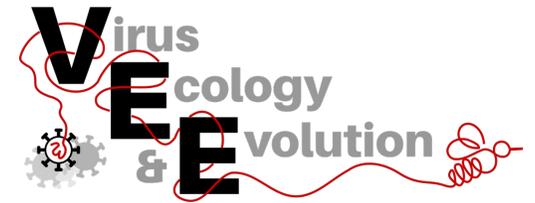




university of
 groningen

faculty of science
 and engineering

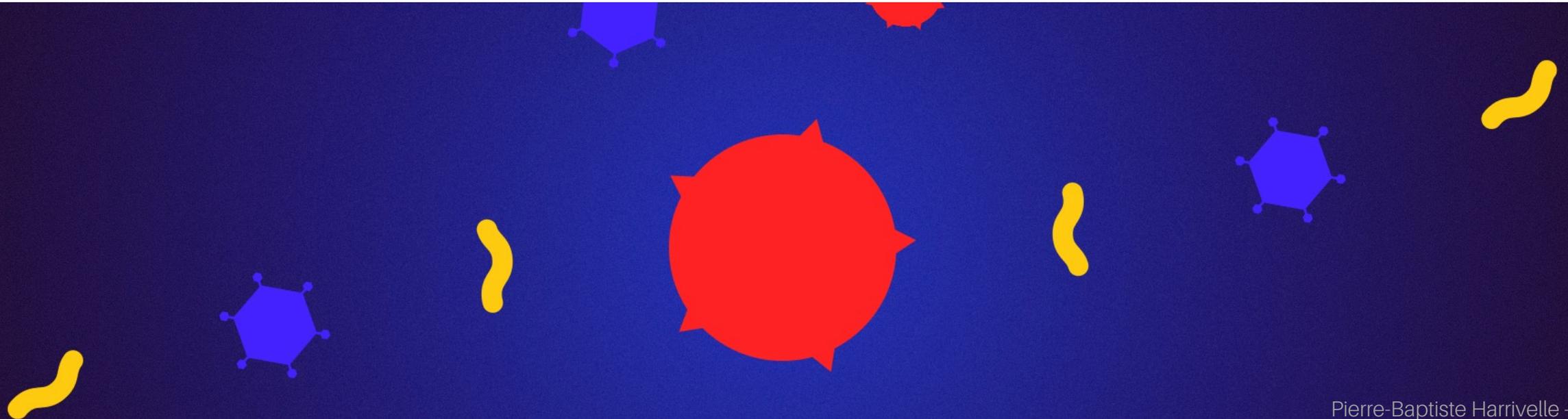
groningen institute for
 evolutionary life sciences



The constant change of viruses

– evolutionary biology in action

Sebastian Lequime (Assistant professor) s.j.j.lequime@rug.nl



Outline

1 What are viruses?

2 SARS-CoV-2

3 How do RNA viruses evolve?

4 Evolution and future of SARS-CoV-2

Outline

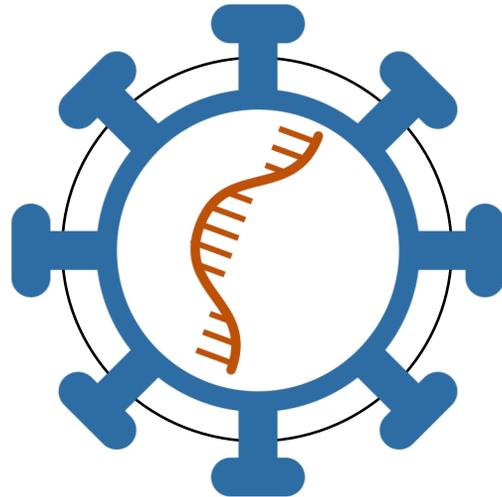
1 What are viruses?

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“A virus is a piece of (bad) news wrapped in protein”.
– Peter Medawar (Nobel Prize 1960)



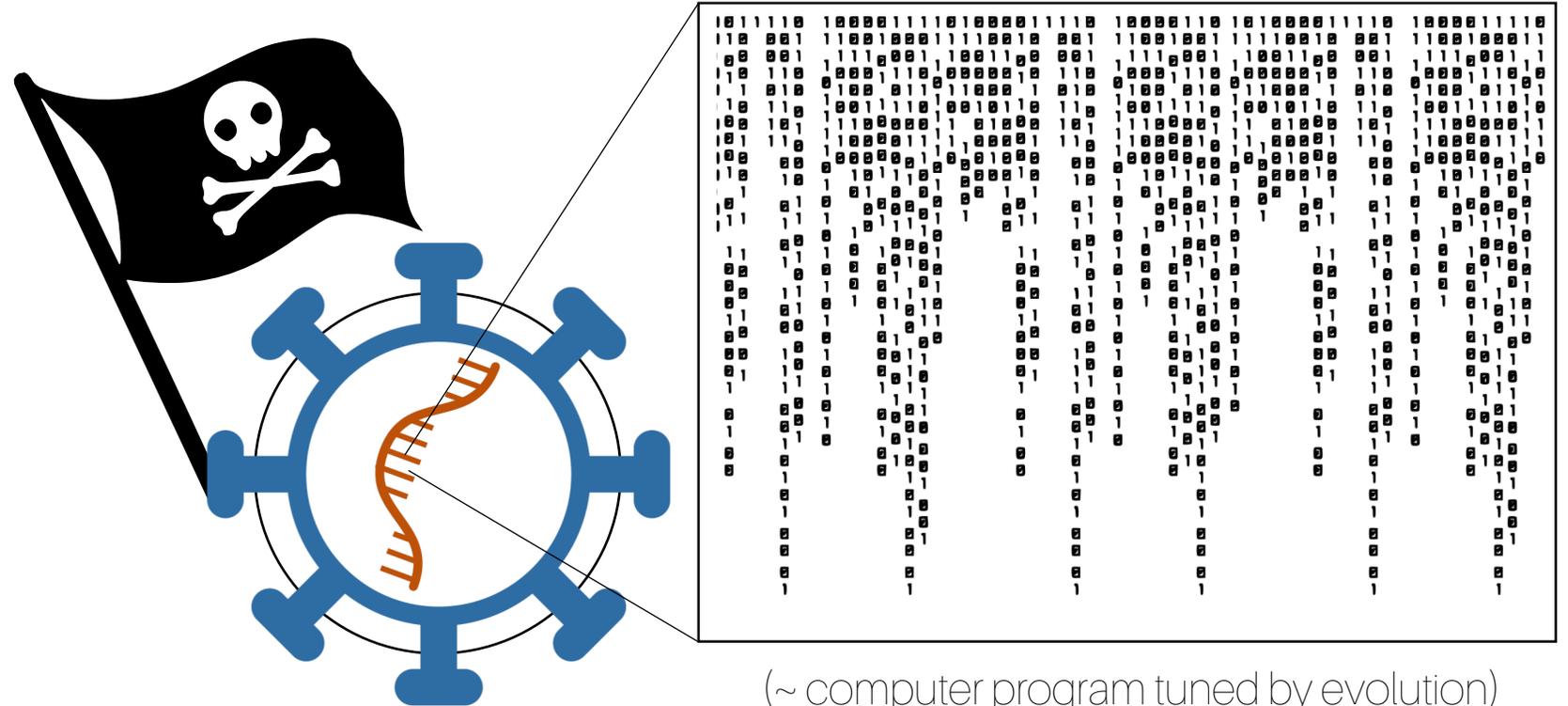
“Viruses appear to be **obligate parasites** in the sense that their reproduction is **dependent** on living cells”.

– Thomas Milton Rivers (1926)



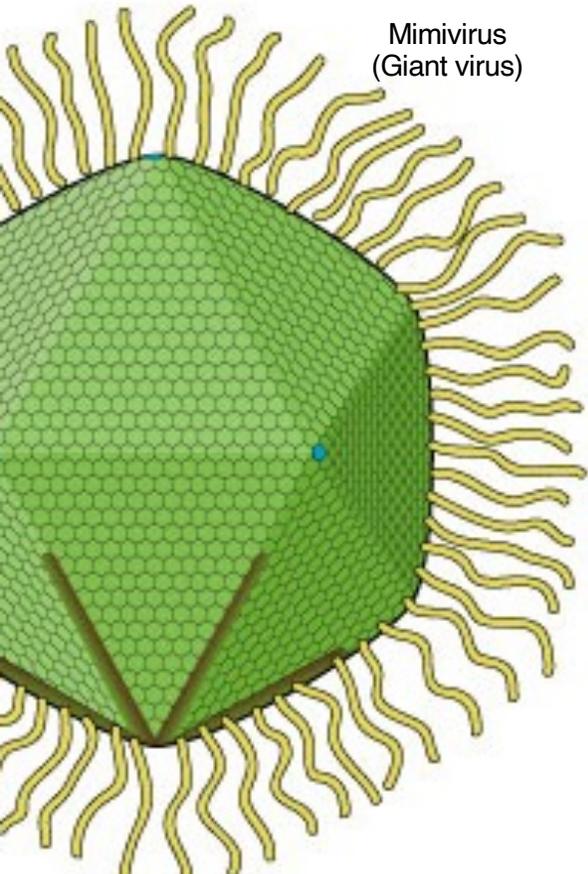
Viruses are passive agents!

– Vincent Racaniello (at least 2012)

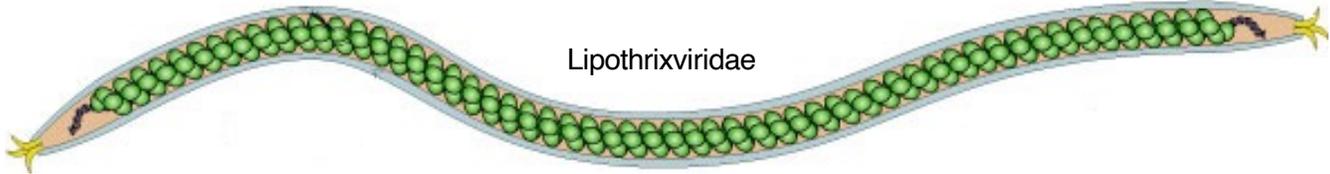


(~ computer program tuned by evolution)

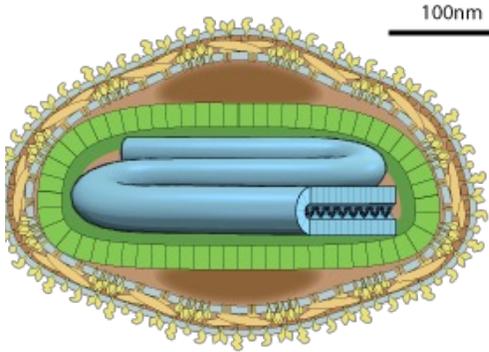
Diversity



Mimivirus
(Giant virus)

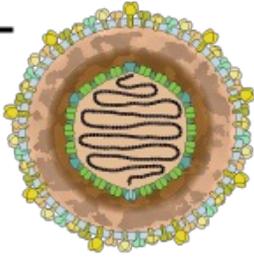


Lipothrixviridae

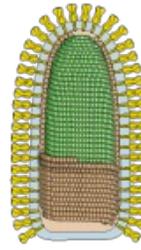


100nm

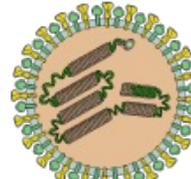
Variola virus
360nm



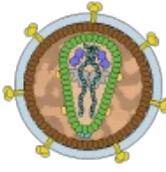
Herpesvirus
200nm



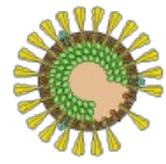
Rabies
180x80nm



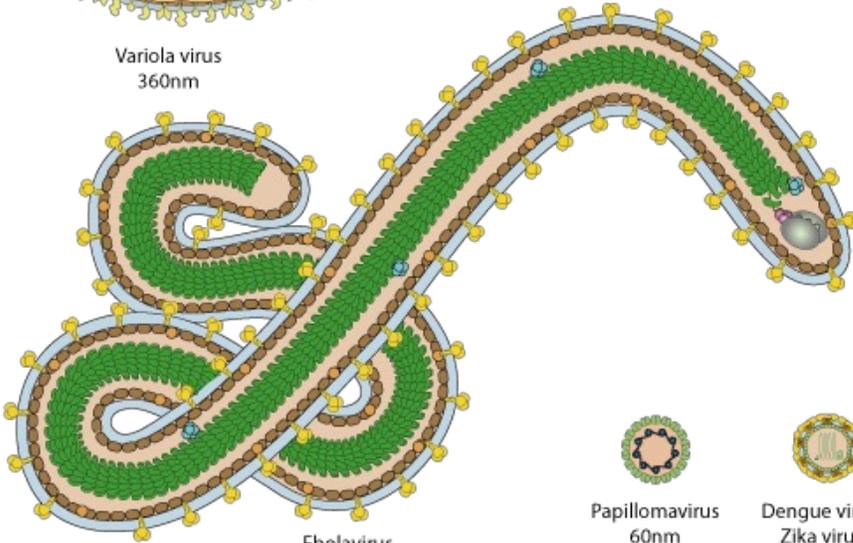
Measles
150nm



HIV-1
120nm



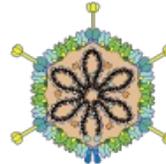
SARS
120nm



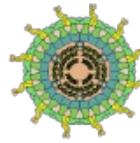
Ebolavirus
80x970nm



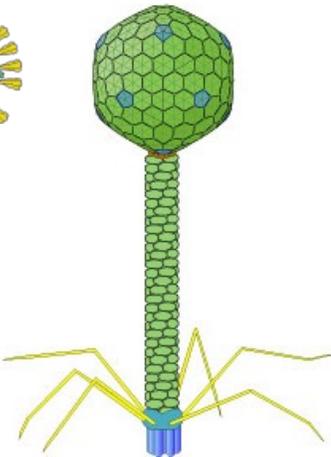
Influenza virus
100nm



Adenovirus
90nm



Rotavirus
80nm



Bacteriophages



Papillomavirus
60nm



Dengue virus,
Zika virus
50nm



Hepatitis C virus
50nm



Hepatitis B virus
42nm



Hepatitis A virus,
Poliovirus
30nm



Parvovirus
20nm



Abundance

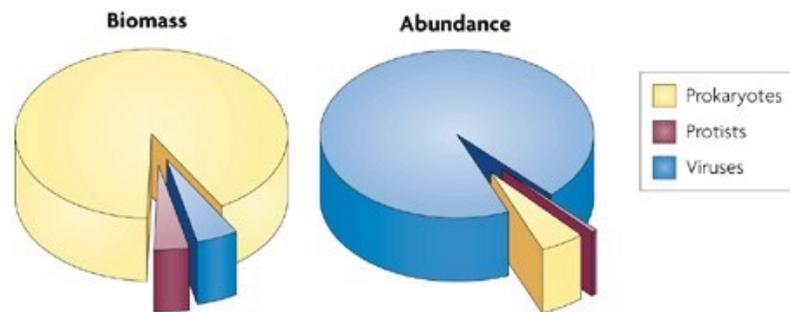
All three domains of life have been found infected by viruses

For example, marine viruses:

10^{30} viruses in the entire marine biota (estimate)

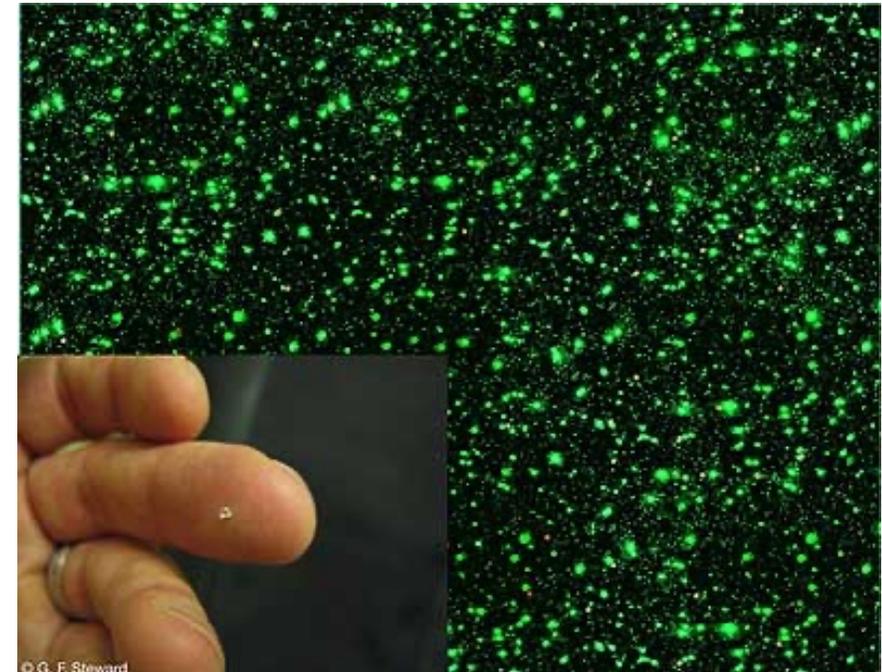
10^{23} viral infections every second (estimate)

Viruses kill about 20% of the total microbial biomass every day forcing a constant and large-scale turnover



Suttle 2005 Nature
<https://www.nature.com/articles/nature04160>

Wietz et al 2017 Nature
<https://www.nature.com/articles/nature23295>



© G. F. Steward

Abundance

Gray whale $\sim 10^6$ calicivirus per gram of feces

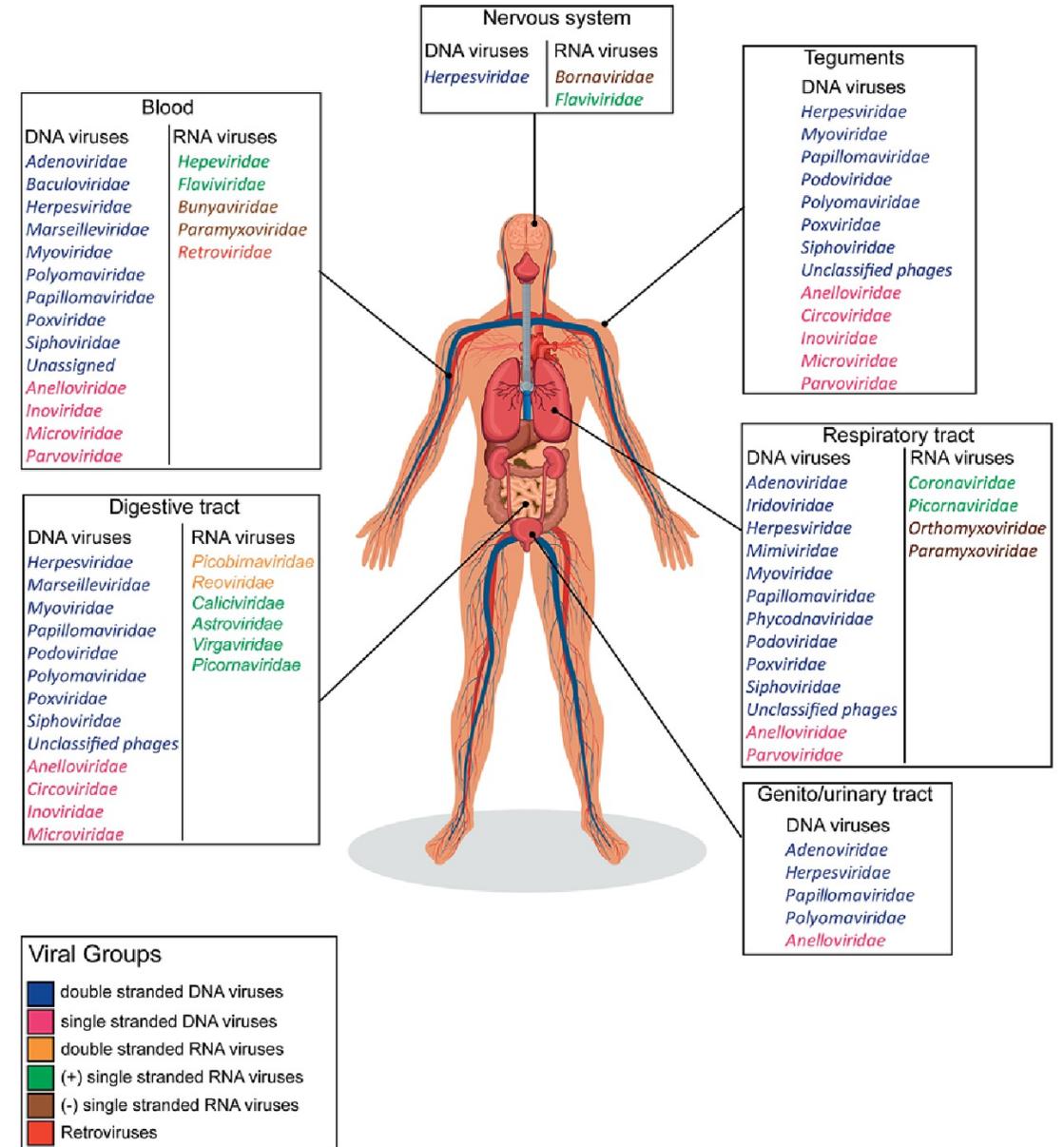
Excretes 10^{13} (10,000,000,000,000) viral particles every day

Abundance

Viruses are part of any microbiome

Infecting directly the host (e.g. Herpesviruses)

Infecting other members of the microbiome





Viruses...

...are everywhere

Especially when you study biology :

- Molecular biology
- Cell biology
- Genetics
- Ecology
- Evolution
- Medical sciences (diseases and treatments)
- Biochemistry
- Epidemiology
- Computational biology

Outline

1 What are viruses?

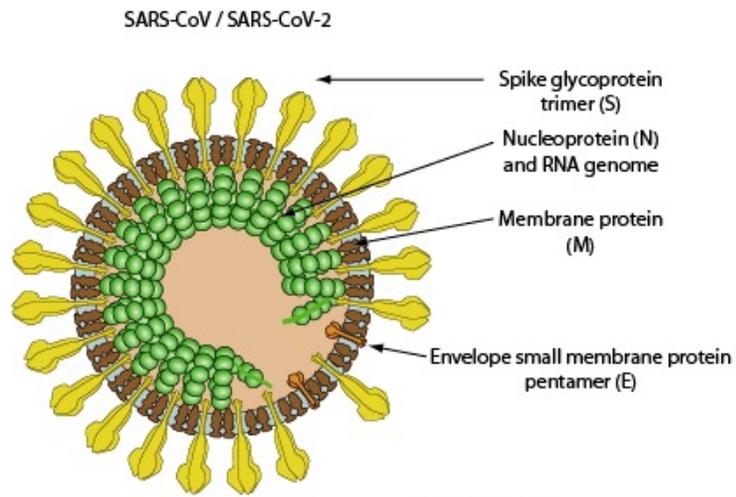
2 SARS-CoV-2

3 How do RNA viruses evolve?

4 Evolution and future of SARS-CoV-2

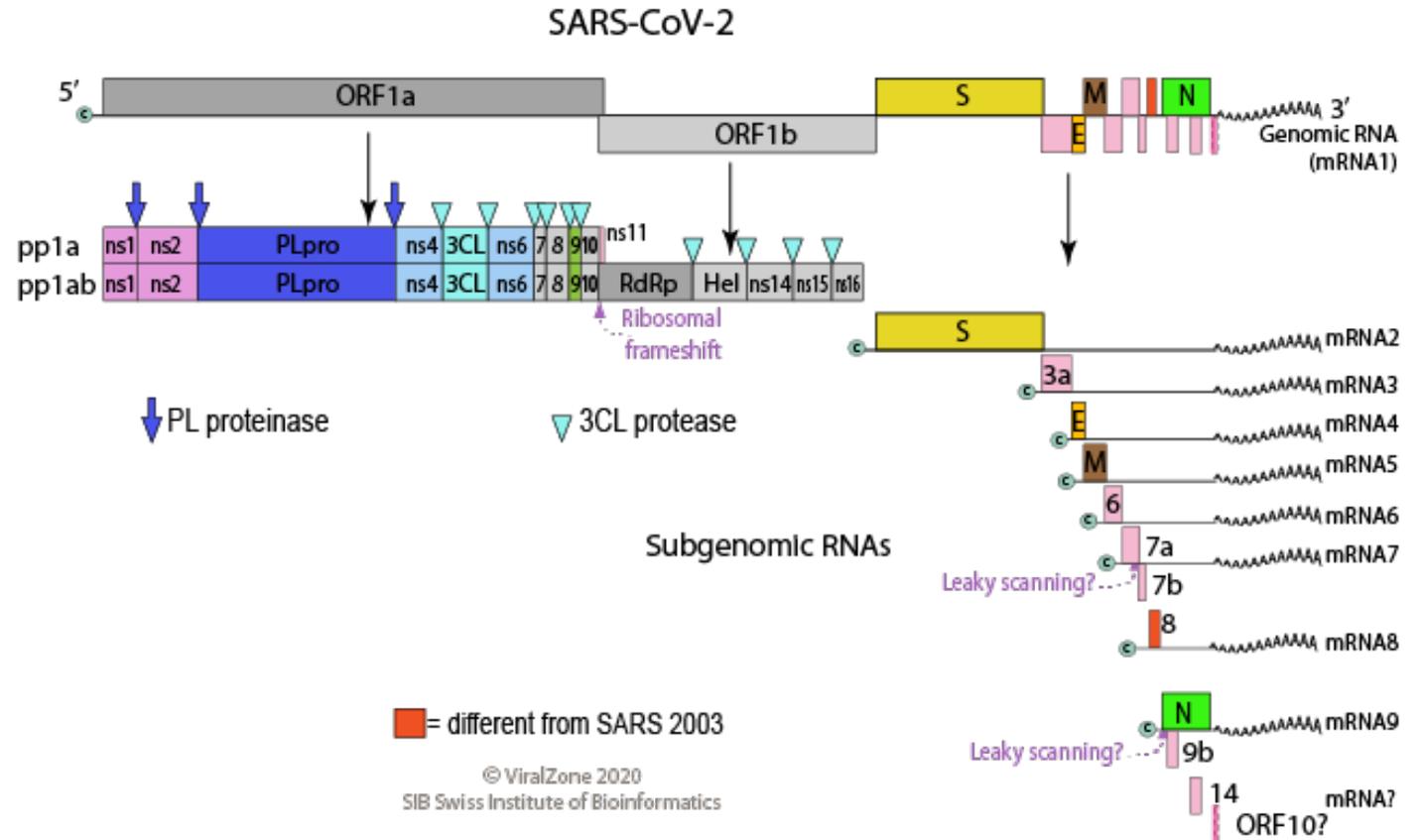
SARS-CoV-2

Betacoronavirus



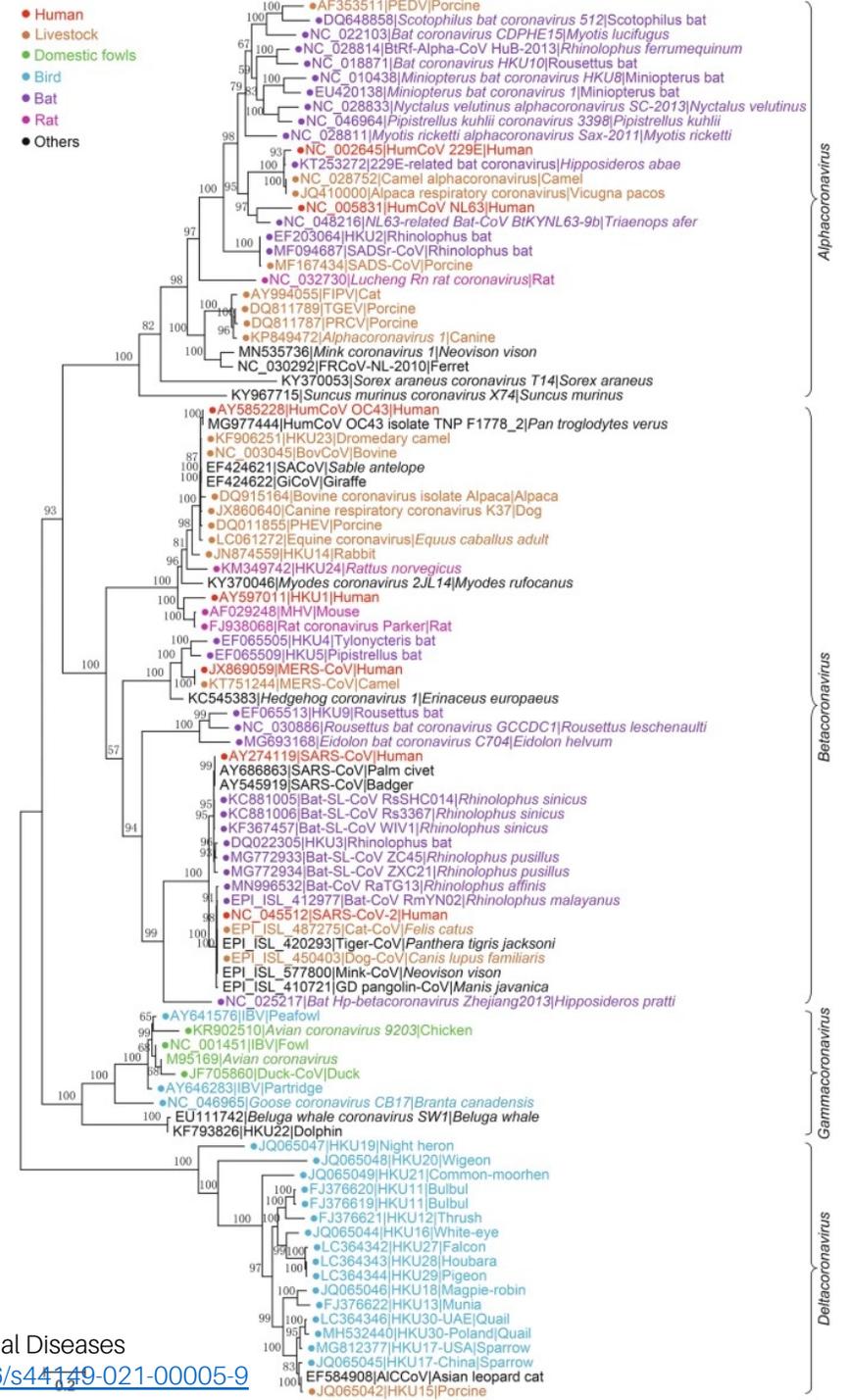
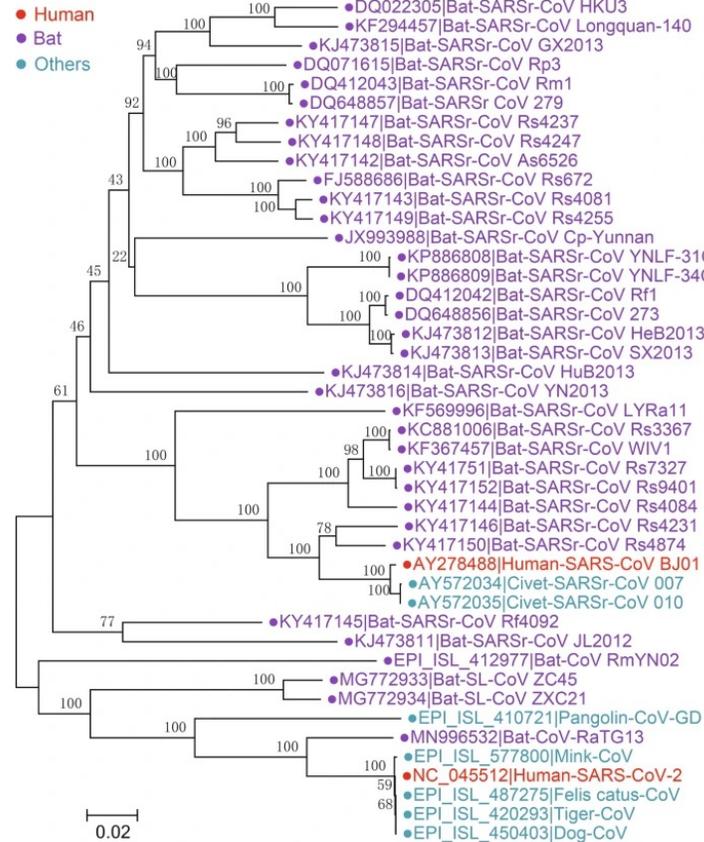
© ViralZone 2020
SIB Swiss Institute of Bioinformatics

Monopartite
Linear ssRNA(+) genome
29.9 kb in size
13 Open reading frames



Betacoronavirus

Diverse sets of hosts (mammalians)



Outline

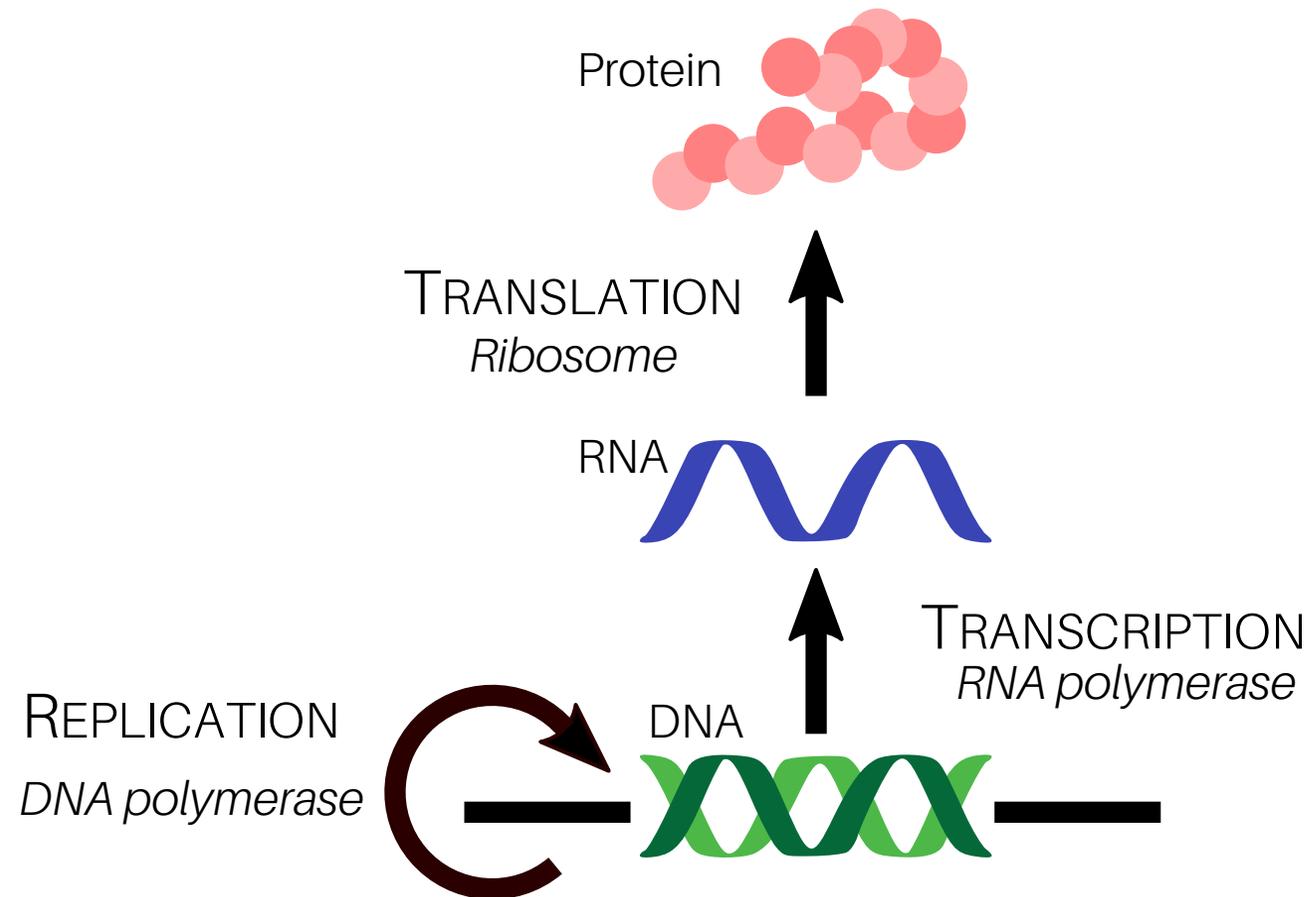
1 What are viruses?

2 SARS-CoV-2

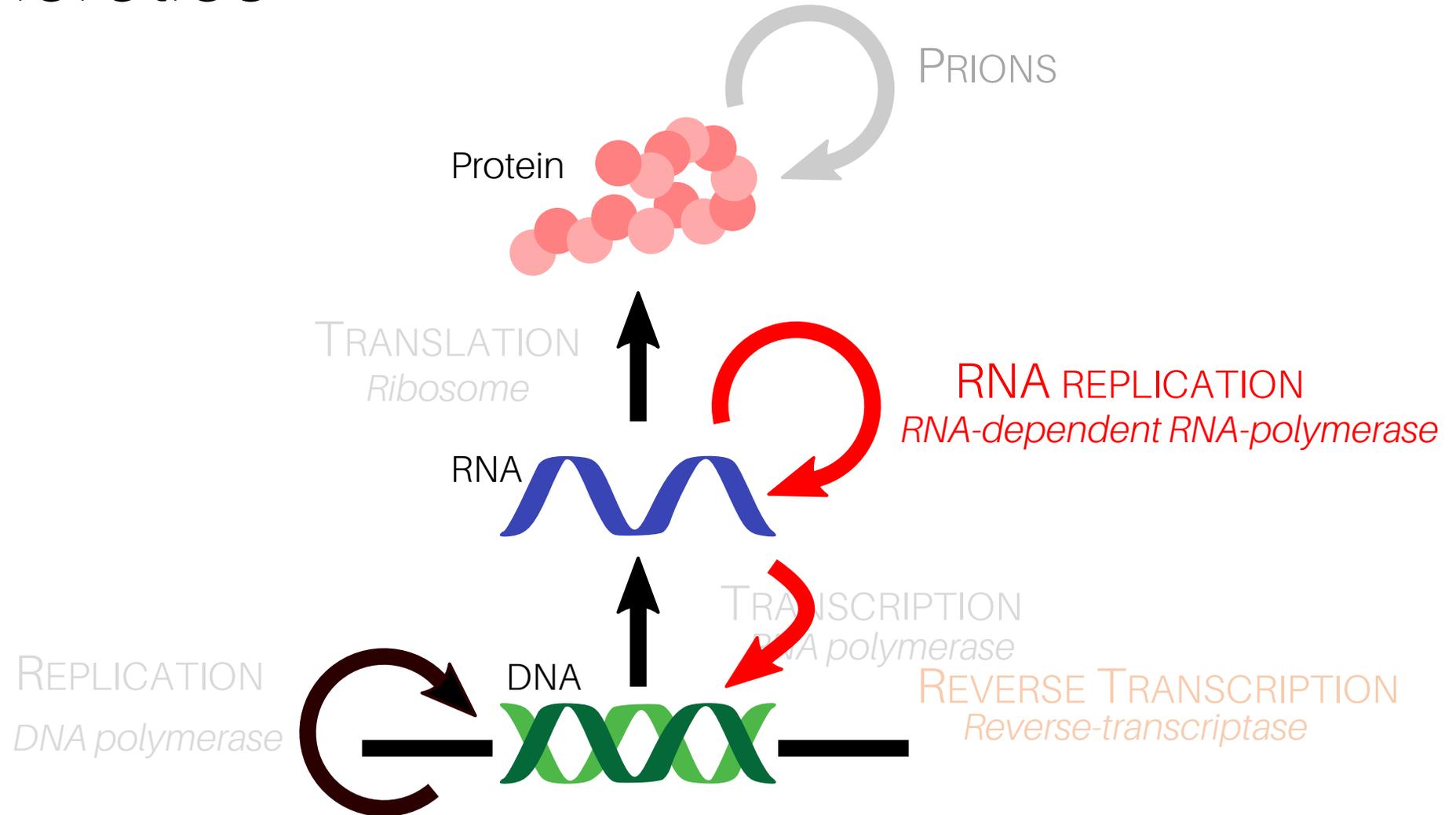
3 How do RNA viruses evolve?

4 Evolution and future of SARS-CoV-2

Central dogma of molecular biology



Viral heretics



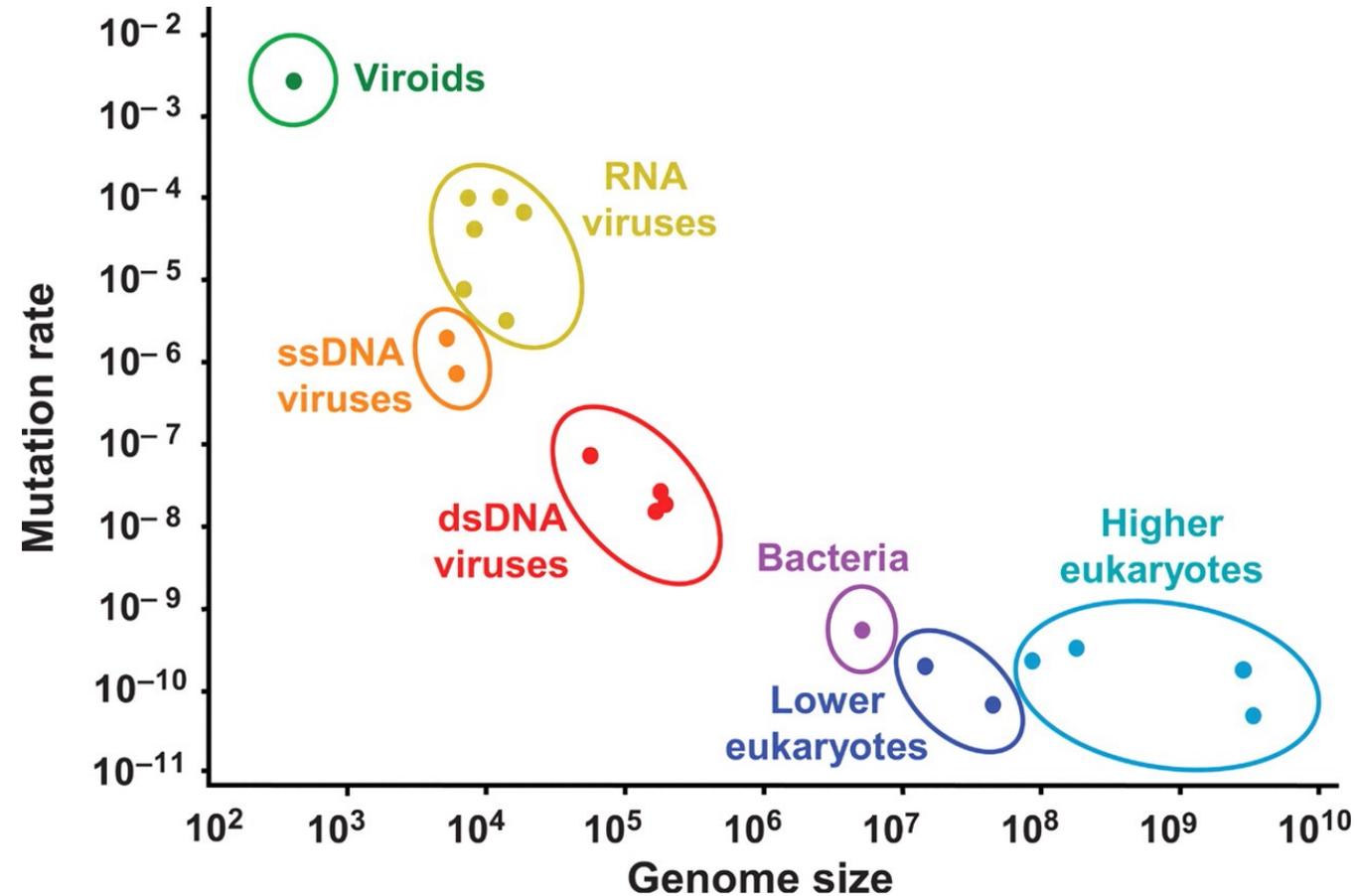
RdRP is error-prone

DNA polymerase: 10^{-7} to 10^{-9} error/nt replicated

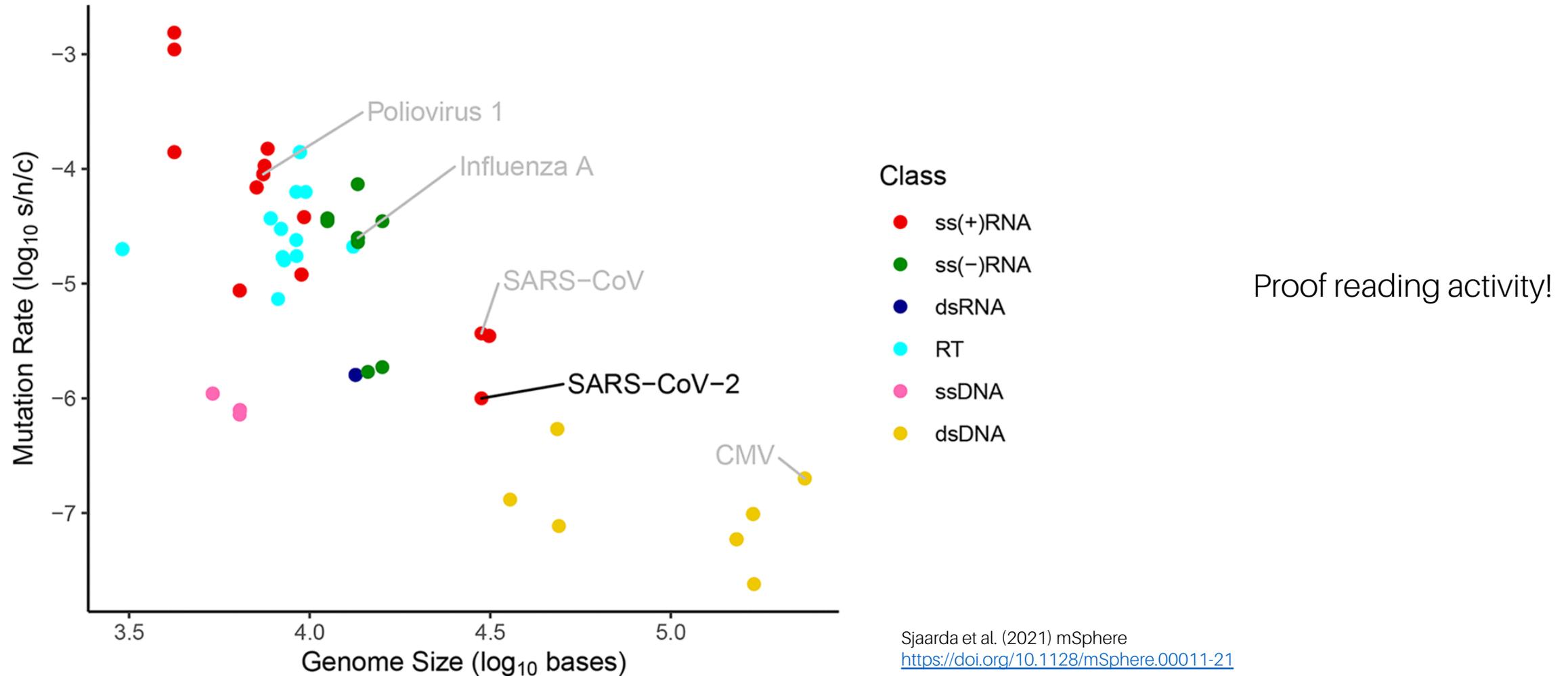
RdRP: 10^{-3} to 10^{-5} error/nt replicated

lack of proofreading ability in RNA polymerases

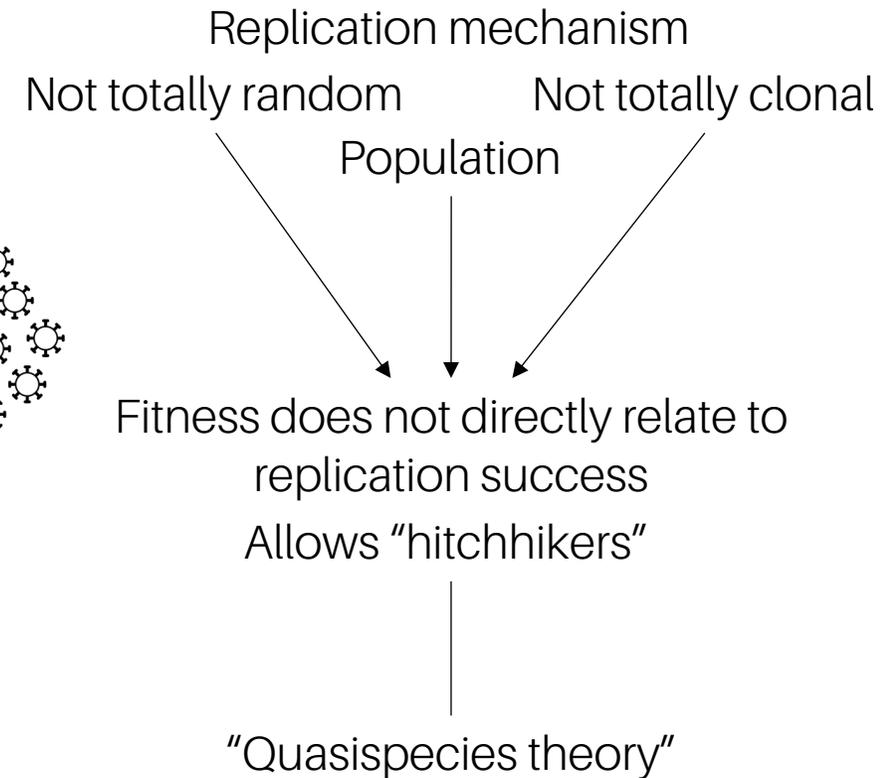
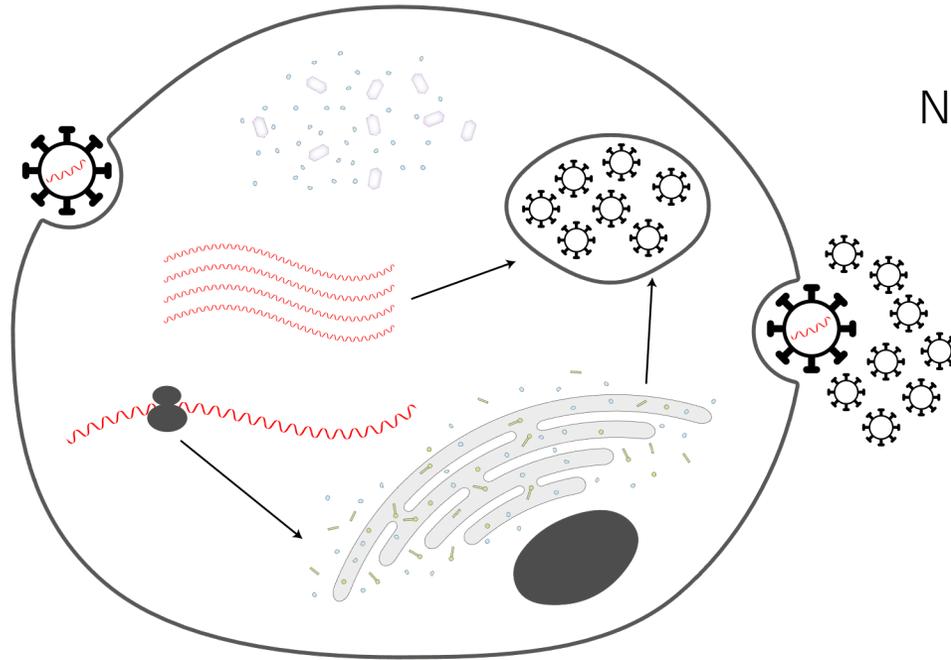
Virus mutation rate



SARS-CoV-2's RdRP is slightly less error-prone



Within-host evolution



Lauring and Andino (2010) PLoS Pathogens

Between-host evolution

Viral population is shaped by:

Bottleneck,

Immune response,

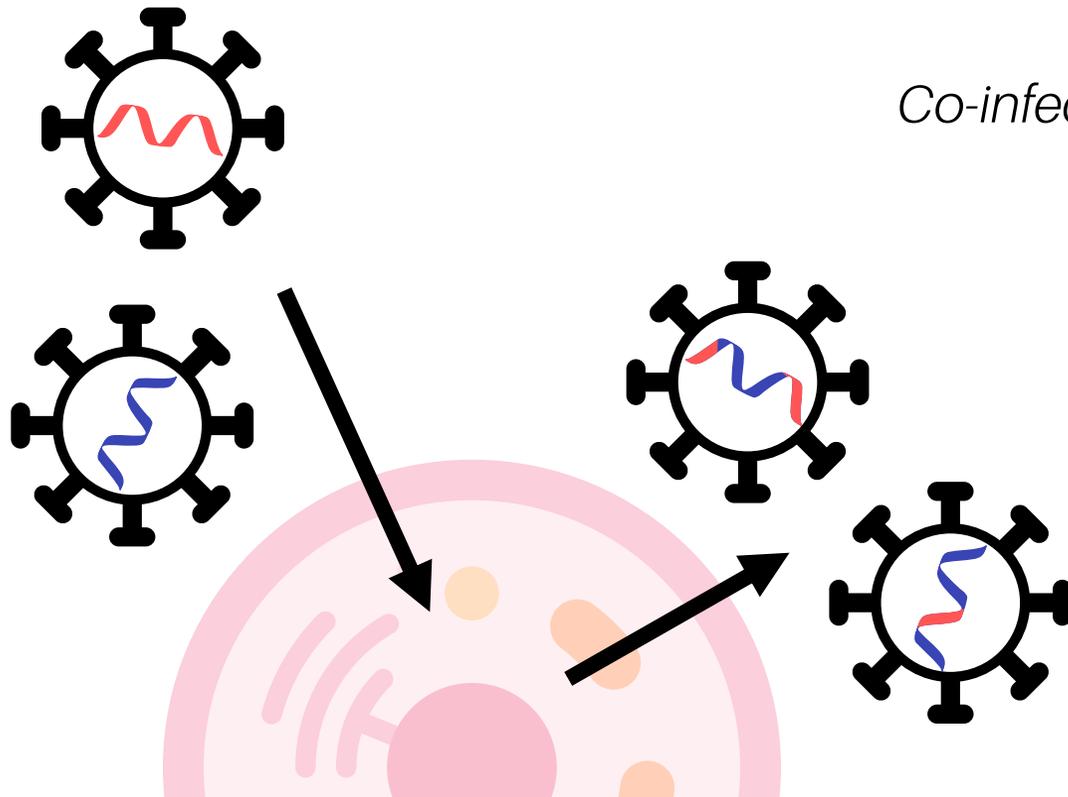
Host genetic background & physiology,

Environment...

~ It's a complex mess.

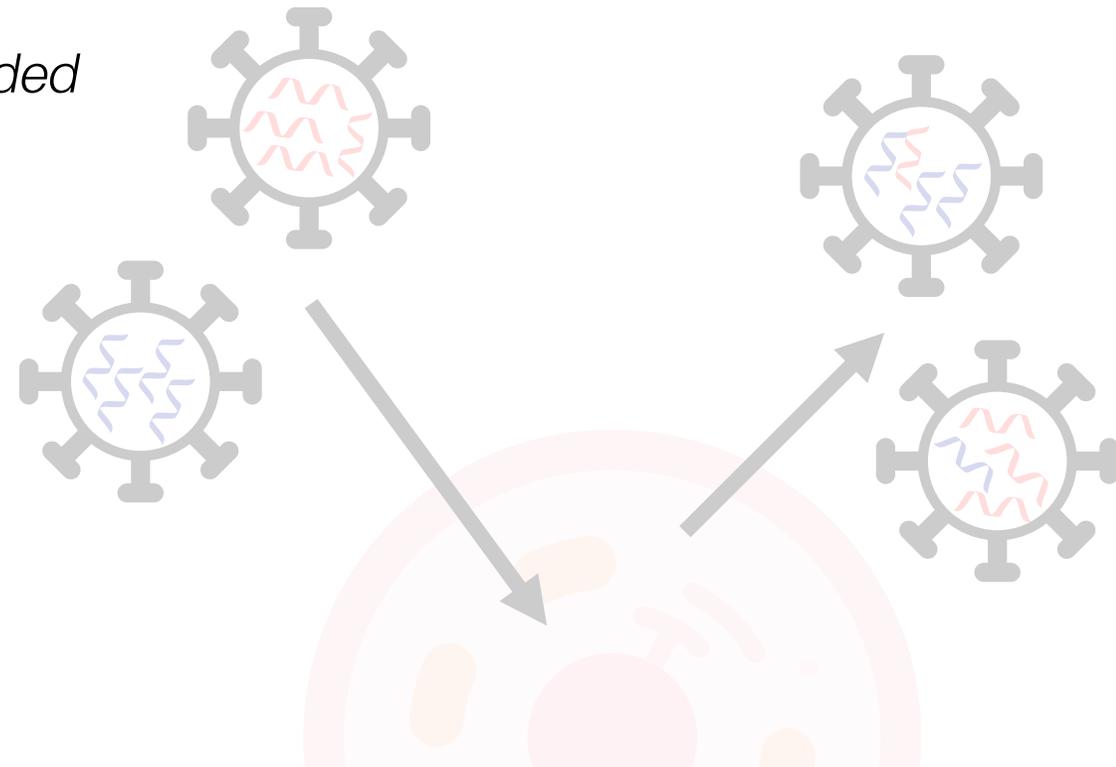
Other mechanisms of virus evolution

Recombination

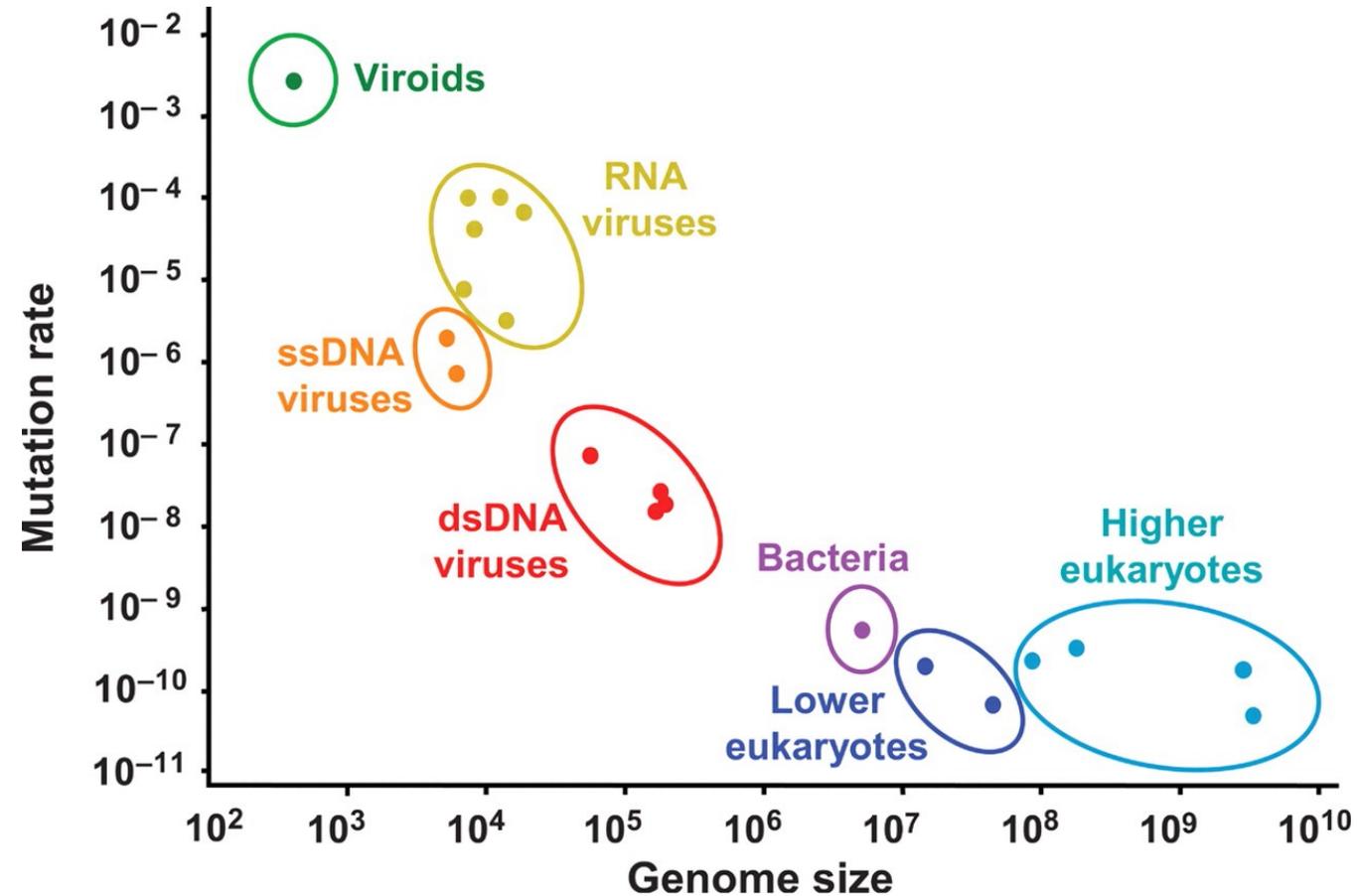


Co-infection is needed

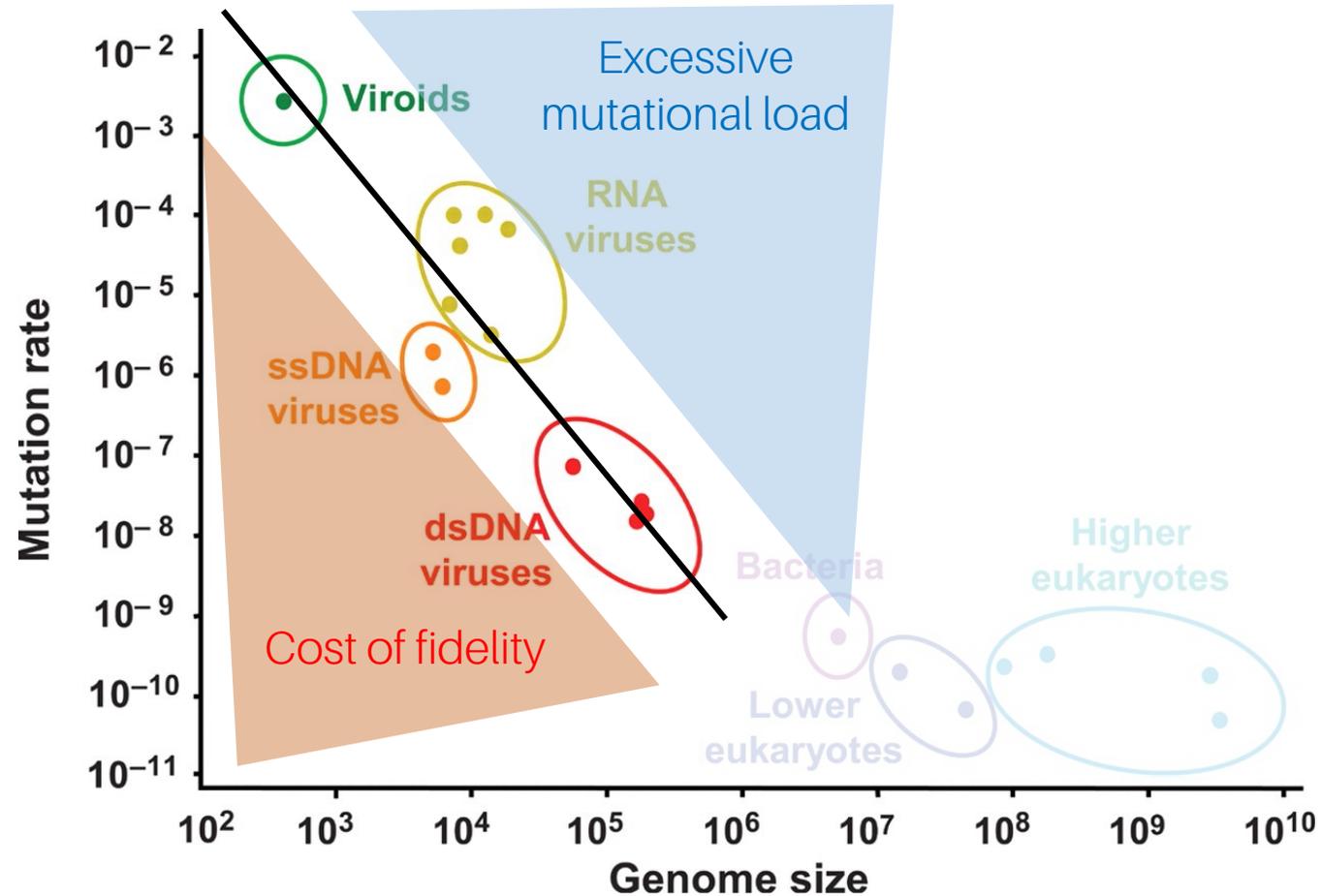
Reassortment



Virus mutation rate



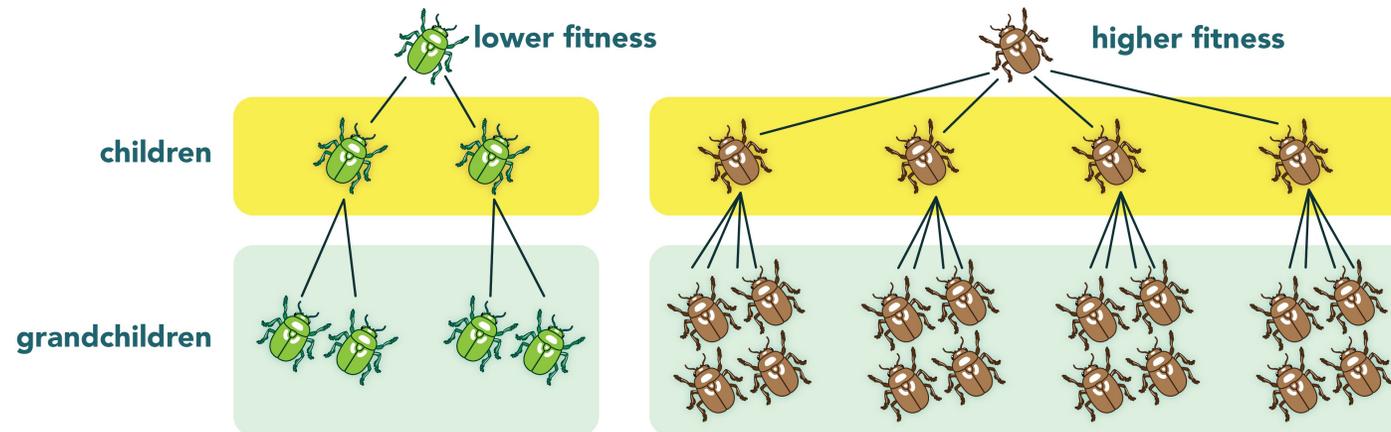
Constraints on virus evolution



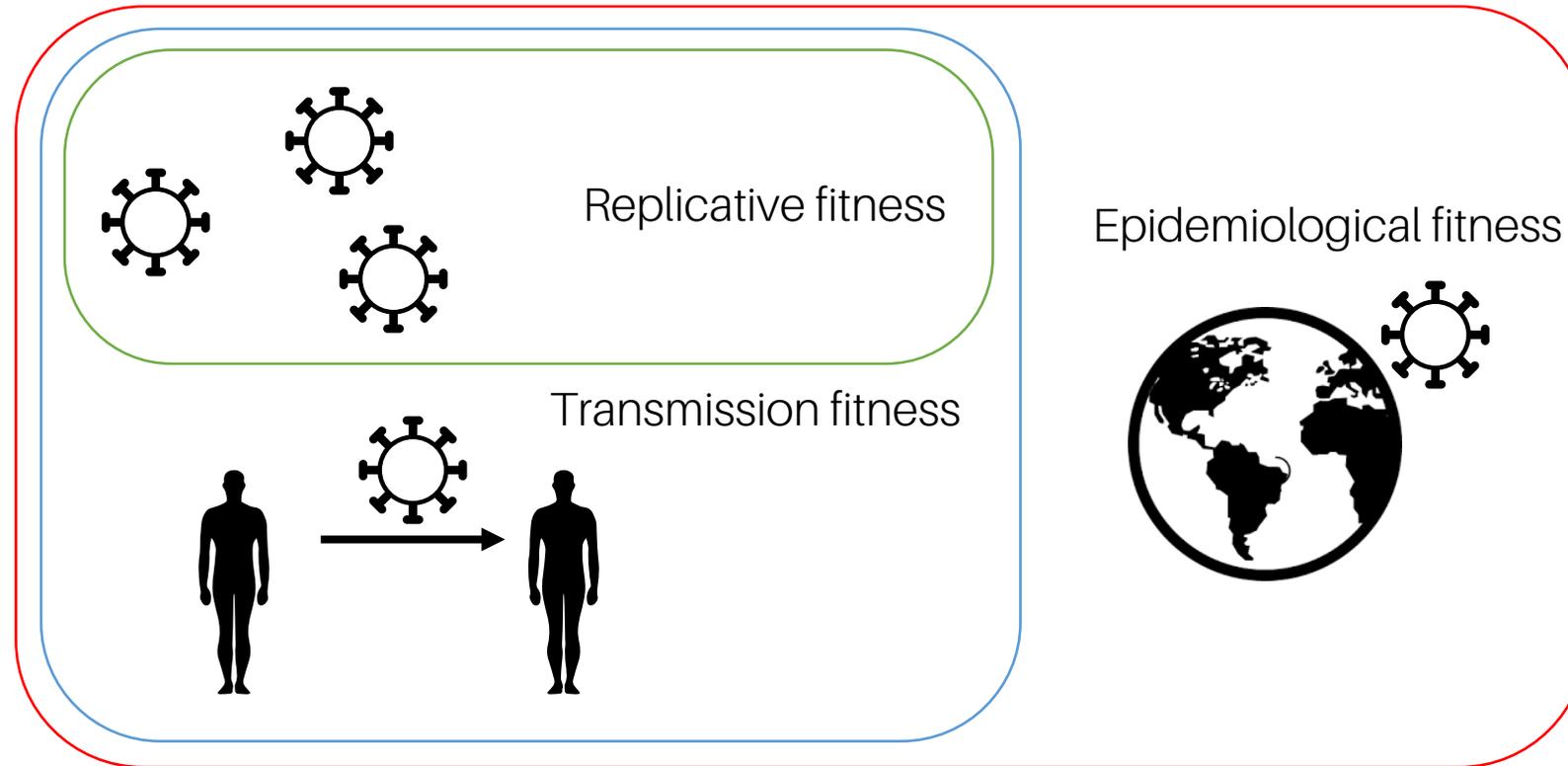
Fitness?

Evolutionary biologists use the word fitness to describe how good a particular genotype is at leaving offspring in the next generation relative to other genotypes

Of course, fitness is a relative thing.



Fitness of viruses



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Why study virus evolution?



<https://nextstrain.org/>

For what it leads to

Genetic flexibility

Adaptation
Emergence

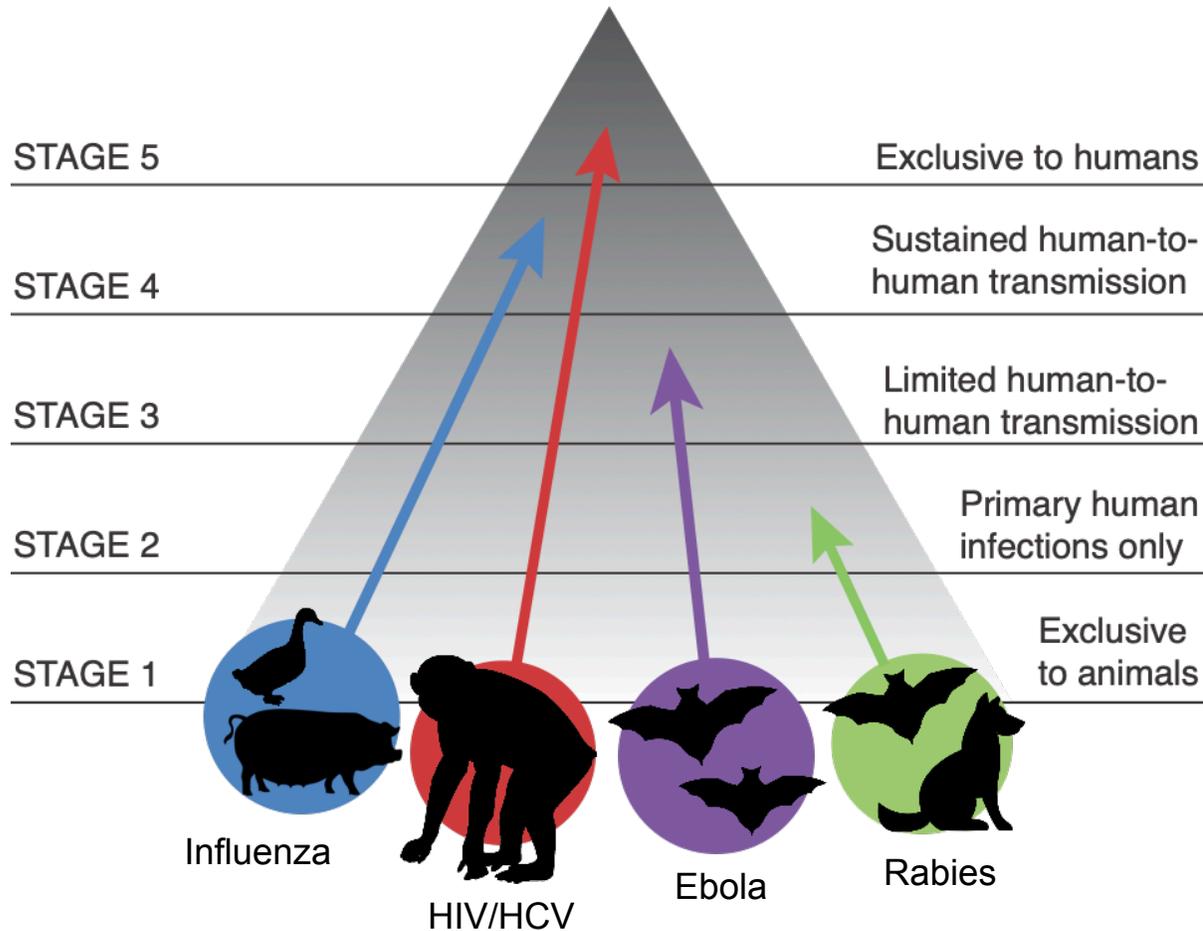
Drug resistance

For what it tells us

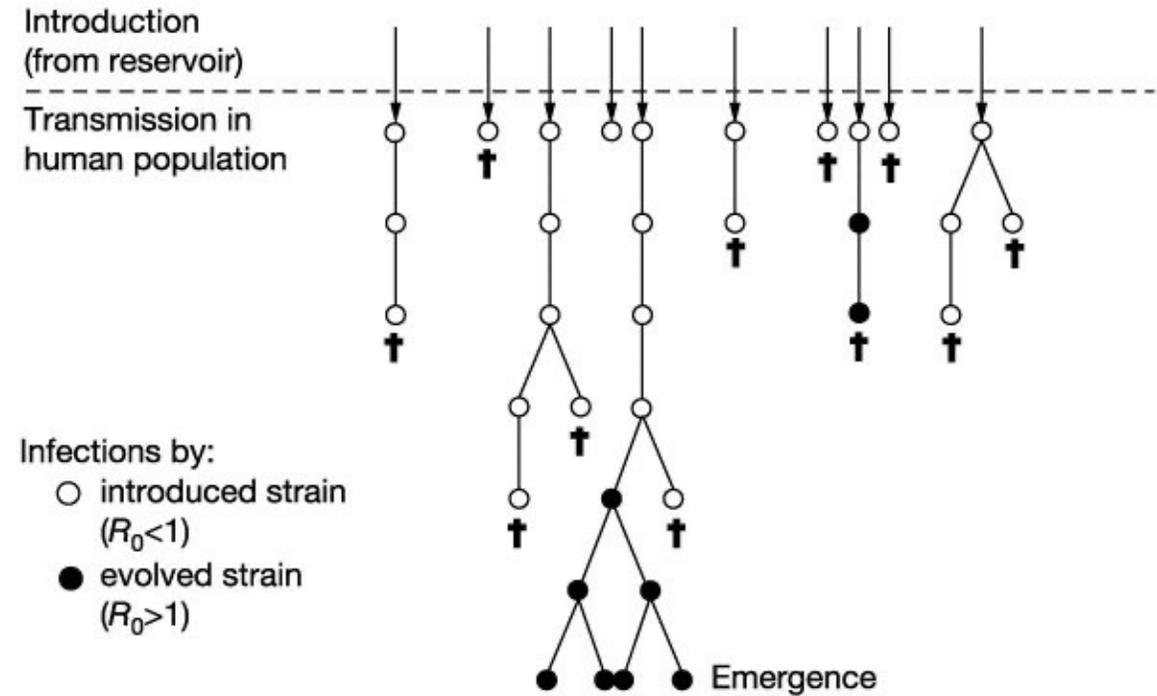
Insights into their epidemiology

Understanding the trajectory of SARS-CoV-2

Genetic changes (can) trigger/follow epidemiological change

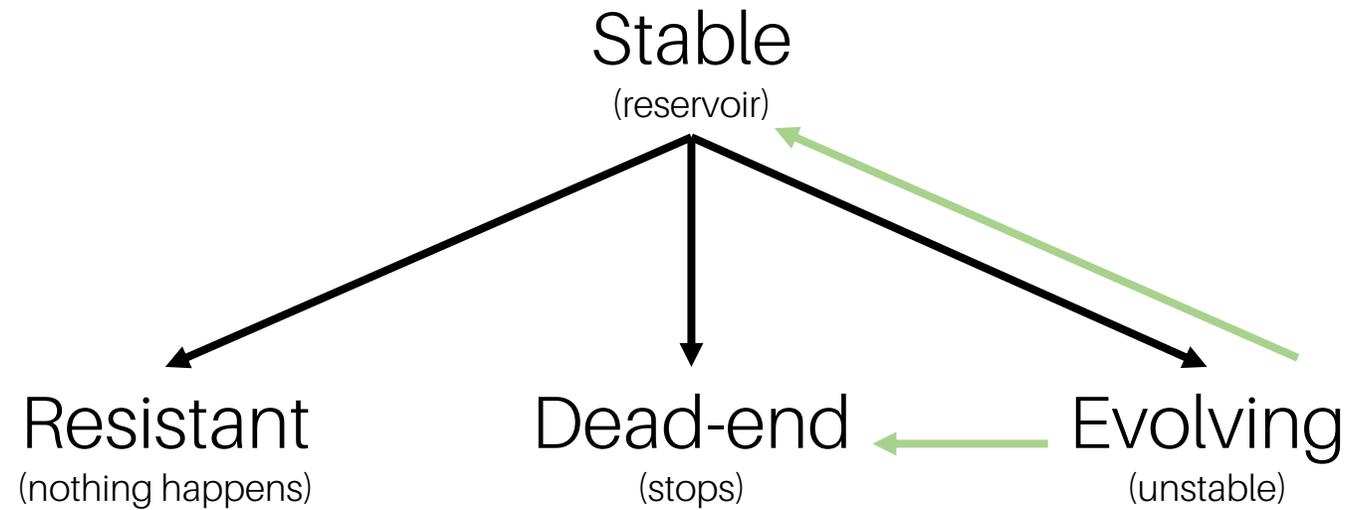


Wolfe et al. Nature 2007 <https://doi.org/10.1038/nature05775>
Pike et al. CID 2010 <https://doi.org/10.1086/652860>



Antia et al. 2003 Nature
<https://doi.org/10.1038/nature02104>

Virus-host interaction



May take some time!

Transmission and emergence

 R_0

“R nought” or “R zero”

Reproduction number
(in an idealized, naïve population)

 R_t

Effective reproduction number
(takes into account immunity, etc)

average number of people who will contract the disease from one infected person

 $R_0 < 1$

Decline, eventually dies out

 $R_0 = 1$

Maintenance, endemicity

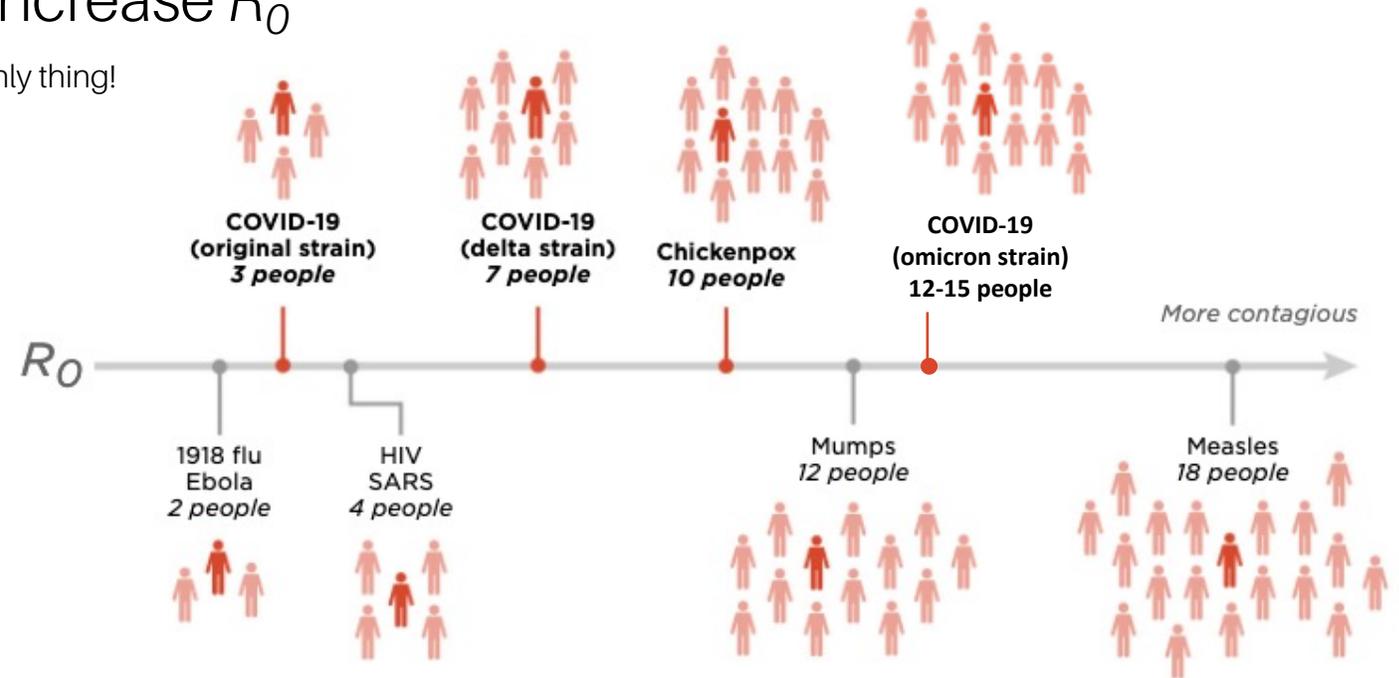
 $R_0 > 1$

Epidemic

Transmission and emergence

Increasing transmission can increase R_0

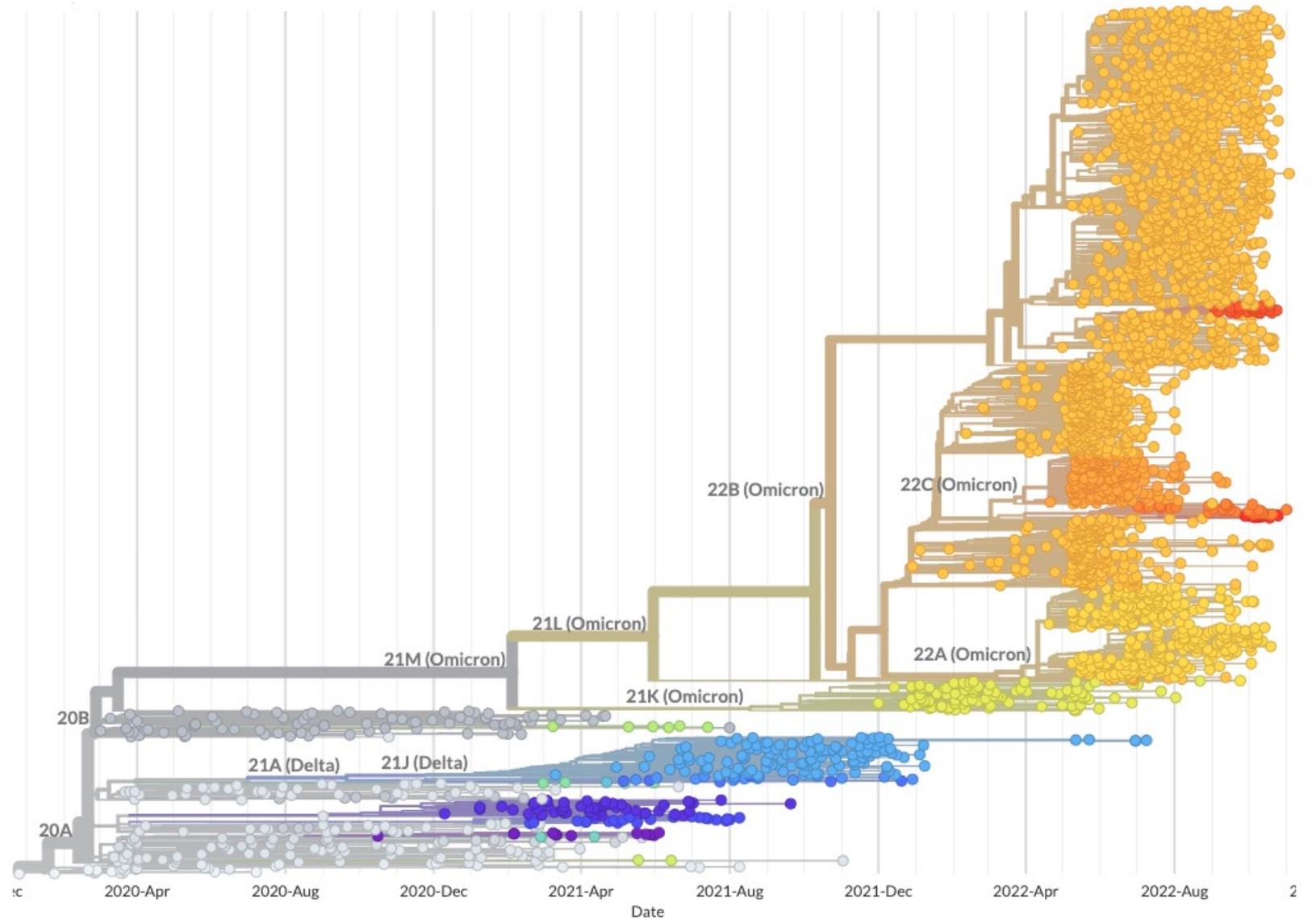
BUT it's not the only thing!



Michaeleen Doucleff, Alyson Hurt and Adam Cole/NPR, [link](#)

It is also dynamics; changes in the virus or else can change R_0

SARS-CoV-2 variants

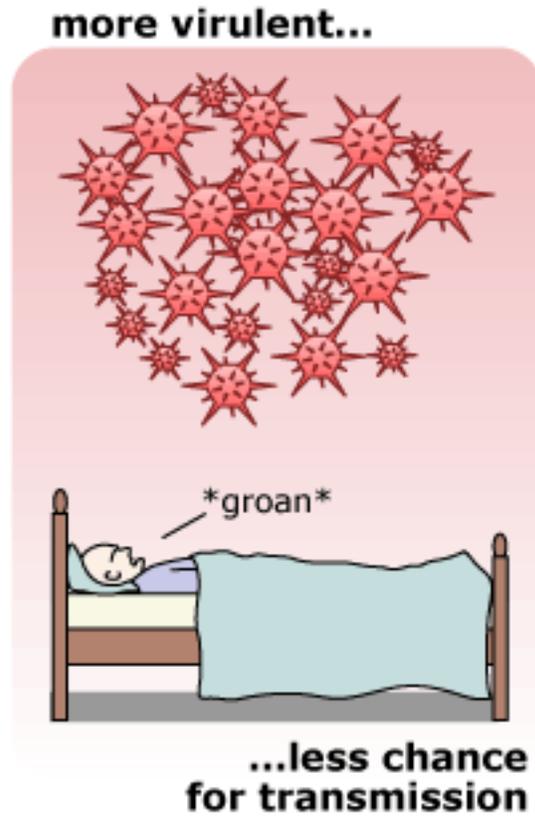


SARS-CoV-2 variants



It's just a mild flu...

Future of COVID



Why is it hard to treat viral infections?

Why so few antivirals?

Reason 1 Inhibiting virus growth can affect the host cell

Virus replication engages host function Side effects

Reason 2 Difficult to grow or have an animal model (or dangerous)

Reason 3 A compound must block virus replication completely

Partial inhibition is not acceptable

Also...

Acute infections are short

When patient feels ill, usually too late

Antivirals for these infections must be given early or prophylactically

But safety issues?

Giving drugs to healthy people?

One counter example though?

Resistance

Resistance to ANY antiviral drug must be anticipated

Special concern for chronic infection

Patient cannot be treated with the same drug

If no other drug available... infection cannot be stopped

Viral mutants resistant to every antiviral drug in arsenal

Genetic analysis of resistance provides insight into mechanism, and may reveal new strategies to reduce or circumvent problem

High mutations rates

RNA viruses have an error prone RNA polymerase

no correction mechanism

Except one order (Nidovirales)...

One mutation in $10^4 - 10^5$ nucleotide

in RNA viruses of ~10kb, that makes 1 mutation per 1 to 10 genomes.

DNA viruses: most DNA polymerase have proofreading mechanisms

Slower evolution

Maths of drug resistance

Consider a unique drug resistance provided by a single mutation

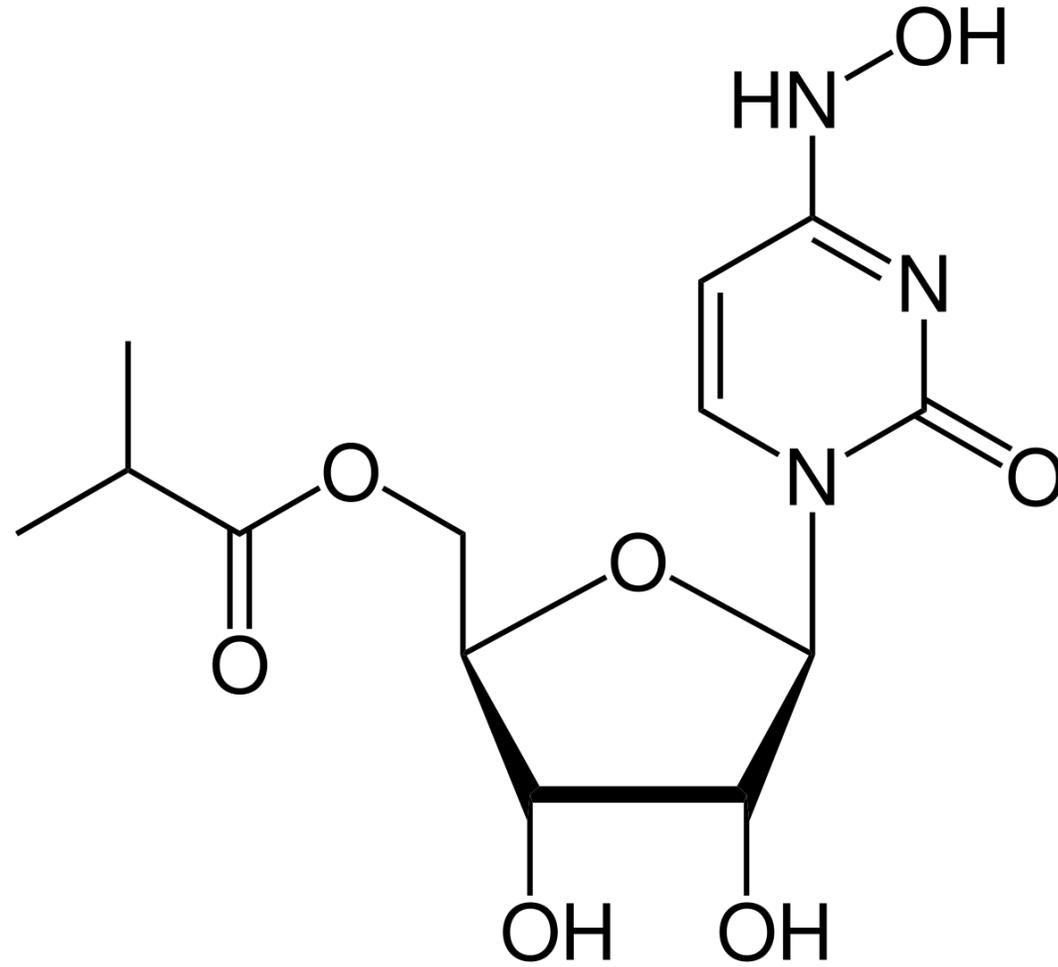
$\mu = 10^{-4}$ mut/base Each base is substituted in every 10^4 viruses

Each person has 10^9 - 10^{11} virions during peak viremia (SARS-CoV-2)

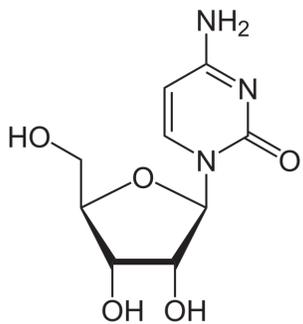
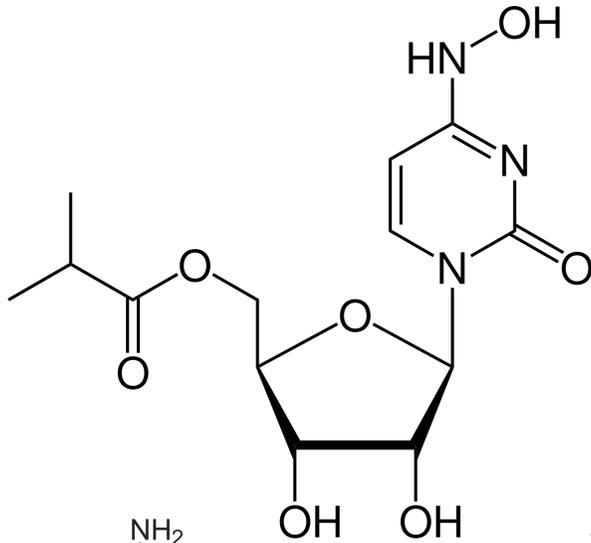
Sender et al. 2021 PNAS
<https://doi.org/10.1073/pnas.2024815118>

$$\frac{10^{10}}{10^4} = 10^6 \text{ viruses with resistance to the one drug...}$$

Molnupiravir (Lagevrio[®])_{MSD}



Molnupiravir (Lagevrio[®])_{MSD}



Cytidine

As soon as possible after diagnosis of COVID, within 5 days of the start of the symptoms, for 5 days



EUROPEAN MEDICINES AGENCY
SCIENCE MEDICINES HEALTH

// About one month after treatment started 7.3% of patients (28 out of 385) who took Lagevrio compared with 14.1% (53 out of 377) of patients who took placebo (a dummy treatment) had been hospitalised or had died; none of the patients in the Lagevrio group died compared with eight patients in the placebo group.

<https://www.ema.europa.eu/en/news/ema-issues-advice-use-lagevrio-molnupiravir-treatment-covid-19>

//

Molnupiravir (Lagevrio[®]_{MSD})

Incorporates into replicating RNA

Induces C→U mutations

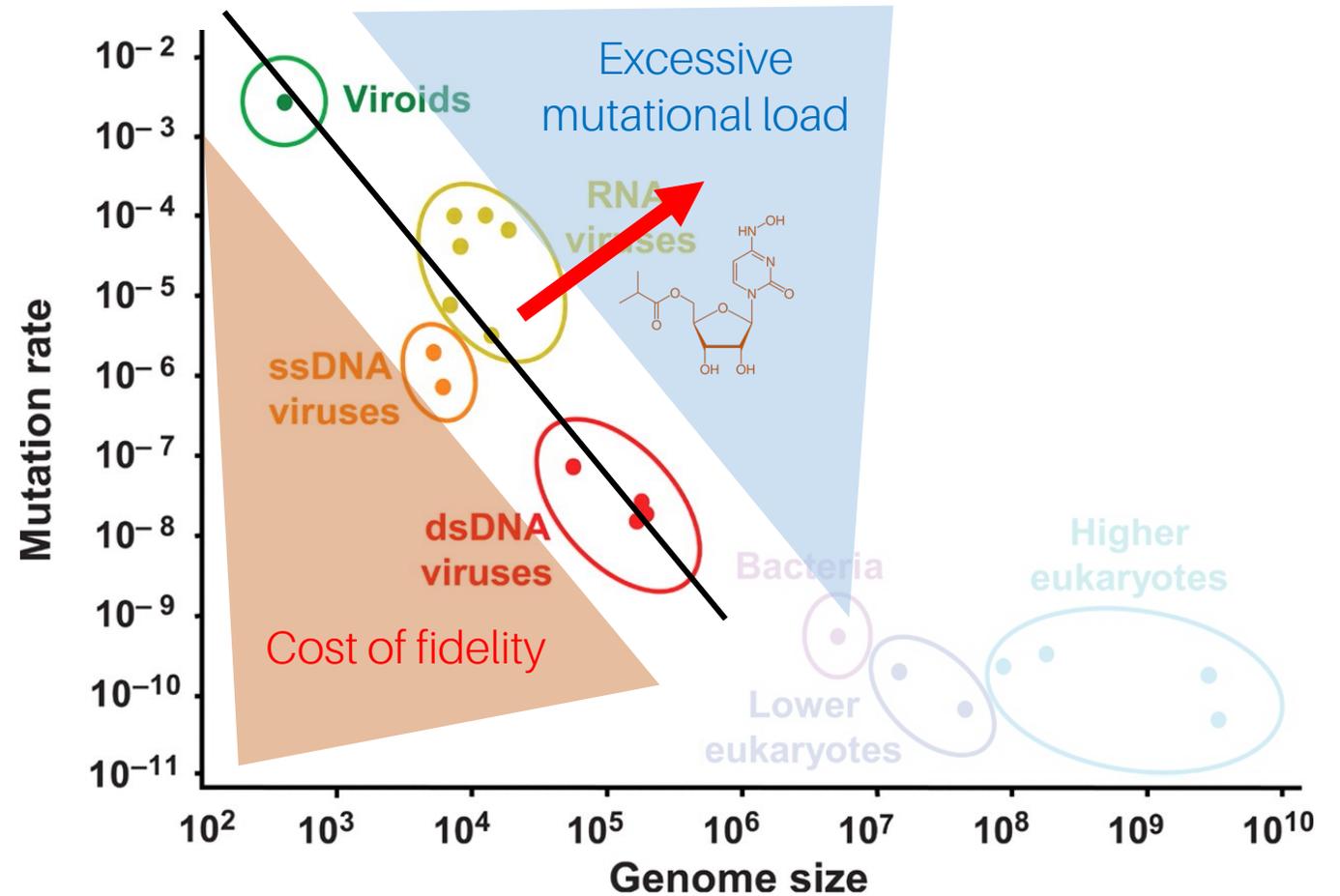
Mutagenic!

Molnupiravir (Lagevrio[®])_{MSD}

Incorporates into replicating RNA

Induces C→U mutations
Mutagenic!

Lethal mutagenesis
“error catastrophe”
“mutational meltdown”

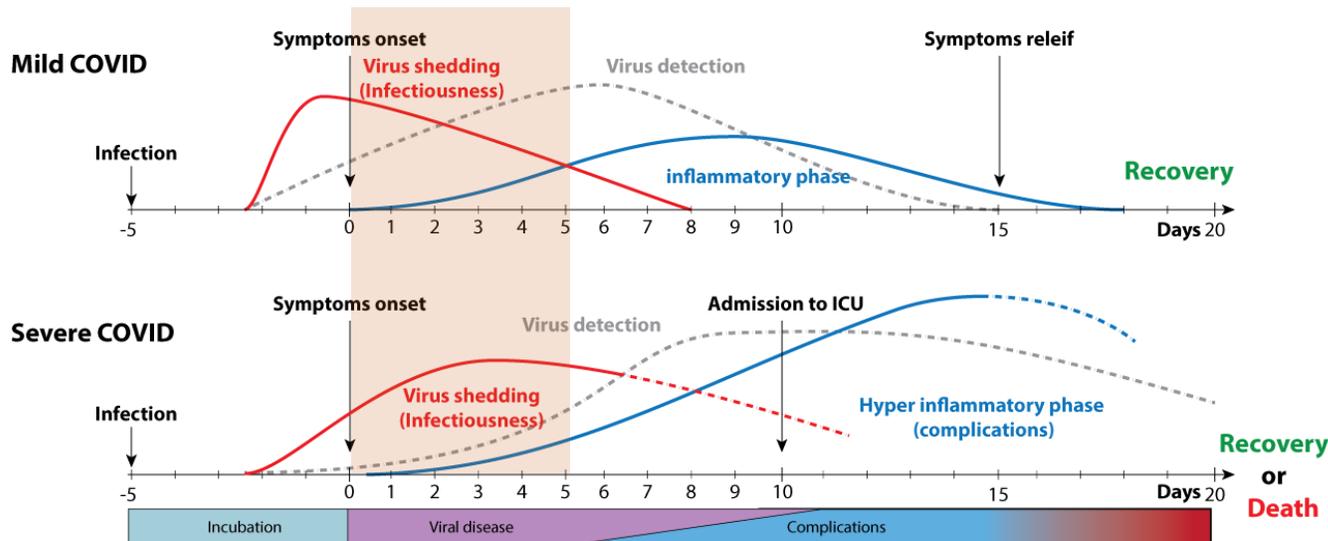


Molnupiravir (Lagevrio[®])_{MSD}

What about low drug concentration?

increase the mutation rate without error catastrophe: sublethal mutagenesis

Peak viral shedding is likely to coincide with low initial drug concentration



Molnupiravir has a short plasma half-life.

1 hour

Sequence content limits mutation rate elevation.

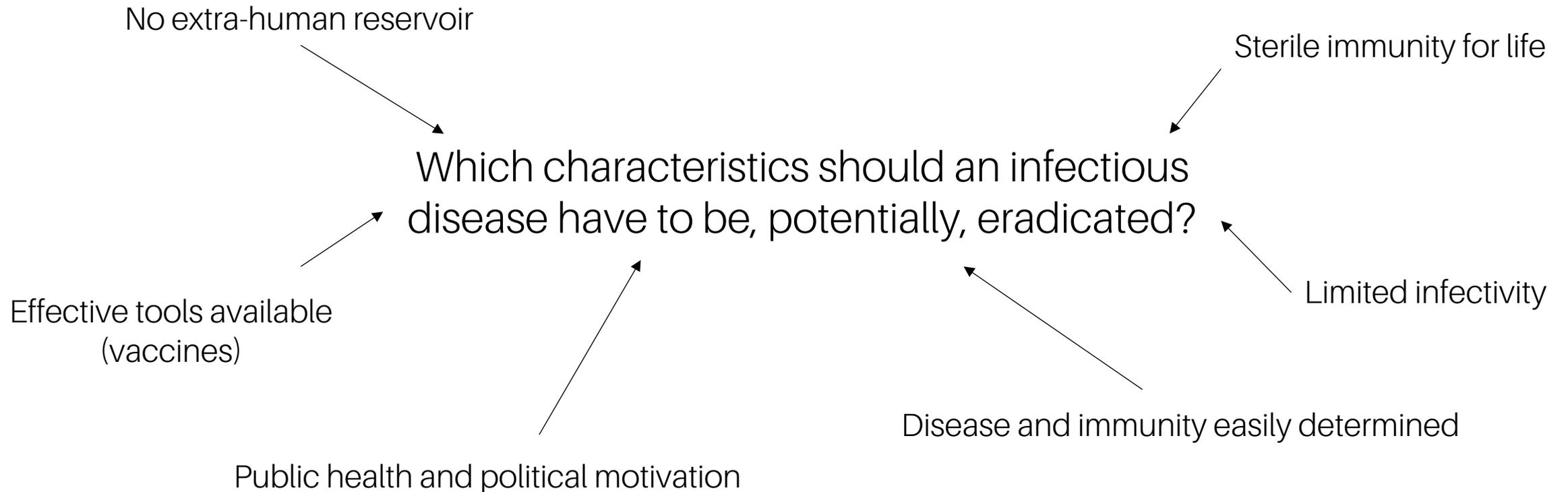
Pre-existing bias for C→U mutations
genomic G:C content of 38%
plus-strand C content of 18%

Eradicating SARS-CoV-2

Eradication of infectious diseases

Which characteristics should an infectious disease have to be, potentially, eradicated?

Eradication of infectious diseases





Virevo

virevo.lequimelab.eu