

Misinterpretation Virus II beginning and end of the corona crisis by Dr. Stefan Lanka

The definition of SARS and Corona or Covid-19 states that atypical pneumonia is regarded as the clinical picture characterising the disease. If known pneumonia pathogens can be detected, the pneumonia is considered a typical, if not an atypical pneumonia. One of two decisive facts for SARS and the corona crisis is that at least 20-30% of all pneumonia is atypical. The causes of atypical pneumonia are clearly known and therefore must NOT be claimed as the cause of an unknown virus.

This fact is suppressed by infectiologists and virologists and is the basis of the current fear and panic, because the impression is created among those affected, the public and politicians that atypical pneumonia would be particularly dangerous and often fatal because there are no drugs or vaccines for the allegedly new disease.

From the time when a test procedure for the alleged new virus is offered, which, which is concealed by those involved, also tests healthy people "positively", the number of cases is increased automatically. At first, people with typical pneumonia are also included, then more and more people with other diseases. This is regarded as practical proof for the spread of the virus. Automatically more and more other diseases are added to the original disease "atypical pneumonia" and this "syndrome" is displayed as "the new virus disease".

The other decisive fact, not only for SARS and the corona crisis, is that virologists who claim that viruses cause illness suppress an openly lying situation for understandable reasons. The virus test procedure offered is a genetic detection method. The gene sequences they use for the detection test are not isolated from a virus. They isolate typical gene sequences that are released in increased amounts when tissue and cells die. These generally short gene sequences, components of the human metabolism, are the basis for further laboratory work. With the help of computer programs, virologists are only able to construct long genetic material strands from many short gene sequences. These are then output as real, viral DNA strands. This is the reason why positive test results are repeatedly obtained even in healthy individuals.

In order to avoid refuting themselves, these virologists consistently disregard two rules prescribed by science. One is to consistently verify all claims themselves. The other is to test all assumptions and methods used by means of control experiments. If they would carry out the control experiments, they would find out that ALL of the short gene sequences which they only mentally link to a virus genome strand, originate from the human metabolism and not from outside, from a claimed virus.

The momentum of the corona crisis was triggered by a message of a young ophthalmologist on 30.12.2019 in the internet, which spread immediately and very quickly. He told friends that in his hospital several people were under quarantine, seven cases of SARS were confirmed, they should be careful and protect themselves. Prof. Christian Drosten of the Charité in Berlin heard about this, immediately started the development of test procedures for SARS viruses before it was even clear and could be made clear whether the report from China about SARS was true and proven, and especially before the Chinese virologists published their results.

The authoritative virologists of the Chinese Disease Control Commission (CCDC) published their results on 24.1.2020 and 3.2.2020. They report on the isolation of many short gene sequences, which, when strung together, could represent a genetic strand of a new type of virus. The authors expressly point out - and all other virologists involved to date - that the absolutely necessary experiments have not yet been carried out, which would make it possible to claim that this is indeed a genetic strand of a pathogenic virus. On the contrary, the Chinese virologists even explicitly point out that the constructed genetic strand bears up to 90% similarity to genetic strands of harmless and for decades known, main corona viruses in bats.

On 21.1.2020 (3 days before the first publication of the CCDC!) the WHO recommended all nations to use the test procedure developed by Prof. Drosten. By claiming that he had developed a reliable test procedure for the rapidly spreading virus in China, Prof. Drosten, disregarding 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, has caused the increase and globalization of the Chinese epidemic panic.

1. the beginning of the corona crisis

When the young ophthalmologist Li Wenliang informed seven doctors in Wuhan via WhatsApp on 30.12.2019 that several people were quarantined in his hospital, seven cases of SARS had been confirmed, that they should be careful and protect themselves, he did not intend to cause a panic. If he had, he would have posted the announcement on the Internet and warned the public. One of the seven recipients of this private WhatsApp message published a "screenshot", i.e. a photo of the message, on the Internet without being aware of the possible consequences. Of course, this information spread very quickly within China and then also worldwide.

This communication 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 "worldwide threat" on March 12, 2003. As a result, the Government in Beijing sent a "rapid reaction force" consisting of epidemiologists and virologists from the Chinese Disease Control Center (CCDC) to Wuhan on 31 December 2019 to support the local health authorities and the surrounding Hubei Province. The aim was to check and verify the allegations about the outbreak of an epidemic. If an outbreak had indeed 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 of Patients with Pneumonia in China, 2019"¹, no accumulation of cases of atypical pneumonia ("patients with pneumonia of unknown cause") is reported. They report that the existing patients can be grouped into a "cluster", a group with common characteristics. The common feature was the more or less frequent visit of 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 of only four patients took smears and fluids of the lower respiratory tract in order to search for known and unknown pathogens.

In the meantime the panic in Wuhan and the surrounding area increased extremely. Even the measures of the police, who asked the ophthalmologist Li Wenliang on January 3, 2020, to commit himself in writing by signing a declaration of discontinuance, which was proven to be punishable by law, not to spread anything more about a possible SARS outbreak, could not slow down the dangerously worsening dynamics of panic any longer. On 10.1.2020 Wenliang, and shortly afterwards also his parents, developed the symptoms of pneumonia. Li Wenliang isolated himself because he was convinced that he had been infected with the SARS virus the day before in an asymptomatic patient. This also increased the panic.

The attending doctors carried out a large number of different tests, all of which were negative. As his state of health deteriorated and more and more people showed public sympathy for his fate, the tests were continued until a first SARS test was assessed as "positive" on 30 January 2020. The disaster of the escalating SARS panic, which mutated into a global corona crisis, took its course.

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 settled, finally diagnosed."

This announcement increased the already existing panic. Everything got completely out of control when he published his cease-and-desist declaration of 3.1.2020, which he had signed, on the Internet. This publication of his cease-and-desist declaration, which was dangerous for him, was and still is considered by all panicked people as proof that there is a new SARS epidemic because a doctor who is himself affected continues to inform and warn the public despite the threat of penalties. The panic increased further because Li Wenliang's health deteriorated despite the intensive use of a variety of antibiotic substances and the public regularly took part in this. The situation was on the verge of escalation because the reporting of his death was more than chaotic and contradictory. This was and still is the central reason why the Chinese and global public assumed that another SARS outbreak had occurred in Wuhan, which was recently transformed into a new epidemic, a pandemic with a new Name, Covid-19.

2. the one, of two possible causes of fear of Li Wenliang

The fear of the ophthalmologist Li Wenliang is based on the events of 2003 in China, when western scientists claimed that an accumulation of atypical pneumonia had occurred in southern China. Two days after the intellectual creation of a genetic strand of the allegedly new virus

(SARS-CoV-1), in which Prof. Drosten was significantly involved,² Prof. Drosten offered an alleged test procedure for this alleged virus.³ Approximately 800 people with atypical pneumonia, i.e. pneumonia in which no known pathogens are detected, but who tested "positive" with Prof. Drosten's test, therefore died - possibly incorrectly and over-treated - with the diagnosis of SARS instead of "atypical pneumonia".

The basis for the fact that the fear of SARS was maintained and increased until 2019 is two publications in 2013⁴ and 2017⁵, which triggered speculation about the possibility of the appearance of new SARS corona viruses. The authors of both publications state that in healthy

bats provides evidence for the existence of short gene sequences that can be interpreted as components of a virus. These short gene sequences would have similarities with those short gene sequences that were declared to be components of the alleged SARS corona virus-1 (SARS-CoV-1) in 2003. SARS stands for Severe Acute Respiratory Syndrome, which is another description of the symptoms of atypical pneumonia.

It is said about these mental (converted to reality) genetic strands that it is possible that they could also develop in reality and form a real virus. Such a virus, which is claimed to be present in bats and other wild animals but is still harmless, could jump over to humans by bite, contact or consumption and become a deadly killer. In humans, this harmless virus could, through changes (mutations), turn into a new SARS corona virus that could actually cause a disease. Such an event and the resulting wave of diseases, such as atypical pneumonia, must be expected at any time.

To date, virologists have not been able to isolate a SARS virus from a patient, bat, other animal, or in the laboratory, nor have they been able to identify an intact and complete genetic strand of a SARS virus. The assumption of the virologists that there are also viral genetic strands in reality, which are constructed in the same way as the genetic strands composed of short gene sequences, has not yet been confirmed. Although the very simple standard techniques for determining the length of genetic sequences have been available for a long time, it has not been possible to prove the existence and presence of a complete genetic strand of a SARS virus in any other way.

The fears massively stirred up by such false claims were the basis for the fears of the ophthalmologist Li Wenliang, as well as other physicians and infectiologists not only in Wuhan. These allegations are the reason why the epidemiologists and virologists of the CCDC have been focused on finding similar gene sequences since December 31, 2019, which were identified as components of SARS corona viruses in 2003 (see further details below).

3. the second of the possible causes of fear by Li Wenliang

The SARS and Corona crises started with the claim in the media that there is an accumulation of patients with atypical pneumonia. This allegation was never substantiated. It was only claimed 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 assumption that an unknown virus could be the cause of atypical pneumonia, known facts described in medical and scientific literature were suppressed.

There are several and wide spectra of non-infectious causes of atypical pneumonia. These atypical pneumonia is more fatal than typical pneumonia for several reasons.

Among the causes are the inhalation of toxic fumes, solvents and substances. Also the penetration of food, drinks or stomach contents, which enter the lungs in case of swallowing disorders or unconsciousness, can cause severe pneumonia (aspiration pneumonia). Water alone is sufficient if it enters the lungs of drowning persons to cause severe atypical pneumonia. A further cause is the recognized spectrum of immunological malfunctions, such as allergies and autoimmune reactions. It is also known that radiation triggers an inflammation of the lungs in cancer, which cannot be distinguished from typical pneumonia. Congestive pneumonia is particularly well known in older people. They develop due to water retention (edema), prolonged bed rest, heart and/or kidney weakness, which can lead to inadequate ventilation and blood circulation in the lungs and, as a direct consequence, to inflammation of the lungs, i.e. atypical pneumonia.

Logically, a combination of otherwise low-threshold causes also causes the atypical pneumonia. An atypical pneumonia can change very quickly into a typical one if a secondary colonization of the inflamed lung occurs. This is the reason why the percentage of atypical pneumonia is probably higher than the estimated 20-30%.

The studies of the five people documented in the two publications relevant to the corona crisis,⁶ did not investigate the possible presence or history, signs, mechanisms and effects of these known causes of atypical pneumonia. Virologists usually do not do this anyway, and the members of the CCDC were not able to do so even under the given circumstances of panic. Excluding the mention of atypical pneumonia is a serious medical malpractice and prevents correct treatment of patients. The affected persons run the risk of being mistreated with a cocktail of antibiotic substances with many side-effects, which, especially in the case of overdosage, is capable of causing the death of patients on its own.⁷ It must be clear to all that extreme panic, especially in cases of respiratory problems, can cause death on its own. Panic can even be fatal in a very short time, not only in cases of cardiovascular problems.

The answer to the crucial question of whether a new virus has actually been detected or whether only short pieces of genetic material produced naturally in the body are being passed off as components of a virus or misinterpreted as such, is decisive for whether the corona crisis can be brought to a rapid end. As with H1N1, the causers of the corona crisis say that it can only be ended by vaccination. But the idea of vaccination has been disproved just like the idea of viruses.

Helpful for the evaluation and classification of the events surrounding the triggering and maintenance of the Corona Crisis is the memory of the meanwhile forgotten swine flu pandemic of 2009, when the majority of the population was prepared to be vaccinated against the alleged swine flu viruses. Then there was a delay in the announced delivery of the vaccines. The vaccines could not be filled in ready-to-use syringes because the novel active substance enhancers used for the first time damaged the vaccine mixture and made it unusable. Therefore, the vaccine was filled in ampoules for 10 persons each, into which the active substance enhancers could only be added shortly before the act of vaccination.

During this time it became known that the active substance enhancers, called adjuvants, without which a vaccine could not unfold its effect, are novel and untested. It became known that these novel drug amplifiers consist of nanoparticles. It is known that nanoparticles are very reactive due to their tiny size and are therefore used as catalysts in many chemical reactions. In technical processes, for example, they cause the surfaces to behave completely differently than can be achieved by conventional methods. Then it became known that the German Chancellor Angela Merkel and the German Armed Forces should receive this vaccine but without the novel nanoparticle active ingredient, whereas the police and the population should receive the vaccine with the untested nanoparticles.

As a result, 93% of the population rejected the vaccine produced for them. Only 7% of Germans have had the vaccine administered. The human metabolism cannot metabolise and excrete nanoparticles. Because of this refusal of almost the entire population, the swine flu actually disappeared from one evening to the next morning, as if by magic, from the media and the vaccines into a blast furnace. (A small polemic is allowed: astonishingly, the swine flu virus H1N1 took off at a gallop, did not affect other people, did not make the people in the decorated ones ill, and stopped its media presence. Perhaps the swine flu virus has turned into fish flu viruses, to swim up the rivers in the bodies of salmon, only to strike again at the fish market in Wuhan with bundled strength).

The epidemiologists, infectiologists and virologists involved have learned from the failure of the pandemic plan, which did not reach the peak of vaccination. They analysed the causes and published their findings and recommendations for the future in issue No. 12, December 2010 of the *Bundesgesundheitsblatt*. The meaningful title of this issue: "Pandemics. Lessons learned" Which means as much as: The lessons we have learned from the H1N1 swine flu debate.

Some of the articles contained in this issue are available on the Internet,⁸ but the most important ones are not. The key recommendations for pandemic management are

- Ensuring that experts do not contradict each other in public discussions.
- Early involvement of leading and social media.
- Control of the Internet. This in order 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. The compelling arguments which have made it into the public domain and which are based on the assumption of a pandemic are simply not

addressed. Only one expert, Prof. Drosten, is heard in the media and politics. The only "criticism" of him, presented by an HIV virologist, had the function of strengthening the central claim of existence of a new type of virus, SARS-CoV-2.

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

Prof. Christian Drosten from the Charité in Berlin claims that from 1.1.2020 he has developed a genetic detection method with which he can reliably prove the presence of the new corona virus in humans.⁸ On 21.1.2020, the WHO recommended the test method he had developed to the Chinese and all nations as a reliable test procedure for detecting the spread of the alleged new corona virus.¹⁰

In order a) to be able to understand which assumptions and which actions form the basis of Prof. Drosten's claims and b) to check whether his conclusions to have developed a safe test procedure for the new corona virus are logically and scientifically proven or not, or even refuted, it is necessary to explain the terms and techniques used, to present his argumentation and to analyse the two decisive 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 known as PCR, RT-PCR and real-time RT-PCR work?
- When may the detection of the presence of sequences in humans be used as proof 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, which is unique to that virus.
- The genetic material of a virus is also called the viral genetic strand, the viral genetic molecule or its genome. - The viral genetic material of a virus contains, in sequence, the various genetic sequences for the formation of the various viral proteins known as viral genes.
- The genetic material of a virus can consist of either the two types of genetic molecules, DNA or RNA.
- Corona viruses are characterized by the fact that they consist of a specific molecule of RNA surrounded by an envelope.
- The genetic material of a certain virus is defined by its precisely determined length and the exact determination of the structure of the viral genome strand.
- The composition of the genetic material of a virus results from the exact determination of the number and the specific sequence of the four building blocks of which a genetic material consists. 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 genetic sequence.
- Disease-causing viruses are characterized 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 be present in its pure form, in accordance with the laws of thought and the logic which precedes every science as a fundamental rule, so that gene sequences which are not cell-specific are misinterpreted as components of a virus.
- It is only possible to determine the sequence of a genetic substance if it is present in the form of a DNA.
- In order to determine the sequence of a genetic substance which is present in the form of 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 as "RT".

The techniques used by Prof. Drosten and first conclusions

- The presence and length of a genetic material is determined by separating it lengthwise in an electric field. Short pieces migrate faster, longer pieces slower. At the same time, in order to determine the length of the genetic material to be examined, different lengths of genetic material

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 to be detected by the technique of "gel electrophoresis", it can be increased at will by the technique of unlimited multiplication of DNA, called polymerase chain reaction. In this way, undetectable DNA can be made visible by gel electrophoresis. This is a prerequisite for making genetic material accessible for further investigations, especially for the subsequent decisive determination of its length and sequence. This method is also known as PCR for short.

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The inventor of the PCR technique, Kary Mullis, who was awarded the Nobel Prize for Chemistry in 1993 for this technique, pointed out early on that this technique, his is very error-prone. In his Nobel Prize speech, which is documented on the website of the Nobel Prize Committee, he also pointed out that there is no verifiable, actually scientific proof that the genetic substance, which is called the genome of HIV, actually causes an immune deficiency or one of the various diseases, which are inadmissibly summarized under the term "AIDS" and treated with highly toxic chemotherapy. He pointed out that there is only a consensus among participating scientists that "HIV" would trigger an immune deficiency.

In order to be able to reproduce a DNA with the PCR technique, it is necessary to know the composition, the sequence of the DNA. A DNA can only be multiplied by PCR if short, artificially produced gene fragments bind to the beginning and the end of the DNA, which correspond exactly to the sequence of the beginning and the end of the DNA to be multiplied. These short pieces of artificially produced DNA are therefore called primers, the starter molecules of the PCR. They are on average between 24 and 30 nucleotides (the building blocks of the genetic substance) long.

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Thus, PCR cannot be used to detect unknown sequences or unknown viruses. Only the determination of the sequence of a virus makes it possible to develop a PCR test for the detection of a gene sequence originating from a virus. - In the early days of PCR, it was only possible to determine the amount of amplified DNA by gel electrophoresis after the PCR amplification reaction had been stopped. In the meantime, certain dyes are added to the enzymes and substances required for the PCR. The detection of these dyes during the course of the PCR shows approximately which concentrations of artificially propagated DNA have been produced

and how much DNA was actually present at the start of the PCR. Since the amount of artificially produced DNA can be determined approximately while the PCR technique is still running, this extension of the PCR technique is called "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 RT-PCR".

- Prof. Drosten uses the technique of "real-time RT-PCR" in the test he has developed for the detection of the new corona virus. For this purpose, he has selected short genetic sequences from a data pool on the Internet on 1.1.2020 that 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 decisive for the PCR, in order to detect the "still" unknown virus in China with his "real-time RT-PCR".

When on 10.1. and 12.1.2020, preliminary compilations of sequences appeared on the Internet which were subsequently modified and published on 24.1.2020 and 3.2.2020,¹¹ this represented the result of the first two attempts to identify the still unknown virus. The virologists of the CCDC used computer programs to combine the sequences of short gene fragments theoretically into a possible genetic strand together. The virologists of the CCDC state in both publications that there is no evidence that these sequence suggestions can actually cause diseases. On 10.1. and 12.1.2020 the Chinese sequence proposals were still pending and had not yet been subjected to the strict process of scientifically prescribed verification.

The fact that the World Health Organisation (WHO) recommends the PCR detection test developed by Prof. Drosten for the detection of the new virus on 21.1.2020, even before the publication of the publications of the first two Chinese sequence proposals, proves a first fact: Prof. Drosten used scientifically unverified data for his rapidly globalized PCR test of the 2019-nCoV, which was renamed SARS-CoV-2 on February 7, 2020¹² with the participation of Prof. Drosten.

The renaming on 7.2.2020 of the name "nCoV" to "SARS-CoV-2", a mere virus presumption of a possibly defective or harmless virus, into a dangerous pathogen, gave the public the impression that an actual SARS virus had been discovered in China, which causes a dangerous disease, namely SARS, and killed the new idol of China, Li Wenliang, who dwarfed the party leadership. With this, Prof. Drosten and his colleagues of the virus nomenclature group fulfilled the expectations of the population which was terrified to the core: "nally diagnosed", "finally diagnosed". This expectation was awakened by the momentum of the mass panic triggered by Dr. med. Li Wengling and apparently fulfilled by Prof. Drosten. The decisive factor in evaluating this act is the fact that at that time all the virologists directly involved testified - and still testify today - that there is no evidence that this new virus actually causes disease. Or does it only occur in parallel in diseases, in healing processes, after healing processes, in some healthy people, in many healthy people or in all people?

This alone proves that Prof. Drosten has crossed the clearly recognizable border of scientifically justified action to a recognizable and momentous fraud. He will also not be able to excuse himself by using a journal for the publication of his test procedure on January 23, 2020¹³ which does not check the statements made in it before going to press.

5. those for a quick termination of the Corona crisis decisive questions

The central and all-decisive question is whether Prof. Drosten has fulfilled his scientific obligation, which is part of his employment contract,¹⁴ to himself and consistently verify all the assertions made in his publication about the detection method he developed and the public statements based on it.

Three central questions arise from this central scientific responsibility:

I. Did Prof. Drosten check whether the gene sequences, which are the basis of his test procedure and which he received from Chinese virologists, are actually sequences that originate from a virus?

II. Did Prof. Drosten carry out the control experiments which are mandatory in science and which prove whether the sequences he used actually originate from a virus? Did he carry out the control experiments to prove whether the sequences he ascribes to the new virus are in fact sequences which are produced in every metabolism, perhaps even in plants such as Tanzanian papayas¹⁵ or which are produced in a metabolically increased form in diseases?

III On the basis of which assumptions, experiments and control experiments can Prof. Drosten claim that his test procedure, with which he only detects partial areas of 2 (two) genes from the

genome of a total of 10 (ten) genes of the corona virus, detects a whole, active and disease-causing virus? 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 gene masses of our chromosomes?

The answers result from the documented actions of Prof. Drosten during the development of the test procedure and from the documented non-actions of Prof. Drosten until today. The virologist Prof. Drosten, who developed the detection method for the new corona virus (first called 2019-nCoV then, from 7.2.2020 on called SARS-CoV-2), describes the development of the test method in a publication published on 23.1.2020.16 On page 3 of this article, left column, 8 lines from below, he describes the first and decisive step of his approach:

"Before the announcement of public virus sequences from 2019-nCoV cases, we relied on reports from the social media announcing the detection of a SARS-like virus. "Therefore, we have assumed that a SARS-related CoV 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 re-lated CoV is involved in the outbreak.) This means that Prof. Drosten and his colleagues have assumed, based on reports in the social media, that a SARS-related corona virus could be involved in the alleged outbreak of atypical pneumonia. At that time, no clinical data were available to support such a suspicion. What was his next step?

"We downloaded all complete and partial (average length >400 nucleotides) of SARS-related viral quences available on the GenBank on January 1, 2020." Continue in the right column of page 3, third row from the top:

"We aligned these sequences [Note from me, SL: against a given standard SARS virus 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 (Figure 1). ("We downloaded all complete and partial (if >400 nt) SARS-re-lated 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 rst 2019-nCoV sequence at virological.org, three assays were selected based on how well they matched to the 2019- nCoV genome (Figure 1).

From his explanations, clear answers, conclusions and consequences can be drawn:

I. Did Prof. Drosten check whether the gene sequences, which are the basis of his test procedure and which he received from Chinese virologists, are actually sequences that originate from a virus? The answer is no! He was not able to check whether the sequences offered originated from a virus, because the two decisive publications describing the extraction of the gene sequences used by him were not available to him before the market launch of his test.

II. Did Prof. Drosten carry out the control experiments which are mandatory in science and which prove whether the sequences he used actually originated from a virus? Did he carry out the control experiments to prove whether the sequences he ascribes to the new virus are in fact sequences that occur in every metabolism, perhaps even in plants, or whether they occur in increased numbers in the metabolism of diseases?

The answer is: No! Neither he, nor the virologists of the CCDG, nor others have demonstrably carried out these necessary control experiments to date and if they have, they have not published them. For these decisive control experiments short gene sequences of the metabolism of healthy persons have to be used to sequence them. These short gene sequences, like the gene sequences from sick people, must be assembled with the same computer programs to form a long genetic strand of a virus. This experiment was either never carried out or never published. There is not even a mention of this compulsory control attempt resulting from the laws of thought and the logic of virology - in order to control one's own results consequently. The moment this attempt is carried out and published, the Corona crisis is immediately over.

The other control test, which is based on scientific logic, is the intensive testing of clinical samples from people with diseases other than those attributed to the virus using the developed PCR method (re- al-time RT-PCR). These further control experiments, which are logically necessary to establish a test procedure, are validate, i.e. to check whether it is valid and has a conclusive force, have not been carried out to date, nor have they even claimed to have been carried out. For this reason, the developers and

producers of these test procedures have ensured themselves by means of corresponding information on the package inserts, e.g. 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 release increased gene sequences from the tissue type of squamous epithelia, e.g. kidney patients, will be tested 100% "positive" with the PCR developed by Prof. Drosten at the latest when their smear quantity is multiplied and concentrated a little. It is very likely that all organisms can even be tested positive.

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

The costs for the performance of the control experiments are covered if I and neutral observers are allowed to be present during the performance of the control experiments and each step is documented. Please contact the publishing house for contact. The results will end the corona crisis immediately. It is of no use if only I present the results of the control experiments.

III. On the basis of which assumptions, experiments and control experiments can Prof. Drosten claim that his test procedure, with which he only detects partial areas of only 2 (two) genes from the genome of a total of 10 (ten) genes of the corona virus, detects a whole, active and disease-causing virus and not just fragments of a virus, after a pleasantly successful battle 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 do not appear anywhere in his publications and claims. The detection of only short gene sequences from a long genome strand of a virus can never prove the presence of an intact and therefore multipliable virus. In order to be allowed to call such a PCR test a *va- lide*, studies would first have to be undertaken whose results show that the detection of short gene sequences automatically proves the presence of a whole and intact genetic strand of a virus. Such logically compelling studies have not been carried out or mentioned to date.

Prof. Karin Mölling, the leading virologist in the field of cell-associated viruses, which are considered endogenous, harmless, incomplete or defective, described the measures taken at the beginning of the corona crisis as unjustified. She has shown in publications and in a book¹⁷ that half of the genetic material of humans, i.e. half of the sequences of which our chromosomes consist, consists of inactive and defective gene sequences of viruses. What it does not know, or hides, is the fact that metabolism constantly produces a large amount of RNA gene sequences of any composition, which do not appear in the form of DNA sequences in the chromosomes. This fact calls into question the claims of existence of all RNA viruses, such as corona viruses, Ebola virus, HIV, measles virus and SARS viruses. This fact is also the basis why control experiments are used to put an immediate end not only to the Corona crisis but also to the fear and mistreatment by the entire virology of the alleged disease viruses. I can assure you that the actual causes and phenomena of the infection attributed to viruses are proven in the "positive" sense of the word "science". For this I refer to the previous article "Misinterpretation Virus" in the magazine *WissenschaftPlus* No. 1/2020, which can also be purchased as pdf-file. And, of course, to the many previous contributions around this question.

The continuation "Misinterpretation Virus III" will follow.

Sources

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- 13 See 9;
- 14 §2 Principles of Good Scientific Practice: (1) among others "to consistently doubt all results oneself" and "to observe the recognized principles of scientific work in the individual disciplines. In: New version of the Statutes of Charité - Universitätsmedizin Berlin to ensure Good Scientific Practice of June 20, 2012 (AMB Charité No. 092, p. 658) To be found at: https://www.charite.de/leadadmin/user_upload/portal/charite/press/publications/amtl-mitteilungsblatt/2016/AMB_208.pdf;
- 15 For examples of how the public is dealing with the findings that fruits are also tested "positive" for SARS-Cov-2, see: <https://www.zdf.de/nachrichten/panorama/coronavirus-papaya-goat-tanzania-test-100.html>
- 16 See 9;
- 17 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