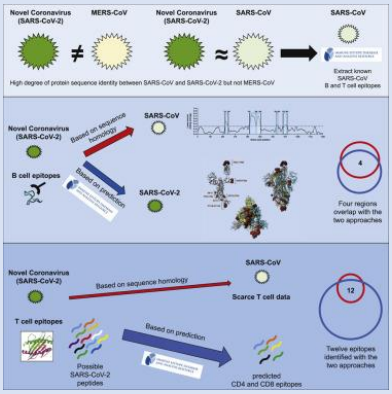
A SEQUENCE HOMOLOGY AND BIOINFORMATIC APPROACH CAN PREDICT CANDIDATE TARGETS FOR IMMUNE RESPONSES TO SARS-COV-2

Abstract:

The Immune Epitope Database and Analysis Resource (IEDB) is used to catalog available data related to other coronaviruses- SARS-CoV-, as there is limited information about (SARS-CoV-2) and the high sequence similarity between them

by identification of specific regions will facilitate effective vaccine design against this virus of high priority.



Keywords:

SARS-CoV; COVID-19; SARS-CoV-2, coronavirus; T cell epitope; B cell epitope; infectious disease; sequence conservation.

Introduction:

we used the IEDB and ViPR resources to compile known epitope sites from other coronaviruses, map corresponding regions in the SARS-CoV-2 sequences, and predict likely epitopes. We also used validated bioinformatic tools to predict B and T cell epitopes that are likely to be recognized in humans and to assess the conservation of these epitopes across different coronavirus species.

Limited information is currently available on which parts of the SARS-CoV-2 sequence are recognized by human immune responses but there is a significant body of information about epitopes for coronaviruses in general, and in particular for BETACORONAVIRUSES like SARS-CoV and MERS-CoV, which cause respiratory disease in humans.

1- Ten experimentally defined regions within SARS-CoV have high homology with SARS-CoV-2.

2-Parallel bioinformatics predicted potential B and T cell epitopes for SARS-CoV-2.

3-Independent approaches identified the same immunodominant regions.

4-The conserved immune regions have implications for vaccine design against multiple CoVs.

Related work:

The Immune Epitope Database and Analysis Resource (IEDB) is a database of epitope-related material curated from clinical literature in the sense of infectious disease, allergy, and autoimmunity (Vita et al., 2019).

The Immune Epitope Database (IEDB, iedb.org) collects experimental evidence contained in scientific literature statistics, text, and charts, making it freely accessible and readily searchable to the public. The IEDB covers immune epitope evidence from all organisms examined and contains antibody, T cell, and MHC binding contexts consistent with bacterial, allergic, autoimmune, as well as transplant-related diseases After being publicly available for more than a decade, the IEDB's recent emphasis has been on enhanced query and reporting capabilities to satisfy our users' needs to view and summarise data that continues to increase in quantity and complexity. We have an update on our existing activities and strategic goals in this section.

In addition, the IEDB offers bioinformatic methods and algorithms for analysing epitope data and predicting possible epitopes from novel sequences. The Virus Pathogen Resource (ViPR) is a complementary repository of knowledge about human pathogenic viruses that combines genome, gene, and protein sequence information with information about immune epitopes, protein structures, and host

The Virus Pathogen Database and Analysis Resource (ViPR, www.ViPRbrc.org) is an interactive archive of data and analysis resources for various virus families funded by the NIAID Bioinformatics Resource Centers (BRC) network. ViPR provides details on human pathogenic viruses from the Arenaviridae, Bunyaviridae, Caliciviridae, Coronaviridae, Flaviviridae, Filoviridae, Hepeviridae, Herpesviridae, Paramyxoviridae, Picornaviridae, Poxviridae, Reoviridae, Rhabdoviridae, and Togaviridae virus families are currently supported, with hopes to add more virus families in the future. ViPR collects a variety of data, including sequence records. Annotations to genes and proteins, 3D protein structures, immune epitope locations, clinical and surveillance metadata, and novel data obtained from comparative genomics research are all available. There are also methods for metadata-driven statistical sequence analysis, multiple sequence alignment, phylogenetic tree building, BLAST comparison, and determining sequence variance. Workflows for data filtering and interpretation may be mixed, and the results stored in personal 'Workbenches' for future use. ViPR instruments and data are provided free of charge to the virology scientific community in order to aid in the creation of diagnostics, prophylactics, and therapeutics for priority pathogens and other viruses.

While no epitope data for SARS-CoV-2 are currently available, there is a substantial body of knowledge about coronavirus epitopes in general, and especially for Betacoronaviruses such as SARS-CoV and MERS-CoV, which cause respiratory disease in humans (de Wit et al., 2016, Song et al., 2019).

Coronaviruses (CoVs) were previously thought to be relatively harmless respiratory pathogens in humans. However, as a result of zoonotic CoVs breaching the species boundary, two cases of severe respiratory tract infection caused by the serious acute respiratory syndrome coronavirus (SARS-CoV) and the Middle East respiratory syndrome coronavirus (MERS-CoV) caused elevated pathogenicity and morality rates in human population. This drew international attention to CoVs and emphasised the importance of monitoring infectious diseases at international boundaries. In this study, we concentrate on our current understanding of the epidemiology, pathogenesis, prevention, and treatment of SARS-CoV and MERS-CoV, as well as the critical structure and role of the spike proteins (S proteins) on the surface of each of the viruses. We compare existing pathogenesis-replicating animal models and summarise the possible function of host receptors in leading to complex host affinity in different organisms. We summarise the study that remains to be done to thoroughly understand the pathogenic mechanism of these viruses, to

create reproducible animal models, and, finally, to establish countermeasures to defeat not only SARS-CoV and MERS-CoV,but also these emerging coronaviral diseases.