

How Our Behaviour Affects Virus Evolution

DR GUL DENIZ SALALI

COVID-19 is caused by the novel coronavirus (Sars-Cov-2), but coronaviruses have been among us for years.

Coronaviruses are a large family of viruses, and different strains (genetic variants) choose different species as their hosts. Many people may have first heard about coronaviruses during the 2002-2004 SARS outbreak, when a strain was able to infect multiple species, including humans, causing at least 774 deaths worldwide. In fact, it was after the SARS outbreak where scientists found that [coronaviruses originate in bats](#). Since then, scientists have reported a diverse range of [SARS-like coronaviruses](#) found in bats in China, Europe and Africa.

But not all coronaviruses have the ability to infect humans.

So, what causes the coronavirus to spill-over into humans (i.e. when a pathogen is transmitted from the “reservoir species” to a new one)? Viruses can only replicate inside living organisms. Therefore, from a virus’ point of view, the more living organisms it can infect the better it can replicate and pass on its genes. Places where various species of animals are found together in great quantities are perfect hotspots for viruses to replicate and potentially evolve to infect more than one species. Although we do not know how exactly the [novel coronavirus jumped from bats to other animals](#) including humans, it is mostly likely the result of our interaction with wildlife. Research papers (like [this one](#)) have warned us to take precautions with wildlife as they foresaw potential future outbreaks. Bill Gates, in his now-famous [2015 TED talk](#), warned us against a very possible future pandemic where a respiratory virus can cause a severe global crisis. The difficulty with respiratory viruses is that they are very contagious (unlike other types of viruses, like ebolaviruses, which spread through direct contact with body fluids).

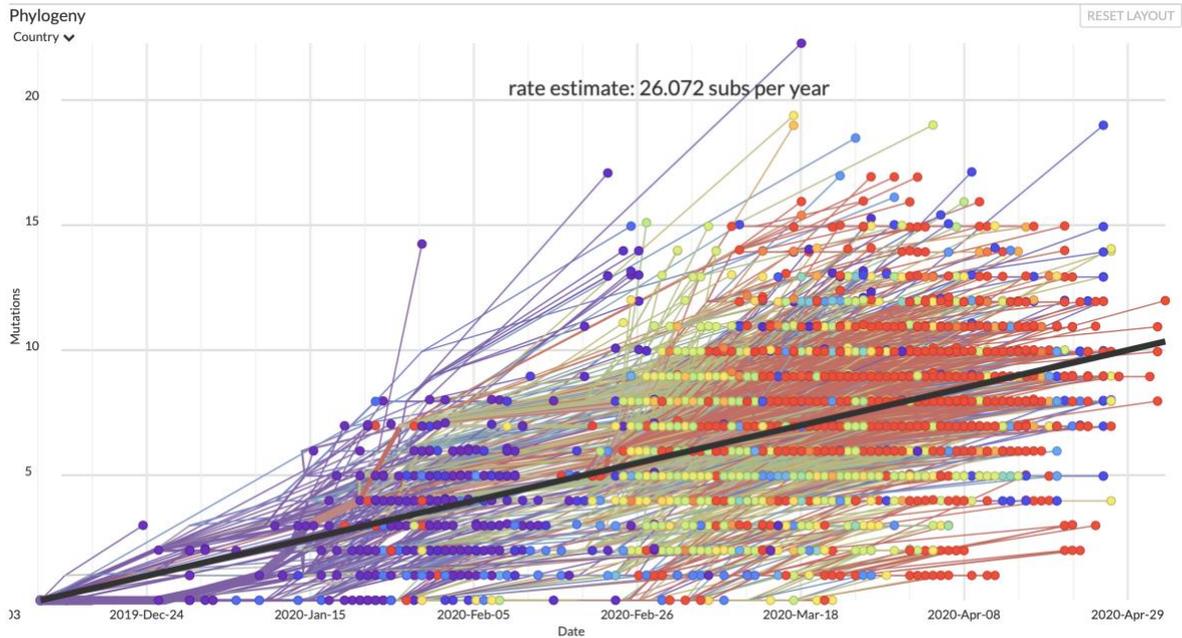
Interaction with wildlife is therefore one factor that can influence the evolution of coronaviruses that infect humans. I have been conducting fieldwork at the heart of the Congo rainforest, where bushmeat is a vital source of protein for local communities. While local and indigenous communities have lived sustainably consuming forest resources for thousands of years, developments such as [industrial logging](#) leads to increasing population sizes from an inflow of workers, resulting in growing demands for bushmeat. It is important to acknowledge that it is not the local communities that are to blame for the origin of new viruses, but increasing consumerism and the consequent need for resource extraction and development. If we were to prevent future pandemics, we all need to change our behaviour- including the consumers who create the demand for industrial logging.



Wild antelope in a meat market in Congo. Photo by: Gul Deniz Salali

Is the novel coronavirus evolving?

[Yes](#), but we do not know yet if the new mutations will make the virus more contagious or deadly. Organisms have different generation times (the length of time between the birth of an individual and the birth of its offspring): while a bacterium can divide every 20 minutes, for us humans the average generation time ranges between 22 to 33 years. Those with shorter generation times evolve faster. This leads to an *arms race* with many pathogens, such as the ones that cause malaria or AIDS, where they evolve to become more resistant to the drugs we use to treat them. Evolutionary approaches to health and disease are of vital importance in tracking the past and the future of the pathogens. By using phylogenetic trees, for example, researchers have been [tracing the origin and evolution](#) of the novel coronavirus. These trees also inform us on when and from where the virus is first introduced to a country. A recent [phylogenetic analysis of 30 SARS-CoV-2 genomes isolated in Turkey](#), for example, showed that the virus is introduced to the country from multiple independent locations and earlier than the first reported case of COVID-19.



A phylogenetic tree showing evolutionary relationships of SARS-CoV-2 viruses from the ongoing novel coronavirus COVID-19 pandemic (source: nextstrain.org).



A possible route of introduction of SARS-CoV-2 viruses to Turkey, obtained by using phylogenetic analyses (source: Adebali et al 2020, BioRxiv)

From an evolutionary point of view, it is advantageous for a virus to multiply as quick as possible to spread its genes – but it also needs to avoid killing its host, since it needs living organisms to multiply and spread. The level of damage a virus causes to its host is called virulence. If a virus is very virulent, it may make the host less mobile and reduce its contact with potential other hosts. Therefore, there is a “virulence-transmission trade-off,” where the virus needs to ensure it can multiply enough without killing its host, so it can spread. The virulence-transmission trade-off can be impacted by the virus’s access to hosts: If there are many potential hosts in close

proximity it can infect (like soldiers staying closely together in the trenches during the World War 1, which [triggered the 1918 influenza pandemic](#)), then the virus may evolve to be more virulent as it can spread easily from host to host, even if it causes the host to demise quickly.



1914, World War 1. Highland Territorials in a trench. Photographer: H. D. Girdwood. Source: [unsplash.com](#)

The chances of the novel coronavirus mutating to a new strain with higher or lower virulence, therefore, partly depends on [how easily it can spread among hosts](#). For now, we are lucky that the SARS-CoV-2 has a [proof-reading](#) mechanism which makes it mutate, and consequently evolve, at a slower rate. In comparison, influenza viruses, which do not have such mechanism, evolve faster. This is why we need to develop new flu vaccines each year. What we can say is that as long as the novel coronavirus is being transmitted happily among its new host- humans, it is less likely to disappear.

ABOUT THE AUTHOR

Dr [Gul Deniz Salali](#) is a British Academy research fellow and lecturer in Evolutionary Anthropology at UCL. She researches human behaviour and health using evolutionary approaches and teaches Evolutionary Medicine Master's course as part of the [Human Behaviour and Evolution \(HBE\)](#), and [BioSocial Medical Anthropology](#) Master's programmes.

REFERENCES

Ewald, P. W. (1993). The evolution of virulence. *Scientific American*, 268(4), 86-93.

Humphreys, M. (2018). The influenza of 1918: Evolutionary perspectives in a historical context. *Evolution, medicine, and public health*, 2018(1), 219-229.

Li, W., Shi, Z., Yu, M., Ren, W., Smith, C., Epstein, J. H., ... & Zhang, J. (2005). Bats are natural reservoirs of SARS-like coronaviruses. *Science*, 310(5748), 676-679.

Andersen, K. G., Rambaut, A., Lipkin, W. I., Holmes, E. C., & Garry, R. F. (2020). The proximal origin of SARS-CoV-2. *Nature medicine*, 26(4), 450-452.

Ge, X. Y., Li, J. L., Yang, X. L., Chmura, A. A., Zhu, G., Epstein, J. H., ... & Zhang, Y. J. (2013). Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. *Nature*, 503(7477), 535-538.

Menachery, V. D., Yount, B. L., Sims, A. C., Debbink, K., Agnihothram, S. S., Gralinski, L. E., ... & Swanstrom, J. (2016). SARS-like WIV1-CoV poised for human emergence. *Proceedings of the National Academy of Sciences*, 113(11), 3048-3053.

Adebali, O., Bircan, A., Circi, D., Islek, B., Kilinc, Z., Selcuk, B., & Turhan, B. (2020). Phylogenetic Analysis of SARS-CoV-2 Genomes in Turkey. *BioRxiv*, 2020.05.15.095794. <https://doi.org/10.1101/2020.05.15.095794>

Dr Vaughn Cooper video on the evolution of SARS-CoV-2:
<https://www.youtube.com/watch?v=MHRGPzoFyEM&feature=youtu.be>