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Beginning and end of the corona crisis

from Dr. Stefan Lanka



Misinterpretation virus

Beginning and end of the corona crisis

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The definition of SARS and Corona or Covid-19 states that atypical pneumonia is considered to be the disease characterizing the disease. If known pathogens can be detected in pneumonia, pneumonia is said to be a typical, if not an atypical one. One of two factors that are decisive for the SARS and the corona crisis is that at least 20–30% of all pneumonia is atypical. The causes of atypical pneumonia are very well known and therefore must NOT be given as the cause of an unknown virus.

This fact is suppressed by infectious diseases and virologists and is the basis of current anxiety generation and panic, because it gives people, the general public and politicians the impression that atypical pneumonia would be particularly dangerous and more often fatal because of the lack of medication or Vaccines for the supposedly novel disease exist.

The number of cases is automatically increased from the time when a test procedure for the allegedly new virus is offered, which, what is concealed by those involved, also tests healthy people "positively". First, people with typical pneumonia are recorded, then more and more people with other diseases. This is considered practical evidence of the spread of the virus. More and more other diseases are automatically added to the original disease "atypical pneumonia" and this "syndrome" is output as "the new virus disease".

The other fact, which is not only decisive for SARS and the corona crisis, is that virologists who claim that they are pathogenic viruses suppress an obvious situation for understandable reasons. The virus test procedure offered is a genetic detection procedure. The gene sequences that they use for the detection test do not isolate them from a virus. They isolate typical gene sequences that are released when tissues and cells die. These generally short gene sequences, components of human metabolism, form the basis for further laboratory work. However, with the help of computer programs, virologists can only construct long strands of genetic material from many short gene sequences using computer programs. These are then issued as real, viral genome strands. That is the reason,

So that these virologists do not refute themselves, they consistently disregard two rules prescribed in science. One is to consistently review all claims yourself. The other is to test all assumptions and methods used by means of control tests. If they carried out the control experiments, they would find that ALL of the short gene sequences that they only mentally link to a virus genome stem from human metabolism and not from the outside, from an alleged virus.

The momentum of the corona crisis was triggered by a message from a young ophthalmologist on December 30, 2019 on the Internet, which spread immediately and very quickly. He told friends that several people were quarantined in his hospital, seven cases of SARS have been confirmed, and they should be careful and protect themselves. Prof. Christian Drosten from the Charité in Berlin heard about it and immediately started developing test procedures for SARS viruses before it was even clear and clear whether the report from China about SARS was true and proven, and above all before the Chinese virologists published their results.

The relevant virologists of the Chinese Disease Control Agency (CCDC) published their results on January 24, 2020 and February 3, 2020. They report on the isolation of many short gene sequences, which, strung together, could represent a genetic strand of a novel virus. The authors expressly point out - including all other virologists involved to date - that the absolutely necessary experiments have not yet been carried out, which would make it possible to assert that the genome is actually a disease-causing virus. On the contrary: The Chinese virologists even explicitly point out that the constructed genetic strand has up to 90% similarity to genetic traces of harmless and known corona viruses in bats that have been known for decades.

On January 21, 2020 (3 days before the first publication of the CCDC!), The WHO recommended all nations to use the test procedure developed by Prof. Drosten. With the claim that he had developed a reliable test method for the virus, which is spreading rapidly in China, Prof. Drosten, in violation of the clearly defined rules of scientific work, which are part of his employment contract, and by violating the laws of thought and logic of virology, the increase and globalization of the Chinese epidemic panic triggered and causes.

1. Beginning of the corona crisis

When on December 30, 2019 the young ophthalmologist Li Wenliang in Wuhan via WhatsApp informed seven friendly doctors that several people were quarantined in his hospital, seven cases of SARS were confirmed, they should be careful and protect themselves, he did not intend one Trigger panic. Otherwise he would have posted this message on the Internet and warned the public. One of the seven recipients of this private WhatsApp message published a "screenshot", ie a photo of this message, on the Internet without being aware of the possible consequences. Of course, this information spread very quickly within China and then worldwide.

This release triggered a wave of fear, panic, and inquiries to Chinese health authorities and the government because of the panic of a SARS crisis in 2003, which the World Health Organization (WHO) classified as a "global threat" on March 12, 2003. The government in Beijing subsequently dispatched a "rapid reaction force" consisting of epidemiologists and virologists from the Chinese Disease Control Agency (CCDC) to Wuhan on December 31, 2019 to support the local health authorities and the surrounding Hubei province. The aim was to review and verify allegations of an epidemic. If an outbreak actually occurred, the situation should be adequately controlled.

In the first authoritative publication by the authors of the CCDC on the results of their research, "A new coronavirus for patients with pneumonia in China, 2019" **no accumulation of cases with atypical pneumonia ("patients with pneumonia of unknown cause")** is reported. They report that the patients found can be combined into a "cluster", into a group with common characteristics. The common feature was the more or less frequent visit to a seafood wholesale market in Wuhan. How small the group of patients with atypical pneumonia actually was can be seen from the fact that the CCDC took swabs and fluids from the lower respiratory tract from only four patients to look for known and unknown pathogens.

In the meantime, panic in Wuhan and the surrounding area increased extremely. The measures taken by the police, who asked ophthalmologist Li Wenliang on January 3, 2020, to sign a punitive cease-and-desist declaration to no longer disseminate anything about a possible SARS outbreak, were no longer able to create the dangerously escalating dynamic of panic slow it down. Wenliang, and shortly afterwards his parents, developed the symptoms of pneumonia on January 10, 2020. Li Wenliang isolated himself because he was convinced that he had been infected with the SARS virus in an eye patient the previous day. That also increased the panic.

The supervising doctors performed a variety of different test procedures, all of which were negative. As his health deteriorated and more and more people showed public concern for his fate, testing continued until a first SARS test was carried out on

January 30, 2020 was rated as "positive". The calamity of the escalating SARS panic that mutated into the global corona crisis began.

Li Wenliang spread 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." "Today the genetic test came back with a positive result, the dust has decreased, finally diagnosed. "

This news increased the already existing panic. Everything got completely out of control when he published his signed cease-and-desist obligation on 3.1.2020 on the Internet. This dangerous publication of his cease-and-desist declaration was and is valid for all panicked people as proof that there is a new SARS epidemic because a doctor who is affected, despite the threat of punishment, continues to inform and warn the public. The panic increased further because Li Wenliang's health deteriorated despite the intensive use of a large number of antibiotic substances and the public regularly took part in it. The situation was on the verge of escalation because the reporting of his death was more than messy and contradictory.

2. One of two possible causes of Li Wenliang's fear

On the one hand, the fear of the ophthalmologist Li Wenliang is based on the events in China in 2003, when western scientists claimed that an accumulation of atypical pneumonia had occurred in southern China. Two days after the intellectual creation of a genetic line of the supposedly new virus (SARS-CoV-1), in which Prof. Drosten was significantly involved, ^{2nd} Prof. Drosten offered an alleged test procedure for this alleged virus. ^{3rd} Approx. 800 people with atypical pneumonia, i.e. a pneumonia in which no known pathogens are detected, but who were tested with the test by Prof. Drosten "positive", therefore died - possibly incorrectly and overtreated - with the diagnosis SARS instead of "atypical pneumonia". "

The basis that the fear of SARS was maintained and increased until 2019 is based on two publications in 2013^{4th} and 2017⁵, started speculation about the possibility of new SARS corona viruses. The authors of both publications state that it is healthy



Bats provide clues for the existence of short gene sequences that can be interpreted as components of a virus. These short gene sequences would be similar to those short gene sequences that were declared components of the alleged SARS Corona Virus-1 (SARS-CoV-1) in 2003. SARS stands **for S heavy A kutes R expiratory S syndrome, which is another description of** the symptoms of atypical pneumonia.

It is stated about these intellectual (fictitious) genomic strands that it is possible that they could also arise in reality and form a real virus. Such a virus, which has been claimed in bats and other wild animals but is still harmless, could spread to humans through bite, contact or consumption and could become a deadly killer. In humans, this harmless virus could, through changes (mutations), turn into an actually new and disease-causing SARS corona virus. With such an event and the resulting wave of diseases such as

eg atypical pneumonia, must be calculated at any time.

To date, the virologists have neither succeeded in isolating a SARS virus from a patient, a bat, another animal, or in the laboratory, nor have they identified an intact and complete genetic strand of a SARS virus. The assumption of the virologists that there are actually viral genome strands that are structured like the genome strands that are composed of short gene sequences has not been confirmed to date. In other ways, too, it has not been possible to date to prove the existence and presence of a complete genome of a SARS virus, although the very simple standard techniques for determining the length of genetic sequences have long been available.

The fears massively aggravated by such false claims were the basis of the fears of the ophthalmologist Li Wenliang, as well as other doctors and infectiologists, not only in Wuhan. These claims are the reason why the CCDC's epidemiologists and virologists from

12/31/2019 focused on finding similar gene sequences that were defined as components of SARS corona viruses in 2003 (see explanations below).

3. The second of the possible causes of Li Wenliang's fear

The SARS and Corona crises started with the media claim that there is an accumulation of patients with atypical pneumonia. This claim has never been substantiated. The only claim was that the atypical pneumonia that occurred could be explained by the assumption of the appearance of a new virus because some of the people with atypical pneumonia had contact with animal markets. To confirm the suspicion that an unknown virus could be the cause of atypical pneumonia,

known facts described in the medical-scientific literature were suppressed. There are several broad spectra of non-infectious causes of atypical pneumonia. This atypical pneumonia is more likely to be fatal for several reasons than is the case with typical pneumonia.

The causes include inhalation of toxic fumes, solvents and substances. The penetration of food, drinks or stomach contents, which get into the lungs when swallowing or loss of consciousness, can cause severe pneumonia (aspiration pneumonia). Water alone is sufficient if it gets into the lungs of drowning people to cause severe atypical pneumonia. Another cause is the recognized spectrum of immunological misconduct, such as allergies and autoimmune reactions. Cancer radiation is also known to cause inflammation of the lungs, which cannot be differentiated from typical pneumonia. Stagnant pneumonia is known especially in older people. These arise due to water retention (edema), if you are bedridden for a long time,

Logically, a combination of otherwise subliminal causes also causes atypical pneumonia. An atypical pneumonia can quickly change into a typical one, if there is secondary colonization of the inflamed lungs. That is why the proportion of atypical pneumonia is likely to be higher than the estimated 20-30%.

In the investigations of the five people, which are documented in the two **publications relevant to the Corona crisis,**⁶

no possible presence or history, signs, mechanisms and effects of these known causes of atypical pneumonia have been investigated. Virologists usually don't do this anyway and the CCDC members were not able to do so due to the circumstances of the panic. Excluding the mention of atypical pneumonia proves a serious medical malpractice and prevents correct treatment of the patient. Those affected therefore run the risk of being mishandled with a cocktail of antibiotic substances that is rich in side effects and which, especially when overdosed, is capable of independently **causing the death of patients.**⁷

Everyone must be aware that extreme panic, especially with breathing problems, can cause death on its own. Panic can even be fatal in a very short time, not only for cardiovascular problems.

The answer to the crucial question of whether a new virus has actually been detected or whether only the body's own, short pieces of genetic substances are given out as components of a virus or misinterpreted as such is decisive for whether the corona crisis can be ended quickly. As with H1N1, the causes of the corona crisis say that this can only be ended by vaccination. The idea of vaccination is just as refuted as that of the virus.



The memory of the swine flu pandemic of 2009, which has since been forgotten in the meantime, is helpful for assessing and classifying the events surrounding the initiation and maintenance of the corona crisis. The majority of the population at the time was willing to vaccinate themselves against the alleged swine flu virus. Then there was a delay in the announced delivery of the vaccines. The vaccines could not be filled into pre-filled syringes because the novel drug enhancers used for the first time damaged the vaccine mixture and made it unusable. For this reason, the vaccine was filled into ampoules for 10 people each, into which the drug enhancers were only allowed to be added shortly before the vaccination act.

During this time it became known that the drug enhancers, called adjuvants, without which a vaccine would not work, were novel and untested. It became known that these novel drug enhancers consist of nanoparticles. It is known about nanoparticles that their tiny size makes them very reactive, which is why they are used as catalysts in many chemical reactions and, for example, in technical processes cause the surfaces to behave very differently than can be achieved with conventional methods. Then it became known that Chancellor Angela Merkel and the German Armed Forces were to receive this vaccine without the novel nanoparticle drug enhancer, whereas the police and the population received the vaccine with the untested nanoparticles.

As a result, 93% of the population rejected the vaccine they were made for. Only 7% of Germans had this vaccine administered. Human metabolism cannot metabolize and excrete nanoparticles. Because of this refusal by almost all of the population, the swine flu actually magically disappeared from one evening to the next morning from the media into the sink and the vaccines into a blast furnace. (A small polemic is allowed: Astonishingly, the swine flu virus H1N1 broke away in a swine gallop, no longer infected other people, did not let the infected get sick, its media presence immediately stopped.

The epidemiologists, infectiologists and virologists learned from the failure of the pandemic planning, which did not come to the peak of the vaccination. They analyzed the causes and published their findings and recommendations for the future in issue no. 12, December 2010 of the Federal Health Gazette. The telling title of this issue: "Pandemics. Lessons learned" Which means something like: The lessons we learned from the swine flu H1N1 debacle!

Some of the articles in this issue are available on the Internet,^{8th} but the essential ones are not. The key recommendations for pandemic management are:

- Ensuring that experts do not contradict each other in public discussions.
- Early integration of key and social media.
- Control of the Internet. This is to prevent claims and criticism from jeopardizing the consensus and acceptance of the measures in politics and society.

These recommendations have now been successfully implemented! The Internet is censored, critics are excluded by insults, among other things. Mandatory arguments that have contradicted the pandemic assumption and have made it into the public eye are simply not dealt with. Only one expert, Prof. Drosten, is heard in the media and politics. The only "criticism" of him, put forward by an HIV virologist, was to strengthen the central existence claim of a novel virus, SARS-CoV-2.

4. The globalization of the Chinese SARS virus panic and course setting for the corona crisis by Prof. Drosten

Prof. Christian Drosten from the Charité in Berlin claims that from January 1, 2020 he developed a genetic detection procedure with which he can **reliably detect the presence of the new corona virus in humans.**^{9th} On January 21, 2020, the WHO recommended the test method it had developed to the Chinese and all nations as a reliable test method to **determine the spread of the allegedly new corona virus.**^{10th}

In order to a) understand which assumptions and actions underlie Prof. Drosten's claims and b) to check whether his conclusions have developed a safe test procedure for the new corona virus, are logically and scientifically proven or not, or even refuted, it requires an explanation of the terms, techniques used, the presentation of his reasoning and the analysis of the two crucial publications to which Prof. Drosten refers.

- How are a virus and a corona virus defined?
- How are sequences defined in this context?
- How do the detection methods of sequences called PCR, RT-PCR and real-time RT-PCR work?
- When can evidence of the presence of sequences in humans be given as evidence of the presence of a virus?
- How is the existence of a virus scientifically proven?

Terms

- In science, a virus is defined by its specific genetic material that only belongs to this virus.
- The genetic material of a virus is also referred to as a viral genetic strand, as a viral genetic molecule or as its genome.
- The viral genetic material of a virus successively contains the various genetic sequences for the formation of the various viral proteins, which are referred to as viral genes.



- The genetic material of a virus can consist of either the two types of DNA or RNA.
- Corona viruses are defined by the fact that they consist of a specific molecule of RNA that is surrounded by an envelope.
- The genetic material of a particular virus is defined by its precisely defined length and the exact determination of the structure of the viral genome.
- The composition of the genome of a virus results from the precise determination of the number and the specific sequence of the four building blocks that make up a genetic material. The four building blocks of a genetic material are called nucleotides.
- The process of determining the specific sequence of the four building blocks of a genetic material is called sequencing.
- The result of determining the sequence of the building blocks of a genetic material is called a sequence or a genetic sequence.
- Pathogenic viruses are defined by the fact that their sequence is unique and does not occur in healthy organisms.
- In order to be able to detect and determine the presence of the genetic material of a virus, this virus must be isolated and in pure form in accordance with the laws of thought and the logic that precedes every science as a fundamental rule, so that cell-specific gene sequences are not misinterpreted as components of a virus.
- The sequence of a genetic substance can only be determined if it is in the form of a DNA.
- In order to be able to determine the sequence of a genetic substance that is in the form of an RNA, it must first be biochemically converted into DNA.
- The process of converting a genetic substance from RNA into DNA is called "reverse transcription" and is abbreviated to "RT".

The techniques used by Prof. Drosten and first conclusions

- The presence and length of a genetic material is determined by lengthwise separation in an electrical field. Short pieces move faster, longer pieces more slowly. At the same time, in order to be able to determine the length of the genetic material to be examined, pieces of genetic material of different lengths of known length are added. This reliable standard technique for the detection and determination of the length of genetic material is called "gel electrophoresis".
- If the concentration of a certain genetic material is too low, so that it cannot be detected using the technique of "gel electrophoresis", this can be increased at will by the technique of unlimited propagation of DNA, called the polymerase chain reaction. In this way, undetectable DNA can be made visible in gel electrophoresis. This is a prerequisite for making genetic substance accessible for further investigations, especially for the subsequent, decisive determination of its length and sequence. This method is also called PCR for short.

The inventor of the PCR technique, Karry Mullis, who received the Nobel Prize in Chemistry for this in 1993, pointed out early on that his, his, for clean room analysis in computer chip factories

developed method is very prone to errors. He also pointed out in his Nobel Prize speech, which is documented on the Nobel Prize Committee website, that there is no verifiable, indeed scientific, evidence that the genetic substance called the genome of HIV is actually an immunodeficiency or one of several Triggers diseases that are summarized under the term "AIDS" and are treated with highly toxic chemotherapy. He pointed out that there is only a consensus among the scientists involved that "HIV" would trigger an immune deficiency.

In order to be able to multiply a DNA with the PCR technique, one needs to know the composition, the sequence of the DNA. A DNA can only be amplified with the PCR if short, artificially produced gene pieces bind to the beginning and the end of the DNA, which exactly correspond to the sequence of the beginning and the end of the DNA to be amplified. These short pieces of artificially produced DNA are therefore called primer molecules in PCR. They are on average between 24 to 30 nucleotides long (the building blocks of the genetic substance).

With the PCR, therefore, no unknown sequences and no unknown viruses can be detected. Only the determination of the sequence of a virus makes it possible to develop a PCR test for the detection of a gene sequence that originates from a virus.

- In the early days of PCR, it was only possible to determine the amount of DNA amplified by means of gel electrophoresis only after the PCR amplification reaction had stopped. In the meantime, certain dyes have been added to the enzymes and substances required for PCR. The detection of these dyes during the course of the PCR roughly indicates which concentrations of artificially increased DNA have arisen and how much DNA was actually present at the start of the PCR. Because the determination of the amount of artificially generated DNA can be roughly determined while the PCR technique is running, this extension of the PCR technique is referred to as "real-time PCR". A "real-time PCR", which is preceded by another step, the conversion of RNA into DNA by means of "reverse transcription" (RT), is therefore called "real-time RTPCR".

- Prof. Drosten uses the "real-time RT-PCR" technique in the test he developed to detect the new corona virus

1.1.2020 offered short genetic sequences selected, which are attributed to SARS viruses. On the basis of these sequences of short gene fragments, which are interpreted as possible components of SARS viruses, he designed the PCR primer sequences that are decisive for the PCR in order to use this to identify the "still" unknown virus in China with its "real-time RT-PCR".

As on 10.1. and 12.1.2020 on the Internet *preliminary* Compilations of sequences appeared, which were changed afterwards and were published on January 24th, 2020 and on February 3rd, 2020, ¹¹

this was the result of the first two attempts to identify the as yet unknown virus. For this purpose, the CCDC virologists theoretically set the sequences of short gene fragments into a possible genetic strand using computer programs



together. The CCDC virologists testify in both publications that there is no evidence yet about these sequence suggestions that they can actually cause disease. On 10.1. and on January 12th, 2020 the Chinese sequence suggestions were still preliminary and had not yet been subjected to the strict process of scientifically prescribed review.

The fact that the World Health Organization (WHO) recommends the PCR detection test developed by Prof. Drosten for the detection of the new virus on January 21, 2020, even before the publication of the publications of the first two Chinese sequence suggestions, is a first Evidence: Prof. Drosten used scientifically untested data for his fast globalized PCR test of the **2019-nCoV, which took place on 7.2.2020¹² with the collaboration of Prof. Drosten** was renamed SARS-CoV-2.

With the renaming of "nCoV" on "7.22020" to "SARS-CoV-2", a mere virus suspicion of a possibly defective or harmless virus, into a dangerous pathogen, the public was given the impression that in China an actual SARS virus has been discovered that triggers a dangerous disease, SARS, and has killed China's new idol, Li Wenliang, who has overshadowed the party leadership. Prof. Drosten and his colleagues in the virus nomenclature group thus fulfilled the expectation of the population who was terrified to the bone: "finally diagnosed", "finally diagnosed." med. Li Wengling aroused mass panic and apparently fulfilled by Prof. Drosten. The decisive factor in evaluating this deed is the fact that at that point all of the virologists directly involved testified - and still testify - that there is no evidence that this new virus actually causes disease. Or only occurs in parallel with illnesses, with healing processes, after healing processes, with some healthy people, with many healthy people or with all people?

This alone proves that Prof. Drosten has exceeded the clearly recognizable limit of scientifically justified action for a recognizable and serious fraud act. Nor will he be able to excuse himself by publishing his test procedure on

January 23, 2020¹³ used a magazine that did not check the statements made therein before going to press.

5. The crucial questions for a quick end to the corona crisis

The central and all-important question arises whether Prof. Drosten has **fulfilled his scientific duty, which is part of his employment contract,**¹⁴ to independently and consistently review all claims in his publication about the detection method developed by him and his public statements based on it.

This central scientific obligation raises three key questions:

I. Has Prof. Drosten checked whether the gene sequences, which are the basis of his test procedure and which he was provided by Chinese virologists, are actually sequences that originate from a virus?

II. Has Prof. Drosten carried out the control experiments that are mandatory in science and prove whether the sequences he uses actually come from a virus? Did he carry out the control experiments to determine whether the sequences he uses, which he attributes to the new virus, are in fact sequences that arise in every metabolism, perhaps even in plants, **such as in Tanzanian papayas¹⁵ or which arise in the metabolism with diseases?**

III. On the basis of what assumptions, experiments and control attempts, Prof. Drosten can assert that with his test procedure, with which he only detects sections of 2 (two) genes from the genome of a total of 10 (ten) genes of the corona virus, a whole, active and disease-causing virus is detected? And not just fragments of a virus, after an assumed successful fight of the immune system or the presence of "defective" or "incomplete" or "harmless" viruses in our genetic material, which are typical and make up 50% of the genetic mass of our chromosomes?

The answers stem from Prof. Drosten's documented actions during the development of the test procedure and from Prof. Drosten's documented failure to do so far. Virologist Prof. Drosten, who developed the detection method for the new corona virus (first called 2019-nCoV then, from 7.2.2020 as SARS-CoV-2), describes the development of the test method in a publication that was published on January 23 .2020 was released.¹⁶ On page 3 of this article, left column, 8 lines from below, he describes the first and decisive step of his procedure:

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

That is, Prof. Drosten and his staff have based on reports in social media *accepted*, that the alleged outbreak of atypical pneumonia *may involve* a corona virus associated with SARS. At that time, no clinical data were available that could have been the basis for such a presumption. What was his next step?

"We downloaded all complete and partial (average length> 400 nucleotides) of SARS-linked virus sequences that were available on GenBank on January 1st, 2020." The right column of the page continues



"We aligned these sequences [note from me, SL: based on a given SARS virus standard sequence] and used the aligned sequences to develop our tests (Figure S1 in the supplement to this publication)."

"After the publication of the first 2019 nCoV sequence on virological.org, we selected three tests based on how well they matched the 2019 nCoV genome (Fig. 1)." ("We downloaded all complete and partial (if > 400 nt) SARS-related virus sequences available in GenBank by 1 January 2020. [...] These sequences were aligned and the alignment was used for assay design (Supplementary Figure S1). Upon release of the first 2019-nCoV sequence at virological.org, three assays were selected based on how well they matched to the 2019nCoV genome (Figure 1).)

The clear answers, conclusions and consequences follow from his remarks:

I. Has Prof. Drosten checked whether the gene sequences, which are the basis of his test procedure and which he has been provided by Chinese virologists, are actually sequences that originate from a virus? The answer is no! He was unable to check whether the sequences offered came from a virus because the two crucial publications describing the generation of the gene sequences he used were not available to him before the launch of his test.

II. Has Prof. Drosten carried out the control experiments that are mandatory in science and prove whether the sequences he uses actually come from a virus? Has he carried out the control experiments as to whether the sequences he uses, which he attributes to the new virus, are really not sequences which arise in every metabolism, perhaps even in plants, or which arise more frequently in the metabolism when there are diseases?

The answer is: no! Neither he, nor the CCDC virologists, nor others have been proven to have carried out these necessary control attempts to this day, and if so, have not published them. For these crucial control experiments, short gene sequences of the metabolism of healthy people have to be used to sequence them. These short gene sequences, like the gene sequences from sick people, have to be put together using the same computer programs to form a long genetic line of a virus. This attempt was either never made or never published. There is no mention of this compulsory attempt at control resulting from the laws of thought and the logic of virology - in order to consistently control your own results. In that moment,

The other control experiment resulting from scientific logic is the intensive, using the developed PCR method (real-time RT-PCR), with clinical samples from people with diseases other than those attributed to the virus and with samples from healthy people, Animals and plants to test whether these samples are also tested "positive". These further control experiments, which are logically essential to a test procedure

Validation, that is, to check whether it is valid and meaningful, have not been carried out to date and have not even been claimed to have been carried out. For this reason, the inventors and producers of these test methods have confirmed the relevant information on the instruction leaflet, for example that the test is only to be used for study purposes and is not suitable for diagnostic purposes.

I can predict with certainty that people who increasingly release gene sequences from the tissue type of squamous epithelia, for example kidney patients, will be tested 100% at the latest with the PCR "positive" developed by Prof. Drosten if their swab volume multiplies and concentrates a little becomes. It is very likely that all organisms can be tested positive.

I call on biochemists, bioinformaticians, virologists and cell culture specialists to carry out these control tests, to publish them and to inform myself about them. I designed a control experiment in which the excuse that the sample material used had been contaminated with the SARS-Cov-2 virus before or during the control experiment is excluded from the outset.

The costs for carrying out the control experiments are covered if I and neutral observers are allowed to be present when the control experiments are carried out and every step is documented. Please contact the publisher to contact us. The results immediately end the corona crisis. It is no use if only I present the results of the control tests.

III. On the basis of what assumptions, experiments and control attempts, Prof. Drosten can assert that with his test procedure, with which he detects only partial areas of only 2 (two) genes from the genome of a total of 10 (ten) genes of the corona virus, a whole, active one and disease-producing virus is detected and not just fragments of a virus, after an assumed successful fight of the immune system or through the presence of the numerous "defective", "incomplete" and "harmless" viruses in our genetic material?

Prof. Drosten did not consider these logical questions at all, because they are nowhere to be found in his publications and claims. The detection of only short gene sequences from a long strand of genetic material from a virus can never prove the presence of an intact and thus reproducible virus. In order to be able to call such a PCR test valid, studies would first have to be carried out, the results of which show that the detection of short gene sequences automatically also detects the presence of a whole and intact genetic strand of a virus. To date, such logically compelling studies have not been carried out or mentioned.

At the beginning of the corona crisis, the virologist, Prof. Karin Mölling, the leading virologist in the field of the cell's own harmless, incomplete or defective viruses, described the measures taken as unjustified. She has in **publications and in a book** ¹⁷⁶ **demonstrated that half of the human genetic makeup, i.e. half of the sequences,**



that make up our chromosomes, inactive and defective gene sequences from viruses. What she does not know or does not mention is the fact that the metabolism constantly produces a large amount of RNA gene sequences of any composition that do not appear in the form of DNA sequences in the chromosomes. This fact questions the existence claims of all RNA viruses, such as corona viruses, Ebola virus, HIV, measles virus and the SARS viruses. This fact is also the reason why control experiments not only end the corona crisis, but also the fear and mistreatment caused by the entire virology of the alleged disease viruses. I can assure you that the actual causes and phenomena of the infection that are attributed to viruses are proven in the "positive" sense of the word "science". I refer to the previous article "Misinterpretation of Virus" in the magazine WissenschaftPlus No. 1/2020, which can also be purchased as a PDF file. And, of course, the many previous articles on this issue.



The sequel "Misinterpretation of Virus III" follows.

sources

¹ A Novel Coronavirus from Patients with Pneumonia in China, 2019. N Engl J Med 2020; 382: 727-33. DOI: 10.1056 / NEJMoa2001017. Published on 1/24/2020.

^{2nd} The responsibility of a virologist. Is Christian Are victims or perpetrators at risk? Published in the blog of peace activist Peter Frey, peds-ansichten.de on May 26th, 2020.

^{3rd} SARS, Wikipedia. https://de.wikipedia.org/wiki/Schweres_akutes_Atemwegssyndrom (entry from 29.5.2020);

^{4th} Xing-Yi Ge et al., Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. Nature. Volume 503, 2013, pp. 535-538, doi: 10.1038 / nature12711;

⁵ 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;

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⁷ 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);

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⁹ Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR. Prof. Christian Drosten and staff. Euro Surveill. 2020; 25 (3): pii = 2000045. <https://doi.org/10.2807/1560-7917.ES.2020.25.3.2000045>. Published on 1/23/2020.

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¹² 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>;

¹³ See 9;

¹⁴ §2 Principles of Good Scientific Practice: (1) among other things "consistently questioning all results yourself" and "to adhere to the recognized principles of scientific work in the individual disciplines." In: New version of the statutes of the Charité - Universitätsmedizin Berlin to ensure good scientific practice from 20.06. 2012 (AMB Charité No.

092, p. 658) To be found at: https://www.charite.de/fileadmin/user_upload/portal/charite/presse/publikation/amtl-mitteilungsblatt/2016/AMB_208.pdf;

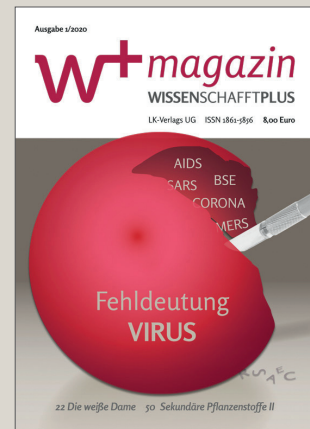
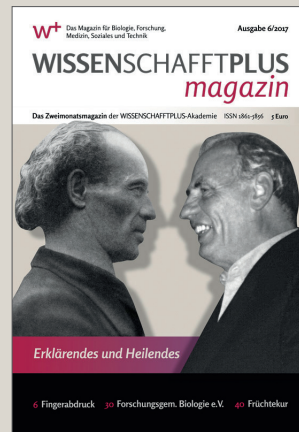
¹⁵ You can find an example of how the public is dealing with the fact that fruit has also tested "positive" for "SARS-Cov-2" here: <https://www.zdf.de/nachrichten/panorama/coronavirus-papaya-goat-tanzania-test-100.html>

¹⁶ See 9;

^{17th} See the book by Karin Mölling with the interesting title "Viruses: More Friends Than Foes", 420 pages, which was also published in German in 2016.

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