The big picture (HL)

Higher level (HL)

? Guiding question(s)

- How can viruses exist with so few genes?
- In what ways do viruses vary?

Keep the guiding questions in mind as you learn the science in this subtopic. You will be ready to answer them at the end of this subtopic. The guiding questions require you to pull together your knowledge and skills from different sections, to see the bigger picture and to build your conceptual understanding.

In 1980, the World Health Organization (WHO) announced the eradication of smallpox, a contagious viral disease that was estimated to have existed for over 3000 years, and was thought to have killed 3 out of every 10 people it had infected. This was a momentous feat, and one of the most notable in public health history.

But why is it that we could eradicate smallpox, but still have relatively little power over other viral diseases? For example, influenza (the 'flu') is estimated to be responsible for between 290 000 and 650 000 respiratory-related deaths worldwide each year, and although flu vaccines do exist, they need to be reformulated and updated annually, and even then are only considered to be around 40–60% effective.

How are the smallpox and influenza viruses similar? How are they different? What impact do their structural differences have on the diseases they cause and our ability to protect against these viruses? The more we know about these infectious agents, the better our understanding of how we can prevent and treat viral diseases. But there are also other reasons to study viruses:

- Viruses can also give us clues into the mechanisms of evolution. Viruses can exchange genetic material with their host cells (indeed, about 8% of your DNA will be viral!), which means that viruses can evolve and rapidly adapt to new environments. This can give scientists useful insights into the mechanisms of evolution.
- Viruses also have the potential to be used as tools for treating diseases, such as in gene therapy, cancer treatment and the development of vaccines. Studying vaccines gives us an understanding of new ways in which they can be used to benefit human health.

An electron micrograph of variola virus virions, the particles responsible for the eradicated disease smallpox, is shown in **Figure 1**. The influenza virus is shown in **Figure 2**.

Overview (/study/ap 422- cid- 755105/o

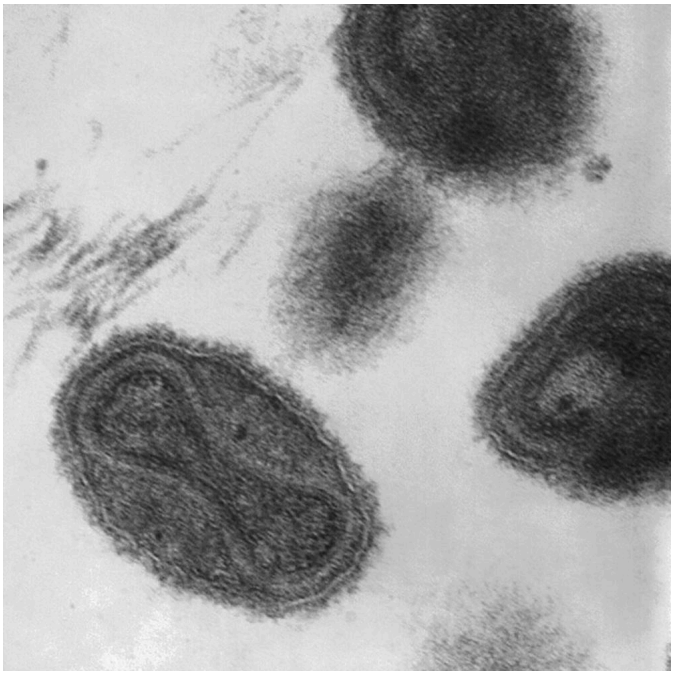


Figure 1. Variola virus virions viewed with an electron micrograph, magnified approximately 370 000×.

Source: "Smallpox virus virions TEM PHIL 1849 (https://commons.wikimedia.org/wiki/File:Smallpox_virus_virions_TEM_PHIL_1849_(crop).png)" by CDC/ Dr. Fred Murphy; Sylvia Whitfield is licensed under CC BY-SA 4.0 (https://creativecommons.org/licenses/by-sa/4.0/deed.en)

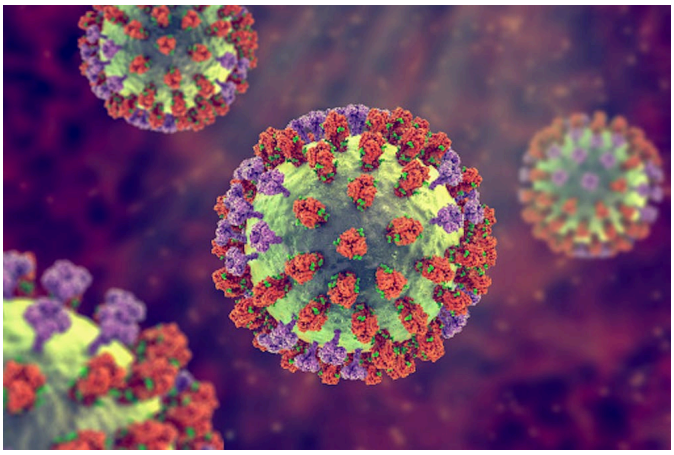


Figure 2. A tiny influenza virus, measuring 80—100 nm in diameter is capable of invading, infecting and hijacking the machinery of its human host cell, ciliated tracheal epithelial cells. These cells measure around 60 µm in length and contain a genome 200 000 larger than that of the influenza virus. How many times bigger is the ciliated tracheal epithelial cell than the influenza virus?

Credit: KATERYNA KON/SCIENCE PHOTO LIBRARY, Getty Images (https://www.gettyimages.co.uk/license/1386012927)

Prior learning

Before you study this subtopic make sure that you understand the following:

- Some viruses use RNA as their genetic material (see section A1.2.1 (/study/app/bio/sid-422-cid-755105/book/nucleic-acids-and-their-structure-id-43580/)).
- Viruses are considered to be non-living (see section A1.2.1 (/study/app/bio/sid-422-cid-755105/book/nucleic-acids-and-their-structure-id-43580/)).

Student view

Viral structure (HL)

Higher level (HL)

Learning outcomes

By the end of this section you should be able to:

- Outline the features that are shared by all viruses.
- Outline examples of diversity in viral structure.

Features shared by all viruses

Viruses are small infectious particles that can range in size from 20 nm to 500 nm (**Figure 1**).

All viruses contain **either** DNA or RNA as their genetic material, a capsid made of protein and few or no enzymes. Some of those that carry RNA are called retroviruses. Non-retrovirus RNA viruses include influenza, coronavirus, West Nile virus, and Zika. Unlike retroviruses, RNA viruses have a simple structure and directly use their RNA to replicate and produce viral proteins. Retroviruses, on the other hand, use DNA intermediates to replicate. Unlike cells, viruses do **not** contain cytoplasm or a plasma membrane.

Viruses range in size from around 20 to 500 nm. By contrast, the size of a typical bacterial cell ranges from 1 to 10 µm (that's 1000–10 000 nm), and typical eukaryotic cells can be between 10 and 100 µm in size (that's 10 000–100 000 nm!). This means that viruses are too small to be seen by light microscopy (with the exception of some large virions of the poxvirus family) but can be viewed with an electron microscope.

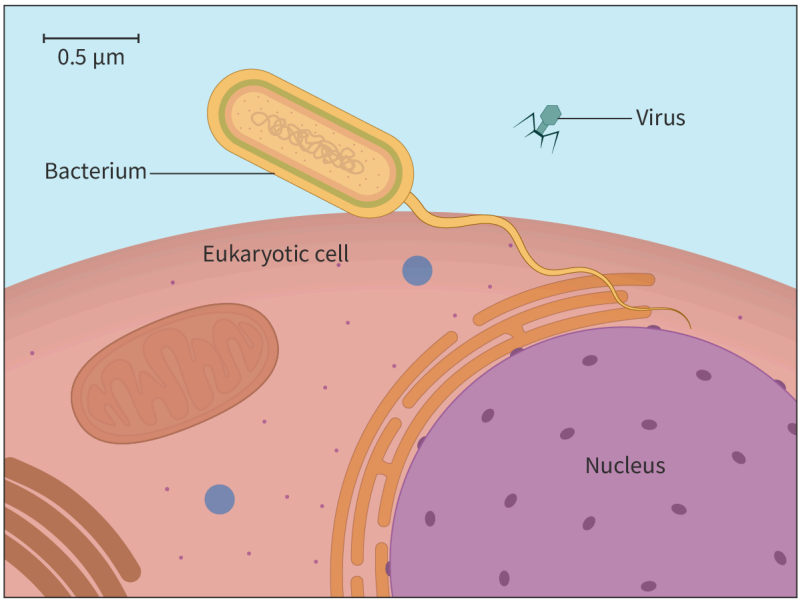


Figure 1. Comparative sizes of a virus, a bacterium and a eukaryotic cell.

More information for figure 1

Overview (/study/ap 422-cid-755105/o

The image is a diagram that visually represents the comparative sizes of a virus, a bacterium, and a eukaryotic cell. The diagram illustrates a small virus adjacent to a larger bacterium and an even larger eukaryotic cell structure.

1. **Virus**: Represented as a small structure with a geometric shape and tail, indicating its micro size relative to the others.
2. **Bacterium**: Shown as a rod-shaped cell with an internal squiggly line, depicting its slightly larger size compared to the virus.
3. **Eukaryotic Cell**: Illustrated with parts of its internal structures visible, such as the nucleus and other organelles, signifying its substantial size relative to both the virus and bacterium.
4. **Labels and Scale**: The diagram includes labels pointing to each cell type with a scale bar labeled "0.5 µm" to provide an idea of size differences among the structures.

[Generated by AI]

Diversity in viral structure

Viruses are highly diverse in their shape and structure. All viruses have a structure called a capsid, a protein sheath that surrounds and protects the genetic material. Some viral capsids are simple and spherical, like the capsid of the influenza virus, and some are much more complex, such as the multilayered complex-shaped capsid of the bacteriophage.

Although all viruses contain genetic material, this may be either RNA or DNA (never both), and can be either single- or double-stranded. Examples of viruses with different genome types are listed in **Table 1**.

Table 1. Viruses with different genome types.

Viral genome	Examples of viruses
Single-stranded RNA	HIV, influenza, coronaviruses
Double-stranded RNA	Rotaviruses
Single-stranded DNA	Parvovirus
Double-stranded DNA	Bacteriophage lambda, variola virus, herpes viruses (herpesviridae)

There is great diversity in the size of viral genomes. Some viruses contain as little as four genes, and others have many more – a recently discovered ‘giant’ virus is estimated to contain 2500 genes. By comparison, the human genome is estimated to contain around 20 500 genes.

Study skills

Usually DNA is a double-stranded molecule and RNA is a single-stranded molecule; however, some viruses contain single-stranded DNA, and some groups of viruses may have double-stranded RNA.

Some viruses, such as HIV and influenza are enveloped. An envelope is a membrane that surrounds the capsid, and is made of lipids and proteins. The virus acquires the envelope from the host cell membrane when it is released. This envelope helps to protect the capsid and provides an additional layer of protection of the viral genome. It also helps to disguise the virus from the immune system of the host cell and helps the virus to attach and enter new host cells.

Student view

Overview (/study/ap 422-cid-755105/o

Other viruses, such as norovirus, adenovirus and bacteriophage lambda are not enveloped. Viruses without an envelope may be more stable and resistant to environmental factors than enveloped viruses, as lipid envelopes may become damaged by heat, light and chemicals (see **Figure 2**).

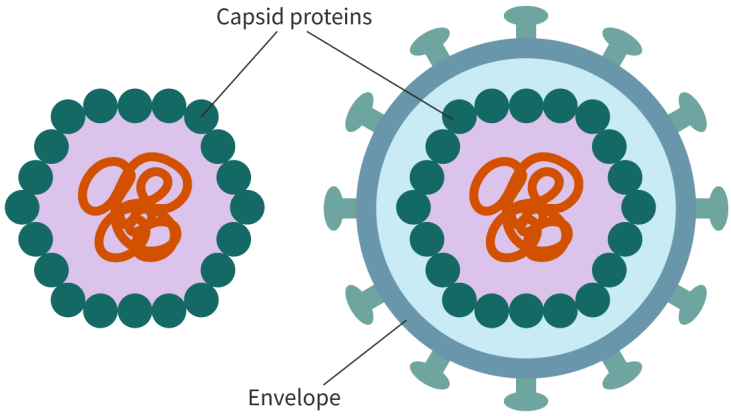


Figure 2. Some viruses are enveloped, containing a lipid and protein membrane that surrounds the capsid. This envelope is derived from the host cell membrane. Other viruses are not enveloped, and therefore the capsid is their outermost layer.

More information for figure 2

The image is a diagram comparing an enveloped virus and a non-enveloped virus. On the left, the non-enveloped virus is shown with its outermost layer being the capsid proteins, depicted as a series of green dots forming a circle. Inside this circle is a representation of genetic material, indicated by a tangled orange line. Labels point to "Capsid proteins."

On the right, the enveloped virus is larger and includes an additional outer layer called the envelope, represented by a grey-blue circle with protruding extensions. Inside this envelope is the capsid, which mirrors the structure of the non-enveloped virus, including the same arrangement of dark green circles and orange tangled line to symbolize the genetic material. Labels indicate both "Capsid proteins" and "Envelope." The diagram illustrates the structural difference between viruses that have an envelope and those that do not.

[Generated by AI]

Interactive 1 shows the structural features of HIV, coronavirus and bacteriophage lambda.

Interactive 1. The Structures of HIV, Coronavirus and Bacteriophage Lambda.

More information for interactive 1

The interactive illustrates the structural differences among three viruses: HIV, SARS-CoV-2, and Bacteriophage lambda, with labeled diagrams on three slides.

Student view

Overview (/study/ap 422-cid-755105/o

Slide 1 — HIV (Human Immunodeficiency Virus)

The image shows a spherical, enveloped virus. Green glycoproteins (lollipop-shaped) on the envelope help the virus attach to host cells. Inner capsid protects the viral contents. Orange RNA strands (single-stranded) are inside the capsid. Enzymes are shown as small colored circles.

The text on the left side of the image says, “The virus responsible for the disease AIDS in humans has an envelope, derived from the host cell plasma membrane. On the envelope are many glycoproteins, which are used by the virus to gain access into the host cell. HIV contains an unusual, cone shaped capsid, within which is single-stranded RNA and three enzymes that help the virus to infect a host cell, including reverse transcriptase, which converts the viral RNA into DNA using the host cell machinery.”

Slide 2 — SARS-CoV-2 (Coronavirus)

Spherical, enveloped virus with a cross-sectional view. The outer lipid envelope has embedded spike proteins (large protrusions) that give the virus its crown-like appearance. Membrane and envelope proteins support structure. The single-stranded RNA genome is shown as orange curls. Nucleocapsid proteins bind to RNA, forming a helical structure.

The text about SARS-CoV-2 reads as “The virus responsible for the disease COVID-19. Like HIV and influenza, SARS-CoV-2 contains a single stranded RNA genome. The virus is enveloped and contains membrane proteins and envelope proteins on its surface, as well as larger spike proteins which give the coronavirus their name ‘crown-like’. The coronavirus capsid is made up of multiple copies of the nucleocapsid protein, which binds to the RNA genome and forms a helical structure.”

Slide 3 — Bacteriophage Lambda

Virus with a complex, geometric shape that infects E. coli. The icosahedral capsid head contains double-stranded DNA. The short collar connects the head to a long contractile tail.

Sheath is present to inject DNA. Tail fibers on the baseplate help to attach to bacterial surfaces. Baseplate with spikes for penetrating host.

The text next to the image reads “The virus that infects the bacterium Escherichia coli has a complex structure, including an icosahedral-shaped capsid head, within which is the double-stranded DNA. Bacteriophage lambda has a short collar, a tail and tail fibres to attach to the cell it is infecting, and the virus contains a number of enzymes including holin, which helps the bacteriophage to make holes in the cell wall of the bacterium it is infecting. See Section A1.2.14 for more information about how this virus was used to demonstrate that DNA is the genetic material in cells.”

Creativity, activity, service

Strand: Creativity and Service
Learning outcome: Demonstrate the skills and recognise the benefits of working collaboratively

The fight against communicable viral diseases includes: education and awareness on the prevention of infections and diseases; health awareness and promotion activities; control measures to reduce the risk of transmission of infections and diseases.

Working with a partner, select one of the viruses mentioned in this section. Find a micrograph of that virus and develop it into a work of art.

You might find some inspiration from Ernst Haecke (https://mymodernmet.com/ernst-haeckel-art/).

You can work individually or collaborate with your peers to educate and raise awareness about the structure of your chosen virus and the prevention of infectious diseases.

One possible outcome for this CAS experience is to gather your artwork to create an exhibition of artworks or infographics to raise awareness about the impact of viruses on human health. This could be set up within the school community or by liaison with a local NGO working within the health industry.

Study skills

The NCBI is an example of a data bank. When you complete your Individual Assignment (sometimes called the Individual Investigation), or if you choose to complete an Extended Essay in Biology, you

Student view

might want to consider collecting secondary data from a data bank.

Try this activity to find out more about different types of viruses and the size of their genomes.

Activity

- **IB learner profile attribute:** Inquirer
- **Approaches to learning:** Research skills — Using search engines and libraries effectively
- **Time required to complete activity:** 20 minutes
- **Activity type:** Individual activity

In this activity you will research some different types of viruses, with the aim of completing **Table 2**. To research the length of viral genomes, use the genome size check on the NCBI (https://www.ncbi.nlm.nih.gov/datasets/) database.

Instructions for using the database:

1. Column one in the Activity: Enter your species to be researched into the “NCBI Datasets” search bar in the middle of the page. For example, “HIV-1” Select from the drop-down menu.
2. Column three in the Activity: The next page will show the type of genetic material (“Genome type”) Scroll down to “Genome,” and select “Browse all 499 assembled genomes.”
3. Select any one you wish to review and click on the “Assembly” code in the left column.
4. Column four in the Activity: On the next page, scroll down to “Assembly Statistics” and then to “Genome size.”

If you get stuck with names of different viruses, read through the examples given in this section, or search the database.

Table 2. Features of different viruses.

Virus	Disease caused by virus	Type of genetic material	Length of genome (bases)	Diagram of virus with structures labelled
Example: HIV	AIDS	Single-stranded RNA	9181	

5 section questions

Lytic and lysogenic cycles (HL)

Higher level (HL)

Learning outcomes

By the end of this section you should be able to:

- Describe how viruses rely on a host cell for energy supply, nutrition, protein synthesis and other life functions.
- Outline the phases in the lytic and lysogenic cycles using the example of bacteriophage lambda.

Dependency on the host cell

Viruses are made of only protein and one type of nucleic acid – they do not contain the organelles and cell structures necessary to replicate themselves and cannot reproduce outside the host cell. Viruses are known as obligate intracellular parasites because they are dependent on the host cell. Some of the ways in which viruses are dependent on the host cell are:

- **Energy**: Viruses do not have their own source of energy like living cells do, and they must rely on the host cell to provide the energy needed for viral replication.
- **Nutrients**: Viruses do not have the ability to obtain their own nutrients and must rely on the host cell for the necessary building blocks for viral replication.
- **Replication machinery**: Viruses do not have the machinery needed to replicate their own genetic material. Instead, they must rely on the host cell's machinery, such as ribosomes and enzymes, to transcribe and translate their genetic material into viral proteins.
- **Transport**: Some viruses use the host cell's transport machinery to move to different parts of the body or to spread to other host cells.

Theory of Knowledge

Because viruses are not able to carry out the eight processes of life they are considered to be non-living (see section A2.1.2—6 (/study/app/bio/sid-422-cid-755105/book/the-origins-of-cell-hl-id-43955/)).

By labelling viruses as non-living we make it more difficult to understand their origin from living organisms or their ability to evolve. Labels can be helpful for experts while hindering understanding in other communities of knowers. To what extent do the names and labels that we use help or hinder the acquisition of knowledge?

Accessing the host cell

Viruses need to gain access into the host cell to take over the host cell machinery (**Figure 1**). There are different ways in which viruses can do this. Some viruses can be taken up by a host cell endosome (an invagination of the host cell membrane). Other viruses bind to receptors on the host cell membrane and then fuse directly with the host cell membrane in a process known as receptor-mediated fusion. Bacteriophage lambda carries out receptor-mediated fusion, binding to a specific receptor on the host cell membrane and then injecting its genetic material directly into the host cell (see section A1.2.14 (/study/app/bio/sid-422-cid-755105/book/investigation-id-43956/)).

Overview (/study/ap 422-cid-755105/o

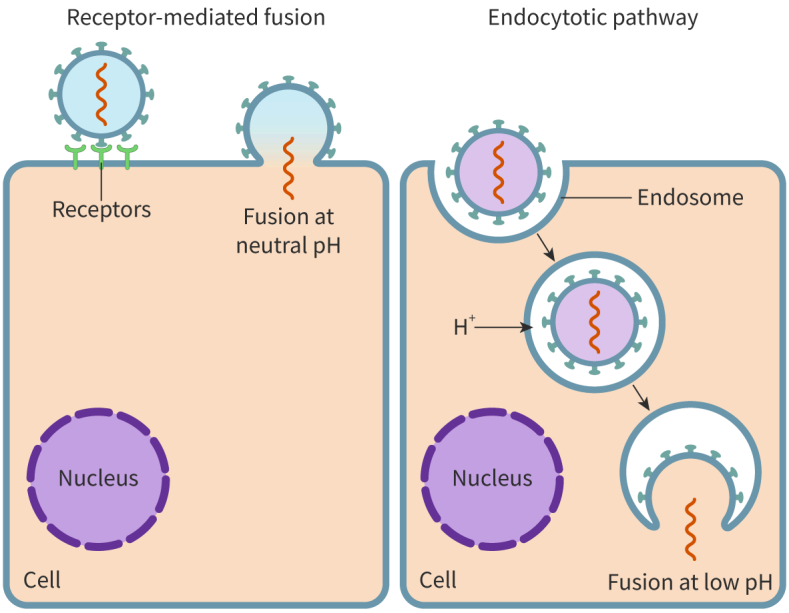


Figure 1. Different viruses have different methods of gaining access to the host cell.

More information for figure 1

The image is a diagram that illustrates two methods viruses use to gain entry into host cells. On the left side, labeled "Receptor-mediated fusion," a virus particle is shown attaching to cell surface receptors. This process, termed as fusion at neutral pH, demonstrates the viral membrane fusing directly with the host cell membrane, allowing genetic material to enter the cell's interior.

On the right side, labeled "Endocytotic pathway," the diagram illustrates a virus being engulfed by the host cell forming an endosome. As the endosome matures, it acidifies (as indicated by the presence of H+ ions), leading to fusion at low pH, which releases the viral genetic material inside the host cell.

Both sections of the diagram include representations of the cell, nucleus, receptors, endosomes, and pathways demonstrating the flow of viral entry.

[Generated by AI]

Lytic and lysogenic cycles

Once the virus, or in some cases, only the viral genome has entered the host cell, the viral genome will undergo replication. There are two main methods of viral genome reproduction inside the host cell, the lytic cycle and the lysogenic cycle.

Some viruses use only the lytic or lysogenic cycle, and some viruses switch between the lytic and lysogenic cycles, when exposed to certain environmental conditions such as UV light or chemical stressors. An example of a virus that can utilise both lytic and lysogenic cycles is bacteriophage lambda, a virus that infects the bacterium *Escherichia coli*.

In the lytic cycle, the bacteriophage genome takes over the host cell machinery, which causes new viral particles to be produced rapidly. The virus particles lyse or burst the host cell, destroying it and causing the new viral particles to be released into the environment (**Figure 2**).

Student view

Overview (/study/ap 422-cid-755105/o

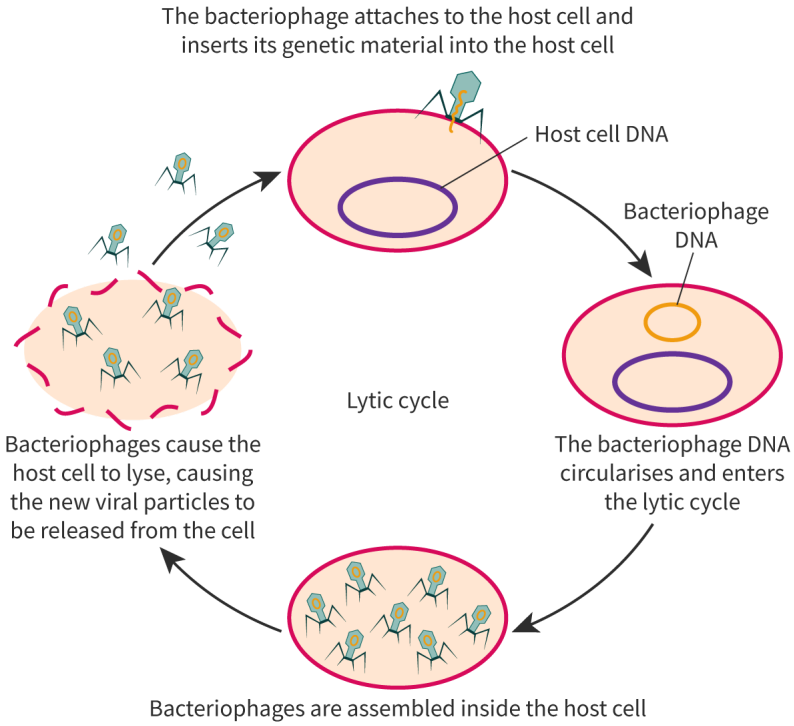


Figure 2. The lytic cycle of bacteriophage lambda.

More information for figure 2

The image is a diagram illustrating the lytic cycle of a bacteriophage in four main steps. It begins with the bacteriophage attaching itself to a host cell and injecting its genetic material. The host cell's DNA is present as a circular structure inside the cell. The next step shows the bacteriophage DNA circularizing and entering the lytic cycle, marked within the host cell. Subsequently, new bacteriophages are assembled inside the host cell, depicted as several bacteriophage structures within the cell. The final step shows the host cell lysing, releasing the newly formed bacteriophage particles into the environment. Arrows between these steps indicate the flow of the cycle, labeled as "Lytic cycle," with accompanying text explanations near each stage.

[Generated by AI]

In contrast, in the lysogenic cycle, no viral particles are produced and the host cell is not destroyed. The lysogenic cycle tends to take place over a longer period of time, during which the virus remains in a dormant state.

In the lysogenic cycle, once the bacteriophage genome has entered the host cell it becomes integrated with the host genome. As the host cell reproduces, each new cell will contain the bacteriophage genome, which is now called a prophage. Occasionally, the prophage genome will be excised from the host cell genome, form bacteriophages and begin the lytic cycle (**Figure 3**). Sometimes when this happens some of the prophage genome is left behind in the host cell genome, or some of the host cell genome is taken with the prophage.

Student view

Overview (/study/ap 422-cid-755105/o

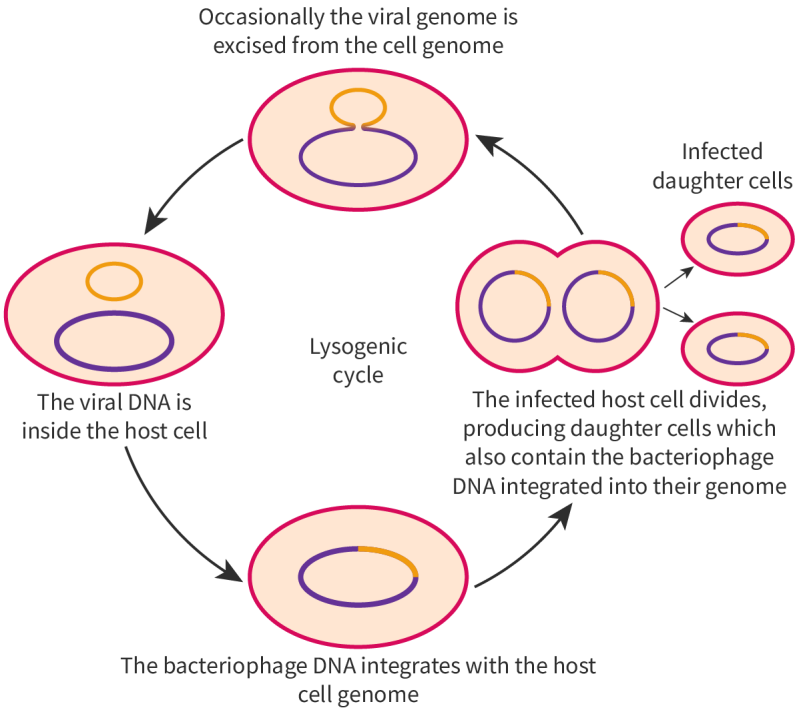


Figure 3. The lysogenic cycle of bacteriophage lambda.

More information for figure 3

The image shows a flow diagram of the lysogenic cycle of bacteriophage lambda. It consists of several labeled stages connected by arrows indicating the cycle's progression:

1. "The viral DNA is inside the host cell" - Shows a host cell with viral DNA inside.
2. "The bacteriophage DNA integrates with the host cell genome" - Displays the integration of viral DNA into the host's genome.
3. "The infected host cell divides, producing daughter cells which also contain the bacteriophage DNA integrated into their genome" - Illustrates cell division resulting in two daughter cells, both containing integrated viral DNA.
4. "Occasionally the viral genome is excised from the cell genome" - Describes the step where the viral genome may be removed from the host genome, potentially leading to the start of the lytic cycle.

The diagram visually represents the continuation of this cycle with arrows forming a circular path, emphasizing the repetitive nature of the lysogenic cycle.

[Generated by AI]

Try the activity below to test your understanding of the lytic and lysogenic cycles of a virus.

Activity

- **IB learner profile attribute:** Thinker
- **Approaches to learning:** Thinking skills — Combining different ideas in order to create new understandings
- **Time required to complete activity:** 15 minutes
- **Activity type:** Individual activity

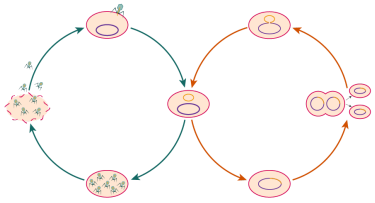
Look at **Interactive 1.**

1. In the middle of each cycle, drag and drop the labels ‘lytic’ or ‘lysogenic’ into the correct cycle.

Student view

Overview (/study/ap 422-cid-755105/o

2. For each of the stages in the cycles, drag and drop the descriptor that explains that stage of the process.
3. A student writes that all viruses can have either lytic or lysogenic cycles. Write a sentence explaining why this statement is incorrect.



Many bacteriophages produced rapidly by host cell	Host cell lyses, releasing bacteriophages	Bacteriophage inserts DNA into host cell	Lysogenic
			Lytic
Bacteriophage DNA integrates with host cell DNA	Bacteriophage DNA circularises and can enter either cycle	As host cell divides, bacteriophage DNA is replicated	Occasionally bacteriophage DNA is excised from host cell

Check

4. **Interactive 1.** The Lytic Cycle of Bacteriophage Lambda.

More information for interactive 1

The interactive illustrates a drag and drop activity with two interconnected life cycles of a virus represented by circular diagrams.

The left-side cycle depicts the lytic bacteriophage life cycle, starting with phages infecting a bacterial cell, leading to phage replication within the cell, lysis of the cell, and the release of numerous new phages.

The right-side cycle shows the lysogenic bacteriophage life cycle, where the phage DNA integrates into the bacterial chromosome, replicates along with it during cell division, and can eventually transition into the lytic cycle.

The two cycles are connected by a central bacterial cell that can either be infected by phages by entering the lytic cycle or contain integrated phage DNA by being part of the lysogenic cycle.

There are nine drag-and-drop options given: Many bacteriophages produced rapidly by host cell; Bacteriophage DNA integrates with host cell DNA; Host cell lyses, releases bacteriophages; Bacteriophage DNA circularises and can enter either cycle; Bacteriophage inserts DNA into host cell; As host cell divides, bacteriophage DNA is replicated; Lysogenic, Lytic, Occasionally bacteriophage DNA is excised from host cell.

Read below for the solution:

The option bacteriophage DNA circularizes and can enter either cycle should be placed in the center of the two cycles. The left side cycle depict the lytic cycle, so the option lytic should be placed in the left side cycle. The other three options for the lytic cycle, from top to bottom, are: the phage inserts its DNA into a host cell, the host cell is then used to rapidly produce many bacteriophages, and finally, the host cell lyses, releasing the newly formed phages.
The right-side cycle illustrates the lysogenic cycle, so the option "Lysogenic" fits there. The other three correct options for the lysogenic cycle, from top to bottom, are: the bacteriophage DNA integrates with the host cell DNA and as the host cell divides, bacteriophage DNA is replicated. Occasionally bacteriophage DNA is excised from the host cell.

Student view

5 section questions

The origins and evolution of viruses (HL)

Higher level (HL)

Learning outcomes

By the end of this section you should be able to:

- Outline the possible origins of viruses.
- Outline reasons for very rapid rates of evolution in some viruses.

The possible origins of viruses

Viruses exhibit huge diversity in their structure and genetic material. This diversity suggests several possible origins. The possible origins of viruses include:

- Viruses may have originated from ancient RNA or DNA molecules that became encapsulated in a protective protein coat. The encapsulated genetic material or 'proto-virus' may have been able to replicate and evolve, eventually forming the viruses that we know today.
- Viruses may have evolved from viroids, which are small infectious agents that consist only of a short strand of RNA and infect angiosperms (flowering plants).
- Viruses may have originated from transposons, which are genetic elements that can move around within an organism's genome.
- Viruses may have evolved from ancient cells that lost their ability to live independently and became dependent on other cells for reproduction.

Theory of Knowledge

The genetic code is **universal** — all living organisms contain the same four DNA bases: adenine, thymine, cytosine and guanine, and use the same cellular machinery to utilise the instructions in the genetic code to produce proteins.

How does the universality of the genetic code among all forms of life, and also viruses, support the idea of descent from a common ancestor?

How does the universality of the genetic code among all forms of life support the idea that the genetic code is a fundamental and essential aspect of the proper functioning of all living organisms and viruses?

The possibility of convergent evolution in viruses

The structural features that viruses share could be regarded as convergent evolution. Convergent evolution is the process by which unrelated organisms independently evolve similar traits as a result of adapting to similar environments or selective pressures.

Viruses are thought to demonstrate convergent evolution in several ways, including:

- Some viruses that infect different cell types have evolved similar mechanisms for entering and replicating within those cells.

- Some viruses that infect different types of host organisms have evolved similar mechanisms for evading the host's immune system and spreading to new hosts.
- Some viruses that infect different types of host organisms have evolved similar shapes and sizes.

It is likely that this convergent evolution occurred because there are only a limited number of ways that viruses can effectively infect and replicate within host cells, and only a limited number of shapes and sizes that are optimal for infecting and replicating within host cells. It may be because of this that different viruses have arrived at similar solutions through different evolutionary pathways.

Rapid rates of evolution in viruses

Evolution in viruses is described as the process by which they change and adapt over time. Viruses evolve at a much faster rate than most organisms. This occurs because :

- Many RNA viruses are retroviruses and have high mutation rates because they copy their genetic material using error-prone mechanisms such as reverse transcriptase enzymes and RNA polymerases, which are much less accurate than DNA polymerases. HIV, influenza and hepatitis C are all RNA-based viruses which can have a mutation rate that is up to 10 000 times higher than those of DNA viruses. These mutations can then be passed onto the next generation of viruses. DNA replication is covered in section D1.1.3 (/study/app/bio/sid-422-cid-755105/book/polymerase-chain-reaction-and-gel-electrophoresis-id-43957/).
- Viruses can exchange genetic material with each other through processes such as recombination and horizontal gene transfer. This can allow them to rapidly acquire new traits or adapt to new environments.
- Viruses have short generation times and high reproductive rates — they can produce many offspring in a short period of time, allowing for more opportunities for evolution to occur.

Viruses with a higher mutation rate are harder to treat and vaccinate against. It is also much harder for the host's immune system to recognise and control these viruses.

Case study: rapid evolution in HIV

Human Immunodeficiency Virus (HIV) is a Retrovirus that was first identified in the early 1980s. The virus is transmitted through infected body fluids and primarily infects CD4+ cells of the immune system, leading to the disease Acquired Immunodeficiency Syndrome (AIDS). AIDS is now considered to be a global pandemic, with millions of people worldwide living with the disease. Although there are preventatives available, as well as treatments to slow the progress of the disease, there is currently no cure for AIDS, in part due to the high rate of evolution in the HIV virus.

HIV reproduces very quickly, and each time it does so, there is a chance that mutations will occur in its genetic material. HIV is an RNA virus, which means that reproduction of the genetic material requires the use of reverse transcriptase, an enzyme that is considered to be many times more error-prone than DNA polymerases. These mutations can lead to the emergence of new HIV strains that may be more or less virulent, more or less transmissible, or more or less able to evade the immune system or antiviral drugs. HIV is also able to carry out recombination, exchanging genetic material with other viruses or its host cell, acquiring new genes and traits which can further increase its adaptability.

HIV transmission and infection is covered in more detail in sections C3.2.11 (/study/app/bio/sid-422-cid-755105/book/hiv-and-aids-id-43958/) and C3.2.12 (/study/app/bio/sid-422-cid-755105/book/antibiotics-and-antibiotic-resistance-id-43959/).

For an overview of HIV, strategies to reduce infections and worldwide data, you can explore WHO's Global HIV Programme (https://www.who.int/health-topics/hiv-aids#tab=tab_3) page.

Overview (/study/ap 422- cid- 755105/o

Case study: rapid evolution in influenza

Like HIV, influenza or the 'flu' is an RNA virus, meaning that it has a less accurate means of replicating its genetic material than DNA viruses or living organisms. High mutation rates in the haemagglutinin and neuraminidase surface proteins can make it more difficult for the host immune system to identify and protect against the virus, and is also a contributing factor to why flu vaccines tend to have a relatively low effectiveness compared with other vaccinations. Remember in The big picture (/study/app/bio/sid-422-cid-755105/book/big-picture-hl-id-43527/), where you learned that flu vaccines need to be updated every year and remain only around 40–60% effective? It is important to note, however, that the flu vaccine still plays an important role in preventing the spread and reducing the severity of influenza infections. Vaccines are covered in more detail in section C3.2.16 (/study/app/bio/sid-422-cid-755105/book/vaccinations-and-more-id-43960/).

Influenza can carry out a process known as reassortment. This occurs when an influenza virus infects a host cell that is already infected with a different strain of influenza, and the two viruses exchange genetic material, leading to the emergence of new strains that may have new or different characteristics. Reassortment is thought to be responsible for many of the global influenza pandemics.

You can learn more about the coordinated effort into the monitoring and control of influenza with previous reports and current information on WHO's Influenza updates (https://www.who.int/teams/global-influenza-programme/surveillance-and-monitoring/influenza-updates) page.

Case study: rapid evolution in SARS-CoV-2

COVID-19 is an infectious disease caused by the SARS-CoV-2 virus (**Figure 1**), which, like HIV and influenza, is an RNA virus, and is therefore more prone to mutations than DNA viruses. The spike proteins on the surface of the virus give the coronavirus their name, 'crown-like', and play a key role in recognition of the host cell and fusion with the host cell membrane. Although some mutations will have a deleterious effect (harmful or damaging to the virus) or no effect, some mutations in the sequence of these spike proteins have been shown to increase transmissibility, reduce vaccine efficacy and aid the virus in evading the host cell immune system.

As with HIV and influenza, SARS-CoV-2 is considered to have a high replication rate, meaning it makes many copies of itself inside a host cell in a set period of time, increasing the likelihood that mutations will occur and accumulate.

When genetic recombination and mutations accumulate that make a virus sufficiently different to the original virus, these new viruses are known as 'variants', such as the SARS-CoV-2 Delta and Omicron variants. Because changes in the RNA sequence of SARS-CoV-2 are so frequent, they can be used to track the transmission of the virus, which can be helpful in developing public health measures to limit the spread of the disease.

You can find lots more information about COVID-19, including global statistics, research and strategies for ending the acute phase of the pandemic on WHO's Coronavirus disease (COVID-19) pandemic (https://www.who.int/emergencies/diseases/novel-coronavirus-2019) page.

Student view

Overview (/study/ap 422-cid-755105/o

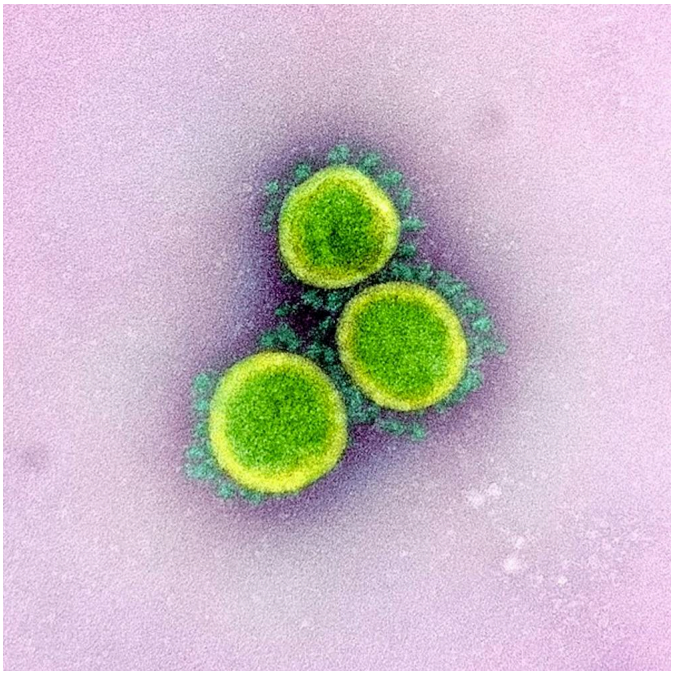


Figure 1. A transmission electron micrograph showing SARS-CoV-2, the virus that causes COVID-19.

Try the activity below to check your understanding of the origins and evolution of viruses.

Activity

- **IB learner profile attribute:** Communicator
- **Approaches to learning:** Communication skills — Clearly communicating complex ideas in response to open-ended questions
- **Time required to complete activity:** 30 minutes
- **Activity type:** Group activity

Take 10 minutes to reread the content from this section, making notes for the following questions. Then carry out a class discussion centred around the questions. Each student should prepare at least two points for each discussion question.

- What are the implications of the various theories about the origins of viruses for our understanding of the evolution of life on Earth?
- What are the potential consequences of convergent evolution in viruses?
- How does the high rate of evolution in viruses impact our ability to control and prevent viral diseases?

5 section questions

Student view

A2. Unity and diversity: Cells / A2.3 Viruses (HL)

Summary and key terms (HL)

Higher level (HL)

- Viruses are small, simple, non-living entities that are composed of nucleic acid (either DNA or RNA, and either single-stranded or double-stranded) and a protective protein capsid.
- There is great diversity within viruses, including in genome size, which can range from a few to thousands of genes, and in the complexity of their capsid structure, which can range from simple and spherical, to multilayered and complex-shaped.
- Viruses are considered to be obligate intracellular parasites — they depend on the host cell for many vital functions including replication, and cannot survive outside of the host cell.
- There are two main methods of viral genome reproduction inside the host cell: the lytic cycle and the lysogenic cycle. The lytic cycle involves rapid production of many virus particles which lyse and destroy the host cell. In the lysogenic cycle, the virus remains dormant, integrating its genome into the host cell genome. Some viruses, including bacteriophage lambda, are able to switch between lytic and lysogenic cycles when exposed to certain environmental conditions.
- There are several possible origins of viruses, including that they have originated from ancient genetic material that became encapsulated in protein, that they evolved from viroids, that they evolved from transposons (genetic elements that can move about within a genome) and that they may have evolved from ancient cells that lost their ability to live independently.
- The structural features that viruses share, including how they enter and replicate within cells, how they evade the host's immune system and transmit to new cells, and the similar shape and size of viruses that infect different host organisms could be regarded as convergent evolution.
- Viruses evolve rapidly. RNA viruses, known as retroviruses, copy their genetic material using error-prone mechanisms, which are more likely to result in a mutation that will be passed on to the virus progeny. Some viruses can exchange genetic material with other viruses and with their host cells, altering their genetic makeup, and because viruses have short generation and high reproductive rates, there are more opportunities for evolution to occur.

Overview (/study/ap 422-cid-755105/o

Key terms

Review these key terms. Do you know them all? Fill in as many gaps as you can using the terms in this list.

1. All viruses contain material and a protective protein . Viruses are considered to be non-living.
2. Viruses are intracellular parasites because they are dependent on the cell for many functions, including energy, nutrients, replication machinery and transport.
3. There are two main methods of viral reproduction: the lytic cycle and the lysogenic cycle. The cycle involves the rapid production of new viruses, which lyse and destroy the host cell. The cycle involves the integration of the viral genome into the host cell genome.
4. Because of the high diversity in the structure and genetic material of viruses, many possible of viruses have been suggested.
5. Viruses exhibit high rates of , which makes it harder to treat and prevent viral diseases.

origins | lytic | capsid | genetic | obligate | evolution | host | lysogenic

Check

Interactive 1. Viruses (HL): Key Concepts and Terminology.

A2. Unity and diversity: Cells / A2.3 Viruses (HL)

Checklist (HL)

Section | Student... (0/0) | Feedback | Print (/study/app/bio/sid-422-cid-755105/book/checklist-hl-id-43929/print/) | Assign

Higher level (HL)

What you should know

After studying this subtopic you should be able to:

- Outline the features that are shared by all viruses.
- Outline examples of diversity in viral structure.
- Describe how viruses rely on a host cell for energy supply, nutrition, protein synthesis and other life functions.
- Outline the phases in the lytic and lysogenic cycles using the example of bacteriophage lambda.
- Outline the possible origins of viruses.

Student view

- Outline reasons for very rapid rates of evolution in some viruses.

Overview (/study/ap 422-cid-755105/o

Investigation (HL)

Section Student... (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/investigation-hl-id-43930/print/) Assign

Higher level (HL)

- **IB learner profile attribute:** Thinkers
- **Approaches to learning:** Thinking skills — Providing a reasoned argument to support conclusions
- **Time required to complete activity:** 20 minutes
- **Activity type:** Individual activity

Your task

This is a text analysis task. Read through the case study on the smallpox virus and consider the information that you have been given previously in this subtopic.

Smallpox

Smallpox is a highly contagious and deadly disease caused by the variola virus. The variola virus has a small, brick-shaped structure, a large, double-stranded DNA genome and a lipid envelope. On the surface of the envelope are many viral envelope proteins which play a critical role in the ability of the virus to enter the host cell (**Figure 1**).

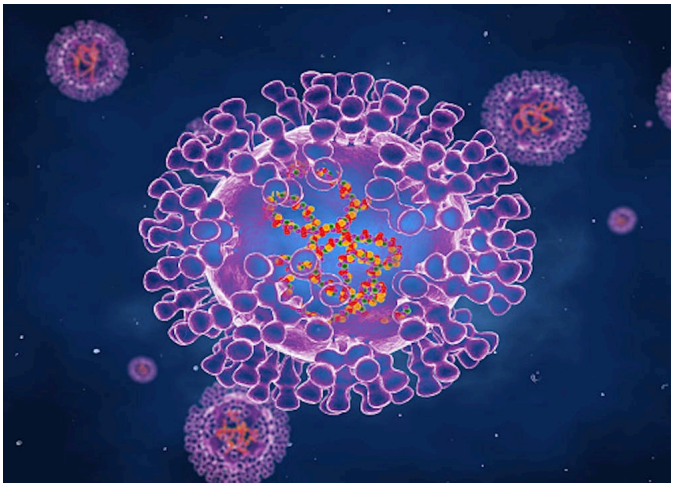


Figure 1. Like monkeypox and chicken pox, the virus responsible for smallpox is a type of pox virus.
Credit: ROGER HARRIS/SCIENCE PHOTO LIBRARY, Getty Images

Smallpox is transmitted through infected droplets, such as those produced by coughing or sneezing. When these infected droplets are inhaled by another person, they can enter the respiratory tract and infect the host cells. The virus typically incubates for between one and two weeks, after which time the infected person will develop symptoms such as fever, headache and a distinctive rash.

Student view

Overview (/study/ap 422-cid-755105/o

In the 20th century, smallpox was a major public health threat, with outbreaks occurring regularly in many parts of the world. In the late 1960s, WHO launched a global vaccination campaign to eradicate smallpox. The campaign was based on the use of a vaccine that had been developed in the 18th century by an English scientist named Edward Jenner (https://www.jenner.ac.uk/about/edward-jenner). The vaccine was administered to people in countries all around the world, and over the course of several decades, the number of smallpox cases began to decline.

The smallpox vaccine is considered to have a success rate of 95% in people who were not previously infected, and is considered to help to reduce the severity of the disease and prevent complications in people who had previously been infected.

The smallpox vaccine was administered to people in areas where smallpox was known to be present and people who had been in contact with infected individuals were vaccinated to prevent the spread of the disease. The smallpox eradication campaign was funded and organised by the WHO, and supported by governments and international organisations.

Smallpox was declared eradicated in 1980, making it the first and only disease in human history to have been eradicated through vaccination.

International Mindedness

The eradication of smallpox was a coordinated global project. It exemplifies the power of international cooperation and the importance of developing and nurturing an international mindset in addressing global health challenges.

However, interestingly, there are other vaccines that are considered to be more effective than the smallpox vaccine. By comparison, two doses of the Measles, Mumps and Rubella (MMR) vaccine results in 97% effectiveness against measles and 97% effectiveness against rubella. It also offers 88% effectiveness against mumps.

Theory of Knowledge

To what extent do personal beliefs, and cultural and societal views shape the effectiveness of vaccination campaigns?

Questions

1. Use the genome size check on the NCBI (https://www.ncbi.nlm.nih.gov/assembly/help/genome-size-check/) database to find out the length of the variola virus genome, and the number of genes contained within the genome. See section A2.3.1 (/study/app/bio/sid-422-cid-755105/book/viral-structure-hl-id-43924/)—2 (/study/app/bio/sid-422-cid-755105/book/viral-structure-hl-id-43924/) for instructions on how to use the database.
2. Explain why the smallpox virus can exist with so few genes.
3. Why was it possible to eradicate the variola virus — the causative agent of smallpox — but it has not been possible to do the same with measles, mumps and rubella? You can find out more about the MMR vaccine using this link (https://www.who.int/news-room/spotlight/history-of-vaccination/history-of-measles-vaccination#:~:text=In%201971%20Hilleman%20combined%20the,make%20the%20combined%20MMRV%20vaccine
4. The influenza vaccine is considered to reduce the risk of flu by 40—60% in a given flu season. Suggest why the effectiveness of this vaccine is much lower than that of the smallpox vaccine. You can find out more about the influenza virus and its effectiveness using this link (https://www.cdc.gov/flu/vaccines-work/vaccineeffect.htm#doe_flu_vax_effect_vary_by_type_subtype).

Student view

Overview (/study/ap 422-cid-755105/o

A2. Unity and diversity: Cells / A2.3 Viruses (HL)

Reflection (HL)

Section Student... (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/reflection-id-46866/print/) Assign

Teacher instructions

The goal of this section is to encourage students to reflect on their learning and conceptual understanding of the subject at the end of this subtopic. It asks them to go back to the guiding questions posed at the start of the subtopic and assess how confident they now are in answering them. What have they learned, and what outstanding questions do they have? Are they able to see the bigger picture and the connections between the different topics?

Students can submit their reflections to you by clicking on 'Submit'. You will then see their answers in the 'Insights' part of the Kognity platform.

Higher level (HL)

Reflection

Now that you've completed this subtopic, let's come back to the guiding question introduced in The big picture (/study/app/bio/sid-422-cid-755105/book/big-picture-hl-id-43527/).

- How can viruses exist with so few genes?
- In what ways do viruses vary?

With these questions in mind, take a moment to reflect on your learning so far and type your reflections into the space provided.

You can use the following questions to guide you:

- What main points have you learned from this subtopic?
- Is anything unclear? What questions do you still have?
- How confident do you feel in answering the guiding questions?
- What connections do you see between this subtopic and other parts of the course?

⚠ Once you submit your response, you won't be able to edit it.

0/2000

Submit

Student view

Overview
(/study/ap
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cid-
755105/o

Rate subtopic A2.3 Viruses (HL)

Help us improve the content and user experience.

☆ ☆ ☆ ☆ ☆

Student
view