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RESEARCH ARTICLE OPEN ACCESS

Molecular Structure and Some Properties of Viruses

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ABSTRAC

The paper involves general information about the general characteristics of viruses and the types of diseases and harms they cause. It also provides information about the molecular structure of viruses and the importance of DNA or RNA, which is the genetic information, in causing disease, and the important role that prions play in maintaining the infectivity of the virus.

Keywords: Viruses, prions, polymers, morphology, hepatitis virus, COVID-19.

INTRODUCTION

Although both bacteria and viruses can harm our bodies, they differ biologically. Bacteria are small, single-celled organisms considered living because they can reproduce without needing a host cell. Due to these differences, diseases caused by bacteria and viruses are treated differently. For example, antibiotics are only effective against bacteria, not viruses.

Viruses are tiny, infectious structures that can only reproduce by infecting a host cell. They invade host cells and use them as a resource to produce new viruses. Because viruses cannot reproduce without a host organism, they are not considered living organisms. They also do not have cells of their own: viruses are much smaller than living cells and are made up of proteins and nucleic acids.

However, viruses do have some characteristics similar to living, cell-based organisms. For example, like us, they also possess genetic material in the form of nucleic acids and have a genome. Additionally, they are highly diverse and have the ability to evolve. Although viruses do not display all the characteristics of life, they are still considered a “questionable” form of life [4].

Viruses are microscopic, infectious agents that can replicate only by infecting a host cell. They hijack the host’s cellular machinery to produce new virus particles, utilizing the cell’s resources for their own replication. Because they are incapable of independent reproduction without a host, viruses are generally not classified as living organisms. Moreover, viruses lack cellular structure; they are significantly smaller than living cells and are composed primarily of proteins and nucleic acids.

Despite this, viruses exhibit several traits similar to those of cellular life forms. For instance, they contain genetic material—either DNA or RNA—organized into a genome, and their replication is governed by a genetic code similar to that of living organisms. Furthermore, viruses are highly diverse and possess the ability to evolve over time. Although they do not fulfill all the criteria typically associated with life, viruses remain a subject of ongoing scientific debate regarding their classification as living or non-living entities.

Virology is the study of viruses and virus-like agents, including, but not limited to, their taxonomy, disease-producing properties, cultivation, and genetics. Virology is often considered a part of microbiology or pathology. During the early years of virology, this discipline was dependent upon advances in the chemical and physical sciences; however, viruses soon became tools for probing basic biochemical processes of cells. Viruses have traditionally been viewed in a rather negative context as agents responsible for diseases that must be controlled or

eliminated. However, viruses also have certain beneficial properties that can be exploited for useful purposes, as is evident in both gene therapy and vaccinology.

In general, viruses contain only one type of nucleic acid (either DNA or RNA) that carries the information necessary for viral replication. Nevertheless, it is clear now that some viruses contain other nucleic acid molecules; for example, in retroviruses, cellular transfer RNAs are essential for the action of the enzyme reverse transcriptase.

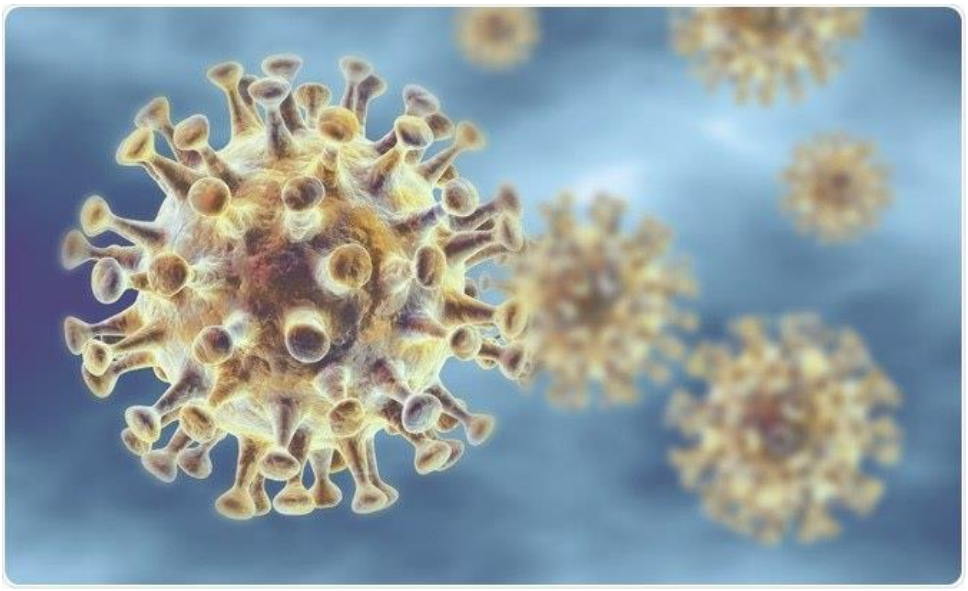
The chemical composition of viruses varies between different virus families. For the simplest of viruses, the virion is composed of viral structural proteins and nucleic acid; however, the situation becomes more complex with when dealing with enveloped viruses. The latter types of viruses mature by budding through different cellular membranes that are modified by the insertion of viral proteins. Several properties should be considered most important in constructing a scheme for the classification of all the viruses. These include the nature of the nucleic acid present in the virion, the symmetry of the protein shell, dimensions of the virus particle, as well as the presence or absence of a lipid membrane.

The International Committee on Viral Taxonomy (ICTV), which was given the task of developing a universal taxonomic scheme for all the viruses, has put an emphasis on the viral genome, which is a blueprint for producing new virusesm as a basis of all classification decisions. In formal virus taxonomy, families, subfamilies, and genera are always written in italics, with the first letters of the names capitalized. Instead of formal names (e.g. Parvoviridae), common names are often used for viruses, as can be seen in the various different kinds of medical literature (e.g. parvoviruses) [1].

Theoretical bases. Even from the earliest times, it was clear that the filterable agents could not be cultivated on artificial media. Even today, virus isolation in cell culture is still considered the gold standard against which other assays must be compared.

Still, the most obvious method of virus detection and identification is direct visualization of the agent. The morphology of most viruses is sufficiently characteristic to identify the image as a virus and to assign an unknown virus to the appropriate family (Picture.1). Furthermore, certain non-cultivable viruses can be detectable by electron microscopy. The culture of animal cells typically involves the use of a culture medium containing salts, glucose, vitamins, amino acids, antimicrobial drugs, buffers, and, typically, blood serum, which provides a source of necessary cellular growth factors. For certain cell-lines, defined serum-free media have been developed, which contain specific growth factors without requiring the addition of blood serum into the medium.

Serological tests are used to show the presence or absence of antibodies to a specific virus. The presence of certain antibodies indicates exposure to the agent, which may be due to a current clinical condition or as a result of an earlier unrelated infection. Some tests that can be used to identify viral antibodies include hemagglutination, complement fixation tests, radioimmunoassays, immunofluorescence, enzyme-linked immunosorbent assay (ELISA), radioimmune precipitation, and Western blot assays.



Picture 1. The morphology of virus.

Molecular techniques such as polymerase chain reaction (PCR) are also widely used for both the detection of an active virus as well as to determine whether any antibodies against the virus are present. Some of the different applications of PCR tests can be found in diagnostic clinical virology, as well as for research purposes. The use of such nucleic acid-centered technology offers substantial advances in the detection of viruses and can be further enhanced with the incorporation of certain nucleic acid hybridization techniques [2].

We look at some Hepatitis virus kinds in the below.

Hepatitis C is caused by hepatitis C virus (HCV), which has a 50-nm enveloped virion that contains a single strand of linear RNA. HCV is a member of the family Flaviviridae. It is transmitted by use of contaminated needles (drug use, tattoo parlors), by in utero transmission from mother to fetus, or through organ transplantation. It is rarely sexually transmitted because HCV requires blood-to-blood contact. Screening for HCV is performed by detection of anti-HCV antibodies. Positive results are then confirmed by HCV nucleic acid amplification to determine viral load. Worldwide, hepatitis C has reached epidemic proportions, with about 70 million people chronically infected. In the United States, HCV is the most common chronic blood-borne infection; approximately 3 million persons are chronically infected and 20,000 new cases occur annually. Like HBV, HCV infection can cause hepatocellular carcinoma. HCV is currently the leading reason for liver transplantation in the United States. There are six major genotypes with genotype 1 the most common, followed by genotype 3. Treatment for genotype 1 disease is with the drug combination of sofosbuvir (a nucleotide analogue polymerase inhibitor) and ledipasvir (an HCV replication inhibitor). A 12-week treatment with this drug combination results in complete cure of the virus from the host. Other genotypes are also usually treated for 12 weeks with sofosbuvir, coupled with velpatasvir, which has a similar mechanism to ledipasvir.

Hepatitis delta virus (HDV) was discovered in 1977 and the disease hepatitis D was designated. There are eight known genotypes of HDV: Genotype 1 has a worldwide distribution; genotypes 2 and 4 exist in East Asia; genotype 3 is found in South America; and genotypes 5 through 8 are in Africa. All genotypes can cause acute as well as chronic liver disease. HDV is a satellite virus that is dependent on hepatitis B virus to provide the surface protein (HBsAg) for its own replication. HDV's dependence on HBV means that HDV only replicates in liver cells coinfected with actively replicating HBV. HDV is spread only to persons who are already infected with HBV (superinfection) or when HBV and the satellite are transmitted together (coinfection). The negativestrand RNA of HDV is smaller than the RNA of the smallest picornaviruses, and its circular conformation differs from the linear structure typical of animal negative-strand RNA viruses. The primary laboratory tools for diagnosis of an HDV infection are serological tests for anti-HDV antibodies. Treatment of patients mirrors that of HBV-infected patients. About 5% of all those with hepatitis B are coinfected with HDV. Prevention and control involve

the widespread use of the hepatitis B vaccine.

Hepatitis A. Hepatitis A (infectious hepatitis) usually is transmitted by fecal contamination of food or drink, or shellfish that live in contaminated water. The disease is caused by hepatitis A virus (HAV) of the genus Hepatovirus in the family Picornaviridae. Recall that while all hepatitis viruses can cause liver disease, they are not taxonomically related (table 37.1). HAV is an icosahedral, linear, positive-strand RNA virus that lacks an envelope. Once in the digestive system, the virus multiplies within the intestinal epithelium. Usually only mild intestinal symptoms result. Occasionally viruses are found in the blood (viremia) and may spread to the liver. The virus reproduces in the liver, enters the bile, and is released into the small intestine. This explains why feces are so infectious. After about a 4-week incubation period, symptoms develop that include anorexia, general malaise, nausea, diarrhea, fever, chills, and jaundice. Most cases resolve in 4 to 6 weeks and yield a strong immunity, although some patients relapse, exhibiting symptoms for 6 months or more. The mortality rate is low (less than 1%), and about 40 to 80% of the U.S. population has antibodies, though few are aware of having had the disease. Control of infection is by simple hygienic measures, the sanitary disposal of excreta, and the HAV vaccine. The number of new cases has been dramatically reduced since the introduction of the hepatitis A vaccine in the 1990s. This vaccine is recommended for travelers (see table 35.2) going to regions with high rates of hepatitis A.

Hepatitis E. Hepatitis E caused by hepatitis E virus (HEV) genotypes 1 and 2 is implicated in many epidemics in countries with limited clean water and sanitation, while genotypes 3 and 4 are found in Europe and, to a lesser extent, the United States. The single, positive-strand RNA viral genome (7,900 nucleotides) is linear. The virion is spherical, nonenveloped, and 32 to 34 nm in diameter (table 37.1). Infection with HEV genotypes 1 and 2 usually is associated with feces-contaminated drinking water, whereas genotypes 3 and 4 are transmitted by contaminated food (particularly undercooked pork). HEV enters the blood from the gastrointestinal tract, replicates in the liver, is released from hepatocytes into the bile, and is subsequently excreted in the feces. Like hepatitis A, an HEV infection usually runs a benign course and is selflimiting. The incubation period varies from 15 to 60 days, with an average of 40 days. The disease is most often seen in patients who are 15 to 40 years of age. Children are typically asymptomatic or present mild signs and symptoms, including abdominal pain, anorexia, dark urine, fever, enlarged liver, jaundice, malaise, nausea, and vomiting. Case fatality rates are low (1 to 3%), except for pregnant women (15 to 25%), who risk death from fulminant hepatic failure. Diagnosis of HEV infection is by detection of anti-HEV antibodies or reverse transcriptase PCR. There are no specific measures for preventing HEV infections, other than those aimed at improving the level of health and sanitation in affected areas.

Ebola Virus and Marburg Diseases

Ebola virus disease (EVD) is caused by Ebola viruses, first recognized near the Ebola River in the Democratic Republic of the Congo in Africa. They are members of the genus Ebolavirus in the family Filoviridae, a group of filamentous, negative-strand RNA viruses (figure 37.23). Six Ebola species are known: Sudan ebolavirus, Tai Forst ebolavirus (formerly Côte d'Ivoire ebolavirus), Bundibugyo ebolavirus, Zaire ebolavirus, Bombali ebolavirus, and Reston ebolavirus. Members of the first five species cause disease in humans. The sixth, Reston ebolavirus, was first discovered in 1989, and to date Reston viruses have caused disease only in nonhuman primates and pigs. Only Reston virus is spread by aerosol transmission. All Ebola virus that infect humans are transmitted by contact with body fluids. Convalescing patients continue to harbor virus in body fluids and in rare instances there has been sexual transmission through infected semen up to 17 months after recovery. Bats are thought to be the natural reservoir for Ebola viruses, although the exact species is not known.

Viral hemorrhagic fever (VHF) is the term used to describe the severe, multisystem syndrome seen in Ebola epidemics. Because the host vascular system is damaged, vascular leakage of fluids into body tissues accompanied by the blood's diminished ability to clot (coagulopathy) occurs. The incubation period for EVD ranges from 2 to 21 days and is characterized by abrupt fever, headache, joint and muscle aches, sore throat, and weakness, followed by diarrhea, vomiting, and stomach pain. Signs of infection include fever, rash, red eyes, bleeding, and hiccups—symptoms alerting of internal hemorrhage. There is no standard treatment for Ebola infection. Patients receive supportive therapy consisting of balancing patients' fluids and electrolytes, maintaining their oxygen status and blood pressure, and treating any complicating infections. Convelscent sera, collected from Ebola survivors, and experimental antibody cocktails demonstrated promising

success in the 2014 treatments of ebolaviruspatients. A highly effective vaccine is now used to control outbreaks.

Marburg disease is caused by a genetically unique RNA virus also in the Filoviridae family. Marburgvirus (MARV) similarly causes a hemorrhagic fever. It is a rare, severe type of hemorrhagic fever that affects both humans and nonhuman primates. MARV was first recognized in 1967, when outbreaks of hemorrhagic fever occurred simultaneously in laboratories in Marburg and Frankfurt, Germany, and in Belgrade, Serbia. The first people infected had been exposed to African green monkeys or their tissues. MARV is indigenous to Africa, and the reservoir host of MARV is the African fruit bat, Rousettus aegyptiacus. The average incubation period for Marburg hemorrhagic fever is 5 to 10 days. The disease symptoms are abrupt, marked by fever, chills, headache, myalgia, and a maculopapular rash (i.e., discolored with bumps). Nausea, vomiting, chest pain, sore throat, abdominal pain, and diarrhea may also occur in infected patients. Symptoms become increasingly severe and may include jaundice, delirium, liver failure, pancreatitis, severe weight loss, shock, and multiorgan dysfunction [3].

CONCLUSION

Human immunodeficiency virus (HIV) is pandemic. HIV has also brought changes that are not so obvious. For example, HIV research led to much of our current understanding of the immune system, which in turn is yielding new and promising cancer treatments. HIV disrupted the pharmaceutical industry as developing nations began manufacturing their own life-saving antiretroviral drugs that were otherwise too expensive to provide to their citizens.

Viruses have significant biological and economic importance. They cause numerous diseases, including HIV/AIDS, influenza, COVID-19, and other infectious illnesses in humans. In animals, viruses can also harm livestock and forest plants. Viruses play an important role in ecosystems as well, as they help regulate the growth and decline of certain plant and animal populations [5].

In addition, viruses are used as valuable tools in biotechnology—for example, in genetic modification, vaccine production, and other scientific research.

The taxonomy of viruses is of great importance because it provides a framework that places and connects all viruses according to their clinical, biological, and evolutionary characteristics. This concept has significant practical implications. For example, when a virus emerges in humans from an animal reservoir, from a taxonomic perspective, it helps us better understand how it originated, from which host it emerged, how it replicates, how it causes disease, and how humans respond to infection. As a result, we are in a much better position to develop treatments and produce vaccines [6].

A current example is the novel coronavirus causing the COVID-19 pandemic, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Taxonomy has helped us understand that the natural host of this virus may be bats and that its genetic material (genome) has evolved through the combination of different parental genomes (genetic recombination). Additionally, knowing that the new coronavirus is closely related to the SARS coronavirus that emerged in 2003 allowed for the reuse of antiviral drugs such as remdesivir in the treatment of COVID-19.

Conclusion: This article has covered the transmission of diseases through viruses, what symptoms they cause, and how to protect yourself from them, especially by gathering information about the harmful effects of dangerous viruses on the body.

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