THE INVENTED PANDEMIC, the lack of VIRUS ISOLATION and the INVALID COVID-19 test

At the request of some of my English speaking friends, I am posting here the document on the fake pandemia, on the lack of isolation of the virus and of the complete unreliability of the swab Covid-19 test...This document is attached to my interview on the ByoBlu online TV, which has now had more than 200,000 views and downloads...
Pubblico qui la versione inglese del documento legato alla mia intervista su ByoBlu, che ha superato le 200,000 visualizzazioni, anche su richiesta di alcuni amici che vogliono condividerla con i loro amici stranieri...

THE INVENTED PANDEMIC, the LACK of VIRUS ISOLATION and the INVALID COVID-19 test

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By now, deaths attributed to Covid-19 are reduced to ridiculous numbers (still, pumped up and exploited as much as possible by the corrupted media). So, the problem of the pandemists has become how to extend the fake pandemic? The main goal is possibly to extend it at least until the next US presidential elections, with the hope that the fake pandemia and the ensuing economic crisis will weaken President Trump's chances of being elected. Their dream would be to extend the pandemic indefinitely, as this would allow them to reshape society in the direction of a tyrannical polity with no freedoms and people living in constant fear. And so they invented the new pathology of asymptomaticity, which consists of testing positive with the Covid-19 swab, even if you are perfectly healthy. In fact, the reality has been even worse, as the CDC, last May, circulated a new definition of "probable case" of Covid-19: you only need to live in a State labelled by his/her Governor as a Covid-19 emergency State (epidemiological criterion) and have either just a cough, or a combination of two other symptoms, such as headache and chills, or rigors and myalgia, to be defined as a probable Covid-9 case, fully equated with a confirmed Covid case, which is then multiplied by involving all the people the "probable" Covid case has been in touch with.

At the center of the pandemic project stands the Covid swab test, which is based on the RT-PCR (Reverse Transcriptase- Polymerase Chain reaction): a sample of organic material is taken from the throat, or more rarely from the broncho-alveolar fluid, of the individual, and then the presence of the SARS-Cov-2 virus in the sample is tested. This is done by using the same RT-PCR methodology used to originally "isolate" the virus from the patient zero. Thus, the Covid test depends essentially on the original isolation, or lack thereof, of the SARS-Cov2 virus, the original PCR isolation of the virus constituting the golden standard necessary to validate any subsequent Covid test.

The problems with the original virus isolation, and thus with the ensuing swab test, are many, and they all point to the truth that **the SARS-Cov2 virus has never been isolated and never tested for its pathogenicity**. As it is well known, at the base of microbiology stand the famous **Koch's Postulates**, which establish common sense principles of microbiological research: to determine that a microorganism is responsible for a disease, one must procede through 4 basic steps: a) physically isolate the micro-organisms, through filtering methods, from a patient; b) grow the isolated micro-organisms in a culture broth; c) inject this broth of microorganisms in a guinea pig, and evaluate if the symptoms generated by that injection are similar to the symptoms of the original patient; d) isolate the microorganism from the newly infected patient and grow it in a broth culture. These postulates were applied to actual microorganisms, bacteria, but as they are logical postulates, they apply also to non-organisms such as viruses, which are non living particles made of a strand of RNA (or DNA) covered by a lipoprotein capside.
Well, even though at least one article has been published claiming that the Koch's postulates were fulfilled, the reality is that the SARS-Cov2 virus has never been isolated and tested. I looked at all the studies claiming that they isolated and even tested the virus, but they all have done something very different: they have taken the faringeal or bronco-alveolar liquid of the patients, then they ultra-centrifuged it to separate the bigger/heavier from the smaller/lighter molecules, they took the supernatant (the upper portion of the centrifuged material) and they call that the "isolate" to which they then apply the RT-PCR (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).

It's technical, but I will try to simplify: the supernatant contains all sorts of molecules, billions of different micro and nano particles, including what are called extra-cellular vesicles (EVs) and exosomes, useful particles produced by our own body and absolutely indistinguishable from viruses:

"Nowadays, **it is an almost impossible mission to separate EVs and viruses by means of canonical vesicle isolation methods**, such as differential ultracentrifugation, because they are frequently co-pelleted due to their similar dimension." (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.

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

Well, you do not, it's impossible, and so you "recreate" the virus through the RT-PCR: you take two primers, two previously existing genetic sequences available in genetic banks, and put them in touch with the supernatant broth, until they attach (anneal) to some RNA in the broth, thus creating an artificial DNA molecule, which is then multiplied though a certain number of PCR runs: each run doubles the quantity of DNA, but the higher is the number of the runs necessary to produce enough "virus" material, the lower the reliability of the PCR - meaning its ability to actually "get" anything at all meaningful from the supernatant -

above 30 runs the result tends to be meaningless, and all the studies, as well as the current swab tests, always use more than 30 runs.

The first unanswered question is: the primers are constituted of 18-24 bases (nucleotides) each; the SARS-Cov2 virus is supposedly composed of 30.000 bases; so the primer represents only the 0.07% of the virus genome. How is it possible to select the specific virus you are looking for on such a minute ground, and moreover in a sea of billions of virus-like particles? It would be like searching for an elephant by looking for a very small grey coloured hair of its tail: by searching the grey coloured hair you could find grey cats, grey dogs, greying human beings, and so on.

But there is more. As the virus you are looking for is new, there are clearly no ready genetic primers to match the specific fraction of the new virus; so you take primers that you believe may be closer to the hypothesised virus structure, but it's a guess, and when you apply the primers to the supernatant broth, your primers can attach to anyone of the billions of molecules present in it, and you have no idea that what you have thus generated is the virus you are looking for. It is, in fact, a new creation made by the researchers, who then call it SARS-Cov2, but there is no connection whatsoever with the presumed "real" virus responsible for the disease.

That the RT-PCR methodology is fraught with fundamental problems is the reason why they are now trying to develop a new technology, called NGS (new generation sequencing), which s still full of limitations, limitations of which are aware also the more honest researchers:

"The most commonly used PCR-based methodologies require the knowledge of the microorganism's genome sequences; however, **this knowledge is not always available. A typical case is represented by the outbreaks of emerging pathogens**…Because random/unbiased amplification amplifies the host nucleic acids along with the microbial ones, **searching for the microbial nucleic acids is like looking for a needle in a haystack**." (

And this, which corresponds to what I have said so far, concerns both RT-PCR and NSG. This is also because many studies have shown that up to 99.6% of the virus-like particles present in the body of patients belong to the genome of the patient him/herself:

"the identification of pathogens' nucleic acids in clinical samples is complicated by the presence of the usual preponderant host background…In the study by Brown and coworkers, **only 0.4% of the total reads could not be assigned to the human genome**." (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).

Which confirms my metaphor of the patient's faringeal or broncho-alveolar liquid as a sea with billions of viral-like particles, most of which, such as extracellular vesicles and exosomes, belong to the patient's own genome

And that raises the next question: if you have no idea of what is the virus, how it is made, how can you say that it is responsible for anything? Yet, they even tried to prove the

pathogenicity of the virus. In a specific Chinese study, they took the supernatant of the faringeal liquid (not the isolated virus, being impossible to isolate it), and they injected it into mice, comparing it with a placebo. Now, even tough not isolated, if there was a virus responsible for the disease, it would still be present in the supernatant of the patient's liquid, so once injected it should have still produced some devastating effect on the animals. But the worst effect it produced was some "slight bristle" and an 8% weight loss (maybe the virus should be suggested as a weight loss aid?) on the genetically modified mice, compared to **no effects whatsoever on the wild type (WT), not genetically modified, mice**. The genetically modified mice were grown to hyper-produce the special ACE2 enzyme, whose hyper production could explain some of the light symptoms found in the genetically modified mice (ACE2 cleaves, or disaggregates, the hormone ghrelin, which is responsabile for the hunger stimulus, so ACE2 hyper-production 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).

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

As this (non pathogenic) virus has never really been isolated, and so there is no gold standard to compare any further study or test, no standard to bind, anyone is free to build their own private SARS-Cov2 virus! This is the reason why there are now, in the GISAID genome bank, the organisation that collects an stores all the genomic sequences, about 70.000 genomic sequences of the SARS-Cov2, each claiming to be the real one. To adjust for this madness, they now say that the virus mutates, and that is why there are so many different sequences. But is it credible that 70.000 different generic structures all correspond to the same virus? It would be as if I have a John, of whom there are 70.000 different pictures, in each of which he looks like a man, then a woman, then a dog, then a snake, and so on, yet you would want to convince me that they are all still John!

This, by the way, raises a further, very important issue: if the presumed virus mutates so much as to have produced 70.000 different genetic sequences, which one will be selected for the vaccine? And how can the vaccine cover anything if the other 69.999 sequence are not covered and the virus, in any case, is supposed to constantly mutate?

And here we come to the issue of the swab test, the very engine of this fake pandemics. As we explained at the beginning, the swab test uses the same technique used for the "isolation", starting from the possibly infected liquid from the patient. This liquid is centrifuged, and then inserted in the pre-arranged test that should have the standard, that is the isolated virus, incorporated. But if the virus has never been isolated, what is the

standard used? Various studies found many mutations and variations among the different geographical strains: an article, which includes also Robert Gallo among the authors, found tens of mutations growing over time and with the presumed spread of the virus from Asia to Europe to the USA (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); while another author, by analysing 85 SARS-Cov2 genomic sequences available at GISAID, found 53 different SARS-Cov2 strains from various areas of China, Asia, Europe and the USA (Phan Tung, *Genetic diversity and evolution of SARS-CoV-2*, Infection, Genetics and Evolution, 81 (2020), 104260.). So, which one of these strains is the Covid test looking for? If the virus constantly mutates (assuming that there is a virus to mutate, which has never been proven), then the test is useless, because it goes to look for a previous virus different from the one currently present and mutated. This alone would be enough to understand that the Covid-19 swab test is completely, 100%, fallacious.

This is indeed what happens in reality. The “Drosten PCR Test” and the “Institute Pasteur test”, the two tests considered the most reliable (though neither of them has been externally validated), both use a E-gene assay, even though the Drosten test (Corman VM et al., *Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR*, Euro Surveill. 2020 Jan 23; 25(3): 2000045) uses it as a preliminary test, while the Institut Pasteur uses it as a confirmatory test. According to the authors of the Drosten test , the E-gene assay is capable to detect all Asian viruses, thus being at the same time very unspecific (all) and limited to a geographical area (Asia). Yet, the Institut Pasteur test, one the most adopted in Europe, uses the E-Gene assay as a final test, even though it is now known that the SARS-Cov2 virus (or viruses) supposedly present in Europe are different from the Asian ones. And then in April, the WHO changed the algorithm “…recommending that from then on a test can be regarded as “positive” even if just the E-gene assay (which is likely to detect all Asian viruses!) gives a “positive” result.” (Engelbrecht T, Demeter K., *COVID19 PCR Tests are Scientifically Meaningless*, Jun 27 2020, p.21) . Clearly this is only good to fuel false positive and the social panic associated with the explosion of the Covid asymptomatic disease!

That the Covid-19 swab test is bound to produce many false positives was already found at the beginning in China, when an article was published on March 5, 2020 (thus referring to tests done in February), and reporting a number of **80.3% of false positives** (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: 10.3760/cma.j.cn112338-20200221-00144). Interestingly, after the “pandemic” exploded, the Chinese journal withdrew and retracted the article! But the official sanctioning of the inefficacy and complete unreliability of the Covid-19 test has come from a most unexpected quarter, that of the European Union. In an official document of April 16, that is after the peak of the pseudo-pandemia had already been experienced, the EU Commission states:

*"Timely and accurate COVID-19 testing is an essential part of the management of the COVID-19 crisis…after being placed on the market the performance of devices may be validated, i.e. confirmed by additional testing that the manufacturer's specifications are indeed satisfied, e.g. in reference laboratories, academic institutions or national regulatory agencies. Such validation is not legally obligatory but highly recommended for public health decision making" (*European Commission, Working Document of Commission Services, *Current performance of COVID-19 test methods and devices and proposed performance criteria,* April 16 2020.)

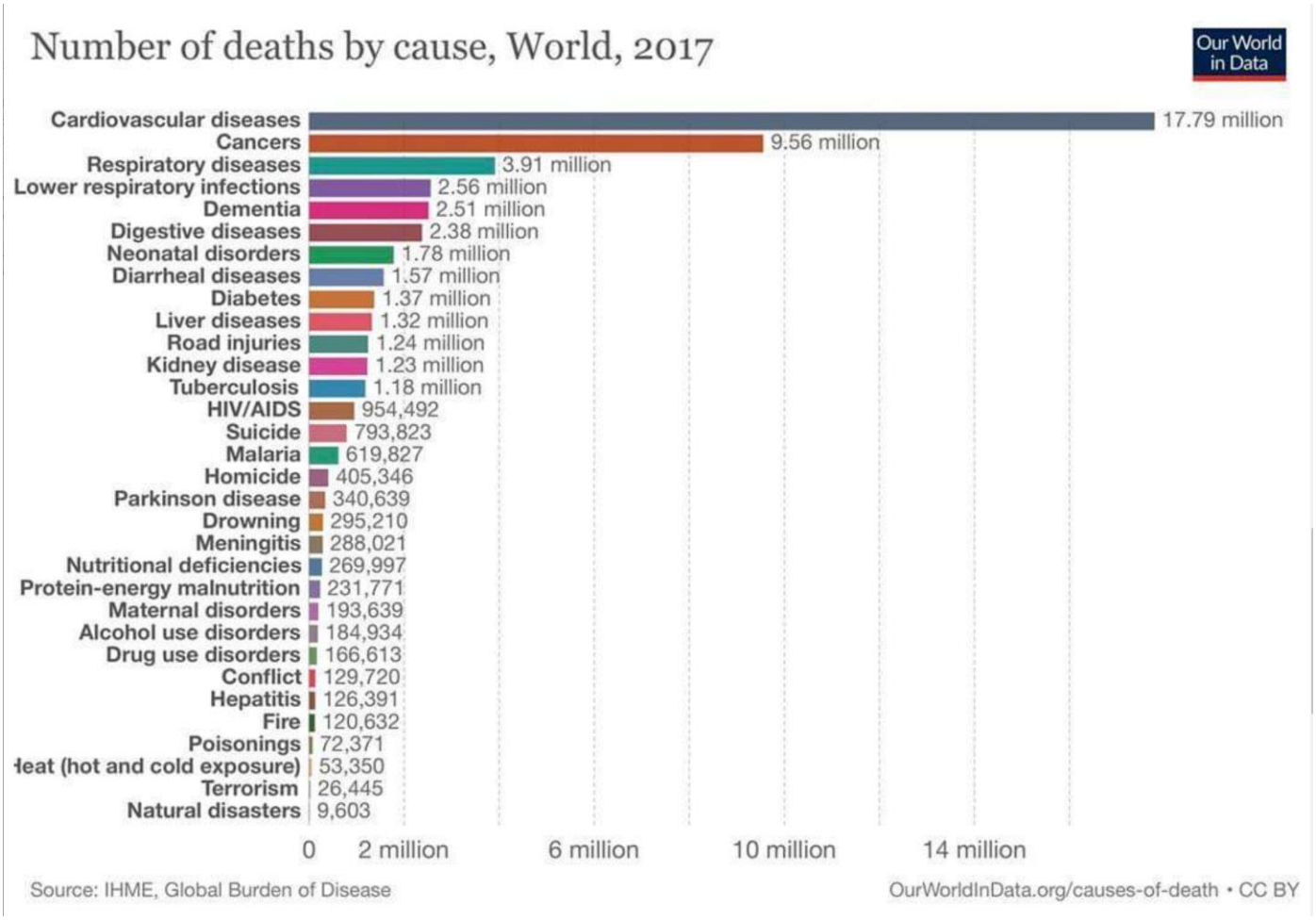
One would expect one standard, and so one fundamental testing methodology, both validated and pre-authorized: we are not talking about a voluptuary product left to the free market forces, but of a tool that has been essential to justify the power of the Government to enforce the worst dictatorial closure of civil an economic rights that a living man can remember! Instead, this is the situation as described by the very EU Commission:
"In total, **78 devices based on RT-PCR…**101 for the detection of antibodies and 13 for the detection of antigens were assessed."

Of these 78 devices, also imported from China, each never checked or inspected, let alone validated, beforehand, only 3, "…*the ones from the Institut Pasteur, the Hong Kong Faculty of Medicine and the Charité were in-house validated*", that is certified to be valid by the manufacturer itself, which is same as saying that even they have never been validated, let alone authorized, by any independent or governmental body. Moreover:
"The most crucial information concerning RT-PCR based methods developed for the detection of SARS-CoV-2 are **the sequences of the oligonucleotides (primers and probe) used for the amplification of the cDNA**……except for a few cases, **no information on the actual sequences of the primers and probes in the device could be found**."

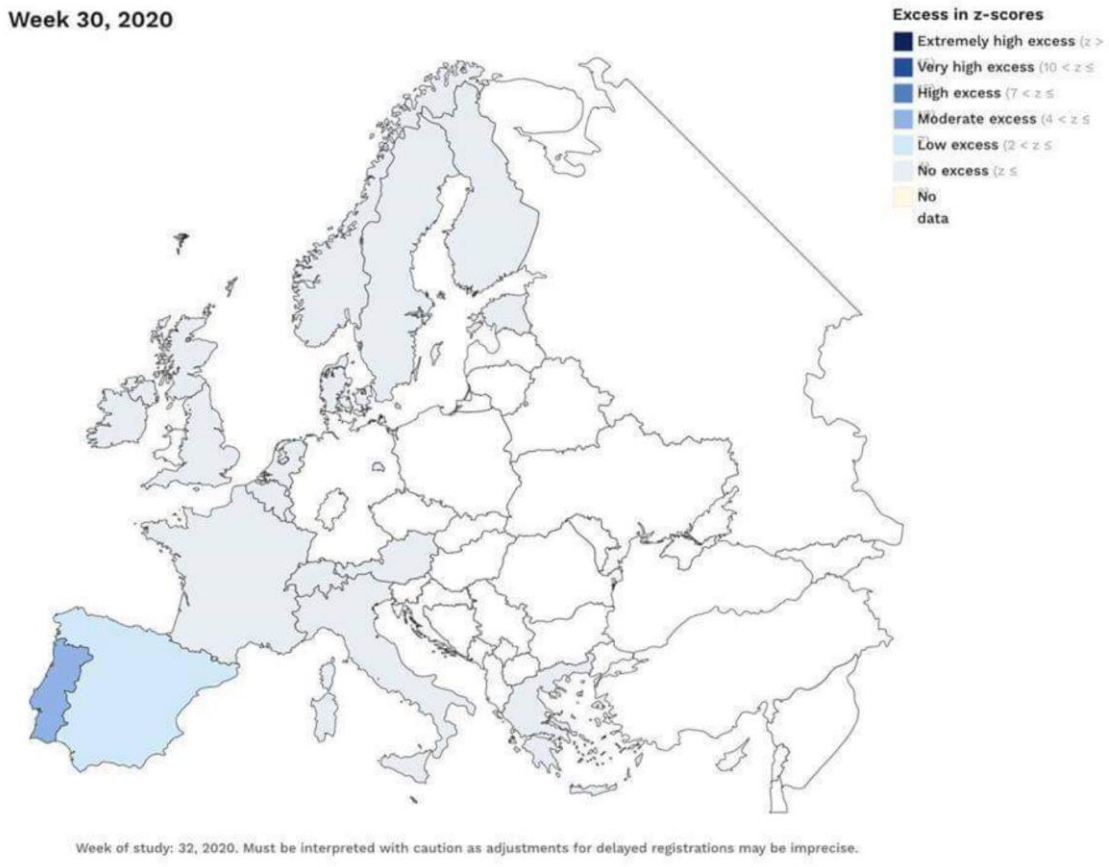
In other words, the testing devices could contain anything, as far as authorities know. Yet, we entrusted the end of our liberty to such unchecked, non validated and never authorised tests.

All the media in the world scream about the fact that this presumed pandemic has already caused more than 750.000 deaths. We know that even this number has been greatly inflated: very old (80+ years) and very sick (2-3 fatal pathologies) people, who died of whatever serious pathologies they were affected by, have been attributed to Covid-19 only because the patients, even after post-mortem, tested positive or even without any test being done. However, even 750.000 deaths for COVID-19 is clearly within the normal range of deaths for respiratory diseases, as shown by the following graphic:

Yearly, as this official statistics shows, in the world almost 7 million people die of respiratory pathologies. The 750.000 deaths attributed to Covid-19 in the last 6 months, even if they were to be doubled (which they shouldn't, as the current death count is decreasing worldwide), would make for approximately 1.5 million death, still well below the almost 7 million yearly deaths for respiratory issues.



And finally, even EU statistics confirm that the current level of death is absolutely normal:



At the end of July 2020, according to EuroMoMom, the official agency that supervises the mortality within the EU, the whole of Europe, except for slight increase in Spain, and including countries in theory very badly affected by the pandemic, such as Italy and the UK, there was no excess deaths whatsoever. All is well, that is, if it weren't for merely political-economic dictatorial decisions.

Link:

https://m.facebook.com/nt/screen/?params=%7B%22note_id%22%3A1288025411544761%7D&path=%2Fnotes%2F%7Bnote_id%7D&_rdr