MRET Treated Water as a Possible Agent for Inhibition of Coronavirus Life Cycle.

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Introduction:

Researchers worldwide are racing to develop potential vaccines and drugs to fight the new coronavirus, called SARS-Cov-2. Now, a group of researchers has figured out the molecular structure of a key protein that the coronavirus uses to invade human cells, potentially opening the door to the development of a vaccine, according to new findings. Previous research revealed that coronaviruses invade cells through so-called “spike” proteins, but those proteins take on different shapes in different coronaviruses. Figuring out the shape of the spike protein in SARS-Cov-2 is the key to figuring out how to target the virus, said Jason McLellan, senior author of the study and an associate professor of molecular biosciences at the University of Texas at Austin. Though the coronavirus uses many different proteins to replicate and invade cells, the spike protein is the major surface protein that it uses to bind to a receptor — another protein that acts like a doorway into a human cell. After the spike protein binds to the human cell receptor, the viral membrane fuses with the human cell membrane, allowing the genome of the virus to enter human cells and begin infection. So “if you can prevent attachment and fusion, you will prevent entry,” McLellan told Live Science.

The overall structure of 2019-nCoV S resembles that of SARS-CoV S, with a root mean square deviation (RMSD) of 3.8 Å over 959 Cα atoms. One of the larger differences between these two structures (although still relatively minor) is the position of the RBDs in their respective down conformations (Fig.1). Despite this observed conformational difference, when the individual structural domains of 2019-nCoV S are aligned to their counterparts from SARS-CoV S, they reflect the high degree of structural homology between the two proteins, Despite this observed conformational difference, when the individual structural domains of 2019-nCoV S are aligned to their counterparts from SARS-CoV S, they reflect the high degree of structural homology between the two proteins. [1]

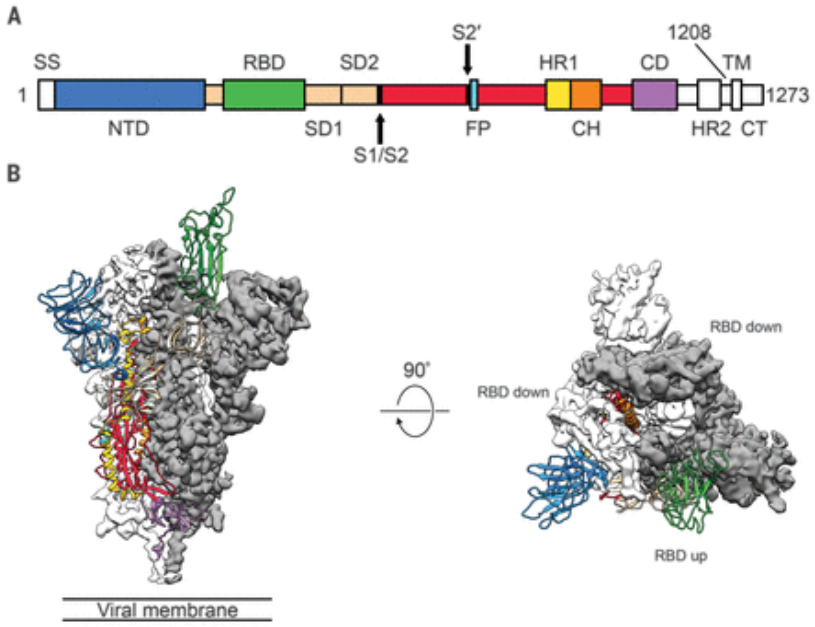

Fig.1 Structure of 2019-nCoV S in the pre-fusion conformation [1].

The snapshot of this interaction, captured through cryogenic electron microscopy by Qiang Zhou of the Westlake Institute for Advanced Study and colleagues, reveals some of the chemistry behind how the coronavirus hijacks angiotensin converting enzyme (ACE2), an enzyme involved in blood pressure regulation. The researchers think that the structure could lead to the development of antibodies that block this interaction ACE2 is the first in a string of enzymes that convert the hormone angiotensin into its active form. When cleaved by enzymes, angiotensin makes blood vessels contract. The SARS-CoV-2 spike protein has two key elements involved in infecting human cells. A string of amino acids in the S1 subunit directly binds to the protein-cleaving part of ACE2 called the peptidase domain. The S2 subunit of the spike protein helps the virus fuse to the human cell. The scientists found that the protein-cleaving part of ACE2 binds the spike through polar interactions formed from a bridge-like structure on the enzyme. Both ends of the receptor binding domain stick to ACE2 through hydrogen bonding and van der Waals forces. McLellan says that SARS-CoV-2 binds ACE2 more strongly than does the virus that caused the severe acute respiratory syndrome outbreak in 2003. Zhou's research shows the subtle amino acid changes that create salt bridges and improve van der Waals interactions that might underlie this stronger interaction, he says [2].

Hypothesis:

Water is the natural background in the scope of which all biochemical processes are running. In nature, only four types of interactions (strong, weak, electromagnetic, and gravitational) are known. Two of the interactions are purely nuclear, and the gravitational one reveals itself only on the cosmic scale. Therefore, it is clear that only the electromagnetic interaction is essential in the scope of any biological system. For the sake of simplicity, we notice that the whole specificity of any biological process is

eventually reduced to certain electromagnetic interactions. Just for this reason, the electromagnetic properties of water, which play the decisive role in its self-organization and in its influence on other objects, must be comprehensively investigated. These properties are revealed in all, without exception, biochemical and biophysical processes.

Specific features of the electrodynamic characteristics of water [first of all, a very great value of its dielectric permittivity $\varepsilon(\omega)$] are the reason for the natural dissociation of molecules of many chemical compounds and the formation of the necessary ion composition of vitally important microelements. Otherwise, the normal operation of many systems of a living organism (in particular, the operation of selective membranes) would be impossible.

The change in the dispersive properties of water can render very strong influence (by means of modification of the electrostatic forces between separated charges and forces of the van der Waals type defining the interaction of the systems of neutral atoms and molecules) on the long range interaction of basic elements of living systems such as cells, viruses, biological macromolecules, enzymes, etc.[5]

The coronavirus, SARS-CoV, the primary cause of SARS, gains entry into pulmonary endothelial cells by membrane fusion on binding to this ectoenzyme. This interaction is mediated by the SARS-CoV spike protein. This conclusion is further supported by recent observations that pulmonary endothelial cells express high levels of ACE2.

Though the coronavirus uses many different proteins to replicate and invade cells, the spike protein is the major surface protein that it uses to bind to a receptor — another protein that acts like a doorway into a human cell. After the spike protein binds to the human cell receptor, the viral membrane fuses with the human cell membrane, allowing the genome of the virus to enter human cells and begin infection.

The stability of spike protein structure is based on the overall interactions of van der Walls weak electrodynamic forces and hydrogen bonding. The pre-fusion spike protein stability needs certain medium that supports required van der Walls interactions and hydrogen bonding to form the protein spike chain by coronavirus. It is obvious, that such medium is a water-based one, since all biochemical formations of proteins requires presence of water molecules in biological systems. The following transition of pre-fusion spike protein to post-fusion protein also requires specific water-based medium to support correct transition and formation of the bridges to help coronavirus fuse with the human cell membrane.

The van der Waals forces among atoms and molecules generally act over relatively short distances, and are proportional to the inverse of the seventh power of the intermolecular distances for molecules and atoms. For two spheres of the same radius R, the interaction energy, W, as a function of the particle separation distance, D, is:

$$W(D) = -\frac{A_{131}\ R}{12\ D} \qquad (1)$$

where the Hamaker constant, A_{131}, depends on the relative dielectric constants of the material 1 and medium 3.

The equation (1) yields for the significant role of the medium relative dielectric constant for the value of van der Waals interaction energy.

Thus, modification of water –based medium electrodynamic parameters can lead to significant change of van der Walls interactions and hydrogen bonding that may result in the inhibition and interruption of proper formation of spike proteins chains. Such scenario obviously disables coronavirus life sequence of attachment and fusion with human cell membranes.

We suggest such agent which can interrupt coronavirus life sequence is MRET water with anomalous electrodynamic characteristics. MRET water can be consumed on the regular basis by human subjects to prevent coronavirus infection.

The studies conducted at AltheaDx Technology, USA confirm that MRET activated water based medium did not affect the cells on genetic level; it affected the morphology of normal PBMC cells in a positive way increasing their viability. [6]

MRET Activated Water is produced with the help of patented in the USA Molecular Resonance Effect Technology (MRET, US Patent # 6022479). MRET water activator is the stationary source of subtle, low-frequency, resonant electromagnetic field with composite structure. The origin of the low-frequency composite electromagnetic field is the intensive electrical activity inside the nano-circles formed by linear molecular groups of MRET polymer compound (volumetric fractal geometry matrix) when polymeric body is exposed to the external electromagnetic fields of specific frequency and wavelength. The significant reduction of values of electrical conductivity and dielectric permittivity confirms the relatively high, long-range dynamic structuring of water molecules in activated water produced with the help of MRET activation process. The long-term storage of activated water (up to 5 hours at 20˚C) did not significantly affect its modified electrodynamic characteristics, thus confirming the ability of MRET activated water to keep its anomalous properties for rather long period of time in case of 30 minutes activation, and even higher level of “long-term water memory” phenomenon in case of 60 minutes activation. The significant level of reduction of dielectric permittivity and electrical conductivity kept by MRET water activated for 30 minutes after it was heated to 72˚C confirms its stability to thermal effects. It demonstrates the anomalous behavior of electrodynamic characteristics (dielectric permittivity and electrical conductivity) of MRET water subject to applied EMF (electromagnetic field) in the area of very low range of frequencies in order to provide some evidence regarding polarized-oriented multilayer structuring of MRET activated water and the possible effect of MRET water on the proper function of cells in biological systems.

Proof of hypothesis:

Severe acute respiratory syndrome (SARS) is a febrile respiratory illness. The disease has been etiologically linked to a novel coronavirus that has been named the SARS-associated coronavirus (SARS-CoV), whose genome was recently sequenced. Since it

is a member of the Coronaviridae, its spike protein (S2) is believed to play a central role in viral entry by facilitating fusion between the viral and host cell membranes. The protein responsible for viral-induced membrane fusion of HIV-1 (gp41) differs in length, and has no sequence homology with S2. Infection by many enveloped viruses requires fusion of the viral and cellular membranes. A viral envelope protein mediates this membrane fusion process. These proteins are synthesized as precursors (ENV in Retroviridae, and E2 in Coronaviridae) that are later processed into a transmembrane subunit (gp41 in the retrovirus HIV-1, and S2 in the coronavirus SARS-CoV) that is responsible for viral-induced membrane fusion, and a surface subunit that is responsible for the interaction with the cellular receptor/s. This study points to a similar mode of action for the two viral proteins, suggesting that anti-viral strategy that targets the viral-induced membrane fusion step can be adapted from HIV-1 to SARS-CoV (Fig.2). Recently the FDA approved Enfuvirtide, a synthetic peptide corresponding to the C-terminal heptad repeat of HIV-1 gp41, as an anti-AIDS agent. Enfuvirtide and C34, another anti HIV-1 peptide, exert their inhibitory activity by binding to a leucine/isoleucine zipper-like sequence in gp41, thus inhibiting a conformational change of gp41 required for its activation. We suggest that peptides corresponding to the C-terminal heptad repeat of the S2 protein may serve as inhibitors for SARS-CoV entry.[3]

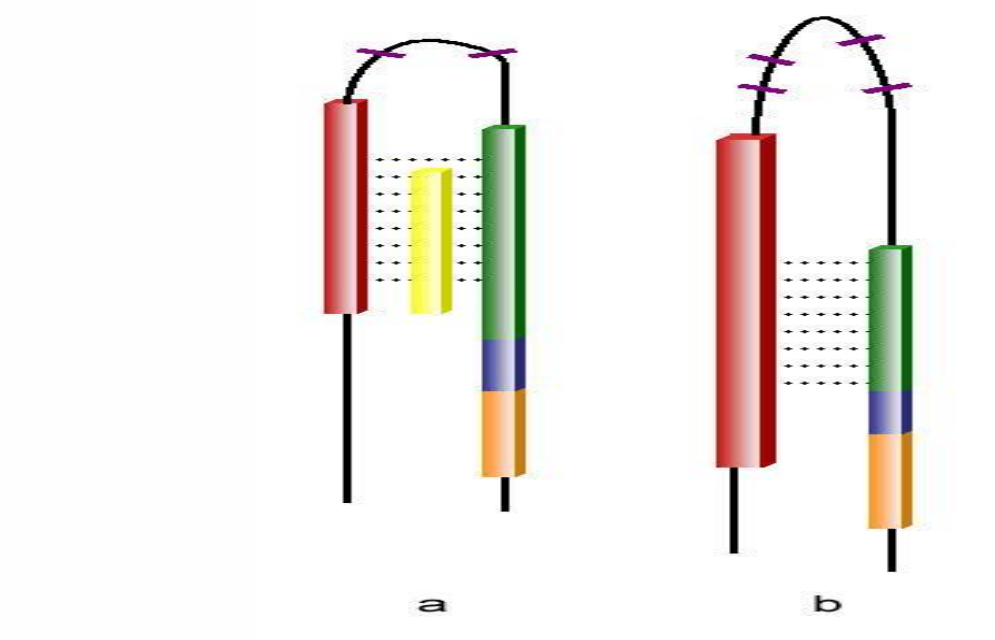

Fig.2 Similarity between the fusion proteins of HIV-1 and SARS-CoV. The HIV-1 gp41 (a) and the equivalent S2 protein from the SARS-CoV (b) are shown. A Leucine/Isoleucine heptad repeat adjacent to the N-terminus of both proteins appears in red. The C-terminal heptad repeat is in green. Cysteine residues (purple) confining a loop structure is located between the two heptad repeats. An aromatic residues-rich motif is marked blue, and the transmembrane segment is in orange. A peptide corresponding to the C-terminal heptad repeat, which acts as potent inhibitor of HIV-1 entry into the cell, appears in yellow.[3]

The clinical observation was performed at Thammarakniwet Foundation, WAT Phrabaat

namphu, Lopburi Province, Thailand. The investigation was conducted under the supervision of Dr. Peerayot Trongsawad, MD, Director of AIDS Control Department, Bangkok Metropolis.
The study was conducted on 38 AIDS patients during August, 2004 - August, 2005. All patients were consuming 1.5 liters of MRET activated water per day as a complimentary treatment in addition to the prescribed Anti-HIV medications. During the course of clinical observation all 38 patients were tested on a regular basis for CD4 counts and required to submit weekly reports regarding their health conditions.
There was simultaneous observation of other group of AIDS patients during the same period of time (control group). They were on the same type of prescribed Anti-HIV medication, but without the complimentary consumption of MRET water. [4]

First method: collection and analysis of the weekly health condition reports and CD4 counts reports;
Second method: group interviews and personal interviews with patients which participate in this observation.
38 patients of the age between 19 and 49 years old were selected for the clinical trial.
Summarizing the observation results we can indicate that in compliance with the studied gradations of AIDS patients health conditions 36 patients showed significant improvement and 2 patients did not show any improvement of their health condition.
Two patients were selected to undergo two tests at the Bangkok Pathology Laboratories due to budget limitation. One test was the reading of the level of CD4 counts (immune system) and the other was Viral Load (the amount of virus in the body) For CD4 reading, a healthy body should have a range of 800 – 1200 cells / microliter.
For Viral Load, the instrument has the ability to measure from 50 – 5000 copies / ml. The lower the number, the lesser the virus in the body, and subsequently lesser it attacks the patient's body.

Patient Mr. Sa-ad


Before MRET water consumption August 2004.


After MRET water consumption September 2004.


After MRET water consumption July 2005.

1st Patient Mr. Sa-ad:
His CD4 counts increased from 2 to 840 within 11 months of consumption of MRET activated water. His Viral Load was less than 50.

2nd Patient Mr. Un-ruang:
His CD4 counts increased from 90 to 805 within 3 months of consumption of MRET water. His Viral Load was also less than 50.
Group of patients without MRET water treatment:
The simultaneous observation of the patients which did not consume MRET water (control group) provides evidence that these patients did not show any significant improvement of their health condition.

Conclusion:
We observed positive results of MRET water complimentary treatment for HIV patients during the clinical trial conducted at at Thammarakniwet Foundation, WAT Phrabaat namphu, Lopburi Province, Thailand in 2004 -2005. The recent research data allows to point to a similar mode of action for the two viral proteins, suggesting that anti-viral strategy that targets the viral-induced membrane fusion step can be adapted from HIV-1 to SARS-CoV. We suggest that MRET water consumption by patients can lead to the modification of dielectric permittivity, electrical conductivity and hydrogen bonding of water –based medium in the human body. It leads to the significant change of van der Walls interactions and hydrogen bonding, those results in the inhibition and interruption of proper formation of virus spike proteins chains. Such scenario obviously disables coronavirus life sequence of attachment and fusion with human cell membranes.

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