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A strategy for rapidly making a vaccine and treatment for the disease caused by the Wuhan-Corona Virus (WCV)

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Peptide vaccines have been successfully developed from identifying epitopes that induce antibodies in various diseases. (https://www.who.int/biologicals/vaccines/synthetic_peptide_vaccines/en).

The Wuhan seafood market pneumonia virus isolate Wuha-Hu-1 Corona genome has been completely sequenced. The possible coding has also been elucidated. NC_045512.2) (https://www.ncbi.nlm.nih.gov/nuccore/NC_045512)

An epitope search using the known epitopic sequences for other viruses and the tools available on (https://www.iedb.org/) has elucidated 184 possible similar epitopic peptide sequences coded by the Wuhan Corona Strain.

Most of these epitopes cluster in the Spike protein region of the WCS virus and are homologous to the SARS virus' Spike protein sequences.

Similar locations have been identified in various other viruses (Role of the Spike Glycoprotein of Human Middle East Respiratory Syndrome Coronavirus (MERS-CoV) in Virus Entry and Syncytia Formation

Zhaohui Qian, Samuel R. Dominguez, Kathryn V. Holmes Plos One, 11 October 2013 | Volume 8 | Issue 10 | e76469).

The 184 possible epitopic peptide sequences are listed in Excel tables (Supplementary File)

One or more of these epitopic peptide sequences can be used to induce an immune response if linked to larger immunogenic proteins or structures (see peptide vaccines above).

However, how can we identify the actual and not theoretical epitopic sequence that induces an immune response?

If one can get access to serum and isolate using staph A or staph G columns the antibodies in patients who have survived infection with the WCV, then one can map the binding sequence of these antibodies using recombinant phage display libraries (US patent 5,866,363 and New England Biolabs, phage display library protocols).

These methods will identify a specific peptide sequence which binds an antibody from patients having been infected by WCS. If this peptide sequence corresponds to the 184 identified here, then it gives one a certain sense of confidence that this is the specific peptide sequence part of the induction of the antibodies to the WCS.

This peptide sequence can then also be used as a target for a combinatorial library binding, amplification and purification. This will identify a peptide sequence which will bind the WCS directly. It will act as an antibody mimic but much smaller and can be used for targeting the WCS directly for treating the disease. Let's call this the complementary peptide (CP). CP can be linked to a ligand that can inactivate the WCS virus.

The above strategies can be effectuated within one month and are worth trying.

This paper is dedicated to the memory of Norton Zinder, GP's professor and colleague.

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