

Influence of amino acid exchange on the Covid 19 Spike protein an observation at the nuclear level by neutron espectrumetry.

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Abstract

With available databases, Laboratorio de Medidas Nucleares (LMN) from the Instituto de Engenharia Nuclear (IEN-CNEN-RJ), the neutron cross-sections of the Spike protein of SARS-COV-2 were calculated and verified, interferences of the substitution of some amino acids that lead to the appearance of virus variants.

1.Introduction

The spread of the virus, Covid 19 around the world from 2019, left a concern in health systems to develop vaccines in the short term and, some of them by modern and synthetic processes [1].

In recent research, variants or mutations of the virus have been discovered that are amenable to further study [2].

Conventional physicochemical techniques have been used and great advances have been made in the study of the dynamics of the process involving the interaction of the Spike protein with the host cell, a complementary technique to these, which can clarify differences found in other techniques are measurements with beams of neutrons of a nuclear reactor, thus we propose to use the neutron spectrometry technique developed at IEN using the Argonauta reactor, as a neutron source.

Neutrals are particles suitable for interacting with light elements such as hydrogen, and emphasize their presence compared to other heavier elements.

Thus, when measuring with good quality neutrons, important information is obtained from nuclear interactions that result in obtaining values of cross sections for neutrons, of the atoms in evidence, especially when dealing with hydrogenated materials or with hydrogen bridges as they exist in proteins which are basically composed of amino acids.

Some methods have been developed for this purpose and have been applied to deal with amino acids in relation to the nuclear parameter of the neutron cross section, database then available in the IEN for the necessary calculations to obtain quantitative values, which we hope are related or identify variants of the virus [3].

2. Materials, Methods and Procedures

The methods and techniques used to obtain cross sections when dealing with experimental measurements are the method of neutron transmission by the material, and the diffraction technique to define the neutron energy.

Regarding the theoretical values that are obtained in this work in the first instance, the methods of grouping and splitting (MPA) and the equivalence and similarity of cross sections (MES) method were used in the MPA, the portions that are the amino acids are added to to obtain the value of the cross-section of the protein.

The exchange of one amino acid for another can define a virus variant.

3. Results

Calculation of the Spike protein cross section.

Considering the values of cross sections obtained for the amino acids and values obtained from the literature, the molecular weight of the Spike protein is between 130k and 170k and that with amino acids distributed in 1150 positions.

An average cross-section value of 441 barn for amino acids can be estimated considering values of 188 barn for glycine, up to 672 barn for arginine.

Aminoacids	Cross-Sections(barn)	Differences(barn)
Fernylanin	453	17
Leucine	470	
Histidine	406	69
Valine	475	

Table 1. Differences found in the cross sections of two virus variants.

The sum of all amino acids resulted in an average value for the cross section of 441 barn, as if the protein were composed of amino acids in the same amount.

4. Conclusion and Discussions

These calculations show that, in order to identify a given virus variant, the neutron spectrometry system must have sensitivity to observe cross-section variations of 20 barn in 9K barn, ie, 1 / 450 percent.

For this we must know with greater certainty the amount of each amino acid that makes up the Spike protein and a more exact value for the molecular weight.

Our experimental measurements allow us to determine the cross-sections of isolated amino acids and those with similar chemical formulas, obtain the values of parts of the molecule, such as a radical or an attached molecular group.

However, Spike's samples would have to be pieces of the protein that include the amino acid exchange that results in the virus variant.

In a second step we would make experimental measurements to verify or compare with the calculated data.

These data can be used so that the differences between the Spike protein cross sections composed with the different identified amino acids can be identified.

This is an initial study to contribute to future research on virus variants.

References

[1] LiF.et al., 2015 Structure of SARS coronavirus Spike receptor-binding domain complexed with receptor. Science, 309:1864-1868

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[2] Frost, CDW, Magalis, BR & Kosakovsky Pond, SL Neutral Theory and rapidly evolving viral pathogens Mol.Biol.Evol.35, 1348-1354 (2018).

[3] Evaluation of Interference of Matrix in the Measurements of Neutron Cross Sections of Solutions Containing Aminoacids

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