Felix de Fries c/o Study Group AIDS-Therapy Juliastr. 8 8032 Zürich

Felix.defries@gmail.com
https://www.immunity.org.uk/articles/felix-de-fries/

To those affected
their doctors and caretakers
To Groups and Institutions
To Media

Zürich 19th April 2022

ref. **SARS Cov-2 as product of laboratory experiments**

Dear Sir/Madam

Dear Contemporaries

In an interview that Prof. Christian Drosten had given to the Süddeutsche Zeitung on February 8, he said:
"Things were definitely done in Wuhan that could be described as dangerous. But the Sars-CoV-2 virus could not have come out of it. They have built new properties into bat viruses, but not those that could be considered the predecessors of Sars-CoV-2. »
and..
"Inserting a furin cleavage site would be a theoretically conceivable laboratory experiment. But the natural diversity of these viruses is not well understood. Therefore, while the furin cleavage site is conspicuous, it is not evidence of a non-natural origin of SARS-Cov2-"
as also…
"Project reports have become public showing that the Institute of Virology in Wuhan actually did what is known as gain-of-function experiments in a project run by the US NGO Ecohealth Alliance (Peter Daszak). New spike proteins were incorporated

into bat viruses using genetic engineering. It turned out that the viruses constructed in this way were able to multiply better. It was also revealed that there were plans to incorporate furin cleavage sites, but that was to be done in an American lab and the project was not funded."

The insertion of a furin cleavage site into spikes of SARS-COV viruses has been undertaken by various research groups for several years in their experiments.
The incorporation of a furin cleavage site into the epidemic swine diarrhea virus created a new form of cell-to-cell fusion and increased the ability to infect different cell types, while the incorporation of a furin cleavage site into spikes of the MERS virus caused that it could be activated by human proteases and direct the entry into human cells.

In contrast to all other known SARS-CoVs, SARS-Cov-2 has a special, four-unit PRRA insertion at its spike junction, which creates a furin cleavage site that is highly functional, similar to the one that caused MERS (Middle East Respiratory Syndrome).
The furin cleavage site in the SARS-Cov-2 spikes at the S1/S2 region, which was discovered in January and February 2020, could significantly improve cell penetration and thus greatly increase transmissibility compared to other corona viruses was stated by researchers at that time.
None of the various SARS-Cov-2-like horseshoe bat coronaviruses found in Japan, Cambodia, Thailand, Laos and China exhibited a furin cleft at the S1-S2 junction as found in SARS-Cov-2. In ferrets infected with SARS-Cov-2 viruses without a furin cleavage site, the virus was implemented to a much smaller degree than in original SARS Cov-2 viruses and was not transmitted to ferrets living in the vicinity.

[HTML] **The furin cleavage site in the SARS-CoV-2 spike protein is required for transmission in ferrets**

[HTML] nature.com

The genetically closest spike genes to SARS-Cov-2 in Coronaviruses occurring in armadillos from Guandong, Guangxi and Zoushan have no furin cleavage site at the S1/S2 junction. Leading researchers such as David Baltimore described the occurrence of the furin cleavage site at the S1/S2 interface as extremely unusual. They cannot explain how a furin cleavage site, which occurs in similar forms in other corona viruses occurring in other species, could have gotten into SARS-Cov-2.

The emergence of the spike furin cleavage site in SARS-CoV-2

HTML] oup.comFull View

[HTML] **Furin cleavage site is key to SARS-CoV-2 pathogenesis**

[HTML] nih.govFree from Publisher

Experiments with SARS-Cov-2 mutants without a furin cleavage site in spike proteins showed a significant reduction in pathogenicity in hamsters and mice compared to "original SARS-Cov-2 viruses". Although the furin cleavage site in various SARS-COV viruses was hardly changed under evolutionary pressure, changes in their spatial structure and their electrostatic potential may have significantly increased their ability to digest, accordingly the difference between the SARS-Cov-2 family and other families of corona viruses becomes manifest in furin function, which plays a crucial role in the pathogenicity of SARS-Cov-2, spreading from the salivary gland, lacrimal gland and the lungs to the kidney, the liver and can the gastrointestinal tract, as researchers

from Hangzhou were able to demonstrate.

Virus strain from a mild COVID-19 patient in Hangzhou represents a new trend in SARS-CoV-2 evolution potentially related to Furin cleavage site

[HTML] tandfonline.comFull View

[HTML] Loss of furin cleavage site attenuates SARS-CoV-2 pathogenesis

[HTML] nature.com

[HTML] Furin cleavage of SARS-CoV-2 Spike promotes but is not essential for infection and cell-cell fusion

[HTML] plos.org

The SARS-Cov-2 spike protein has a polybasic furin cleavage site through the insertion of 12 nucleotides at the S1-S2 junction, which ensures greatly improved binding to ACE-2 receptors. Six RBD amino acids are responsible for its binding to ACE-2 receptors and have significantly expanded the number of possible SARS-Cov-2 hosts.

According to structural and biochemical studies, SARS-Cov-2 has high affinity to ACE-2 from humans, ferrets, cats and other species with high receptor similarity. In regard of the high variability in the spikes, it is likely that corona viruses with partial or complete furin cleavage sites can soon be found in other species, said the authors, in a letter to the editor of Nature Medicine dated April 26, 2020, who assumed, a natural origin of the furin cleavage site in SARS-Cov-2 viruses, but the corresponding corona viruses have not been found yet.

Virus strain from a mild COVID-19 patient in Hangzhou represents a new trend in SARS-CoV-2 evolution potentially related to Furin cleavage site

[HTML] tandfonline.comFull View

[HTML] Loss of furin cleavage site attenuates SARS-CoV-2 pathogenesis

[HTML] nature.com

[HTML] Furin cleavage of SARS-CoV-2 Spike promotes but is not essential for infection and cell-cell fusion

[HTML] plos.org

Corona viruses in various animals have a functioning furin cleavage site in spike proteins, which can increase the number of possible host organisms and the pathogenic effect. That, in addition to human-to-human transmission, contagion can occur through animals was shown by experience with ferrets and mink on farms and transmission by cats, while cows and pigs do not seem to transmit the virus to humans.
In 2003-2004, a coronavirus termed as SARS-Cov led to around 8000 cases, mainly in China, which could be contained to 800 deaths through non-pharmaceutical measures, since it only affected the lower respiratory organs but not the upper ones, such as SARS Cov-2 does. SARS-related corona viruses, which in addition to SARS-Cov and SARS-Cov-2 contain a large range of genetically different strains in bats, can infect other mammals and primates in addition to armadillos and bats.

Animals such as dromedaries or alpacas have also been recognized as hosts that can cause infection in humans. Civet cats and raccoon dogs have been identified as possible intermediate hosts for SARS-Cov, while all attempts to find intermediate hosts for SARS-Cov-2 have been unsuccessful.

[HTML] The proximal origin of SARS-CoV-2

HTML] nature.com

Human-to-animal transmissions of SARS-Cov-2 have been reported from various countries over the course of the pandemic. Infection of cats and dogs by sick pet owners led to both mild and severe illnesses. Infections also occurred in herd animals and wild animals

In regard of the millions of pets and breeding animals worldwide and the reinfection by variants of the virus such as omicron, which took place in a certain animal host , new methods must be found in the field of animal husbandry.

In contrast to SARS-Covs, SARS-Cov-2 contains a furin protease cleavage site in its spike proteins, which is responsible for binding and entry into cells and for increased transmissibility, higher pathogenicity and an increased range of possible host organisms.

Modified live vaccines, available for infections in animals since 2008, have remained controversial due to possible antibody induced potentiation of inflammatory responses. Various vaccine candidates against MERS infections in humans and camels including adenovirus vector-based ones were tested. A vaccine with a proxivirus vector was in phase I testing in December 2019. MRNA- and virus vector- vaccines were then urgently approved and widely distributed to humans from the late 2020 on.

Potential zoonotic sources of SARS-CoV-2 infections

PDF] wiley.com

Analysis of new SARS-Cov-2 mutants reveals novel mechanisms of resistance to vaccines and new antibodies, as well as the

ability to utilize ACE-2 receptors from additional species.

Analysis of SARS-CoV-2 variant mutations reveals neutralization escape mechanisms and the ability to use ACE2 receptors from additional species

[HTML] nih.gov

The genetic structures of RATG13, MP789 and RmYNO2, which are closest to the ones occurring in SARS-Cov-2 and only emerged after the onset of the pandemic, have been invoked to support the natural origin of SARS-Cov-2.
The presence of a postulated natural PAA/PAA amino acid insertion at the S1/S2 junction in their spike proteins at the same site where the PRRA insertion in SARS-Cov-2 creates a polybasic furin cleavage site is indicative of RmYNO2 which instead of the claimed insertion shows damage of 6 nucleotides in the same region, so that the insertion of 12 nucleotides in SARS-Cov-2 at the S1/S2 junction remains unique among the corona viruses, not only because of their polybasic furin cleft but also because of the size of the surrounding locus.

SARS-CoV-2′ s claimed natural origin is undermined by issues with genome sequences of its relative strains: Coronavirus sequences RaTG13, MP789 and …

[PDF] wiley.com

Measures to reduce the transmission of SARS-Cov-2 should also reduce the transmission of other endemic respiratory viruses, while its easing also could lead to increased co-infections of SARS-Cov-2 with influenza viruses, syncytial viruses (RSV) and adenoviruses.
An investigation of such co-infections in Covid patients showed 8,4% co-infections with influenza viruses, around 7,5% with syncytial viruses (RSV) and around 4,2% co-infections

with adenoviruses, at all of which the likelihood of mechanical ventilation and mortality decreased significantly. About 15% of those infected with adenoviruses aged 68-71 years who had an average of one previous illness were immunocompromised, as also 37% of those with influenza viruses and 32% of those with RSV viruses.

[HTML] SARS-CoV-2 co-infection with influenza viruses, respiratory syncytial virus, or adenoviruses

HTML] thelancet.com

As a study from China shows, plant substances such as puerarin, quercetin and kaemferol show a high binding capacity to the ACE-2 receptor and thus influence the binding of the SARS-Cov-2 spike proteins to this receptor. Quercetin was also able to block the RBD domain of the spike proteins and thus neutralize the entire SARS-Cov-2 virus.

[HTML] Chinese herbal compounds against SARS-CoV-2: puerarin and quercetin impair the binding of viral S-protein to ACE2 receptor

[HTML] sciencedirect.com

Sulfur-containing polysaccharides such as heparin were able to block SARS-Cov-2 in vitro, while polyunsaturated fatty acids were able to block ACE-2 controlled binding of SARS-Cov-2 and its entry into cells.

[HTML] Sulfated polysaccharides effectively inhibit SARS-CoV-2 in vitro

[HTML] nature.comFull View

[HTML] Polyunsaturated ω-3 fatty acids inhibit ACE2-controlled SARS-CoV-2 binding and cellular entry

[HTML] nature.com

Findings that to date have little impact on the treatment of Covid-19, which continues to be driven by antivirals delivered as mRNA vaccines and virus-vector vaccines built into PEGYlated nanoparticles, or orally, by Pfizer's Paxlovid , which is intended to reduce severe disease progression by 89%, but is not available for high-risk patients in developing countries, as part of research projects or for the production of generics.
However, the many new antiviral drugs that are supposed to work against Covid-19, its pre-existing diseases and its sequelae, which can also be the product of antiviral therapy using mRNA and virus vector vaccines, are now likely to come into play.
They are currently being developed by almost all internationally known pharmaceutical manufacturers using genetic engineering methods and will be brought to market as soon as possible. There is also talk of a new vaccine against the omicron variant, which is due to be launched in the fall, and of combined vaccines against influenza viruses and corona viruses.

By inserting 12 nucleotides at the S1-S2 junction in the Wuhan Institute of Virology, a polybasic furin cleavage site was created in SARS-Cov-2, which ensures a greatly improved binding to ACE-2 receptors, and the expansion of the range of possible SARS-Cov-2 host organisms. With this a new interplay between genetic-engineering modified viruses and a broader happening zoonisis under the condition of higher particulate matter emissions has been brought under way.
Since no internationally valid regulation of genetic engineering experiments with animals and in cell cultures has come about to date, bacteria, viruses and parasites occurring today can be modified at any time through the installation of

new structures by genetic engineering manipulations in such a way that they can spread in species that are not hitherto been attacked by them.
This means that complex balances between different species and their environment can be disturbed at any time. New tests to detect antibodies against such new, experimentally modified pathogens can be developed, as can therapies against them.
This opens a new game of chance with genetic engineering methods and substances in which, as Covid-19 has shown, people can become losers very quickly. In the near future we will see how fast and precisely short-term, medium-term and long-term side effects of substances can be recorded so that causes and effects can be precisely assigned.

Whether we can change the production of everyday goods, our transport of goods and people, waste incineration and the generation of energy within a reasonable time will be decisive for the emission of greenhouse gases and particulate matter particles, which serve viruses as vectors and for the formation of new virus variants. Whether we can farm sustainably so that healthy staple foods are produced for everyone, water and soil are protected and there is enough space for wild animals to live will be decisive for us and our children.

Felix de Fries