SARS-CoV-2 501Y.V2 variants lack higher infectivity but do have immune escape

With the beginning of2020, the corona virus appeared, which led to great loss of life around the world so we had to understand what virus was and what change caused it and the solution to it.

Abstract:

The corona virus has led to some change resulting in many mutations, and experiments on these variants have shown that they don't prevent infertility in multiple cells, the rate of overstimulation as mice. Also as result of those experiment:

The monoclonal experiment was greatly reduce and the ability of serum neutralized and the reason for that neutralization was to link mutation in clone and its resistance.it indicated the possibility of effective variables penetrating antibodies and serums.

Introduction:

Corona virus is a member of the family that carries the largest genome among the RNA viruses and has a checking activity unlike other viruses. This activity, although it prevents them from mutating, but it show some mutations that increase the infection by increasing some of the molecules in protein (s), also appear as other mutations resulting from the antibodies stimulated by SARAS antibody through additional infection, such as vaccinations and linking the receptors, and those transforming the bodies into monoclonal antibody and transporter sera, and some mutations also appeared at the end of the first stage, which led to the spread of the disease significantly and the reason for the difference that was made reformatting it in the amino acid sequence between the different Corona strains, and by mean of amino acid mutation, it is possible to identify the variable that appeared as result of the deletion of a protein and compared to the original protein, it was found that there are four localized mutations of what previously noted for the biological importance of the research was based on pseudo type viruses and a model was formed as an element the assays were judged by analyzing the infection into hyper cellular cells and system-forming proteins. Anti-monoclonal anti-serum.

Related work:

That paper related to many works, each work talk on one point like software or biological data, the collection of that points make this paper, we will discussed some of these work.

The mutations resulting from the Corona virus varied and became transmissible and able to confront the antibodies and the functional response of the antibodies was measured with a powerful tool (Pseudotype neutralization assays: from laboratory bench to data analysis).

These mutations led to a decrease in the effect of the vaccine and from previous studies of those mutations we found that the infection did not change significantly, but it changed the antigen, and the evidence for this is that when it infected mice They had symptoms similar to the Coronavirus and there are some variables that neutralize the ability to bind to the RBD ,referenced paper about this

(Structural basis for neutralization of SARS-CoV-2 and SARS-CoV by a potent therapeutic antibody)this paper has result was:

biochemical and cellular studies it has been shown that (RBD) it prevents corona binding with cell receptors and resulted in highlighting the main role of antibody-based therapeutic interventions in treating Corona, the new paper talk the last paper and added advanced information on it as however the negative effect of (RBD) on the antibodies, that antibodies used in vaccines has the ability to neutralize and maintain the broadest spectrum possible to achieve against the escape of immunity, and thus these sites reduce the sensitivity of the virus. The immunity established early by the virus infection prevented the attack Again by means of the variables that can have a role in immune responses and by monitoring and analyzing them genetically, it clarifies the prevention and control measures against Corona and there are tools used to visualize gene and protein expression data in heat maps and can be recolored and recycled in a dedicated way and provides multiple collection methods for data analysis the software can used for this action

And there are many reference like:

https://www.medrxiv.org/content/10.1101/2020.10.25.20219063v1.abstract

https://science.sciencemag.org/content/369/6511/1603.abstract

In this paper some software are used like (graphpad prism, Microsoft office, heat map referenced paper about this software (HemI: a toolkit for illustrating heatmaps),bio edit, Pymol , ---)

Methodology:-

They studied the possible effects of infection with variants associated with 50 ly-v2 and exposed some cells to pseudotype virus infection. It was noticed that the number of infections in cell lines did not increase. Therefore, they distinguished viruses (which are receptors for many mammals expressing individual plasmid cells containing genes of 14 species) and between the infection. For pseudotype viruses and their presence, all of them are susceptible to SARS infection, so they used the infection of the reference variant as a control element, and then they challenged the receptors of 18 types of pseudotype viruses and did not discover any improvement, and then they noticed that there were three single-residue variants, respectively Rbd that increased the infection to fold What it was, and from here, they intensified efforts around the identification of the serum and they targeted Rbd with 17 types of monoclonal antibodies that led to a decrease in the neutralization of the virus, and they identified from that step on the areas of immune escape and they used a heat map of the interactions of the only antibodies to facilitate the experiments on them and found that the number of mutations is very large And counter-charity is unable to cope, so they made long proverbs that contain polyclonal antibodies and a fortress. And here is Rbd and they added some samples from ten patients and some other ingredients and focused on targeting mutations because they found the immune escape spectrum to be too large

Result:-

They relied on some mutations to create a standard for calculating the viral version number and the plasmid is that criterion. So what did the plasmid answer to the mutation first thing to be able to get it, they inserted an antioxidant codon into eukaryotes and built 14 types of plasmids from different

organisms and each gene of these types is considered to be a codon enhancer Each complex sequence was inserted into the expression vector in eukaryotes to obtain plasmids of different types and after making them increased their number until it became 18 of the type mutated by point mutations and digestion of the polymerase chain reaction led to the classification of bacteria and exclusion of some variables to ensure the integrity of the mutations and they prepared the hypercellular cells in A specific temperature and a specific medium, in addition to preparing the pseudotype viruses sars_cov-2 and for the point mutation, 18 viruses were produced of them, where the first built 10 of them using site mutations in some variables and built three main variables in linking the virus to the cell's receptor, including soly-v2_3, which is part of the composition of Rbd, which is more Variables complex in the SARS molecule that have been discovered to help determine whether cognitive effects and synergies have been conferred. Yeh side by side with the emergence of these three mutations in the double Rbd and others. 18 viruses of the pseudotype were formed and used in experimental infection tests with some purified sera, and by that they extracted a quantitative measurement of the viruses and obtained the virus DNA by copying the reverse, and the plasmid was used as a standard to calculate the viral version number After that, they carried out some neutralization tests to assess the effects of monoclonal antibodies and the pseudotype by detecting the decrease in gene expression.

The main result is the discovery of the genetic makeup of the virus by reverse transcription, the discovery of a criterion for calculating the number of the viral version, and the creation of a scale to evaluate the effects of the antibodies, and through them, they found the best antibodies that should be used in the recovery serum, and the convalescent serum was manufactured.