

# Viruses : where do they come from?

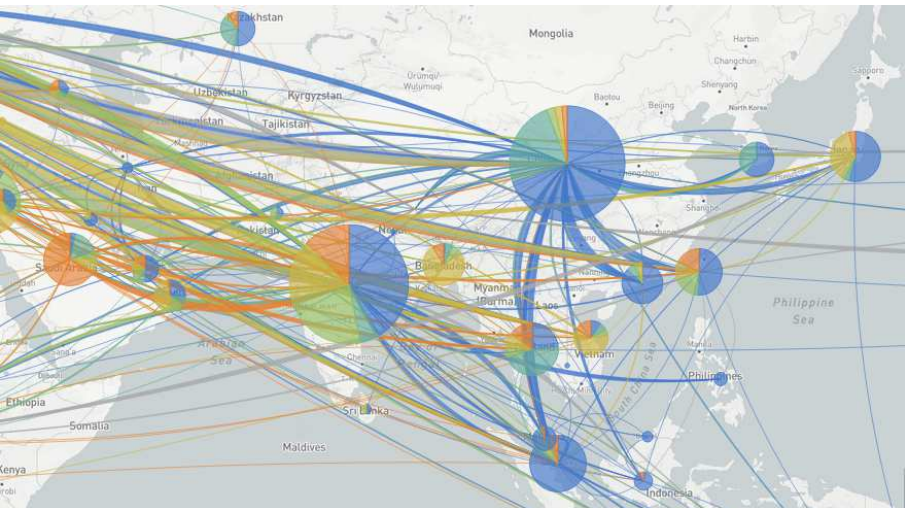
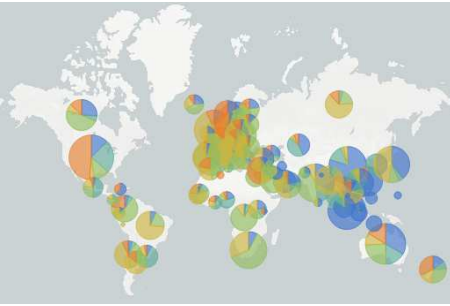
Viruses are infectious particles made up of a core of genetic material (DNA or RNA) wrapped up in protein. Like all viruses, SARS-CoV-2 cannot reproduce outside certain cells in its host. Can we tell where the virus came from? How did these viruses get all over the world? What features does SARS-CoV-2 share with other human viruses? How are they related to other viruses that we know about?



Tree: [tolweb.org](http://tolweb.org)

# Worldwide spread of SARS-CoV-2

SARS-CoV-2 has spread all over the world to cause the CoViD-19 (COrona VIRUS Disease 2019) global pandemic. To understand the geographic spread of the virus, we need to understand how the viruses in different parts of the world are related to each other. Scientists do this by aligning gene sequences of viruses isolated from different parts of the world and analyzing them to get a phylogenetic tree.



Maps: [nextstrain.org](https://nextstrain.org)

# Variation in gene sequences can reveal evolutionary relationships

All genetic material, including the DNA and RNA of viruses, are polymers made up of repeated subunits of sugar, phosphorus, and nucleotides. These nucleotides are arranged in a specific order that makes up the genetic instructions to make the proteins that help grow an organism. Sequences may change over generations such that even individuals in the same species could acquire slightly different sequences and pass them on to their progeny. This variation in sequences allows us to study how populations change and evolve over generations.

We can also use variation that accumulates in the same genetic region of different species to understand the evolutionary relationships of groups of species. This gives insights into the shared history of a species and its relatives, where its ancestors used to live and how it came to be where it is now.

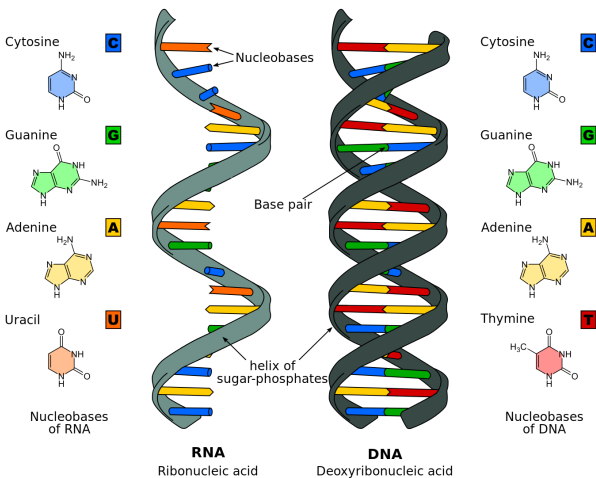


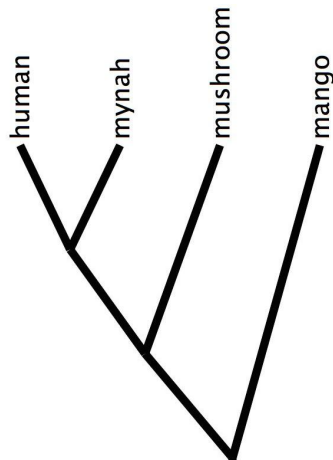
Image: Wikimedia Commons

# How do you make a phylogenetic tree?

To estimate evolutionary relationships, we first align (line up) different sequences to get the best match. We can then identify similarities and differences between the sequences and analyse them to get a family tree called a phylogenetic tree.

The phylogenetic tree is a graph that shows the relationships of sequences – closely related sequences are more closely connected on the tree and distantly related sequences are far apart. In this tree, the human and mynah are more closely related to each other than to any other organism on the tree. The human and mynah are together more closely related to the mushroom than they are to the mango.

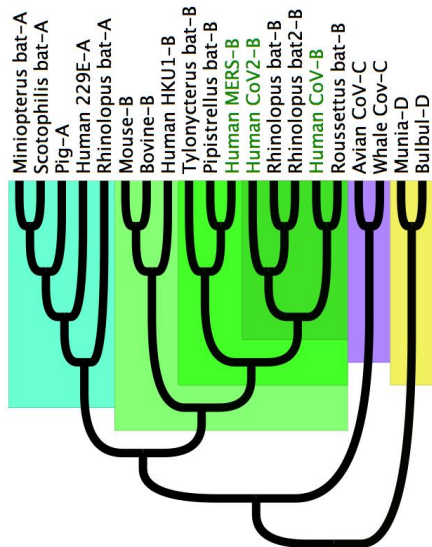
human	A	C	C	T	T	T	G	T	A	G
mynah	A	C	C	T	T	A	G	T	A	G
mushroom	A	C	C	T	T	C	G	T	T	G
mango	A	C	C	T	A	G	G	T	C	C



# Coronaviruses

This tree diagram shows that the closest relative of SARS-CoV-2 is SARS-CoV, which caused the SARS epidemic in 2002-2003. These two SARS viruses are considered to belong to a single species, SARS-CoVs (green). They are closely related to MERS-CoV (which causes a different type of respiratory illness), and HCoV 229E and OC43 (which cause forms of the familiar cold). All of these viruses belong to the same family, Coronaviruses. This large group infect mammals such as humans, bats, civet cats, whales, pangolins (alpha, beta and gamma coronaviruses) and birds (delta coronaviruses).

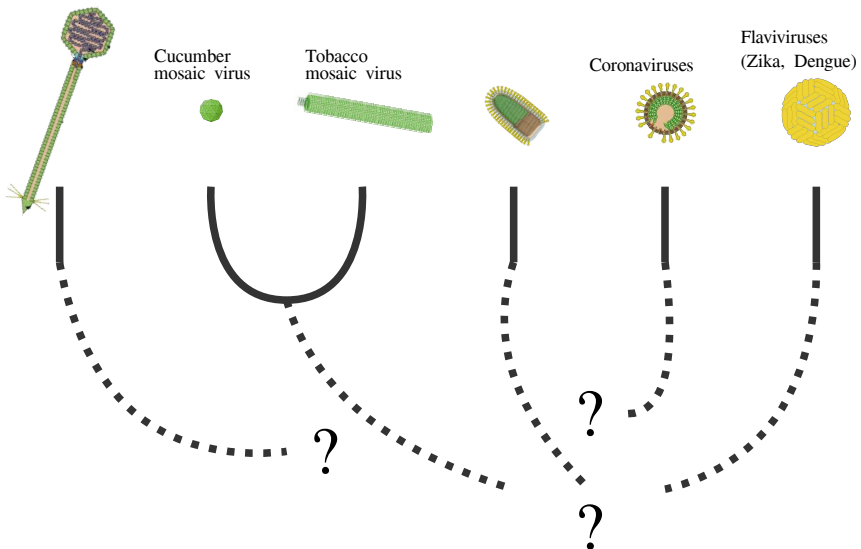
This tree tells us that Alpha- (blue) and Betacoronaviruses (green) commonly infect bats, and that different diseases originate when bat viruses jump to humans, usually via an intermediate host. We also can see the close relationships between the SARS, COVID-19 and MERS viruses.



# How are Coronaviruses related to other viruses?

Like coronaviruses, there are many other groups of viruses (6590 species in 168 families). How are viruses that give you the cold or flu related to coronaviruses? How are they related to viruses that cause dengue or chikungunya? Are viruses that infect humans or other mammals related to the coronavirus?

Gene sequences of coronaviruses have been aligned and analysed to determine relationships among its species. Similar analyses can be done within other families like Flaviviruses which includes Zika and Dengue viruses. Plant viruses like the tobacco mosaic virus and cucumber mosaic virus seem to be related. However, many viruses do not appear to share any genes in common, so it is difficult to determine relationships among them. It is possible that different virus groups arose independently and may not have an origin from a single ancestral virus.



Viron images: ViralZone, SIB Swiss Institute of Bioinformatics

# How are viruses related to us? To insects? To plants? To bacteria?

Organisms like plants, animals and bacteria descended from a common ancestor and are all related to each other in the tree of life. Did viruses evolve from a single ancestor? Would such an ancestor be related to any species on the tree of life? Or are viruses just products of their respective host cells? Are different groups of viruses related to different parts of the tree of life? Can we even place viruses on the tree of life?

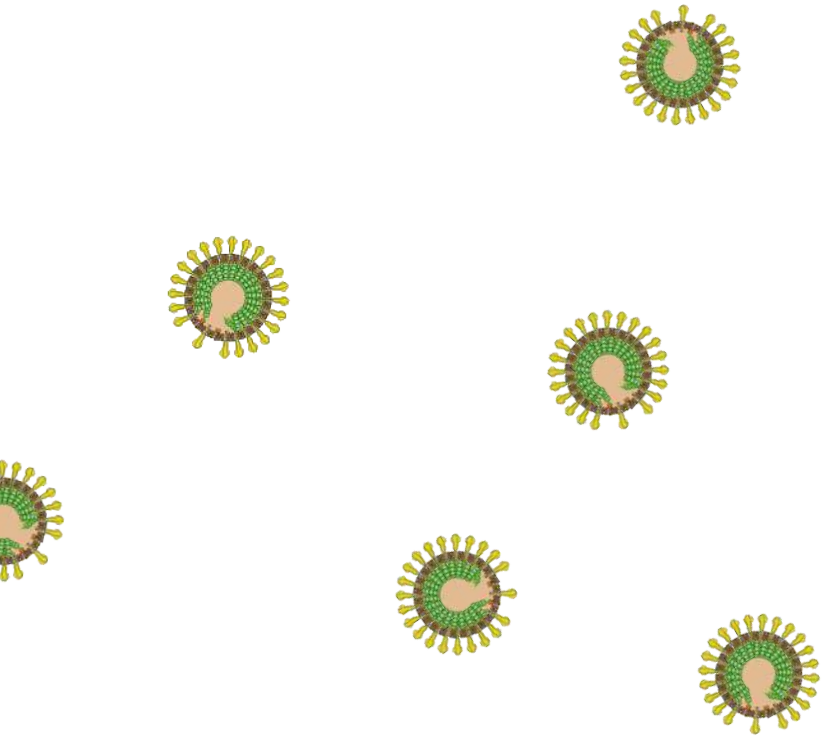
# Are viruses even living organisms?

Viruses do reproduce and evolve, even if this happens only inside their hosts' cells. Is this enough to call them alive? What else do living beings do? They must metabolize, respond to external stimuli and maintain homeostasis. Viruses do none of this. Does that mean viruses are only "partly" alive? Do they need to be alive to be on the tree of life?

Scientists have debated these questions ever since we started studying viruses over 100 years ago. And there are no clear answers yet!

# Why study the evolution of SARS-CoV-2 and other viruses?

Evolution is not just a matter of ancient history of fossils from millions of years ago. Viruses, for example, can evolve very fast, even within months! We can use phylogenetic trees to understand which type of virus might have evolved into the new disease-causing SARS-CoV-2. Reconstructing these phylogenetic trees help us understand the nature of the disease and its epidemiology.



*Viron images: ViralZone, SIB Swiss Institute of Bioinformatics*