research paper. Use big pictures: You may use encyclopedias like Wikipedia to get pictures with the best resolution. At Global Journals, you should strictly follow here.

6. Bookmarks are useful: When you read any book or magazine, you generally use bookmarks, right? It is a good habit which helps to not lose your continuity. You should always use bookmarks while searching on the internet also, which will make your search easier.

7. Revise what you wrote: When you write anything, always read it, summarize it, and then finalize it.

8. Make every effort: Make every effort to mention what you are going to write in your paper. That means always have a good start. Try to mention everything in the introduction—what is the need for a particular research paper. Polish your work with good writing skills and always give an evaluator what he wants. Make backups: When you are going to do any important thing like making a research paper, you should always have backup copies of it either on your computer or on paper. This protects you from losing any portion of your important data.

9. Produce good diagrams of your own: Always try to include good charts or diagrams in your paper to improve quality. Using several unnecessary diagrams will degrade the quality of your paper by creating a hodgepodge. So always try to include diagrams which were made by you to improve the readability of your paper. Use of direct quotes: When you do research relevant to literature, history, or current affairs, then use of quotes becomes essential, but if the study is relevant to science, use of quotes is not preferable.

10. Use proper verb tense: Use proper verb tenses in your paper. Use past tense to present those events that have happened. Use present tense to indicate events that are going on. Use future tense to indicate events that will happen in the future. Use of wrong tenses will confuse the evaluator. Avoid sentences that are incomplete.

11. Pick a good study spot: Always try to pick a spot for your research which is quiet. Not every spot is good for studying.

12. Know what you know: Always try to know what you know by making objectives, otherwise you will be confused and unable to achieve your target.

13. Use good grammar: Always use good grammar and words that will have a positive impact on the evaluator; use of good vocabulary does not mean using tough words which the evaluator has to find in a dictionary. Do not fragment sentences. Eliminate one-word sentences. Do not ever use a big word when a smaller one would suffice.

Verbs have to be in agreement with their subjects. In a research paper, do not start sentences with conjunctions or finish them with prepositions. When writing formally, it is advisable to never split an infinitive because someone will (wrongly) complain. Avoid clichés like a disease. Always shun irritating alliteration. Use language which is simple and straightforward. Put together a neat summary.

14. Arrangement of information: Each section of the main body should start with an opening sentence, and there should be a changeover at the end of the section. Give only valid and powerful arguments for your topic. You may also maintain your arguments with records.

15. Never start at the last minute: Always allow enough time for research work. Leaving everything to the last minute will degrade your paper and spoil your work.

16. Multitasking in research is not good: Doing several things at the same time is a bad habit in the case of research activity. Research is an area where everything has a particular time slot. Divide your research work into parts, and do a particular part in a particular time slot.

17. Never copy others' work: Never copy others' work and give it your name because if the evaluator has seen it anywhere, you will be in trouble. Take proper rest and food: No matter how many hours you spend on your research activity, if you are not taking care of your health, then all your efforts will have been in vain. For quality research, take proper rest and food.

18. Go to seminars: Attend seminars if the topic is relevant to your research area. Utilize all your resources.

19. Refresh your mind after intervals: Try to give your mind a rest by listening to soft music or sleeping in intervals. This will also improve your memory. Acquire colleagues: Always try to acquire colleagues. No matter how sharp you are, if you acquire colleagues, they can give you ideas which will be helpful to your research.

20. Think technically: Always think technically. If anything happens, search for its reasons, benefits, and demerits. Think and then print: When you go to print your paper, check that tables are not split, headings are not detached from their descriptions, and page sequence is maintained.

21. Adding unnecessary information: Do not add unnecessary information like "I have used MS Excel to draw graphs." Irrelevant and inappropriate material is superfluous. Foreign terminology and phrases are not apropos. One should never take a broad view. Analogy is like feathers on a snake. Use words properly, regardless of how others use them. Remove quotations. Puns are for kids, not grunt readers. Never oversimplify: When adding material to your research paper, never go for oversimplification; this will definitely irritate the evaluator. Be specific. Never use rhythmic redundancies. Contractions shouldn't be used in a research paper. Comparisons are as terrible as clichés. Give up ampersands, abbreviations, and so on. Remove commas that are not necessary. Parenthetical words should be between brackets or commas. Understatement is always the best way to put forward earth-shaking thoughts. Give a detailed literary review.

22. Report concluded results: Use concluded results. From raw data, filter the results, and then conclude your studies based on measurements and observations taken. An appropriate number of decimal places should be used. Parenthetical remarks are prohibited here. Proofread carefully at the final stage. At the end, give an outline to your arguments. Spot perspectives of further study of the subject. Justify your conclusion at the bottom sufficiently, which will probably include examples.

23. Upon conclusion: Once you have concluded your research, the next most important step is to present your findings. Presentation is extremely important as it is the definite medium though which your research is going to be in print for the rest of the crowd. Care should be taken to categorize your thoughts well and present them in a logical and neat manner. A good quality research paper format is essential because it serves to highlight your research paper and bring to light all necessary aspects of your research.

Informal Guidelines of Research Paper Writing

Key points to remember:

- Submit all work in its final form.
- Write your paper in the form which is presented in the guidelines using the template.
- Please note the criteria peer reviewers will use for grading the final paper.

Final points:

One purpose of organizing a research paper is to let people interpret your efforts selectively. The journal requires the following sections, submitted in the order listed, with each section starting on a new page:

The introduction: This will be compiled from reference matter and reflect the design processes or outline of basis that directed you to make a study. As you carry out the process of study, the method and process section will be constructed like that. The results segment will show related statistics in nearly sequential order and direct reviewers to similar intellectual paths throughout the data that you gathered to carry out your study.

The discussion section:

This will provide understanding of the data and projections as to the implications of the results. The use of good quality references throughout the paper will give the effort trustworthiness by representing an alertness to prior workings.

Writing a research paper is not an easy job, no matter how trouble-free the actual research or concept. Practice, excellent preparation, and controlled record-keeping are the only means to make straightforward progression.

General style:

Specific editorial column necessities for compliance of a manuscript will always take over from directions in these general guidelines.

To make a paper clear: Adhere to recommended page limits.

Mistakes to avoid:

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- Separating a table, chart, or figure—confine each to a single page.
- Submitting a manuscript with pages out of sequence.
- In every section of your document, use standard writing style, including articles ("a" and "the").
- Keep paying attention to the topic of the paper.
- Use paragraphs to split each significant point (excluding the abstract).
- Align the primary line of each section.
- Present your points in sound order.
- Use present tense to report well-accepted matters.
- Use past tense to describe specific results.
- Do not use familiar wording; don't address the reviewer directly. Don't use slang or superlatives.
- Avoid use of extra pictures—include only those figures essential to presenting results.

Title page:

Choose a revealing title. It should be short and include the name(s) and address(es) of all authors. It should not have acronyms or abbreviations or exceed two printed lines.

Abstract: This summary should be two hundred words or less. It should clearly and briefly explain the key findings reported in the manuscript and must have precise statistics. It should not have acronyms or abbreviations. It should be logical in itself. Do not cite references at this point.

An abstract is a brief, distinct paragraph summary of finished work or work in development. In a minute or less, a reviewer can be taught the foundation behind the study, common approaches to the problem, relevant results, and significant conclusions or new questions.

Write your summary when your paper is completed because how can you write the summary of anything which is not yet written? Wealth of terminology is very essential in abstract. Use comprehensive sentences, and do not sacrifice readability for brevity; you can maintain it succinctly by phrasing sentences so that they provide more than a lone rationale. The author can at this moment go straight to shortening the outcome. Sum up the study with the subsequent elements in any summary. Try to limit the initial two items to no more than one line each.

Reason for writing the article—theory, overall issue, purpose.

- Fundamental goal.
- To-the-point depiction of the research.
- Consequences, including definite statistics—if the consequences are quantitative in nature, account for this; results of any numerical analysis should be reported. Significant conclusions or questions that emerge from the research.

Approach:

- Single section and succinct.
- An outline of the job done is always written in past tense.
- Concentrate on shortening results—limit background information to a verdict or two.
- Exact spelling, clarity of sentences and phrases, and appropriate reporting of quantities (proper units, important statistics) are just as significant in an abstract as they are anywhere else.

Introduction:

The introduction should "introduce" the manuscript. The reviewer should be presented with sufficient background information to be capable of comprehending and calculating the purpose of your study without having to refer to other works. The basis for the study should be offered. Give the most important references, but avoid making a comprehensive appraisal of the topic. Describe the problem visibly. If the problem is not acknowledged in a logical, reasonable way, the reviewer will give no attention to your results. Speak in common terms about techniques used to explain the problem, if needed, but do not present any particulars about the protocols here.

The following approach can create a valuable beginning:

- Explain the value (significance) of the study.
- Defend the model—why did you employ this particular system or method? What is its compensation? Remark upon its appropriateness from an abstract point of view as well as pointing out sensible reasons for using it.
- Present a justification. State your particular theory(-ies) or aim(s), and describe the logic that led you to choose them.
- Briefly explain the study's tentative purpose and how it meets the declared objectives.

Approach:

Use past tense except for when referring to recognized facts. After all, the manuscript will be submitted after the entire job is done. Sort out your thoughts; manufacture one key point for every section. If you make the four points listed above, you will need at least four paragraphs. Present surrounding information only when it is necessary to support a situation. The reviewer does not desire to read everything you know about a topic. Shape the theory specifically—do not take a broad view.

As always, give awareness to spelling, simplicity, and correctness of sentences and phrases.

Procedures (methods and materials):

This part is supposed to be the easiest to carve if you have good skills. A soundly written procedures segment allows a capable scientist to replicate your results. Present precise information about your supplies. The suppliers and clarity of reagents can be helpful bits of information. Present methods in sequential order, but linked methodologies can be grouped as a segment. Be concise when relating the protocols. Attempt to give the least amount of information that would permit another capable scientist to replicate your outcome, but be cautious that vital information is integrated. The use of subheadings is suggested and ought to be synchronized with the results section.

When a technique is used that has been well-described in another section, mention the specific item describing the way, but draw the basic principle while stating the situation. The purpose is to show all particular resources and broad procedures so that another person may use some or all of the methods in one more study or referee the scientific value of your work. It is not to be a step-by-step report of the whole thing you did, nor is a methods section a set of orders.

Materials:

Materials may be reported in part of a section or else they may be recognized along with your measures.

Methods:

- Report the method and not the particulars of each process that engaged the same methodology.
- Describe the method entirely.
- To be succinct, present methods under headings dedicated to specific dealings or groups of measures.
- Simplify—detail how procedures were completed, not how they were performed on a particular day.
- If well-known procedures were used, account for the procedure by name, possibly with a reference, and that's all.

Approach:

It is embarrassing to use vigorous voice when documenting methods without using first person, which would focus the reviewer's interest on the researcher rather than the job. As a result, when writing up the methods, most authors use third person passive voice.

Use standard style in this and every other part of the paper—avoid familiar lists, and use full sentences.

What to keep away from:

- Resources and methods are not a set of information.
- Skip all descriptive information and surroundings—save it for the argument.
- Leave out information that is immaterial to a third party.

Results:

The principle of a results segment is to present and demonstrate your conclusion. Create this part as entirely objective details of the outcome, and save all understanding for the discussion.

The page length of this segment is set by the sum and types of data to be reported. Use statistics and tables, if suitable, to present consequences most efficiently.

You must clearly differentiate material which would usually be incorporated in a study editorial from any unprocessed data or additional appendix matter that would not be available. In fact, such matters should not be submitted at all except if requested by the instructor.

Content:

- Sum up your conclusions in text and demonstrate them, if suitable, with figures and tables.
- In the manuscript, explain each of your consequences, and point the reader to remarks that are most appropriate.
- Present a background, such as by describing the question that was addressed by creation of an exacting study.
- Explain results of control experiments and give remarks that are not accessible in a prescribed figure or table, if appropriate.
- Examine your data, then prepare the analyzed (transformed) data in the form of a figure (graph), table, or manuscript.

What to stay away from:

- Do not discuss or infer your outcome, report surrounding information, or try to explain anything.
- Do not include raw data or intermediate calculations in a research manuscript.
- Do not present similar data more than once.
- A manuscript should complement any figures or tables, not duplicate information.
- Never confuse figures with tables—there is a difference.

Approach:

As always, use past tense when you submit your results, and put the whole thing in a reasonable order.

Put figures and tables, appropriately numbered, in order at the end of the report.

If you desire, you may place your figures and tables properly within the text of your results section.

Figures and tables:

If you put figures and tables at the end of some details, make certain that they are visibly distinguished from any attached appendix materials, such as raw facts. Whatever the position, each table must be titled, numbered one after the other, and include a heading. All figures and tables must be divided from the text.

Discussion:

The discussion is expected to be the trickiest segment to write. A lot of papers submitted to the journal are discarded based on problems with the discussion. There is no rule for how long an argument should be.

Position your understanding of the outcome visibly to lead the reviewer through your conclusions, and then finish the paper with a summing up of the implications of the study. The purpose here is to offer an understanding of your results and support all of your conclusions, using facts from your research and generally accepted information, if suitable. The implication of results should be fully described.

Infer your data in the conversation in suitable depth. This means that when you clarify an observable fact, you must explain mechanisms that may account for the observation. If your results vary from your prospect, make clear why that may have happened. If your results agree, then explain the theory that the proof supported. It is never suitable to just state that the data approved the prospect, and let it drop at that. Make a decision as to whether each premise is supported or discarded or if you cannot make a conclusion with assurance. Do not just dismiss a study or part of a study as "uncertain."

Research papers are not acknowledged if the work is imperfect. Draw what conclusions you can based upon the results that you have, and take care of the study as a finished work.

- You may propose future guidelines, such as how an experiment might be personalized to accomplish a new idea.
- Give details of all of your remarks as much as possible, focusing on mechanisms.
- Make a decision as to whether the tentative design sufficiently addressed the theory and whether or not it was correctly restricted. Try to present substitute explanations if they are sensible alternatives.
- One piece of research will not counter an overall question, so maintain the large picture in mind. Where do you go next? The best studies unlock new avenues of study. What questions remain?
- Recommendations for detailed papers will offer supplementary suggestions.

Approach:

When you refer to information, differentiate data generated by your own studies from other available information. Present work done by specific persons (including you) in past tense.

Describe generally acknowledged facts and main beliefs in present tense.

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Topics	Grades		
	A-B	**C-D**	**E-F**
Abstract	Clear and concise with appropriate content, Correct format. 200 words or below	Unclear summary and no specific data, Incorrect form Above 200 words	No specific data with ambiguous information Above 250 words
Introduction	Containing all background details with clear goal and appropriate details, flow specification, no grammar and spelling mistake, well organized sentence and paragraph, reference cited	Unclear and confusing data, appropriate format, grammar and spelling errors with unorganized matter	Out of place depth and content, hazy format
Methods and Procedures	Clear and to the point with well arranged paragraph, precision and accuracy of facts and figures, well organized subheads	Difficult to comprehend with embarrassed text, too much explanation but completed	Incorrect and unorganized structure with hazy meaning
Result	Well organized, Clear and specific, Correct units with precision, correct data, well structuring of paragraph, no grammar and spelling mistake	Complete and embarrassed text, difficult to comprehend	Irregular format with wrong facts and figures
Discussion	Well organized, meaningful specification, sound conclusion, logical and concise explanation, highly structured paragraph reference cited	Wordy, unclear conclusion, spurious	Conclusion is not cited, unorganized, difficult to comprehend
References	Complete and correct format, well organized	Beside the point, Incomplete	Wrong format and structuring

INDEX

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ISSN 9755896