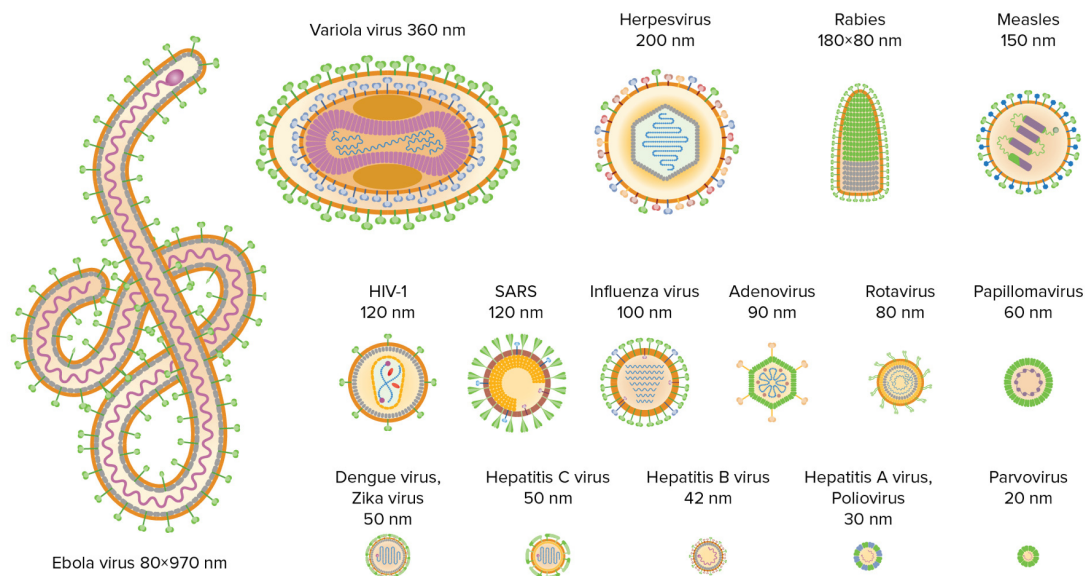


A2.3 Viruses [HL]

Structural features of viruses

- Small size (20 – 300 nm)
- Non-living
- Fixed size (they do not grow in size)
- Cannot replace themselves, nor have metabolic functions
- Enclosed by a protein coat, called capsid
- No cytoplasm
- Need host cells to reproduce inside them
- Have no (to very few) enzymes

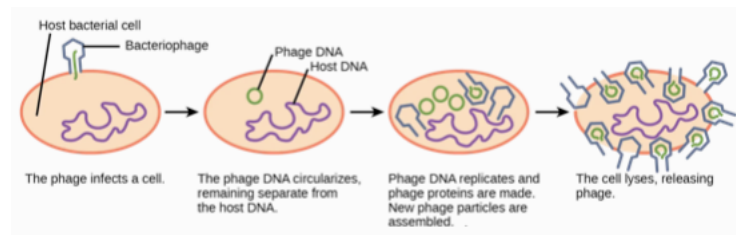
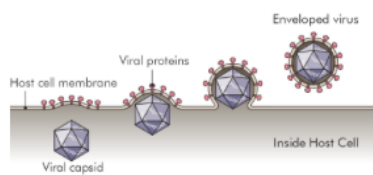
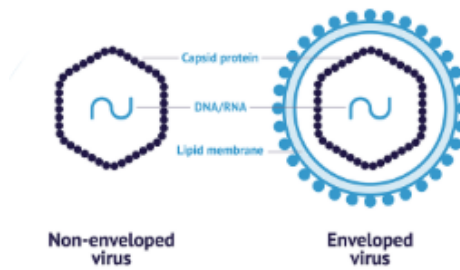


Diversity

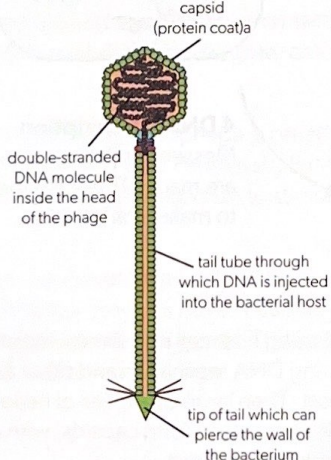
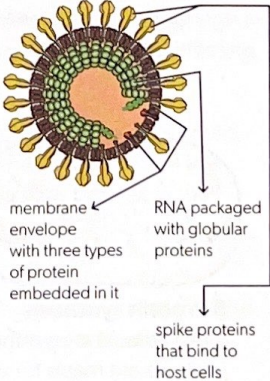
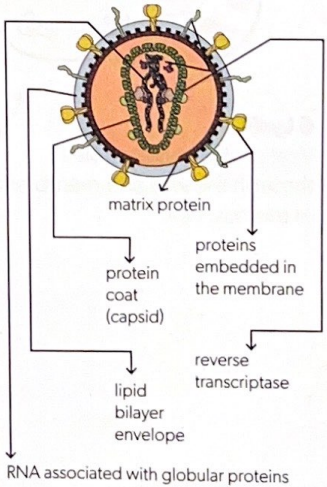
They all descended from a common ancestor

- Genetic material – DNA or RNA
- Genetic material – RNA
 - positive – sense RNA: They use their genes directly as mRNA
 - negative – sense RNA: They transcribe their genes to mRNA
 - Retroviruses: They make double stranded DNA copies of their RNA genes and then transcribe the negative – sense strand of DNA to produce mRNA

- Enveloped and non-enveloped viruses (capsid present or absent)



Structure comparison of bacteriophage lambda, coronaviruses and HIV

	Bacteriophage lambda	COVID-19	HIV
Type of virus	Bacteriophage (a DNA virus that uses either a bacterium or an archaean as its host)	Coronavirus (an RNA virus with a crown-like shape that uses an animal cell as its host)	Retrovirus (a virus that converts its RNA genome to DNA after infecting a host)
Enveloped or non-enveloped	Non-enveloped	Enveloped	Enveloped
Genetic material	One double-stranded DNA molecule with positive and negative sense strands and 48,502 base pairs. There are 32 genes which code for 29 proteins including 4 enzymes.	One single-stranded positive-sense RNA molecule with 29,903 bases. The 16 genes code for 29 proteins, including 4 structural proteins and 6 enzymes.	Two copies of a single-stranded positive-sense RNA molecule of 9,749 bases. There are 9 genes, coding for 15 viral proteins, including 4 enzymes.
Distinctive features	The virus can follow either a lytic cycle (in which it reproduces and then kills the host cell as it bursts out) or a lysogenic cycle (in which it integrates its DNA and does not kill the host).	COVID-19 caused a pandemic, starting in 2020. It is an example of a zoonosis, because it was passed to humans from another species, probably a bat.	The virus contains the enzyme reverse transcriptase which makes a double-stranded DNA copy of the viral RNA genome. This is then integrated into a host cell chromosome.
Host	<i>Escherichia coli</i> —a Gram-negative bacterium	Human cells and possibly cells in other mammals	T-helper cells in the human immune system
	 capsid (protein coat) double-stranded DNA molecule inside the head of the phage tail tube through which DNA is injected into the bacterial host tip of tail which can pierce the wall of the bacterium	 membrane envelope with three types of protein embedded in it RNA packaged with globular proteins spike proteins that bind to host cells	 matrix protein protein coat (capsid) reverse transcriptase lipid bilayer envelope RNA associated with globular proteins proteins embedded in the membrane

▲ Table 1

Lysogenic and Lytic cycle of a virus

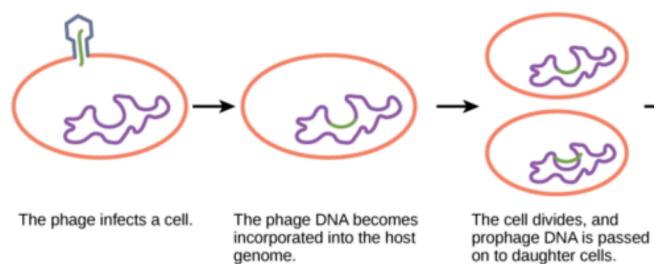
In the lytic cycle, a virus relies on a host cell for energy supply, nutrition, protein synthesis and other life functions. Bacteriophage Lambda are viruses that infect bacteria like *E. coli*

Lambda can alternate between two approaches of infection from the lysogenic to the lytic if exposed to environmental stressors (eg UV light or low nutrient conditions):

- **Lysogenic cycle** – the virus assimilates its genome with the host cell's genome to achieve replication without killing the host

There are five steps to the lysogenic cycle:

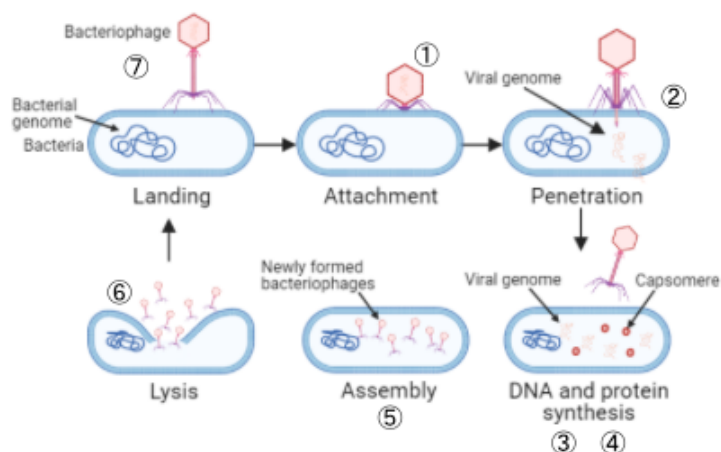
1. Phage attachment to host cell
2. Phage entry into host cell
3. Phage DNA is integrated into host genome
4. DNA replication
5. Cell division



- **Lytic cycle** - the virus reproduces and bursts out of the host cell, killing it

There are seven steps to the lytic cycle:

1. Phage attachment to host cell
2. Phage DNA entry into host cell
3. Phage DNA replication
4. Phage protein synthesis
5. Assembly of new phage viruses
6. Lysis
7. Spread

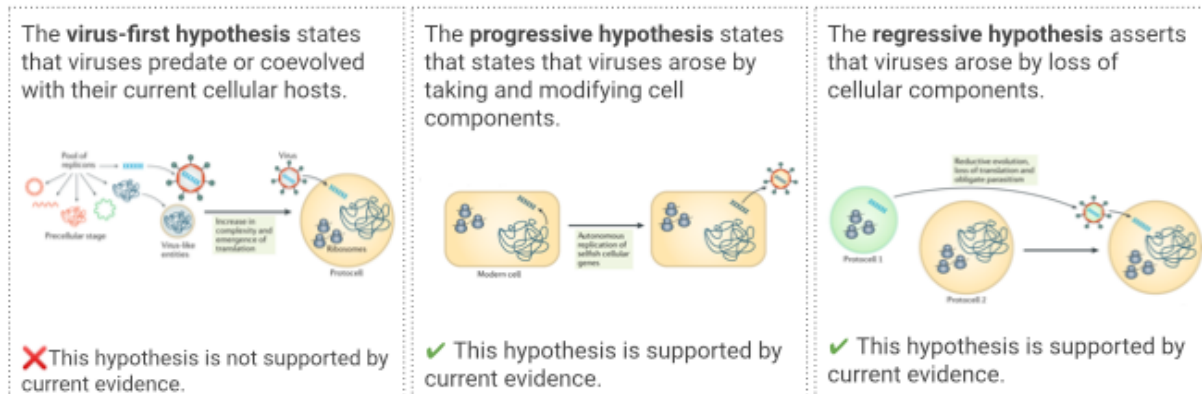


***Note:** A temperate virus can alternate between a lytic and lysogenic cycle.

Evidence for several origins of viruses from other organisms

- Viruses evolved after the origin of cells
- Progressive and regressive hypotheses

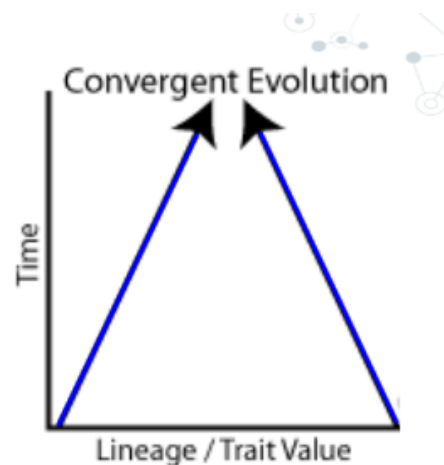
Three main hypotheses have been suggested for the origin of viruses:



- Convergent evolution could result in the common characteristics shared by viruses

The shared features of viruses are likely the result of convergent evolution (A4.1.5). In convergent evolution, different lineages evolve similar features because of selection for function rather than inheritance from a common ancestor.

- Multiple viral lineages ... 
- Have independently evolved similar functional adaptations ...
- Over time.



Where Did Viruses Come From?

<https://www.youtube.com/watch?v=X31g5TB-MRo>

Rapid evolution in viruses

The genome of viruses has rapid rates of evolution, meaning the genetic information changes rapidly in a population of viruses.

- a) **Generation time / Evolutionary change:** It can only happen between one generation and the next, so it is limited by generation time. In humans it is 25 years on average, while in viruses it can be less than an hour.
- b) **High rates of mutation:** RNA viruses such as coronaviruses do not perform any checks or correct any errors when they replicate, so they can mutate quickly.

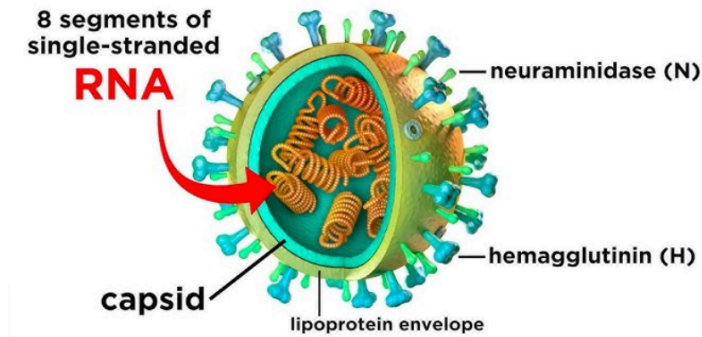
→ The rapid evolution and mutations have important implications for the progression of a disease, treatment of infections and development of vaccines.

HIV and Influenza virus

The human immunodeficiency virus (HIV) is a retrovirus that infects T-lymphocytes causing AIDS as a consequence.

→ HIV has one of the highest mutation rates of any virus. Natural selection can rapidly select for any new variation that help the virus evade the immune system or drug treatments. As a result, infections are hard to cure and developing an effective vaccine has not been possible yet.

Influenza is an enveloped virus with 8 strands of -ssRNA as its genetic material. It has a high mutation rate and can be transmitted between species. This results in the evolution of new strains.



Two proteins on the influenza virus capsid are vital for viral function and detection by the immune system:

- Haemagglutinin (H) is used to bind a host cell for entry
- Neuraminidase (N) helps release new virions from the infected cell

The H and N surface proteins of influenza viruses are "antigens," which means they are recognized by the immune system and are capable of triggering an immune response (C3.2.7). Flu vaccines are designed to target one or more of the surface proteins/antigens of flu viruses.

→ Influenza can evolve through **antigen drift** and **antigen shift**.

Antigen drift consists of small mutations that can lead to changes in the surface proteins of the virus. Changes in H and N accumulate over time, resulting in a flu virus becoming antigenically different. Thus, a person can be re-infected since his/her antibodies will not recognize the new antigens. Because of this antigen drift the composition of the flu vaccines are reviewed and updated annually to keep up with evolving viruses!

Antigenic shift is an abrupt, major change in a flu virus. Shift can happen if the flu virus from an animal population gains the ability to infect humans. Such animal-origin viruses can contain h/N combinations that are very different from human viruses, so most people will not have the immunity to the new virus.

Antigenic shift occurred in 2009 when a H1N1 virus with genes from viruses originating from N. American swine, Eurasian swine, humans and birds emerged to infect people and quickly spread, causing a pandemic.

