Scientific background

Covid-19 anti-docking strategy for the throat

Virus-reducing preventative treatment: gargling H2O2/alcohol at set intervals

Coronaviruses have long been endemic and are known to be the cause of winter infections among children, for example. SARS-CoV-2 is a mutation caused by transmission from bats to pigs – and its high level of infectiousness and pathogenicity now also poses a threat to the human body.

The primary means of infection is the inhalation of droplets released by infected people when they cough or sneeze.

These droplets contain the virus. Due to the physiological centrifugation effect that occurs when they are breathed in, the viruses come into contact with the mucous membrane in the nose and duly accumulate in the nose and throat area.

For reasons relating to respiratory physiology, the number of viruses that reach the lungs directly can be classed as relatively small. This is because hardly any free viruses find their way into the alveoli without first contacting the mucous membranes in the nose and throat area or in the bronchial system.

A viral infection fundamentally depends on the number and pathogenicity of viruses entering the body, as well as the competence and dimensions of the human immune system.

Whenever a new virus appears, the non-specific and – if we consider the primary means of infection with SARS-CoV-2 – the local immune system comprising the mucous membranes in the nose and throat area or in the bronchial system acquire great significance. The defensine system is of primary importance in this context, as it is capable of inhibiting virus replication in the mucous membranes. Additional protection is provided by the non-specific cellular macrophage system, which is activated by alpha- and beta-interferons (for instance) and triggers an inflammatory defensive response that is capable of eliminating viruses.

In fighting SARS-CoV-2 viruses via targeted external measures, we can build on the physiological mechanisms of the immune defence system by using a particular feature of coronaviruses to our advantage.

Coronaviruses are enveloped viruses that use the spike protein on their surface to penetrate into the host cell and dock onto the receptors of a mucous membrane cell (angiotensin-converting enzyme 2: HCoV-NL63, SARS-CoV, sialic acid HCoV-OC43), which in turn enables the fusion between the viral envelope and the cell membrane. The spike protein is also the structure that lends coronaviruses their familiar appearance when viewed under an electron microscope and is indeed the inspiration behind their name.

A team of researchers at the University of Texas has succeeded in decoding the structure of the spike protein and proving that, while it uses the same 'unfolding mechanism' as other coronaviruses, it docks onto the ACE2 receptor of the mucous membrane cells with around 20 times the intensity of spike proteins in previously known coronaviruses (McLellan et al., 2020). This is what makes it more infectious among humans. These findings suggest that it is crucially important to disrupt or prevent the docking mechanism, for example via oxidation with H2O2 or C2H5OH, as virus replication is almost impossible to influence later on in the process.

In the course of docking, which is currently believed to take 2–6 hours (Ziebuhr J., 2008), the spike protein changes its structure and enters into an energetically metastable state. As the process continues, the spike protein is proteolytically split into S1 and S2 proteins.

Two components of the S2 peptide, known as heptad repeats 1 and 2 respectively, are of particular significance. During fusion activation, HR1 and HR2 interactions in the spike protein trimer help form a compact bundle structure (six-helix bundle) typically seen in the stable post-fusion state of the spi-

ke protein. Not only can the initial metastable energetic state of the spike protein be used to destroy the protein via oxidation mechanisms, the HR1 and HR2 interactions can be specifically inhibited and the entry of the virus into the host cell prevented as a result (Ziebuhr J., 2008).

This has inspired the development of an anti-docking strategy involving systematic virus-reducing gargling – a simple measure anyone can perform correctly in order to reduce the viral load in the nose and throat area, support the body's defence mechanisms and prevent these from being overwhelmed.

A 1.5–2% H2O2 solution was chosen for the oxidation mechanism as it is capable of inhibiting the docking process and virus replication.

No toxic effect on mucous membrane cells is to be anticipated with this H2O2 concentration. Instead, targeted oxidative processes are supported through peroxiredoxins that are present in large quantities in every somatic cell and use H2O2 for the oxidation of target proteins such as virus proteins (German Cancer Research Center, Dick T. P., 2014). Another effect that destroys spike proteins is provided by an alcohol component featuring an initial concentration of 70–90%, which is then diluted to 6–8% by volume in the solution.

It is therefore anticipated that the continuous application of a corresponding gargling solution containing H2O2 and alcohol at intervals of 4–6 hours can sufficiently reduce the viral load in the throat so as to prevent severe illness caused by the body being flooded with viruses originating from the throat.

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Responsible for content: Dr Achim Neumayr

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