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THE INVENTED PANDEMIC, THE NEW PATHOLOGY OF ASYMPTOMATICITY, AND NOT VALIDITY OF THE COVID-19 TEST

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By now, the deaths attributed to Covid-19 are reduced to ridiculous numbers (though still pumped and exploited as much as possible by the corrupt media). Hence, the problem for the "pandemists" has it become how to extend the fake pandemic? The target main is possibly to extend it at least until the next elections American presidential elections, with the hope that the false pandemic and the resulting crisis economic problems weaken President Trump and his chance of being re-elected. Their dream would be to extend the pandemic indefinitely, because that would allow them to reshape society in the direction of a civilization tyrannical politics without freedom and with the masses living in constant fear. IS so they invented the new pathology of asymptomaticity, which consists in test positive for Covid-19 swab, even if you are perfectly healthy.

In fact, the reality was even worse, as the CDC, last May, has circulated a new definition of "probable case" of Covid-19: that's enough live in a state labeled by its governor as a state of emergency Covid-19 (epidemiological criterion) and having even just a little cough or one combination of two other symptoms, such as headache and chills, or stiffness and myalgia, to be defined as a "probable case" of Covid-9, and to be so

immediately equated to a confirmed Covid-19 case. After that, the number of positives is multiplied by involving all the people with whom he has been in contact with the "probable" Covid case.

At the heart of the pandemic project is the Covid buffer, which is based on the RT-PCR (Reverse Transcriptase- Polymerase Chain Reaction or Reverse Transcriptase - Polymerase Chain Reaction): A sample of organic material comes taken from the throat, or more rarely from the broncho-alveolar fluid, of the individual tested, and is then subjected to an RT-PCR procedure to check for presence of the SARS-Cov-2 virus in the sample. This is the same RT-PCR methodology used to "isolate" the virus originally from patient zero. Therefore, the test Covid essentially depends on whether or not the original isolation took place of the SARS-Cov2 virus, because the original PCR isolation of the virus constitutes the golden standard required to validate subsequent Covid tests.

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The problems with the isolation of the original virus, and therefore with the resulting swab tests, there are many, and all point to the truth that the SARS-Cov2 virus does not it has never been isolated and never tested for its pathogenicity. As is known, at the base of microbiology there are the famous Koch Postulates, which establish principles of common sense of microbiological research: to determine what a microorganism is cause of a disease you have to proceed through 4 basic steps:

- a) physically isolate the microorganisms, through filtering methods, from a sick patient;
- b) growing the isolated microorganisms in a culture broth;
- c) Inject this broth of microorganisms into a guinea pig, and evaluate if symptoms generated by that injection are similar to the original patient's symptoms;
- d) re-isolate the microorganism from the newly infected patient and culture it in a culture broth.

These postulates have been applied to live microorganisms such as bacteria, but since they are logical postulates they also apply to non-living "non-organisms" such as i viruses, which are non-living particles made up of a strand of RNA (or DNA) covered with a lipoprotein envelope (capsid).

Well, even if at least one article has been published stating that i Koch's postulates have been met, the reality is that the SARS-Cov2 virus is not never been isolated and tested. I looked at all the studies that claim to have isolated and even tested the virus, but they all did something very different: they have took patients' pharyngeal or bronchoalveolar fluid, so they have it centrifuged to separate the larger and heavier molecules from the longer molecules small and lighter, like the alleged viruses; they then took the supernatant (the top of the centrifuged material) and they called that matrix extremely complex "isolated virus" to which they then applied the RT-PCR. [1](#)

It's a pretty technical thing, but I'll try to simplify: the supernatant contains different types of molecules, billions of different micro and nano particles, including what are called extracellular vesicles (EVs) and exosomes, useful particles produced by our body and absolutely indistinguishable from viruses:

“Nowadays, it's a nearly impossible mission to separate vesicles extracellular and viruses through canonical methods of isolation of vesicles, such as that of differential ultra-centrifugation, because they are

[1](#) Zhu N et al, *A Novel Coronavirus from Patients with Pneumonia in China*, 2019, N Engl J Med. 2020 Feb 20; 382 (8): 727-733.

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often co-pelleted (gathered together) due to their size similar. " [2](#)

So how do you isolate a specific virus from this huge mixture of billions of indistinguishable particles, which includes beneficial exosomes?

Well, it is not done, it is impossible, and therefore the virus is "recreated" via the RT-PCR: take two *primers*, two already existing genetic sequences available in gene banks, and put them in contact with the supernatant broth, until you they *anneal* to some RNA fragment in the broth, thus creating an artificial DNA molecule, which is then multiplied with a certain number of strokes of PCR: each run doubles the amount of DNA, so theoretically more runs the greater the amount of DNA produced; but the greater the number of strokes, the less it is the reliability of the PCR, ie its ability to actually "produce" something significant from the supernatant, something that has the least bit to do with it do with the virus you are looking for: over 30 strokes the result is essentially devoid of meaning (as also stated by one of the world's leading PCR experts, the prof. Stephen Bustin). All studies, as well as current swab tests, they always use between 35 and 40 rides.

The first unanswered question is: primers consist of 18-24 bases (nucleotides) each; the SARS-Cov2 virus is presumably made up of 30,000 bases; thus the primer represents only 0.07% of the virus genome. How is You can select the specific virus you are looking for based on a primer so minute, and besides in a sea of billions of virus-like particles? Would be how to search for an elephant using tiny gray tail hairs: looking with such gray hairs you can find gray cats, gray dogs, beings graying humans and so on.

But there is more. Since the virus you are looking for is new, it clearly isn't there they are ready-made genetic primers that match the specific fraction of the new virus; then primers are taken which are thought to resemble the structure of the virus hypothesized, but it's a mere guess, and when you apply primers to the broth of the supernatant, these can attach themselves to any of the billions of molecules present, and there is no certainty that what you have thus generated is the virus what are you looking for. It is, in fact, a new artificial creation made by researchers, which is later called the "SARS-Cov2 virus," but there isn't any connection with the alleged virus responsible for the disease.

² Giannessi F. et al., *The Role of Extracellular Vesicles as Allies of HIV, HCV and SARS Viruses*, Viruses 2020, 12, 571; doi: 10.3390 / v12050571, p.4.

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The standard RT-PCR methodology is plagued by fundamental problems, e this is the reason they are now trying to develop a new one technology, called NGS (new generation sequencing), which is however also full of limitations, limitations that the most honest researchers are aware of:

"The most commonly used PCR-based methodologies require knowledge of the genomic sequences of the microorganism; however, this knowledge is not always available. A typical case is represented by outbreaks of emerging pathogens ...

Because random / unbiased amplification amplifies nucleic acids host together with microbial ones, look for microbial nucleic acids is like looking for a needle in a haystack. "

And this, which corresponds to what has been said so far, concerns both RT-PCR and NSG. This is also because many studies have shown that up to 95% of the particles virus-like present in the patient's body belong to the patient's genome same:

"The identification of pathogen nucleic acids in clinical specimens is complicated by the presence of the usual preponderant guest background ... In the study by Brown and colleagues, it was possible not to assign the human genome only 0.4% of the total readings. "3

Which confirms my metaphor of the pharyngeal or bronchoalveolar fluid of the patient like a sea of billions of viral-like particles, most of the which, such as extracellular vesicles and exosomes, belong to the genome of the patient.

And that raises the next question: if you have no idea what the virus is, how it is made, how can you say that it is responsible for something? However, i Chinese researchers have also tried to prove the pathogenicity of the virus. In one

specific Chinese study, they took the supernatant of the pharyngeal fluid (passing it off as an isolated virus), and injected it into mice, comparing it to a placebo. Now, even if it wasn't isolated, if there really was a virus responsible for the disease, it would still be present in significant quantities

³ Calistri A. Palù G., Unbiased Next-Generation Sequencing and New Pathogen Discovery: Undeniable Advantages and Still-Existing Drawbacks, *Clinical Infectious Diseases*, 2015; 60 (6): 889–91, p. 889.

⁴ Bao L. Et al. The Pathogenicity of SARS-CoV-2 in hACE2 Transgenic Mice, *Nature* (2020) 10.1038 / s41586-020-2312-y.

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in the supernatant of the patient's pathological fluid. Therefore, once injected into the guinea pigs should still produce devastating effects on animals.

But the worst effect it produced was a few "bristles" and one minimal weight reduction of 8% (perhaps the virus should be suggested as help with weight loss?); but even these minimal effects were only obtained on genetically modified mice, while there was absolutely none effect on natural, non-genetically modified or “wild” (WT) mice. This it means that the virus, if there is one, is incapable of doing the slightest bit damage to normal mice, and therefore to normal humans.

The mice were genetically engineered to hyper-produce the special ACE2 enzyme, the overproduction of which could explain some of the mild symptoms found in genetically modified mice.⁵

What is certain is that no effect whatsoever has been produced by the so-called virus on normal mice (normal people). And this is the most important study that demonstrates the pathogenicity of the Covid-19 virus, the article par excellence published on the most important scientific journal, *Nature*!

As this virus has never really been isolated, and therefore there is no *gold standard* to support further studies or tests, no standard to guide them,

anyone is free to build their own private SARS-Cov2 virus! This is the reason so now there are, in GISAID genome bank, the organization that collects and stores all genomic sequences, over 70,000 gene sequences of the virus SARS-Cov2, each of which claims to be the real one.

To adapt to this madness, we are now being told that the virus mutates, and that is why that there are so many different sequences. But it is credible that 70,000 different structures do they all correspond to the same virus? It would be like I had a John, di which are 70,000 different images, in each of which he looks like a man, then one woman, then a dog, then a snake, and so on, yet you'd like to convince me that they are all and always John!

This, among other things, raises a further very important question: whether the alleged virus mutates so much that it has produced over 70,000 genetic sequences different, which of these will be selected for the vaccine? And how can the vaccine cover something if the other 69,999 sequences are not covered and the virus in each case, it keeps changing constantly?

And here we are with the problem of the buffer, the real engine of this pseudo-pandemic. As we explained at the beginning, the swab test uses the same

5 Just to give an example, the ACE2 enzyme breaks down, or breaks down, the hormone ghrelin, responsible for of the stimulus of hunger, therefore the over-production of ACE2 can decrease hunger and contribute to weight loss. Unger T, Ulrike M, Steckelings UM, dos Santos RA (eds.). *The protective arm of the Renin Angiotensin System (RAS): functional aspects and therapeutic implications*, Academic Press. pp. 185–189.

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technique we saw above for pseudo-isolation, starting from the liquid presumptively infected of the patient. This liquid is then centrifuged inserted in the pre-established test that should have the viral standard, that is, the virus isolated, embedded. But if the virus has never been isolated, what is the standard used?

Various studies have found many mutations and variations between the different strains geographic: an article, which also includes Robert Gallo among the authors, found

dozens of mutations increasing over time in parallel with the alleged spread of virus from Asia to Europe to the USA, while another author analyzed 85 different SARS-Cov2 genomic sequences available from GISAID, and found 53 different SARS-Cov2 strains from various areas of China, Asia, Europe and the United States [.7](#)

So which of these viral strains is looking for the swab? If the virus mutates constantly (assuming and not granted that the virus exists), then the test is useless, because it looks for a virus that is always older than the one currently in circulation. This alone would be enough to understand that the Covid-19 buffer the test is completely, 100%, fallacious!

This is really what happens in reality. The “Drosten PCR Test” and the test of the Institute Pasteur, the two tests considered the most reliable (although none of the two has been externally validated), both use an E gene test, although the Drosten test uses it as a preliminary test, while the Institut Pasteur uses it as a definitive test. According to the authors of the Drosten test, the E-gene test is capable of detecting all Asian viruses, thus being very non-specific at the same time (all viral strains) and limited to a geographical area (Asia). Again, the Institut Pasteur, one of the most adopted in Europe, uses the E-Gene test as a final test, although it is now known that the SARS-Cov2 virus (or virus) believed to be circulating in Europe would be different from the Asian ones. And then in April, the WHO changed the algorithm "... recommending that from now on a test can be considered positive even if only the gene E assay (which will probably detect all Asian viruses!) gives a positive result ". [2](#)

[6](#) Pachetti M. et al., *Emerging SARS-CoV-2 mutation hot spots include a! Novel RNA-dependent RNA polymerase variant*, J Transl Med (2020) 18: 179 <https://doi.org/10.1186/s12967-020-02344-6>

[7](#) Phan Tung, *Genetic diversity and evolution of SARS-CoV-2*, Infection, Genetics and Evolution, 81 (2020), 104260

[8](#) Corman VM et al., *Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR*, Euro Surveill. 2020 Jan 23; 25 (3): 2000045.

[2](#) Engelbrecht T, Demeter K., COVID19 PCR Tests are Scientifically Meaningless, Jun 27 2020, p.21. <https://off-guardian.org/2020/06/27/covid19-pcr-tests-are-sc> AR3G6Fuq8C-8XW7szL43scbKOYF78irq52A6ZQCRdZmPMWiHTqD_2jv4Zo

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Clearly all of this is only good for fueling false positives and panic associated with the explosion of the Covid asymptomatic "disease"! That the Covid-19 swab test is set to produce many false positives it already was found early in China when an article was released on March 5, 2020 (therefore referring to the tests carried out in February) and reporting a number of 80.3% of false positives. Interestingly, after the outbreak of the "pandemic", the Chinese newspaper withdrew the article!

But the official sanction of the ineffectiveness and total unreliability of the test Covid-19 came from an unexpected area, that of the European Union. In Working Document of the European Commission of 16 April, that is, after peak of the pseudo-pandemic, the European Commission states:

“ Timely and accurate COVID-19 tests are an essential part of the management of the COVID-19 crisis ... after being placed on the market performance of the devices can be validated, ie confirmed by additional tests confirming the manufacturer's specifications, eg. in reference laboratories, academic institutions or national regulatory agencies. Such validation is not legally mandatory but highly recommended for decision making public health ”.[11](#)

One would expect there to be a standard, a testing methodology essential that it is validated and pre-authorized. This is not about a product voluntarily left to the management of the free market, but of an instrument that is essential to justify governments' power to impose the worst closure dictatorial of civil and economic rights that can be remembered in living memory!

Instead, this is the situation described by the EU Commission itself:

“In total, 78 RT-PCR based devices... 101 for the detection of antibodies and 13 for the detection of antigens were evaluated. ”

Of these 78 devices, some imported from China, none have ever been checked or inspected, let alone validated, in advance. Only 3, “... those of the Institut Pasteur, the Hong Kong Faculty of Medicine and the Charité were internally validated ”, ie certified as valid by the manufacturer himself, the

[10](#) Zonghua L et al. Potential false-positive rate among the 'asymptomatic infected individuals' in close contacts of COVID-19 patients, 2020 Mar 5; 41 (4): 485-488. doi: 10.1370/j.cma.j.cn.11.2338-2020.0221-00144

[11](#) European Commission, Working Document of Commission Services, Current performance of COVID-19 test methods and devices and proposed performance criteria, April 16 2020.

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which is to say that even those have never been validated or authorized by any independent or governmental body. Moreover:

“The most crucial information in relation to RT-PCR methods for detection of SARS-CoV-2 are the sequences of oligonucleotides (primers and probes) used for cDNA amplification... except for a few cases, we could not find any information on the actual sequences of primers and probes used in the devices. ”

In other words, devices in circulation could contain any kind of what, as far as the authorities know.

And the same level of unreliability also applies to serological tests either antibody not only because, as we have seen above, there are over 100 types in circulation different without any prior evaluation or authorization, but why to the basis of the serological test is the same fundamental limit that afflicts the swab, or the absence of a reliable standard due to the lack of isolation of the virus. When we talk about serological we are talking about antibodies, and probably all of them they think there are specific antibodies to each virus. Nothing further from reality: the antibodies that are found with the serological are only two, and only always those, IgG and IgM, the latter early immune responses, while the igG are generated later. Now, if they are always and only two, how do you know if you are refer to SARS-Cov2 and not a cold, or emotional distress, to one contusion, and so on? In theory, these antibodies are extracted from the serum, and they are undergoes the same PCR methodology used for the swab, to see if yes activate in contact with SARS-Cov2. But since, as we have seen, SARS-Cov2

it has never been isolated, and is only an artificial laboratory construction, the result of the serologic test is a mere batch, which probably activates or does not activate randomly, with no real relationship to the alleged virus that is alleged cause of Covid-19.

In short, we have entrusted the end of our freedom to such uncontrolled, never validated and never authorized tests, be they swabs or serological!

All the media in the world are screaming that this alleged pandemic already has caused more than 750,000 deaths. We know this number was a lot too swollen: the deaths of very old people (80+ years) and very sick (2-3 pathologies fatal), death from any serious pathology from which they were affected, have been attributed to Covid-19 only because patients, even after the autopsy, tested positive for unreliable test, or even without any tests.

However, there were also actually 750,000 deaths from COVID-19, would clearly be within the norm of the number of deaths from diseases respiratory, as shown in the following graph:

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Every year, as these official statistics show, nearly 7 million die worldwide from respiratory diseases. The 750,000 deaths attributed to Covid-19 in the last 6 months, even if they have doubled (which is unlikely, since the current mortality from Covid-19 is decreasing sharply around the world), it would result in about 1.5 million deaths, still well below the nearly 7 million deaths per year from respiratory problems (and certainly the deaths declared for Covid-19 they were all dead that in the past years would have been classified as dead for respiratory diseases).

And finally, EU statistics also confirm that the current level of mortality is absolutely normal:

At the end of July 2020, according to EuroMoMo, the official agency that oversees mortality within the EU, across Europe, with the exception of one slight increase in Spain and Portugal, and including countries in theory a lot harder hit by the pandemic, like Italy and the United Kingdom, there has not been no increase in mortality. All good, then, were it not for the devastating and dictatorial political-economic decisions.

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