Review Article

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The First Identification of the Unique Epitope induced by COVID-19 Vaccines

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Introduction

The J&J vaccine was administered to over 2.3 million Americans. The J&J vaccine is a DNA adenovirus vector expressing the COVID-19 Spike protein. The Spike protein is 1.2 thousand amino acids long. The side effects of this vaccine are platelet suppression and blood clots. This was noted in 6 female patients. These 6 patients had antibodies which bound Platelet Factor Four protein (PL4). PL4 is 110 amino acids long. Given these numbers and assuming random nucleotide changes; then, one can calculate that a one nucletotide change (leading to a one amino acid change in the coding of the Spike protein's epitope) is responsible for the antibody binding to a PL4 epitope [1].

This is an example of a vaccine's side effects being a consequence of molecular mimicry. Using molecular mimicry one can then deduce which of the many possible epitopes on the surface of the Spike protein is the true epitope which actually induces the antibody response to the COVID-19 virus and, thereby, cross reacting with the platelets. There are over 184 possible epitopes on the COVID-19 surface [2].

No one has yet mapped or identified the actual unique binding sequence, on the COVID-19 surface, by the induced antibodies by all the vaccines being injected in the world's population. This mappng could have been done as described in Pieczenik's pioneering patents [3]. These patents describe the first combinatorial libraries that allow the complete mapping of monoclonal antibodies to their respective epitopes. However, this has not been done by anyone with any COVID antibodies. No one knows what the actual binding sequence on the COVID-19 virus surface which is induced by the spike protein vaccines.

What is the amino acid sequence on the COVID-19 virus and also the nucleotide change that allows the same antibody to bind PL4 and the COVID-19 surface; and, thereby, depress patient's platelets?

We have identified the amino acid sequences that are almost identical between the COVID-19 amino acid sequence and the Platelet Factor 4 amino acid sequence by using proprietary modifications of the NIH Blast amino acid comparison algorithm [4].

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PL4       5   ------AGFCAS----------------------------------
                    AG CAS
Cov1d19 661 CDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYS
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Having identified these similar sequences in both COVID-19 and PL4 proteins, I then checked to see if these amino acid sequences are known part of known epitopes on both the Spike protein and on Platelet Factor 4 protein using a proprietary modification of the Immune Data Base [5]. https://www.iedb.org/.

It turns out that both sequences are known epitopic sequences from other antibody binding experiments.

The epitopic sequence on the Spike protein is AGICAS. It appears 4 times in the Spike glycoprotein of SARS-COVID 2 ie the COVID-19 viral surface sequence.

The epitopic sequence on surface of the PL4 protein is AGFCAS. The difference can be accounted for by a one-nucleotide change in the coding of I to F or a transversion in the first nucleotide of their respective codons of a transversion of A to U. This is consistent with the predicted number discussed above. A peptide AGFCAS can block the mimicry and blood clots.

This is the first time one can actually identify, using molecular mimicry (a functional test), and the actual epitope, which induces the antibodies in the Spike protein vaccines. This inducing epitope

sequence has never been identified or known.

Now it is known. It is AGICAS. (ALA.GLY.ILE.CYS.ALA.SER) Molecular mimicry with vaccines is a known phenomena. However, it has never been used before to identify the actual binding sequence induced by a vaccine.

One published example of sequence comparisons, but not a functional test, is YQQQGRL which appears in the mumps virus nucleocapsid protein and MHC class II-associated invariant chain [6].

The author has identified proprietary mRNA coding for COVID-19, which would obviate these molecular mimicry side effects, induced by the antibodies the adenovirus vector J&J and Astra Zeneca vaccines and the other mRNA vaccines. His analysis is based on the Theory of Genotypic Selection and his work with Francis Crick, Sydney Brenner (discoverer of mRNA) and Sir Aaron Klug [7,8].

Acknowledgement

Professor Pieczenik is on a union arranged Furlough from Rutgers University, Department of Biochemistry and Microbiology, School of Environmental Biological Sciences, to protect his colleague's employment during this pandemic.

This paper is dedicated to the memory of Prof. William Ward, who recently passed away. We were colleagues in developing the Green Fluorescent Protein marker.

References

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