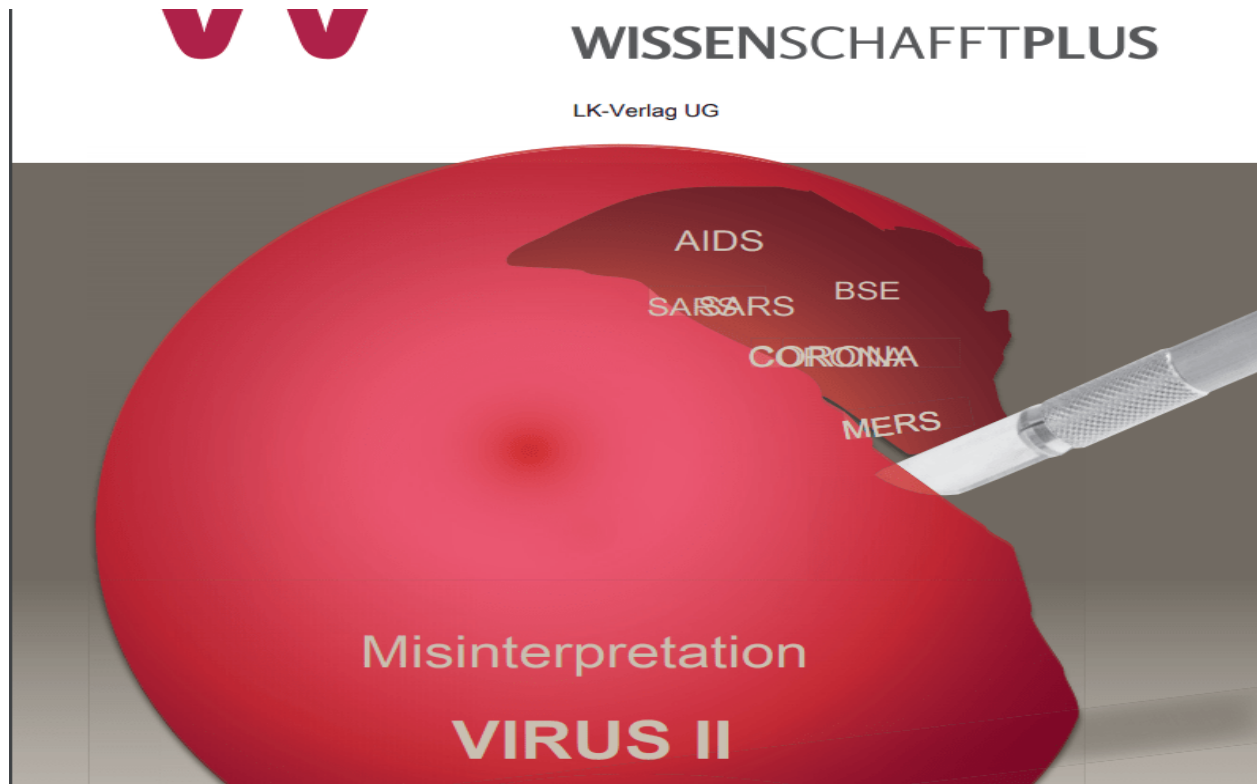


# Misinterpretation VIRUS II (2) by Dr. Stefan Lanka – Beginning and End of the Corona Crisis

<https://yummy.doctor/blog/misinterpretation-virus-ii-2-by-dr-stefan-lanka-beginning-and-end-of-the-corona-crisis/>



## **The Misinterpretation of Viruses Part 2 – The beginning and end of the coronavirus crisis By Dr. Stefan Lanka**

Translated from German by James McKumiskey

The definition of SARS and Corona or COVID-19 states that atypical pneumonia is regarded as the disease characterising symptom. If known pathogens can be proven with pneumonia, it is characterised as a typical pneumonia, if not, then as atypical. The defining factor of SARS, Corona 'virus' and at least 20%-30% of all pneumonias is they are atypical. The causes for atypical pneumonias are well known and should not be claimed to be because of an unknown virus.

This fact is suppressed by Infectious disease experts and virologists and is the basis of the current fear-mongering and panic, because the afflicted, the public and the politicians have the impression that atypical pneumonias are especially dangerous and would be more frequently deadly because there are still no medications nor vaccines for this apparent new type of disease.

From the time that a test for the alleged 'new virus' was offered, healthy people also tested "positive" and the case count was automatically raised, which was covered up by the concerned parties. First, people with typical pneumonias were recorded and then more and more people with other diseases. This is regarded as empirical evidence for the spreading of the virus. More and more diseases are automatically added to the original disease "atypical pneumonia" and this "syndrome" is claimed to be "the new viral disease."

The other defining factor, and not just for the SARS- and the Corona-virus, is that virologists who allege that pathogenic viruses exist suppressed a well-known fact for understandable reasons. The virus test that is used is a genetic test. The genetic sequences which they seek in the test are not isolated from a virus. They isolate typical genetic sequences, which are released in increasing quantities when tissues and cells die. These generally short genetic sequences, which are component parts of the human metabolism need to be studied further. Virologists can theoretically construct, with the help of a computer program, long genetic strands from many short genetic sequences. These are then claimed to be real viral genetic strands. That is the reason why healthy people who are repeatedly tested have a positive test.

Consistently, the virologists ignore two of the prescribed rules of science so that they do not contradict themselves. The first is to consistently verify all assertions oneself. The second is to test all assumptions and methods by means of control experiments. If they would carry out the control experiments, they would discover that all the genetic sequences, which are theoretically connected together to form a viral genetic strand originate from the human metabolism and not from outside, from an alleged virus.

The momentum behind the Corona-virus was triggered by a communication on the internet from a young ophthalmologist on the 30/12/2019, which spread immediately and very quickly. He informed friends that several people in his hospital were under quarantine, seven cases of SARS are confirmed and they should be careful and look after themselves. Professor Christian Drosten from the Charité in Berlin heard about it and immediately started the development of a test process for the SARS-virus before it was clear and could be clear whether the report from China about SARS was true and proven, and above all before the Chinese virologists published their results.

The authoritative virologists from the Chinese epidemic authority (CCDC) published their results on 24/01/2020 and 03/02/2020. They reported isolations of many short genetic sequences that could be theoretically arrayed to one another and could represent the genome of a new type of virus. The authors expressly point out – as do all other concerned virologists to date – that the obligatory experiments were not carried out, so not permitting them to claim that it actually was the genetic strand of a pathogenic virus. On the contrary: the Chinese virologists even

expressly point out that the constructed genetic strand has up to 90% similarity with the genetic strands from harmless Coronaviruses in bats, which were known for decades.

On 21/01/2020 (3 days before the first publication by the CCDC!) WHO recommended that all nations apply the testing method developed by Professor Drosten. Professor Drosten triggered and caused the growth and globalisation of the Chinese epidemic panic, with the claim that he had developed a reliable test process for the rapidly spreading virus in China, by not observing the clearly prescribed rules of scientific work, and by violating the laws of logic and the logic of virology, which are an integral part of his employment contract.

### **The first of two possible causes of Li Wenliang's fear**

The fear of the ophthalmologist Li Wenliang was grounded in the events of 2003 in China when Western scientists claimed that in South China a cluster of atypical pneumonia had occurred. Two days after the theoretical invention of the genome of the allegedly new virus (SARS-COV-1), in which Professor Drosten was the main scientist,[ii] he proposed a test process for this alleged virus.[iii] Around 800 people with atypical pneumonia (that is pneumonia with no known pathogens) tested positive with Professor Drosten's test, and died because of it – by possible mishandling or over-treatment – with the diagnosis SARS, instead of “atypical pneumonia.”

The reasons why the fear of SARS was perpetuated are two publications in 2013[iv] and 2017[v], which set in motion the speculation of a new SARS-Corona-Virus. The authors of both publications stated that there is evidence in bats of the existence of short genetic sequences, which can be interpreted as component parts of a virus. These short genetic sequences had similarities with those short genetic sequences, which in 2003 were explained to be a component part of the alleged SARS-Corona-Virus (SARS-COV-1). SARS stands for Severe Acute Respiratory Syndrome, which is another description of the symptoms of atypical pneumonia.

It is claimed that these theoretical genetic strands (fictitious in reality) could exist in reality and form a real virus. Such a virus, allegedly in bats and other wild animals, or even a harmless virus could jump by biting, contact, or consumption to humans and become a deadly killer. This could be transformed in humans from a harmless virus into a new pathogenic SARS-Corona-Virus. With such an experience, the resulting wave of diseases such as atypical pneumonia was inevitable.

**To date, the virologists have not succeeded in isolating a SARS-virus in the laboratory, neither from a patient, a bat nor any other animal nor detected any intact and independent SARS-Virus genome.**

The virologists' hopes of discovering a viral genome could not be fulfilled to date but were created from the short gene sequences they theoretically patched together. They have not succeeded to prove the existence nor presence of the complete genome of a SARS-virus, although the very simple standard techniques for determining the length of genetic sequences have been long available.

These false allegations fomented terror and sparked fear in the ophthalmologist doctor Li Wenliang, as well as other doctors and infectious disease experts, not just in Wuhan. The allegations are why the CDDC epidemiologists and virologists were focussed from 31/12/19 on finding similar genetic sequences, which were defined in 2003 as a component part of the SARS-Corona-Virus (see the explanations below).

## **1 The Beginning of the Corona Crisis**

When the young ophthalmologist Li Wenliang in Wuhan informed seven of his doctor friends via WhatsApp on 31/12/2019, that several people were under quarantine in his hospital, that seven cases of SARS were confirmed, and that they should be careful and look after themselves, he did not intend to trigger a panic. Otherwise, he would have put the communication on the internet and warned the public. One of the seven recipients of this private WhatsApp message published it on the internet, or rather a “screenshot “or a photograph of it, without being conscious of the possible consequences. Naturally, this information spread very quickly inside China and then worldwide.

This message triggered a wave of fear, panic, and queries to the Chinese health authorities and the government, because of the 2003 SARS panic, which the World Health Organisation (WHO) classified as a “worldwide threat” on 12/03/2003. Thus, the government in Peking sent a “rapid intervention force” to Wuhan, consisting of epidemiologists and virologists from the Chinese epidemic authority (CCDC) in order to support the health authorities locally and in the surrounding province of Hubei. The mission concerned the assessment and verification of the allegations about the outbreak of an epidemic. If there was an actual outbreak, the situation was to be appropriately controlled.

In the first authoritative publication from the CCDC authors about the results of their research: “ A new Coronavirus from patients with pneumonia in China, 2019”[i], there are no reports about a cluster of cases with atypical pneumonia (“patients with pneumonia of unknown cause”). They reported that the patients could be traced to a group with a common feature. The common feature was the more or less frequent visits to a seafood wholesale market in Wuhan. One recognises, how small the group of patients with atypical pneumonia actually was because the CCDC took swabs and fluids from the lower respiratory tract of just four patients in order to look for known and unknown pathogens.

In the meantime, the panic in Wuhan and the surrounding area dramatically rose. Also, the measures of the police could no longer slow down the dangerously escalating momentum behind the panic; they had requested on 03/01/2020 that the ophthalmologist Li Wenliang sign a cease and desist declaration, subject to a fine, and to no longer spread anything about a possible SARS outbreak. On 10/01/2020, Wenliang developed the symptoms of pneumonia and shortly afterward his parents. Li Wenliang isolated himself because he was convinced that he had been infected the previous day by a patient with the SARS-virus. This also heightened panic.

The attending doctors carried out countless different tests, which were all negative. Because his condition worsened and more and more people were interested in his fate, he was further tested, until a SARS test was finally evaluated to be “positive”. The calamity of the escalating SARS panic took its course and mutated into a global corona crisis.

Li Wenliang disseminated this result on the internet with the following words: “Today nucleic acid testing came back with a positive result, the dust has settled, finally diagnosed”.

This message increased the already existing panic. Everything went completely out of control when he published his cease and desist declaration on the internet on 03/01/2020. This publication of his cease and desist declaration, which was personally dangerous for him, was and is used as the evidence that there is a new SARS-epidemic, because a doctor who is afflicted himself, despite the threat of a fine, nevertheless informs and warns the public. The panic further increased because Li Wenliang’s health worsened despite the intensive intake of countless antibiotic substances and the public was regularly informed. This was the situation shortly before the escalation because the reporting over his death was more than chaotic and contradictory. This was and is the central reason why the Chinese and worldwide public accepted that a renewed SARS-outbreak occurred in Wuhan, which was redefined into a new epidemic and a pandemic with the name COVID-19.

### **3 The second of two possible causes of Li Wenliang’s fear**

The SARS- and Corona -crisis started with the allegations in the media that there is a cluster of patients with atypical pneumonia. This allegation was not confirmed. It was just alleged that the atypical pneumonia could only be explained by the acceptance of a new virus because a few of the people with atypical pneumonia had contact with animals for sale. In order to confirm the suspicion that an unknown virus could be the cause of atypical pneumonia, known facts were suppressed which are described in the medical scientific literature. There are actually several causes of atypical pneumonia, which are not “infectious”. This atypical pneumonia is, for several reasons, more frequently deadly than typical pneumonia.

Causes include the breathing in of poisonous fumes, solvents, and other chemical products. Other causes are the intake of food, drink or gastric contents into the lungs because of difficulties in swallowing or by loss of consciousness causing the most severe pneumonia (aspiration pneumonia). Water alone is sufficient if it gets into the lungs. Further causes include the known spectrum of immune disorders, such as allergies and autoimmune reactions. Also, treatments such as the radiation of the lungs for cancer triggers a pneumonia which cannot be differentiated from typical pneumonia. In older people there are known causes for hypostatic pneumonia; this happens because of water accumulation (oedema) from prolonged bed rest, heart or kidney weaknesses, which can lead to a lack of air and blood to the lungs as a direct consequence of their inflammation.

Logically, a combination of different factors can also cause atypical pneumonia. An atypical pneumonia can very quickly transition to a typical pneumonia, if there is a secondary attack on

the inflamed lung. This is the reason, why the percentage of atypical pneumonias is probably higher than the stated 20%-30%.

The examination of the five people, which are documented in both of the publications about the Corona-crisis,[vi]shows that neither the possible presence nor prehistory, signs, mechanism, and effects of these known causes of atypical pneumonia were researched. The virologists do not usually do that and it was not possible for the members of the CCDC because of the given circumstances of the panic. The fact that other causes of atypical pneumonia were excluded proves a severe failure of modern medicine and prevented the correct treatment of patients. The affected patients are in danger of being mistreated by a myriad of side effects from a cocktail of antibiotic substances, which above all are capable of leading to the death of patients by overdosing.[vii] It is clear that extreme panic, especially with breathing problems can on its own cause death. Panic can become deadly in a short amount of time, and not just with heart circulation pains.

The answer to the crucial question as to whether in fact a new virus was proven, or whether short pieces of genes from the body were claimed as such or are misinterpreted as viruses is crucial if the Corona-crisis is to be quickly ended. Just as with H1N1, the promoters of the Corona-crisis say that it can only be ended by vaccination. The concept of vaccination is refuted as much as viruses.

A reminder of the currently forgotten swine-flu pandemic from 2009 is helpful for the evaluation and classification of the events that triggered and perpetuated the Corona-crisis. Most Germans were ready at the time to allow themselves to be vaccinated against the alleged swine-flu virus. Then there was a postponement of the delivery of the vaccine. The vaccine could not be pre-filled into the syringe, because the new type of adjuvant damaged the vaccine mixture and made it unusable. Thus, the vaccine for 10 people at a time was filled into vials, in which the adjuvant was allowed to be mixed just before the vaccination.

It was known at this time, that the adjuvants, without which a vaccine couldn't work, were new and untested. It was known that this new type of adjuvant consisted of nanoparticles.

Nanoparticles are known to be very reactive because of their infinitesimal size and are thus used as catalysts in many types of chemical reactions, for example, to cause surfaces to behave differently than what can be achieved with normal methods. It was then said that Chancellor Angela Merkel and the army would receive this vaccine without the new type of nanoparticle-adjuvant but the police and general population would get the vaccine with the untested nanoparticles.

This led to 93% of the German population refusing the proposed vaccine. Only 7% of Germans would allow this vaccine to be prescribed. The human metabolism cannot metabolize nanoparticles and eliminate them. Because of the refusal of almost the entire population, the swine flu actually disappeared like magic from one evening to the following morning forgotten by the media and the vaccines incinerated.

(A little polemic is permitted: Astonishingly, the swine flu virus H1N1 had galloped into pigs, to no longer infect people, nor to let the infected get sick and its media presence was immediately stopped. Perhaps the swine flu vaccine had transformed itself into a fish-flu virus, in order to swim up the river in salmon's bodies and then to hit back with renewed energy at the fish market in Wuhan).

The participating epidemiologists, infectious disease experts, and virologists learned from the failure of the pandemic planning, which did not reach its climax of mass vaccination. They analysed the causes and published their results and recommendations for the future in Edition 12, December 2010 of the German Federal Health bulletin. The revealing title of this edition "Pandemic, Lessons Learned". It basically means, "The lessons we learned from the swine-flu pandemic – H1N1 debacle".

Some of the sources in this article are viewable on the internet,<sup>[viii]</sup>the main ones are not. The critical recommendations for the management of pandemics are:

- Ensuring that the experts do not contradict themselves in public discussion.
- Early involvement of mass media and social media.
- Control of the internet. This is necessary to prevent claims and criticisms damaging the consensus and acceptance of the measures outlined by politicians and society.

These recommendations were now successfully implemented! The internet is censored. Critics are ostracised by insults. The counter-arguments against the pandemic measures, which have been publicised are not debated. In Germany, in the media and politics, only one expert was heard -Professor Drosten. His only "critic", an HIV-virologist, had the function of strengthening the central assertion about the existence of a new type of virus.

#### **4 The globalisation of the Chinese SARS-Virus-Panic and the agenda-setting of the Corona-Crisis by Professor Drosten**

Professor Christian Drosten from the Charité in Berlin claims that he developed a genetic test from 01/01/2020, with which he can reliably prove the presence of the new Corona-Virus in humans.<sup>[ix]</sup>The WHO recommended his testing process on 21/01/2020 to China and all nations as a reliable test process, in order to be able to determine the spread of the alleged new Corona-Virus.<sup>[x]</sup>

In order to be able to understand a) which assumptions and actions are the basis of Professor Drosten's claims and b) to verify whether his conclusions to have developed a secure test process for the new Corona-virus, are logically and scientifically proven or not or are even refuted, requires the explanation of the applied terms, techniques, presentation of his arguments and the analysis of the two crucial publications which he references.

- How are a virus and a coronavirus defined?
- How are sequences defined in this context?

- How do the test methods for sequences work, which are characterised as PCR, RT-PCR, and as real-time RT-PCR?
- When may the evidence for the presence of sequences in humans be claimed as proof for the presence of a virus?
- How is the existence of a virus scientifically proven?

#### Terms

- A virus is scientifically defined by a specific unique genetic material.
- The genetic material of a virus is referred to as a viral strand, a viral genetic molecule or its genome.
- The viral genetic material contains the various genetic sequences for the formation of the different viral proteins, which are referred to as viral genes.
- The genetic material of a virus can consist of two genetic molecules DNA or RNA.
- Coronaviruses are defined by them consisting of a particular molecule of RNA, which is enclosed by a shell.
- The genetic material of a particular virus is defined by its precisely determined length and the exact determination of its viral genetic strands.
- The characterisation of the genome of a virus is as a result of the precise determination of the number and of the specific sequencing of the building blocks which comprise a genome. The four building blocks of the genome are called nucleotides.
- The procedure for the determination of the specific sequence of the four building blocks of a genome is called sequencing.
- The result of the determination of the building blocks of a genome is called a sequence or a genetic sequence
- Pathogenic viruses are defined by their sequence being unique and that they do not appear in healthy organisms
- In order to be able to prove and determine the presence of the virus genome, the virus has to be isolated and appear in a pure form according to the rules of thought and of logic, which every scientist presumes to be a fundamental rule, so that cellular genetic sequences are not misinterpreted as component parts of a virus.
- The determination of the sequence of genetic material is only possible if it appears in the form of DNA.
- In order to be able to determine the sequence of a genetic substance, which appears in the form of RNA, it has to be previously biochemically transformed into DNA.
- The process of the transformation of a genetic substance from RNA into DNA is referred to as "Reverse Transcription" and is abbreviated by "RT".

#### Professor Drosten's technique and first conclusions

- The presence and length of a genome is determined by it being separated according to length in an electric field. Small pieces go faster, longer pieces slower. Simultaneously, various known lengths of pieces of DNA are added in order to be able to determine the length of the researched DNA. This reliable standard method for proving and determining the length of the DNA is referred to as "Gel Electrophoresis".



– If the concentration of a particular genetic material is so low, that it cannot be proven with the “Gel Electrophoresis” technique, it can be arbitrarily increased by the technique of unlimited increase of DNA called Polymerase-Chain Reaction. Thus, DNA that is not provable by Gel Electrophoresis can be made viewable. That is a precondition to make genetic material available for further research, above all for the following crucial determination of their length and sequence. This method is abbreviated to and is also referred to as PCR.

– The inventor of the PCR-technique, Kary Mullis, who received the Nobel Prize in Chemistry, pointed out that his invention for a clean room analysis in a computer chip factory was prone to failure. He also pointed out in his Nobel prize speech, which is on the website of the Nobel prize committee, that there is no actual verifiable scientific evidence that the genetic substance, which is referred to as the HIV genome, actually causes an immune weakness or the various diseases, which are classified under the term “AIDS” and are treated with highly toxic chemotherapy. He pointed out that there is just a consensus among the concerned scientists that “HIV” would cause a weakness in the immune system.

Knowledge of the composition and sequencing of DNA is required in order to be able to increase DNA with the PCR technique. DNA can actually only be increased with PCR when short artificially manufactured pieces of genetic material are bound to the beginning and end of the DNA, which are in accordance with the exact beginning and end of the DNA being increased. Therefore, these short pieces of artificially manufactured DNA are referred to as the starter molecules of PCR or primers. They are on average between 24 to 30 nucleotides (building blocks of the genetic substance) long.

**Therefore, unknown sequences and viruses cannot be proven with PCR.** First, the determination of the sequence of a virus makes it possible to develop a PCR test for proving a genetic sequence, which comes from the virus.

– At the beginning of the PCR, it was only possible to determine the quantity of increased DNA after stopping the PCR multiplication reaction by using Gel-Electrophoresis. Meanwhile, certain dyes are added to the required enzymes and substances for the PCR. The evidence of the dye by the process of PCR indicates approximately the concentration of artificially increased DNA that has accrued, and how much DNA was actually available at the start of the PCR.

Because the determination of the quantity of artificially created DNA during the course of the PCR-technique can be approximately determined, this development of the PCR technique is referred to as “real-time PCR”. A “real-time PCR” which is preceded by another step, the transformation of RNA into DNA by means of “Reverse Transcription” RT; It is therefore referred to as “real-time RT-PCR”.

Professor Drosten applies the “real-time RT-PCR in his developed test for proving the new Corona-virus. He searched a data-pool on the internet for short genetic sequences, which are ascribed to the SARS-virus. He used these sequences of short pieces of genetic materials for the PCR-Primer sequence, in order to prove the “still” unknown Chinese virus with his “real-time RT-PCR”.

On the 10th January and 12th January provisional compilations of sequences appeared which were subsequently changed and were published on 24/01/2020 and on 03/02/2020, this represented the results of the first two experiments for identifying the still unknown virus. The CCDC virologists theoretically compiled the sequences of short genetic pieces by means of computer programs to a possible genetic strand. The CCDC virologists state in both publications that there is still no evidence that these suggested sequences actually cause disease. On 10/01/20220 and on 12/01/2020 the suggested Chinese sequences were still provisional and had not been through the strenuous process of scientific verification.

The fact that the World Health Organisation (WHO) recommended the PCR test developed by Professor Drosten for proving the new virus, even before the publication of the two Chinese sequencing suggestions, is proven. Professor Drosten used unproven scientific data for his quickly globalised PCR-test for the 2019-nCoV, which was renamed with his participation SARS-CoV-2 on 07/02/2020[xi].

With the renaming of the description of a mere suspicion of a possibly defective or harmless virus “nCoV” to a dangerous pathogen “SARS-CoV-2” the impression was implanted in the public, that an actual SARS-virus was discovered in China, which causes a dangerous disease, namely SARS, and killed the new Chinese idol Li Wenliang, who had defied the party leadership. Thus, Professor Drosten and his colleagues from the Virus-Nomenclature-Group fulfilled the expectation of the shocked population into being “finally diagnosed”. This expectation was triggered by the momentum of the mass panic caused by Dr Li Wenliang and seemingly fulfilled by Professor Drosten. It is crucial to know that at this time all directly concerned virologists stated – and to date still state – that there is no evidence that this new virus actually causes disease. Or, it occurs in parallel with diseases, with healing processes, after healing processes, by a few healthy people, or by many healthy people, or by everyone?

The above proves that Professor Drosten has overstepped the boundary of scientifically justified behaviour to a blatantly successful fraud. He cannot explain away the fact that he used a magazine for the publication of the test-process on 23/01/2020,[xii]which did not verify the statements before printing.

## **5 The crucial question for a rapid ending of the Corona-Crisis**

The central and most crucial question is; did Professor Drosten fulfill his scientific duty, which is a component part of his work contract,[xiii]to personally verify all assertions in his publications and all his public statements about the detection method he developed.

On the basis of this core scientific duty three central questions emerge:

1) Has Professor Drosten verified whether the genetic sequences (which are the basis of his test and which he received from the Chinese virologists) are actually sequences, which originate from a virus?

2) Has Professor Drosten carried out the necessary scientific control experiments, which prove whether his applied sequence actually originates from a virus? Has he carried out the control experiments to determine whether his applied sequences which he ascribes to a new virus, in reality, are not sequences which arise in every metabolism, perhaps even in plants such as for example the Tanzania papayas[xiv], or are in increased amounts in the metabolism of sick people.

3) On the basis of which assumptions, experiments, and control experiments can Professor Drosten claim that a complete, active, and pathogenic virus is proven with his test method, with which he proves only a subset of 2 (two) genes from the genome of in total 10 (ten) genes of the coronavirus? And not just a component part of a virus after a successful battle by the immune system, or the presence of a "defective" or "incomplete" or "harmless" virus in our genes, which are typical and make up 50% of the genes in our chromosomes.

The answers emerge from Professor Drosten's documented actions with the development of his test and from his documented inactions to date.

The virologist Professor Drosten who developed the test process of the new Coronavirus (first named 2019-nCoV, then from the 07/02/2020 SARS-CoV-2), described the development of the test process in a publication, which was published on 23/01/2020.[xv] On page 3 of this article, left column, 8th line from the bottom, he describes the first and crucial step of his process.

"Before the public release of virus sequences from cases of 2019-nCoV, we relied on social media reports announcing the detection of a SARS-like virus. We thus assumed that SARS-related CoV was involved in the outbreak".

That means that Professor Drosten and his colleagues assumed, on the basis of reports in social media, that the alleged outbreak of atypical pneumonia meant a SARS related coronavirus could be involved. At this time, there was no clinical data, which could have been the basis for such a suspicion. What was his next step?

"We downloaded all complete and partial (average length > 400 nucleotide) SARS-related virus sequences which were available on GenBank on 1 January 2020." It continues in the right column on page 3, the third line from the top.

"These sequences were aligned (remark by me, SL: using a SARS -Virus standard sequence) and the alignment was used for assay design (supplementary figures S1) Upon the release of the first 2019-nCov sequence at virological.org, three assays were selected based on how well-matched they were to the 2019-nCoV genome (Figure S1 in the supplement to this publication).

"After the publication of the first 2019-nCov-sequence on virological.org, three assays were selected based on how well they aligned to the 2019-nCoV genome (Figure 1)."

The following clear answers, conclusions, and consequences emerge from his statements.

1) Has Professor Drosten verified whether the gene-sequences, which are the basis of his tests, and were obtained from the Chinese virologists are actually sequences that originate from a virus? The answer is No! He couldn't verify whether the sequences are from a virus, because the two definitive publications, in which the extraction of the gene sequences used by him are described, were not available before the launch of his test.

2) Has Professor Drosten carried out the prescribed control experiments to determine whether the sequences used actually come from a virus? Has been carried out the control experiments to determine whether the applied sequences, which he ascribes to the new virus, are in reality, not sequences that originate in every metabolism, perhaps even in plants and even more so in the metabolism of sick people?

The answer is: **No! Neither he nor the CCDC virologists nor others have demonstrably carried out the necessary control experiments to date and if so, they have not published them.** Short genetic sequences from the metabolism of healthy people must be used in order to sequence them for the crucial control experiments. These short genetic sequences must be put together into a long genetic-strand of a virus with the same computer programme as the gene sequences from sick people. This experiment was neither performed nor published. This necessary control experiment, which arises from pure logic, and the logic of virology was never mentioned. The moment in which this experiment is carried out and published, the corona-crisis is immediately ended.

The other control experiment resulting from scientific logic, using the corona-virus PCR-test (real-time RT-PCR), to test whether or not clinical probes from people with other diseases other than those ascribed to the corona-virus, clinical probes from healthy people, animals, and plants are "positive". These further control experiments, which are logically necessary in order to validate a test process, that is to verify whether it is valid and has authenticity, were not carried out to date and have never been claimed to have been carried out. Thus, the inventor and producer of this test process have ensured on the package insert that the test is only to be only used for study purposes and is not suitable for diagnostic purposes.

I can predict with certainty that people, who have increased genetic sequences for the platen epithelium tissue type, for example, kidney patients, are almost always tested 100% positive with Professor Drosten's PCR test because their smear is multiplied a little and is concentrated. Very probably all organisms can even be tested positive.

I request all biochemists, bioinformaticians, virologists and cell culture specialists to carry out these control experiments, to publish them, and inform me. I conceived a control experiment, which discards from the outset the excuse that the probe might get contaminated with SARS-CoV-2.

The cost of the control experiments will be paid, if I and neutral observers are allowed to be present during the execution of the control experiments, and every step is documented. Please contact me. The results will immediately end the corona crisis. It is not useful if I alone present the results of the control experiments.

3) On the basis of which assumptions, experiments and control experiments can Professor Drosten claim that a complete, active, and pathogenic virus is proven with his test method, with which he only verifies a subset of 2 (two) genes from the genome of in total 10 (ten) genes of the Corona Virus. And not just a component part of a virus after a successful battle by the immune system, or the presence of countless “defective”, “incomplete” and “harmless” viruses in our genes.

Professor Drosten has not taken these logical questions into account as they do not appear in his publications and claims. The evidence of just short genetic sequences from a longer genetic strand of a virus can never prove the presence of an intact virus capable of propagation. In order to be able to characterise such a PCR-test as valid, a study would have to be taken, whose results prove that the evidence of short genetic sequences automatically proves the presence of a complete and intact genome of a virus. Such a logical and necessary study has not been carried out or mentioned to date.

The leading virologist in the area of cellular viruses, classified as endogenous harmless incomplete or defective viruses, Professor Karin Moelling, characterised the measures at the beginning of the Corona-Crisis as unjustified. She has shown in publications and in a book[xvi]that half of the genetic material of the human, that is half of the sequences, from which our chromosomes are comprised, consist of inactive and defective gene sequences from viruses. What she doesn't know, or denies, is the fact, that the metabolism permanently creates a great quantity of RNA-genetic-sequences of arbitrary characterisation, which do not appear in the form of DNA-sequences in the chromosomes. This fact calls into question claims about the existence of all RNA-viruses such as for example, coronaviruses, Ebola virus, HIV, measles-virus, and the SARS virus. With control experiments, not just the corona-crisis but the fear and the misrepresentation by the entire virology sector of all alleged pathogenic viruses is immediately ended. I can assure you that the actual causes and phenomena of infection, which are ascribed to viruses, are proven in the “positive” sense of the word “science”. I refer to this in the previous article “Misinterpretation of Viruses 1” in the magazine WissenschaftPlus Nr 1/2020, which can also be obtained as a pdf, and naturally on the many previous articles about this issue.

The sequel “Misinterpretation of Viruses 111” follows.

[i] A Novel coronavirus from patients with pneumonia in China, 2019. N Engl J Med 2020; 382: 727-733. DOI: 10.1056/NEJMoa2001017. Published on 24/01/2020.

[ii]About the responsibility of a virologist. Is Christian Droster a victim or a perpetrator? Published in the blog of the peace activist Peter Frey, peds-ansichten.de on the 26/05/202.

[iii]SARS, Wikipedi. <https://www.bbc.co.uk/news/health-53320155><https://www.bbc.co.uk/news/health-53320155>

[iv] Xing-Yi Ge et al., Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. Nature. Band 503, 2013, S. 535–538, doi:10.1038/nature12711;

[v] Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. Ben Hu, Lei-Ping Zeng, Xing-Lou Yang et al., PLoS Pathogens. 13(11): e1006698, doi:10.1371/journal.ppat.1006698;

[vi] Siehe Quelle 1 und: A new coronavirus associated with human respiratory disease in China. Nature | Vol 579 | 12 March 2020 | 265-269. <https://doi.org/10.1038/s41586-020-2008-3>. Veröffentlicht am 3.2.2020.;

[vii] Pathological findings of COVID-19 associated with acute respiratory distress syndrome. Lancet Respir Med 2020; 8: 420–22.

Published Online February 17, 2020. [https://doi.org/10.1016/S2213-2600\(20\)30076-X](https://doi.org/10.1016/S2213-2600(20)30076-X);

[viii] Bundesgesundheitsblatt, Ausgabe Nr. 12, Dezember 2010. Pandemien. Lessons learned <https://link.springer.com/journal/103/53/12>

[ix] Bundesgesundheitsblatt, Ausgabe Nr. 12, Dezember 2010. "Pandemien. Lessons learned". Federal Health newsletter, Edition 12, December 2010 "Pandemics, Lessons Leaned". <https://link.springer.com/journal/103/53/12>

[x] Diagnostika: Erster Test für neuartiges Coronavirus entwickelt. Medica Magazin vom 21.1.2020. <https://www.medica.de/de/News/Archiv/Diagnostika>; Diagnostic: First test developed for the new type of Coronavirus Medica Magazine 21.1.2020.

[xi] See 6.

[xii] Severe acute respiratory syndrome-related coronavirus: The species and its viruses – a statement of the Coronavirus Study Group. bioRxiv preprint doi: <https://doi.org/10.1101/2020.02.07.937862>;

[xiii] §2 Grundsätze Guter Wissenschaftlicher Praxis: (1) u.a. „alle Ergebnisse konsequent selbst anzuzweifeln“ und „die anerkannten Grundsätze wissenschaftlicher Arbeit in den einzelnen Disziplinen einzuhalten.“ In: Neufassung der Satzung der Charité – Universitätsmedizin Berlin zur Sicherung Guter Wissenschaftlicher Praxis vom 20.06.2012 (AMB Charité Nr. 092, S. 658) Zu finden

unter: [https://www.charite.de/fileadmin/user\\_upload/portal/charite/presse/publikationen/amtli-mittei-lungsblatt/2016/AMB\\_208.pdf](https://www.charite.de/fileadmin/user_upload/portal/charite/presse/publikationen/amtli-mittei-lungsblatt/2016/AMB_208.pdf):

[xiv] Wie mit den Befunden in der Öffentlichkeit umgegangen wird, dass auch Früchte „positiv“ auf „SARS-Cov-2“ getestet werden ist, finden Sie beispielhaft hier: <https://www.zdf.de/nachrichten/panorama/coronavirus-papaya-ziege-tansania-test-100.html>

[xv] See 9.

[xvi] See the book by Karin Mölling with the interesting title "Viruses: More Friends Than Foes", 420 Pages, which also was published in German in 2016.

<https://onlinelibrary.wiley.com/doi/epdf/10.1002/elan.201900604>

Article in German: <https://wissenschaftplus.de/uploads/article/wissenschaftplus-fehldeutung-virus-teil-2.pdf>