Original article https://telegra.ph/Die-neuen-3D-Abbildungen-des-behaupteten-SARS-CoV-2-beweisen-kein-Virus-01-20 *An auto-translation below*

New 3D images of claimed SARS-CoV-2 does not prove a virus ❗

Corona_Fakten - January 20, 2021

Since 18.01.2021, both local press and representatives of the major mainstream media have been rolling over with joy. The supposed sensational news about the first "REAL" image of the new claimed virus "SARS-CoV-2" keeps everyone in suspense. The media is thrilled to finally be able to present a "real" image and not just computer animations.

Everyone agrees on this: this is what it looks like! The new virus that brings almost the whole world to its knees.

Everyone seemed to be so impressed by this fact that no one even thought of checking how the raw data on which the study is based, from which this 3D image is derived, was obtained. That is exactly what we have been doing, checking which studies this figure is based on and which samples were used for it.

As every scientist is aware, it is assumed that the samples have been subjected to thorough testing, in terms of necessary and obligatory control experiments, isolation of the virus and its verified pathogenicity.

If these prerequisites have not been checked and carried out, the 3D image is merely a counterfeit without any explanatory power. It can convey purely nothing to us and cannot even remotely be considered as proof that the image is a disease-causing virus.

In this article we will show you what publications are involved, what has been done and that the new 3D image, of course, was "constructed" by an algorithm.

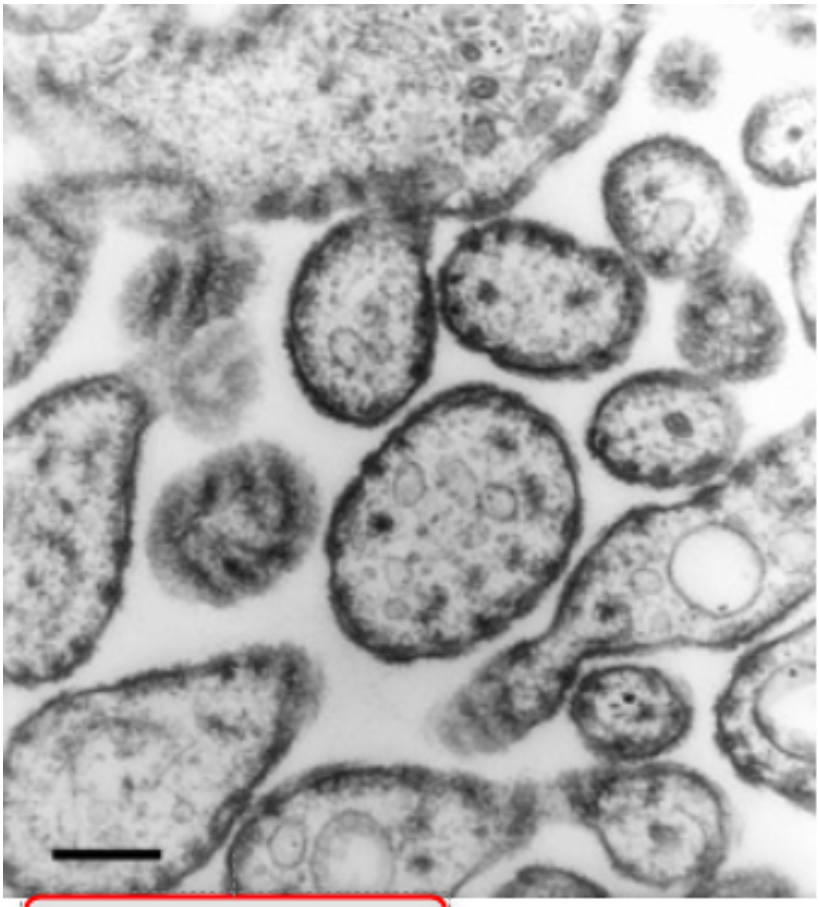
Comment on the photos of viruses claimed to be isolated: When does a picture say nothing about the existence of the one depicted and can only be interpreted as unscientific or even an attempt to deceive?

- *if there is no scientific publication which at least states and describes that the nucleic acid has been determined from a structure shown in a photograph as evidence*

- *no control experiments have been carried out to confirm that the structure is not different from that assumed to exist*

- *if this structure has not been isolated from all other components*

- *e.g. the so-called HIV, measles and smallpox virus images clearly show, as the captions themselves clearly state, that these are cells in which viruses are supposed to be present - so nothing has been isolated!*



Masernvirus in Vero-Zellen.

Quelle: *Hans R. Gelderblom/RKI*

https://www.rki.de/DE/Content/Infekt/NRZ/EM/Aufnahmen/EM_Tab_Masern.html

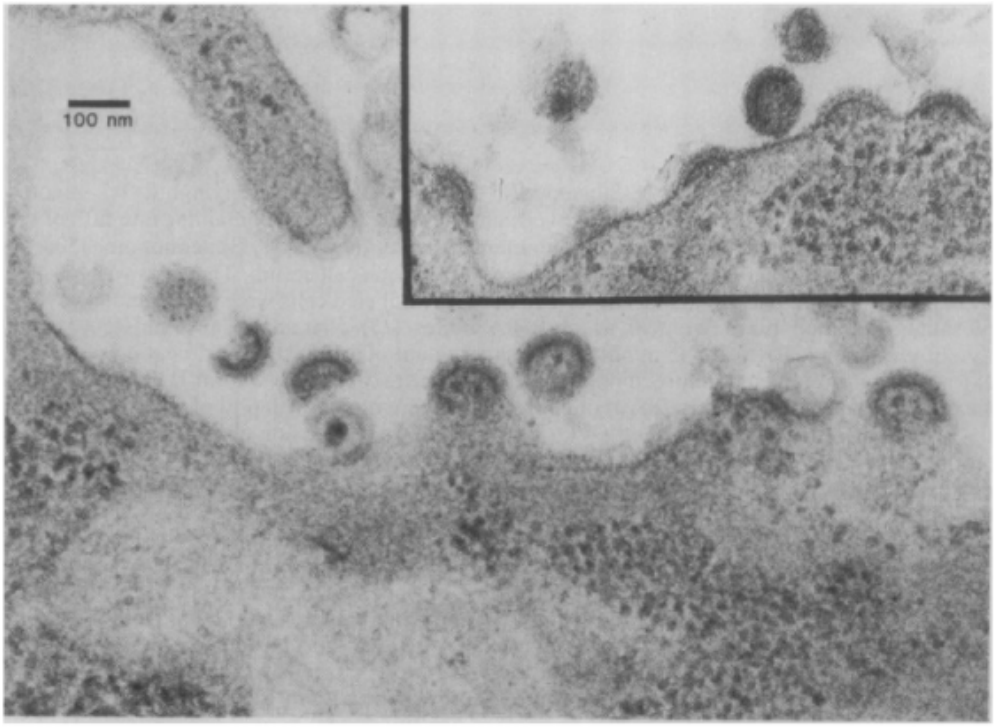


Fig. 2. Electron microscopy of thin sections of virus-producing cord lymphocytes. The inset shows various stages of particle budding at the cell surface.

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Publikation Luc Montagnier - https://www.researchgate.net/publication/8335711_Isolation_of_a_T-lymphotropic_retrovirus_from_a_patient_at_risk_for_acquired_immune_deficiency_syndrome_AIDS

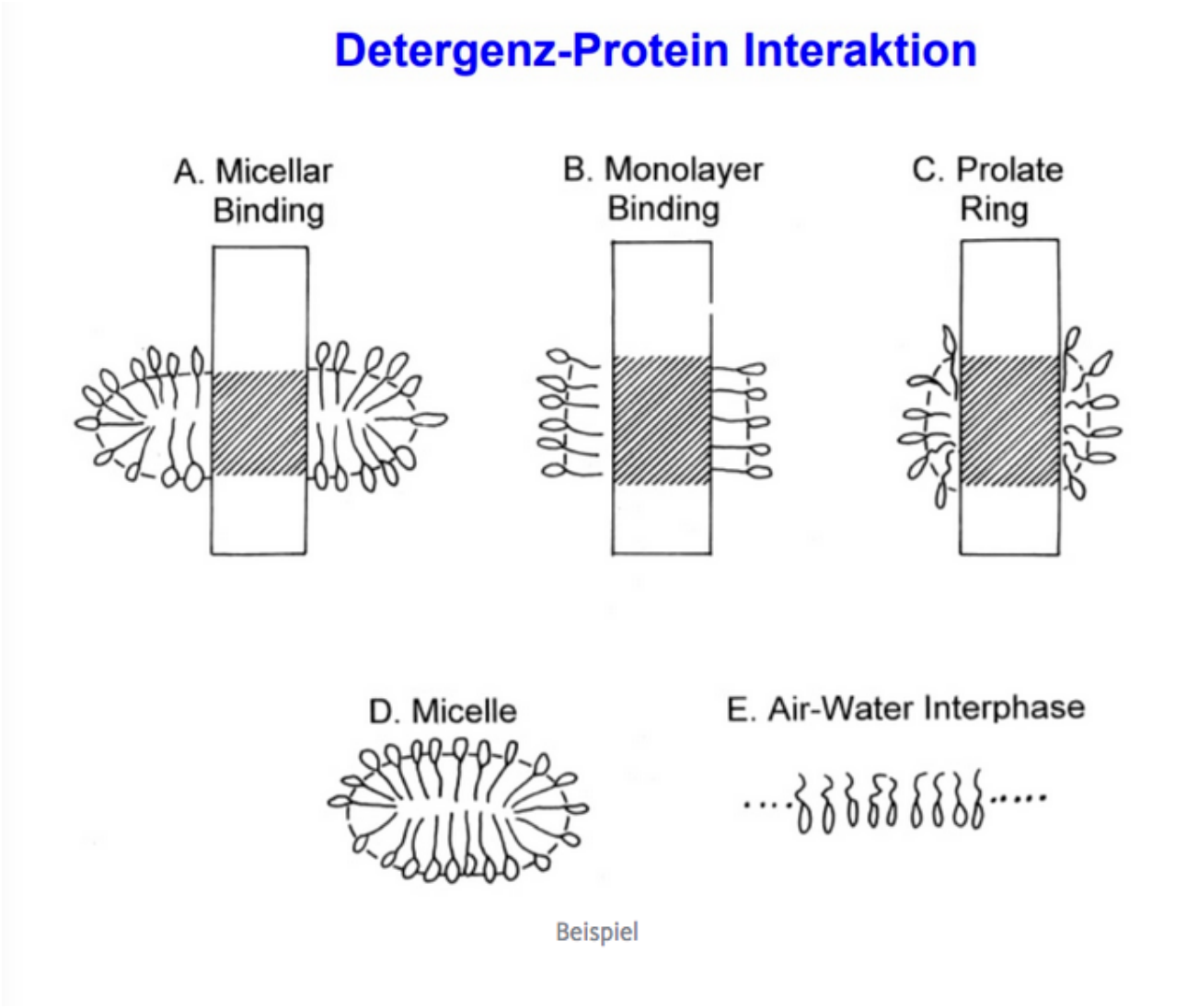
In the case of the new 3D image, which is the first "real" image to be published, none of the points just mentioned were adhered to in the underlying studies. Just for the record: If the specified scientific criteria are missing, such a paper cannot be considered scientific.

Crucial things must be said about EM recordings in general

Structures shown in EM images and published as images of viruses **are never biochemically characterised**. No nucleic acid has ever been taken from such particles and determined. These particles are only passed off as viruses, omitting the information that the same particles of this type are also produced every time "uninfected" cell cultures are treated in the same way as cell cultures defined as “infected." **Non-virologists refer to these particles as, for example, phagosomes, endosomes, exosomes, transport vesicles and, in cross-section, villi, etc. pp.**

You will see the same representation for many differently claimed structures.

EM images **always show only dead**, chemically fixed matter. The image depicts soap micro-cells made of detergents, fats and proteins, preserved by freezing and perhaps only created by this freezing process.



The most important message to the outside world is that only "artefacts" are depicted - **crucial here is:**

1. that these images only come from **cell cultures**, i.e. dying tissue in a test tube, and definitely show nothing that comes from a human being,

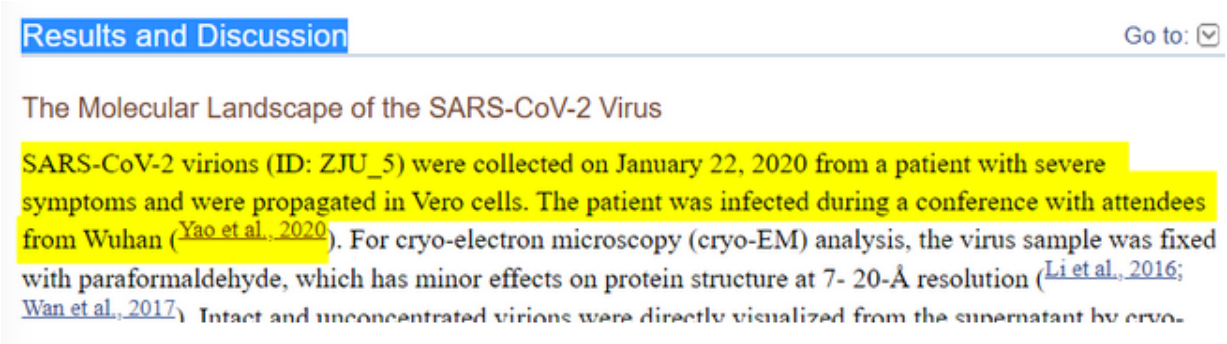
2. that these structures have never been biochemically characterised (sic!),

3. nucleic acids, which are supposed to be the essence of the virus, were never extracted from these structures *(i.e. the nucleic acid was never extracted from a specific structure that is claimed to be a virus).*

A motionless image from electron microscopy never shows the living biological process. What one examines under the EMs has absolutely nothing to do with what happens in the biological organism of a living organism. The results from laboratories can give absolutely no information about the processes within a living organism.

What was really done in the crucial studies that serve as the basis for the new 3D images? In any case, a virus was not detected.

The primary study, which served as the basis, was:



Results and Discussion

Go to:

The Molecular Landscape of the SARS-CoV-2 Virus

SARS-CoV-2 virions (ID: ZJU_5) were collected on January 22, 2020 from a patient with severe symptoms and were propagated in Vero cells. The patient was infected during a conference with attendees from Wuhan (Yao et al., 2020). For cryo-electron microscopy (cryo-EM) analysis, the virus sample was fixed with paraformaldehyde, which has minor effects on protein structure at 7- 20-Å resolution (Li et al., 2016; Wan et al., 2017). Intact and unconcentrated virions were directly visualized from the supernatant by cryo-

Molecular Architecture of the SARS-CoV-2 Virus - Author Sai Li.

In this study we can read which sample material was used, that is claimed to be sample material of the new coronavirus (*SARS-CoV-2*).

It is the study: Yao et. al. - "Patient-Derived Mutations Impact Pathogenicity of SARS-CoV-2

So we have to check what exactly was done in this study and why it is claimed that a new virus was detected here. If this is not the case, the primary study Sai Li et. al. (*which was used for the new 3D images*) is automatically based on a false foundation and has no significance.

So we need to check the following points:

> - Has a structure that is being claimed to be a virus been isolated in pure form *(separated from all other components)?*
>
> - Has this isolated structure been biochemically characterised (its entire structure sequenced)?
>
> - Have all the necessary control experiments been carried out to rule out the possibility that the sequenced structure, i.e. the genetic strand which is assigned to the virus, does not originate from another source and is completely harmless?
>
> - Have all the necessary control experiments been carried out to check the experimental set-up, i.e. the "infection" of a cell culture *(e.g. Vero E6 cells/cells from the kidney of monkeys),* so that it can be ruled out that the treatment of the cell culture is not the cause of an effect that is automatically mistakenly equated with the detection of a virus?

Let's look at what was done and what was omitted in the study from which the samples were taken.

"Epidemiological exposure in Hubei Province was not a prerequisite for suspected cases. All suspected cases were identified by laboratory testing and were based on positive qRT-PCR test results for COVID-19. Patients were excluded if two qRT-PCR tests 24 hours apart both gave

negative results. Clinical samples from patients whose PCR test gave a Ct value of less than 28 were collected for isolation of SARS-Cov-2."

STAR Methods

Experimental Model and Subject Details

Patients with confirmed COVID-19 were admitted in the First Affiliated Hospital from Jan 19 to Mar 5, 2020. The First Affiliated Hospital, located in Hangzhou, Zhejiang Province, China, is one of the major provincial hospitals designated to receive patients with COVID-19 infection across the Zhejiang Province; therefore, patients with severe symptoms outside of Hangzhou were also admitted. Starting Jan 10, 2020, all patients presenting to the hospital's fever clinic were screened by clinical staff for COVID-19 infection utilizing criteria for suspected cases as defined by the National Health Commission of China's clinical diagnosis and management guideline for COVID-19 (China National Health Committee, 2020). Briefly, patients were screened based on their clinical symptoms and their risk of epidemiological exposure, including past travel to Hubei Province or close contact with people who had visited Hubei Province during the COVID-19 outbreak. As the pandemic continued to spread, the probability of transmission outside of Hubei Province increased. The epidemiological exposure to Hubei Province was not a prerequisite for suspected cases. All suspected cases were determined by laboratory tests and based on positive results of qRT-PCR assay for COVID-19. Patients were excluded if two qRT-PCR tests 24 hours apart both suggested negative results. Patients' clinical samples which PCR test C_t value less than 28 were collected to isolate SARS-Cov-2.

https://www.medrxiv.org/content/10.1101/2020.04.14.20060160v2.full-text

We therefore understand that within the study, samples were used that resulted in a positive PCR test. We all know that a PCR test cannot detect a virus, you can read about this in one of our many articles on the PCR test. *[All information with the corresponding links].*

In the methods section we find the following procedure:

"The sputum, stool and nasopharyngeal swab samples were pre-processed by first mixing them with the appropriate volume (sputum, 5-10 volumes; stool, 2 ml/100 mg; nasopharyngeal swab, 1 volume) of MEM medium with 2% FBS, amphotericin B (100 ng/ml), penicillin G (200 units/ml), streptomycin (200 µg/ml) and TPCK trypsin (4 µg/ml). The supernatant was collected after centrifugation at 3000 rpm at room temperature. Before infecting Vero-E6 cells, all collected supernatant was filtered using a 0.45-µm filter to remove cell debris, etc."

https://www.medrxiv.org/content/10.1101/2020.04.14.20060160v2.full-text

Note Corona_Facts:

Even before the cell cultures were infected, the samples were prepared with various chemicals, antibiotics and foetal bovine serum. One looks in vain for a control sample group.

We will come to why these comments are so important.

"For viral infection and isolation, 3 ml of filtered supernatant was added to Vero-E6 cells in a T25 culture flask. After incubation [the time that elapses between infection with a pathogen and the appearance of the first symptoms] at 35°C for 2h to allow binding, the inoculum [infectious material] was removed and replaced with fresh culture medium. The cells were incubated at 35°C [growing cell cultures or microorganisms in an incubator] and observed daily to assess cytopathic effects (CPE). The supernatant was tested for SARS-CoV-2 by qRT-PCR (see below for qRT-PCR protocol). Once the qRT-PCR test shows positive (typically after 4-5 days of incubation), the viral particles were collected from culture supernatant by ultra-speed centrifugation (100,000x g for 2 hours) for downstream sequencing, infectivity assay, and observed under 200 kV Tecnai G2 electron microscope."

https://www.medrxiv.org/content/10.1101/2020.04.14.20060160v2.full-text

Note Corona_Facts:

The typical procedure: Cells are pre-treated with chemicals, antibiotics and fetal bovine serum and the so-called cytopathic effect (CPE) is equated with a replication of a virus. A positive PCR test is then used as a complementary confirmation.

First a short summary, then the explanation:

- Samples were used which were assumed to be a pathogenic virus due to a positive PCR test.

- The material used was pre-treated, which had a direct influence on the experimental set-up.

- No control runs were carried out to rule out the possibility that the experimental set-up and the treatment of the material were not the cause of the effect. *(Although this has been known for decades).*

- A complementary PCR test cannot detect a virus and cannot be used as evidence for this reason *alone. (see all our articles on the PCR test)*

Now the fuller explanation:

1. No actual rigorous negative control has been carried out in which it is ensured that the "potentially infectious agent" or those short gene sequences from which the genetic strand of the claimed viruses is later constructed are not already present in the starting material, the monkey

kidney cells and the chemicals and nutrient solutions used. Both the introduced agents themselves, or these interacting with the cell material, or this alone, or all together with the isolate from the diseased tissue could be responsible for the observed changes interpreted as viral and for the release of short gene sequences from which the virus genome is later constructed computationally.

2. Virologists kill tissue in the lab unnoticed
Virologists do not use the word "isolation" in the true sense of the word isolation and become suspiciously nervous when it is mentioned to them. They understand "isolation" to mean the production of an effect in the laboratory which they simultaneously call
a) infection
b) proof of the presence of a virus
c) proof of its multiplication
d) proof of the destructive power of the supposed virus.
In reality, they kill tissues and cells in the laboratory unnoticed and unknowingly - by starving and poisoning them.
This effect is known as the cytopathic effect.

3. The alleged cultivation of the virus
This confluence is called giant cell formation and a "cytopathic effect". This result of many violent and insane steps is interpreted as central evidence of the "presence, isolation, multiplication, etc." of the suspected virus. Those involved then claim that they have succeeded in cultivating the virus.

Here the compulsive logic to which virologists are subject becomes clear. This manifested itself on **10 December 1954**, when John Franklin Enders was awarded the Nobel Prize for a long-standing misinterpretation of the suspected polio virus. With the Nobel Prize of **10.12.1954,** however, **his speculation** about the suspected measles virus, **published on** 1.6.1954, became a scientific fact overnight, which **has not been doubted** to this day. **Doubt** is the most important scientific commandment and rule to avoid misinterpretations and to recognise and correct existing misinterpretations.

On **1.6.1954** Enders and his colleagues published observations according to which the death of tissues in the test tube could be regarded as the result of the action of presumed viruses, but at the same time refuted this presumption, since he reported **that the same death of tissues in the test tube also occurred without the addition of presumed infected material.** He explicitly warns that the assumption that this effect could prove the presence of a virus must be researched and investigated in the future. As a result of the Nobel Prize of **10.12.1954** awarded to him for a different matter, the admonition and request to examine this technique and precisely not to equate it with the presence of a virus **has not been made to this day**.

You will find all further details with references in our two following articles:

A sincere request to Prof. Ulrike Kämmerer (Explanation of the two studies from China that were largely responsible for the corona crisis. What was done in these publications and what is their significance).

Corona: The comprehensible and verifiable refutation of the virus claims (A review of the authoritative study on SARS-CoV-2 and a historical retrospective)

This study also performed an alignment to construct a genome.

The alignment, the easily recognisable and essential refutation of all viral assumptions.

A method **such as the alignment here**, to calculate a theoretically long gene sequence from very short ones, which is not backed up by control experiments, cannot be called scientific. This is a pretence of science, which, however, is in no way obvious, comprehensible and verifiable for everyone.

From the word alignment, every layman recognises directly that - **as with all so-called disease-causing viruses** - no whole and intact genome strand, i.e. the complete genome, which is assigned to SARS-CoV-2, was found and isolated, **but only very short snippets of nucleic acid were constructed into something new on the basis of an alignment**. The complete genome strand of the alleged SARS-CoV-2 allegedly consists of 29903 nucleotides according to the mental-computational alignment (*Fan Wu et. al.*).

To clarify: Never does the claim appear in the publications of scientists or other literature that even an approximately complete nucleic acid (*in the case of SARS-CoV-2: 29903 nucleotides long*) has been found from a (*viral*) structure or even from an "infected" liquid, whose determination of its molecular sequence would correspond to the whole nucleic acid that has only been theoretically constructed. It is even the case that missing gaps (gene sequences) have to be freely invented, since the many very short gene sequences are not sufficient to construct a new genome.

If you want to know more about alignment, we recommend our two articles just mentioned (*above*).

Summary of the first study Yao et. al. - "Patient-Derived Mutations Impact Pathogenicity of SARS-CoV-2:

- **No structure** or anything even close to a complete nucleic acid was found from an "infected" liquid whose determination of its molecular sequence would correspond to the whole nucleic acid that was constructed only conceptually (29903 bp Fan Wu et. al.).

- The scientifically prescribed and binding control experiments were not carried out.

- The cytopathic effect is not virus-specific and was also not validated by necessary control experiments. These control experiments are an absolute scientific obligation and have been mandatory for all by the DFG since at least 1998.

- The supposedly "infected" samples, which were only considered to be infected with SARS-CoV-2 because a PCR test carried out was positive, cannot themselves provide any conclusion that one is dealing with a disease-causing virus. The PCR test itself only detects 1-3% of the mentally constructed genome. It is itself based on gene sequences that have been given and is subject to the same scientific weaknesses that we have addressed in this article.
The determination of pathogenicity in "animal experiments" or similar was also omitted.

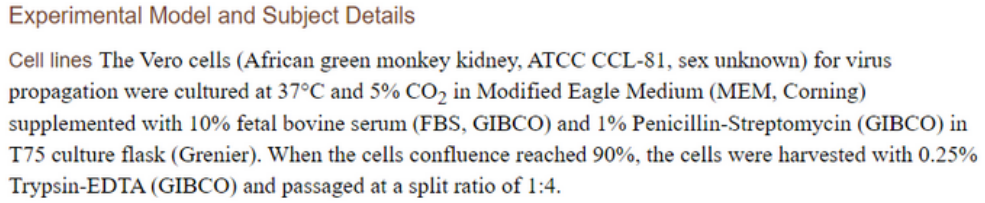
So we can say with one hundred percent certainty that this study has definitely not detected a disease-causing virus. The very fact that the sample material from this study acts as a reference for the "FIRST" real 3D image actually says it all at this point: **the image is certainly not that of a disease-causing virus!**

Let us now turn to the study <u>Molecular Architecture of the SARS-CoV-2 Virus - author Sai Li et. al.</u>

As we have just seen, this study is based on sample material that does not derive from a disease-causing virus. Nevertheless, we will say a few words about the study.

We read in the study in the sample details section:

"Vero cells (African green monkey kidney, ATCC CCL-81, sex unknown) for virus propagation were cultured at 37°C and 5% CO2 in Modified Eagle Medium (MEM, Corning) supplemented with 10% fetal bovine serum (FBS, GIBCO) and 1% penicillin-streptomycin (GIBCO) in T75 culture flasks (Grenier). When cells confluence reached 90%, the cells were harvested with 0.25% trypsin-EDTA (GIBCO) and passaged at a split ratio of 1:4."



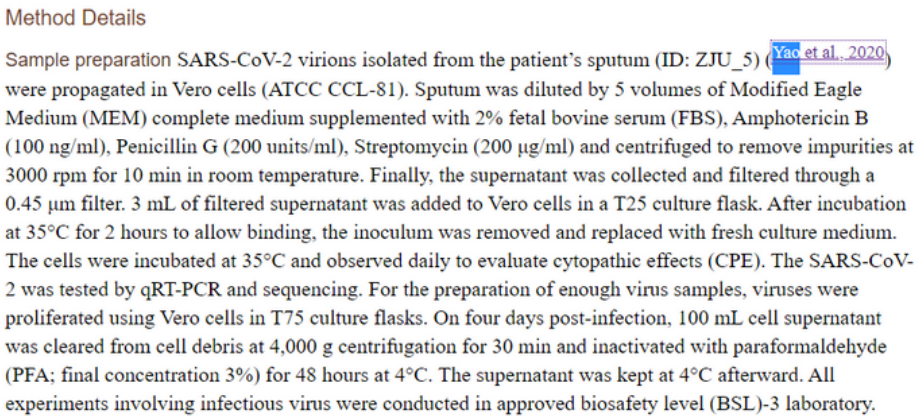
Experimental Model and Subject Details

Cell lines The Vero cells (African green monkey kidney, ATCC CCL-81, sex unknown) for virus propagation were cultured at 37°C and 5% CO_2 in Modified Eagle Medium (MEM, Corning) supplemented with 10% fetal bovine serum (FBS, GIBCO) and 1% Penicillin-Streptomycin (GIBCO) in T75 culture flask (Grenier). When the cells confluence reached 90%, the cells were harvested with 0.25% Trypsin-EDTA (GIBCO) and passaged at a split ratio of 1:4.

Method details

Sample preparation

"SARS-CoV-2 virions (ID: ZJU_5) (Yao et al., 2020) isolated from patient sputum were propagated in Vero cells (ATCC CCL-81). Sputum was diluted with 5 volumes of Modified Eagle Medium (MEM) complete medium supplemented with 2% fetal bovine serum (FBS), amphotericin B (100 ng/ml), penicillin G (200 units/ml), streptomycin (200 μg/ml) and centrifuged at 3000 rpm for 10 min at room temperature to remove contaminants. Finally, the supernatant was collected and filtered through a 0.45 μm filter. 3 mL of the filtered supernatant was added to Vero cells in a T25 culture flask. After incubation at 35 °C for 2 hours to allow binding, the inoculum was removed and replaced with fresh culture medium. Cells were incubated at 35 °C and observed daily to assess cytopathic effects (CPE). The SARS-CoV-2 was tested by qRT-PCR and sequencing. To produce sufficient numbers of virus samples, viruses were propagated using Vero cells in T75 culture flasks. On the fourth day post-infection, 100 mL of cell supernatant was cleared of cell debris at 4,000 g centrifugation for 30 min and inactivated with paraformaldehyde (PFA; final concentration 3%) for 48 h at 4°C. The supernatant was then stored at 4°C. All experiments with infectious viruses were performed in an approved biosafety level (BSL)-3 laboratory."



Method Details

Sample preparation SARS-CoV-2 virions isolated from the patient's sputum (ID: ZJU_5) (Yao et al., 2020) were propagated in Vero cells (ATCC CCL-81). Sputum was diluted by 5 volumes of Modified Eagle Medium (MEM) complete medium supplemented with 2% fetal bovine serum (FBS), Amphotericin B (100 ng/ml), Penicillin G (200 units/ml), Streptomycin (200 μg/ml) and centrifuged to remove impurities at 3000 rpm for 10 min in room temperature. Finally, the supernatant was collected and filtered through a 0.45 μm filter. 3 mL of filtered supernatant was added to Vero cells in a T25 culture flask. After incubation at 35°C for 2 hours to allow binding, the inoculum was removed and replaced with fresh culture medium. The cells were incubated at 35°C and observed daily to evaluate cytopathic effects (CPE). The SARS-CoV-2 was tested by qRT-PCR and sequencing. For the preparation of enough virus samples, viruses were proliferated using Vero cells in T75 culture flasks. On four days post-infection, 100 mL cell supernatant was cleared from cell debris at 4,000 g centrifugation for 30 min and inactivated with paraformaldehyde (PFA; final concentration 3%) for 48 hours at 4°C. The supernatant was kept at 4°C afterward. All experiments involving infectious virus were conducted in approved biosafety level (BSL)-3 laboratory.

We see the same procedure as in the study before. This procedure, as we described earlier, became the scientific standard in 1954 when the Nobel Prize was awarded. Although everyone knew that this was pure speculation, it was never questioned again (with a few exceptions).

We will now give you some examples where the necessary control results have shown that precisely this cytopathic effect is not virus-specific, but has other underlying causes.

1. One of the expert reports, which was carried out within the measles virus trial and presented to the court, proved that the experimental set-up alone, i.e. the pre-treatment of the cell cultures themselves, leads to the cytopatic effect. (see expert opinion 3 - cytopathic effect in monkey kidney cells is not specific to measles virus).

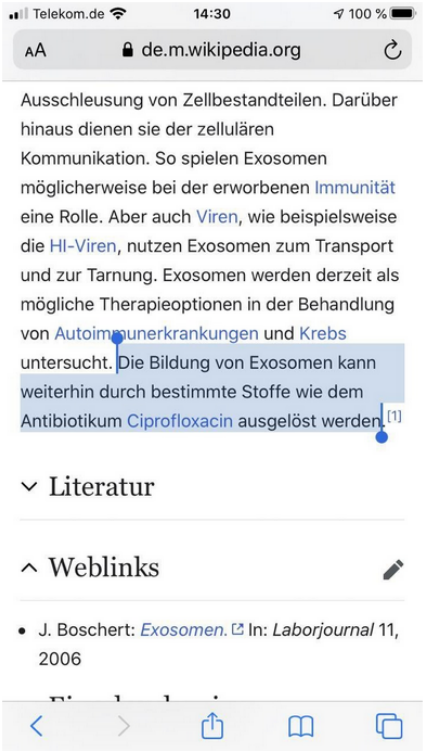
2. Also in the publication by Bech, V. & von Magnus, P. (1958) Studies on measles virus in monkey kidney tissue cultures. Acta Pathologica Microbiologica Scandinavica 42(1):75-85 it is described that the **cytopathic effect is not measles-specific**, but is caused by other factors.
Thus, the publication states on p.80:
"*cytopathic changes similar to those caused by measles virus may be observed also in uninoculated cultures of monkey kidney tissue (Fig. 4-5). These changes are probably caused by virus-like agents, so called 'foamy agents', which seem to be frequently present in kidney cells from apparently healthy monkeys.*"

This sentence is remarkable, as it points to the non-specificity of the very pathological changes that served as the starting point for the visual evidence of infection in the first publication by Enders & Peebles.

3. *Prof. Karlheinz Lüdtke, Max Planck Institute for the History of Science, Early History of Virology, Special Paper 125, 89 pages, 1999. i. K. (A 2) Preprint 1999.*

This reading is so important because it shows how necessary control experiments are in order to recognise that one was wrong. It shows that by 1953 it was clear and well known to every virologist and the scientific community that all the constituents that had hitherto been interpreted as constituents of viruses turned out, **through control experiments**, to be constituents of dead tissues and cells. This is why it is so essential to keep insisting on the lack of control experiments in the publications presented.

4. Another aspect to be mentioned is that there is scientific knowledge that the addition of antibiotics creates exosomes (*RNA sequences*) that were not present before. (Wikipedia 22.01.2021).



Edit I. Buzás, Robert Horvath, Károly Vékey, László Drahos, Sára Tóth: Antibiotic-induced release of small extracellular vesicles (exosomes) with surface-associated DNA. In: Scientific Reports. Band 7, Nr. 1, 15. August 2017, ISSN 2045-2322, S. 8202, doi:10.1038/s41598-017-08392-1 (nature.com [abgerufen am 31. März 2019]).

5. For the very reason that these obligatory control experiments were not carried out, this study must be classified as unscientific and is not worth the paper it was written on. See the rules for scientific work (lege artis) that have been bindingly codified by the DFG since 1998 and signed by all university rectors.

Crucially, here again one pelletised - not isolated - and the pelletised was not biochemically investigated. The photos were calculated on the basis of a predefined model, which is why they do not show a real image.

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