

COVID-19 (COronaVirus disease 2019) background:

First case identified in December 2019 in Wuhan China

caused by SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) virus

SARS-CoV-2 virus is a positive-sense single-stranded RNA virus

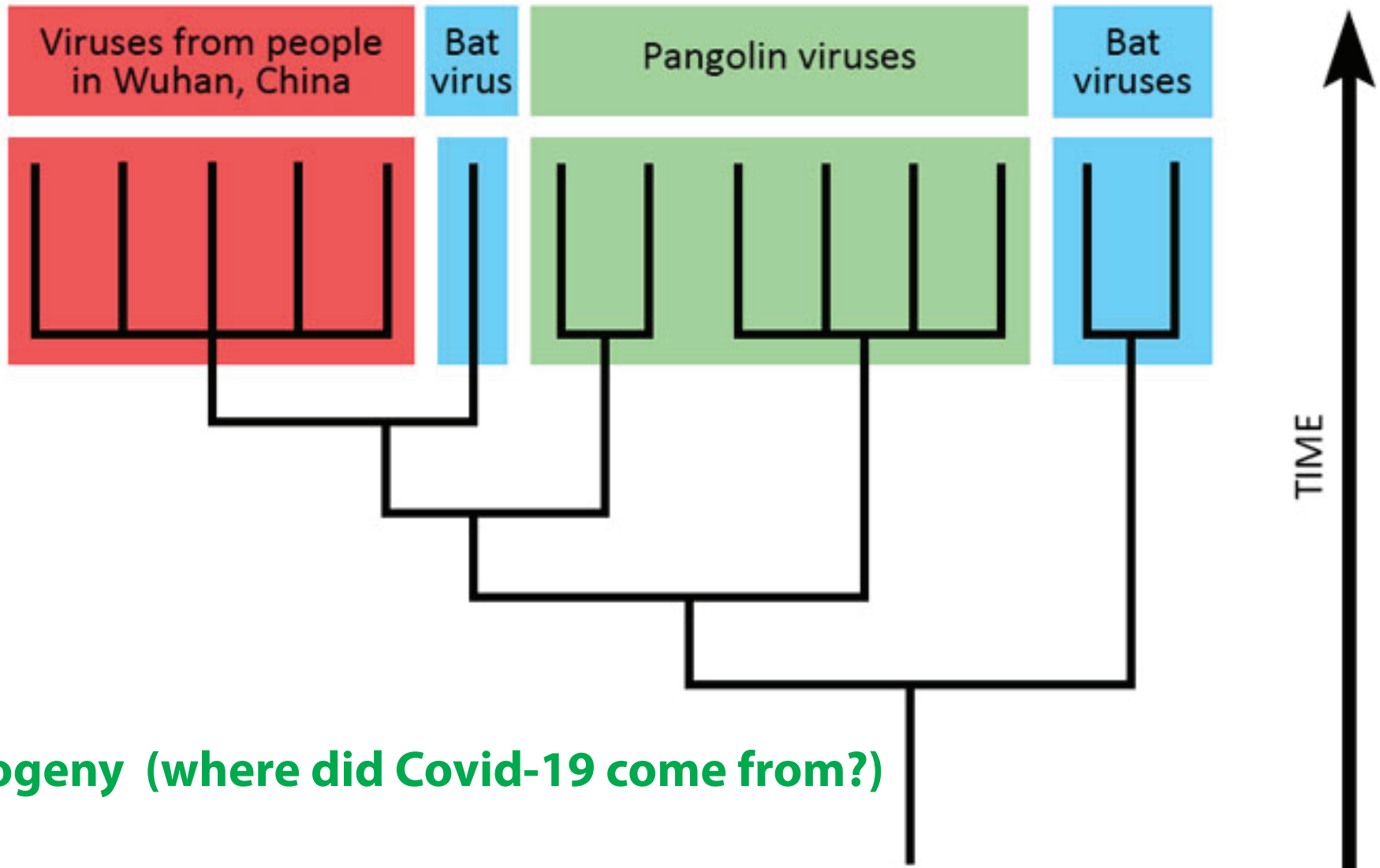
“positive-sense” RNA virus -- can act as mRNA and therefore can be **directly** translated into protein

“negative-sense” RNA virus has genome being complementary to mRNA so that mRNA must be synthesized via RNA-dependent RNA polymerase

SARS-CoV-2 virus:  
29,903 bases  
(Large for RNA virus!)

Human genome:  
about 3.2 billion bases

## CORONAVIRUS EVOLUTIONARY TREE



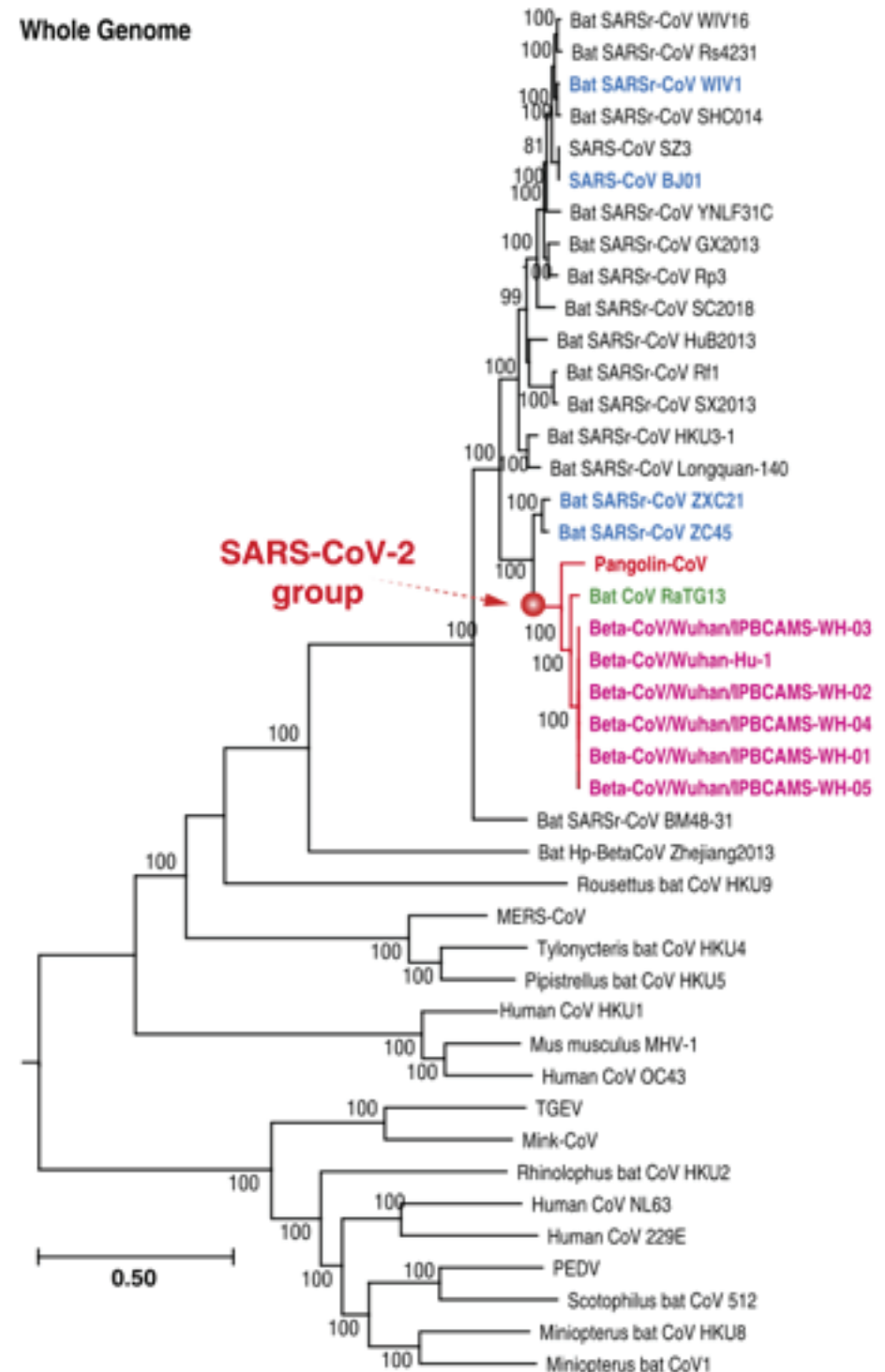
**Phylogeny (where did Covid-19 come from?)**

**Zoonotic Transfer History**

Phylogeny of the SARS-like coronaviruses.  
From: Zhang et al. (Current Biology, 2020)  
[Redirecting]  
(<https://doi.org/10.1016/j.cub.2020.03.022>)  
[copied in turn from Dr. David Rasmussen]

**Update: An “in press” Nature article**  
Cave bats in Laos found to harbor  
closer virus sequences to human  
pandemic sequences than those  
previously known. Also, different  
regions of viral genome of that  
causing human pandemic seem to  
have come from different ancestors  
 (“a mosaic history”).

(Temmam, S. et al. Bat coronaviruses  
related to SARS-CoV-2 and infectious for  
human cells. Nature  
[https:// doi.org/10.1038/s41586-022-04532-4](https://doi.org/10.1038/s41586-022-04532-4). 2022)



# Is Covid-19 genetically engineered?

Andersen et al. 2020. The Proximal Origin of SARS-CoV2. Nature Medicine.

RaTG13 viral sequence from a bat is 96% identical to HCoV-19 genome.

But (!), virus from pangolins is more similar to Receptor Binding Domain (RBD) in HCoV-19 & 6 key RBD residues from pangolin viruses identical to HCoV-19 ones (only 1 of 6 identical to HCoV-19 in closest bat sequence).

RBD binds to human ACE receptor to allow virus to enter cells.

HCoV-19 RBD differs from previously identified optimal RBD sequence

(Also, HCoV-19 genome substantially different than coronavirus genomes studied by molecular geneticists )