

CORONA VIRUS AND ITS MORPHOLOGY

A. Sai Sowmya
Bachelor of Arts, II year
Little Flower Degree College, Uppal
sowmyaakkumahanty@gmail.com

Abstract

Viruses are non cellular, non living infectious agents that are composed of **nucleoproteins** which can multiply inside animal, plant, or bacterial cell. It causes widespread diseases in humans such as common cold, influenza etc, although most viral infections do not result in death. The most recently discovered corona virus causes Corona virus disease COVID-19. The aim of this research is to find the structural design on virus. Before 2003, there were only 10 corona viruses with complete genomes available. After the SARS epidemic, up to Dec 2008, there was an addition of 16 corona viruses with complete genomes sequenced. The present evidence supports that bat Coronaviruses are the gene pools of group 1 and 2 corona viruses, whereas bird coronaviruses are the gene pools of group 3 coronaviruses. There are many ongoing clinical trials evaluating potential treatments. World Health Organization is trying to develop vaccines and medicines to prevent COVID-19. The best way to prevent and slow down transmission is be well informed about the COVID-19 virus, the disease it causes and how it spreads. This research entails construction and diverseness of Coronavirus.

Keywords: Nucleoproteins, SARS, Transmission, COVID, WHO.

Introduction

Viruses are very small, infectious, obligate intercellular parasites. They are cellular and lack metabolism of their own. Structurally they are very simple, with a nucleic acid core protected by a protein capsid. Viruses can be crystallized. Viruses are grouped according to their shared properties and are classified by ICTV system of classification. Viruses are best described as infectious particles. The genome size of this virus is about 30 kb and encodes structural and non-structural proteins like other corona viruses. There is very little known actually about the pathogenesis of the virus; therefore, an immune informatics-based approach to investigate the immunogenic epitopes and vaccine design using data from proteins sequencing of the COVID-19 is required. Largest virus is vaccinia virus and pox virus. All viruses consist of two basic components: a core of nucleic acid that forms the **genome** and the surrounding coat of protein known as **capsid**. The viral genome is replicated and directs the synthesis of other virion components by cellular systems of other virion components. A virus particle contains a single type of nucleic acid, either DNA or RNA. Viruses are obligate intracellular parasites, they cannot multiply unless they invade a specific host cell and instruct its genetic and metabolic machinery to make and

ANNQUEST(9)-1:1-5

release daughter or progeny viruses. In this process, they destroy the host cells causing serious damage and disease in humans, plants and animals. The study of viruses is called Virology.

Corona in Latin means crown, the virus has projections like a crown hence it is called so. Corona viruses are a large family of viruses which may cause illness in animals or humans. In humans, several corona viruses are known to cause respiratory infections ranging from the common cold to more severe diseases such as Middle East Respiratory Syndrome and severe Acute Respiratory Syndrome.

The virus and disease were unknown before the outbreak began in Wuhan, China, in December 2019. There are several ongoing clinical trials of both western and traditional medicines. World Health Organization is trying to develop vaccines and medicines to prevent the COVID-19.

Humans have long been infected by corona virus as it is one of those responsible for the common cold. It is a contagious viral infection that can be spread through inhalation or ingestion of viral droplets as a result of coughing and sneezing and touching infected surface. Studies have shown that COVID-19 virus can survive up to 72 hours on plastic and stainless steel, less than 4 hours on copper and less than 24 hours on cardboard.

Structure

COVID-19 is a spherical or pleomorphic enveloped particles containing single-stranded RNA associated with a nucleoprotein within a capsid comprised of matrix protein. The envelope bears

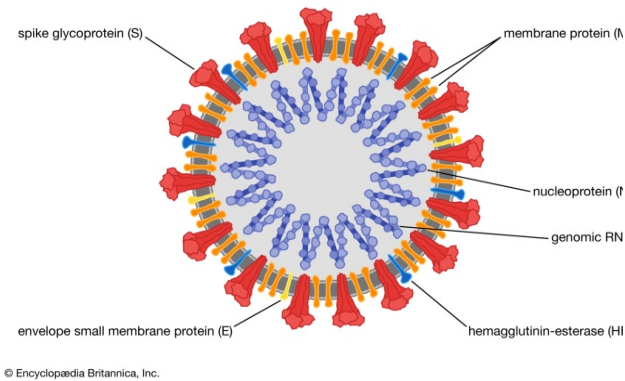
club shaped glycoprotein projections. Some corona viruses also contain a hemagglutinin-esterase protein. Coronavirus possess the largest genomes among all known RNA viruses, with G+C contents varying from 32% to 43%. After the viruses enter the host cell and uncoats, the genome is transcribed and then translated. Coronavirus genome replication and transcription takes place at cytoplasmic membranes and involve coordinated processes of both continuous and discontinuous RNA synthesis that are mediated by the viral replicase, a huge protein complex encoded by the 20-kb replicase gene. A typical CoV contains at least six ORFs in its genome. All the structural and accessory proteins are translated from the sgRNAs of CoVs. Four main structural proteins contain spike(S), membrane (M), envelope(E), and nucleocapsid(N) proteins are encoded by ORFs 10, 11 on the one-third of the genome near the 3'-terminus. These mature proteins are responsible for several important functions in genome maintenance and virus replication.

There are three or four viral proteins in the coronavirus membrane. The most abundant structural protein is the membrane (M) glycoprotein; it spans the membrane bilayer three times. The spike protein (S) as a type I membrane glycoprotein constitutes the peplomers. In fact, the main inducer of neutralizing antibodies is S protein. In the presence of tunicamycin corona virus grows and produces spike less, noninfectious virions that contain M but devoid of S.



ANNQUEST(9)-1:1-5

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)



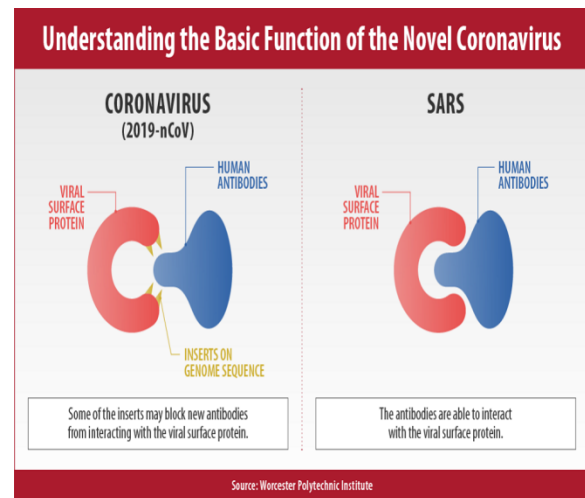
Classification

At present the **International Committee on Taxonomy of Viruses (ICTV)** regulates the norms of classification and nomenclature of viruses. The ICTV scheme has only three hierarchical levels – the **Family, Genus and Species**. The family names end with the suffix 'viridae' while the genus names with 'virus' and the species names are common English expressions describing their nature. Viruses are named after the disease they cause. Using the ICTV system, the virus that causes Acquired Immune Deficiency Syndrome (AIDS) in human beings is classified as Family: Retroviridae, Genus: Lentivirus, Species: Human Immune deficiency Virus (HIV). Example: Coronavirus.

Professor Dmitry Korin and Colleagues reconstructed 3D model of novel coronavirus; findings to provide research community with greater understanding of infection spread and possible treatment.

A Worcester Polytechnic Institute (WPI) has created and unveiled a structural 3D Road map of the new corona virus (2019-nCoV), a major development that potentially holds the key to understanding the spread and treatment

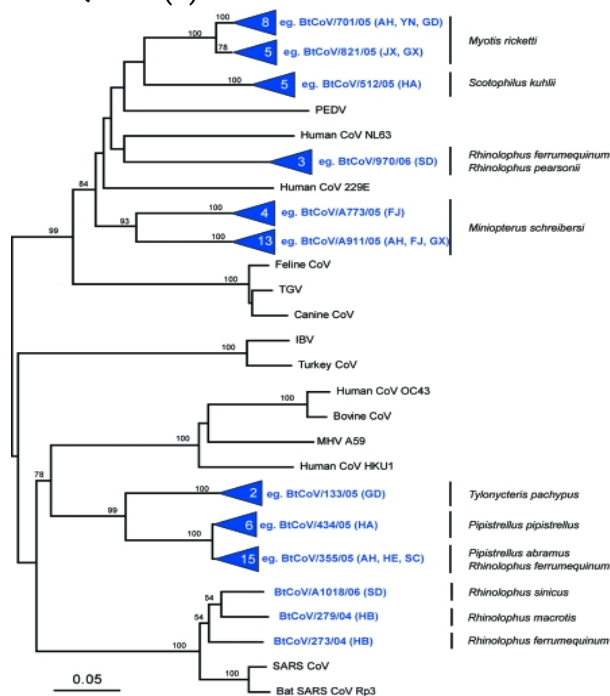
of the deadly virus.(figure1)



Korin and his team used existing public databases to identify Syndrome (SARS), a virus identified in three different isolates, or specimens, in Severe Acute Respiratory Syndrome (SARS), a virus identified in 2003 that also caused worldwide infection and significant deaths. These could be the source of the new virus. According to the World Health Organization, there have been more than 40,000 cases worldwide, with more than 900 deaths, mostly in China-numbers that have been increasing daily as international agencies work to stem the spread of the virus, which began in Wuhan, China, in late December.

Diversity:

ANNQUEST(9)-1:1-5



Phylogenetic relationships of 64 coronaviruses isolated from bats in china. The tree was generated based on 440 nucleotides of the RNA-dependent RNA polymerase region by the neighbor-joining bootstrap values (percent) calculated from 1000 bootstrap replicates. Terminal nodes containing bat coronaviruses isolated in this study are collapsed and represented by a blue triangle with the number of viruses indicated within. (comment 4; refernce need to be added)

Group 1 Coronaviruses (Alphacoronavirus)

Although it has been proposed that group 1 coronaviruses can be subdivided into groups 1a and 1b based on phylogenetic clustering of group 1a coronaviruses and >90% overall genome identity among the members of this subgroup, no additional genomic evidence, such as gene contents, transcription regulatory sequence (TRS) or other unique genomic features, as in the subgroups in groups 2 and 3

coronaviruses. For the group 1b coronaviruses, in addition to the lack of common genomic features, there is no phylogenetic clustering. Therefore, the group 1b coronaviruses are in fact “non-group1a” coronaviruses, rather than having common features that make them a distinct lineage.

Although the present sub-classification of group 1 coronaviruses into groups 1a and 1b may not be ideal, the best documented example of generation of corona virus species through homologous recombination is present in group 1a coronavirus, which is the generation of FCoV type II strains by double recombination between FCoV type I strains and canine coronavirus. It was originally observed that the sequence of S in type II FCoV was closely related to that of CCoV(43, 44) but the sequence downstream of E in type II FCoV was closely related to that of type I FCoV(45,46). This suggests that there may have been a homologous RNA recombination event between the 3' ends of the genomes of CCoV and type I FCoV, giving rise to a type II FCoV genome.

Group 2 Coronaviruses (Betacoronavirus)

Among the three groups of coronaviruses, the greatest improvement in our understanding in coronaviruses phylogeny lies in group 2 coronaviruses. Before the discovery of SARS-CoV, group 2 coronaviruses were considered to include one lineage, with all members possessing haemagglutinin esterase genes and two papain-like proteases in nsp3 of ORF1ab. When SARS-CoV was first identified and its genome sequenced. After more extensive analyses of the amino-terminal domain of S of SARS-CoV were first identified domain of S of SARS-CoV,

ANNQUEST(9)-1:1-5

it was observed that 19 out of 20 cysteine residues were spatially conserved with those of the consensus sequence for group 2 coronaviruses (50). In 2006 and 200, proposed two additional subgroups of group 2 coronaviruses: group 2c and group 2d (33). These two subgroups form two unique lineages, most closely related to, but distinct from group 2a and group 2b coronaviruses. In addition to phylogenetic evidence, there is also clear-cut evidence from gene contents and other genomic features that four subgroups exist in group 2 coronaviruses.

Extensive homologous and heterologous recombination events have been documented in both human and animal group 2 coronaviruses, which has led to the generation of various genotypes and strains within a coronavirus species, as well as acquisition of new genes from other non-coronavirus RNA donors. Among the coronaviruses, MHV is one of the most extensively studied examples of homologous recombination in coronaviruses, and is also the coronavirus in which homologous recombination was first observed.

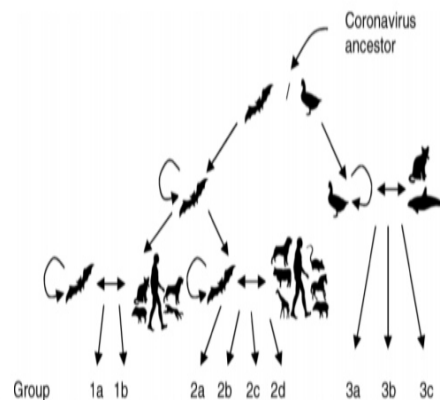
Group 3 Coronaviruses (Gammacoronavirus)

Dramatic improvement in our understanding of the diversity and phylogeny, and potential interspecies jumping, of group 3 coronaviruses occurred in the last year. Since its discovery in 1937, IBV has been the only species of group 3 coronavirus for over 50 years. In the last decade of the last century and the first few years of the 21st century, a few IBV-like viruses, including TCoV have been described in various species of birds with some of

their genomes sequenced (36, 67-69). The sizes, G+C contents, and genome organizations of their genomes were similar.

SWI was discovered from the liver tissue of a dead beluga whale (28). It was the first reported group 3 mammalian coronavirus with complete genome sequence and was phylogenetically distantly related to IBV.

The novel subgroup of avian coronaviruses, group 3c coronavirus, that we recently described consisted of at least three members (BuCoV HKU11, ThCoV hku12, and MuCoV HKU13), infecting at least three different families of birds. These coronaviruses were distantly related to IBV and SWI. Most interestingly, these three **avian coronaviruses** were also clustered with a coronavirus recently discovered in the Asian leopard cat (ALC-CoV).



A model of coronavirus evolution

Coronaviruses in bats are the hypothesized gene pool of group 1 and group 2 coronaviruses and coronaviruses in birds are the hypothesized gene pool of group 3 coronaviruses.

In the past six years of the 21st century, we have witnessed a drastic

ANNQUEST(9)-1:1-5

increase in the number of coronaviruses discovered and coronavirus species and genomes, we are starting to appreciate of coronavirus. Detailed analysis and structures, as well as the receptors for the individual coronaviruses, will enable rational design of experiments to understand the secret behind interspecies jumping at the molecular level.

[researcher-shares-3d-roadmap-coronavirus-scientists- worldwide](#)

Conclusion

There are several drugs against SARS-CoV, MERS-CoV tested in animals, and infected viral cell in lab and protein vaccines. These investigations are in progress but it takes years to develop the vaccines for COVID-19. So far, the infected patient's is growing rapidly. Coronavirus pathogenesis is best understood by discriminating how each of these variables dictates clinical outcomes. Diversity of coronavirus surface proteins likely contributes to epidemic disease, timely topic given the recent emergence of the human SARS coronavirus. These structure predictions have not yet been experimentally verified, but that hope is that by accelerating their release they may contribute to the scientific community understands of how the virus functions and experimental work in developing future treatments.

References

1. <https://www.tandfonline.com/doi/full/10.1080/07391102.2020.1756411?src=ecsys>
2. <https://jvi.asm.org/content/82/5/2515>
3. <https://www.wpi.edu/news/wpi->

