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- In ID, the average number of infections produced by an infected individual in a susceptible population

$R_o < 1$, self-sustaining epidemic is not possible

$R_o \sim 1$, early stochastic events may extinguish invader, but epidemic is possible, typical of endemic disease

Large R_o , Epidemic is virtually certain

- In some diseases R is not a homogeneous value (remember R_o may differ from R)
- Differs from R_e (R_t)

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Main source of susceptible hosts

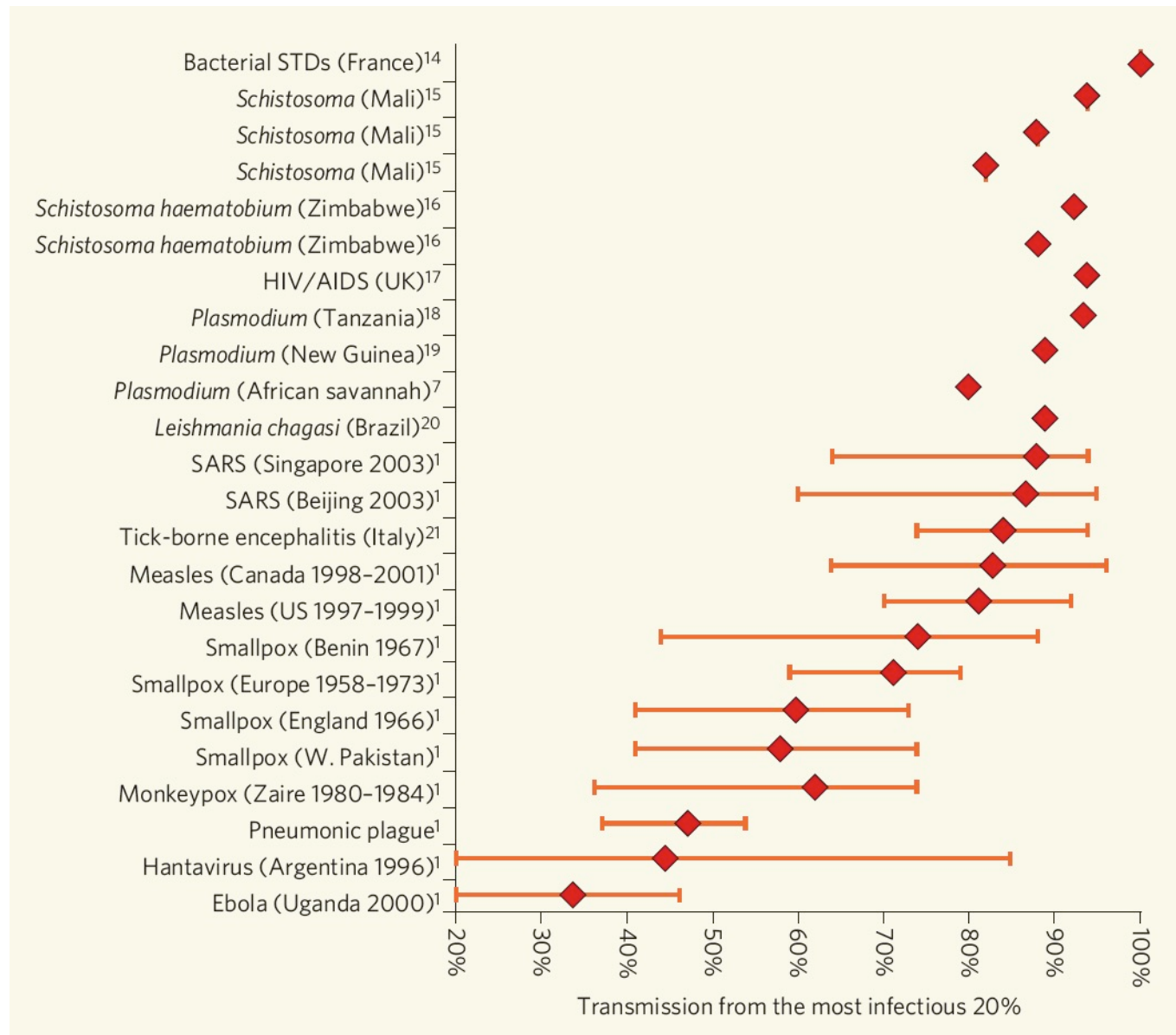
- Newborns (*post maternal protection*)
- Decay of immune memory
- Evolution of antigenicity
- Migration

Ro not a homogenous value
throughout the population?

Superspreaders

- Individuals are not homogeneous in infectiousness
- Superspreading occurs in all diseases (albeit a greater or lesser extent depending on the disease)
- Heterogeneities in patterns of sexual partner acquisition (gonorrhea, HIV) primarily based on contact differences among individuals
- Differences in parasite burdens with helminth infections
- Heterogeneous biting by malaria vectors
- Control efforts should focus on these individuals
- Events are also being classified as “superspreader events” in the COVID-19 pandemic

Heterogeneity in infectiousness for a range of diseases



- The 20/XX index, 20% of the most infectious individuals are responsible for XX% of the transmission

Today, there are ~ 1,400 currently recognized
species of **human** pathogens

500- bacterial

300- fungi

300- helminths

200- viruses

50- protozoa

2- prions

+ Variants

Microbes

Eukaryotes vs.
Prokaryotes

Do you think that this represents
an abundant number of microbes?

A dark, solid black shadow of a person's head and hand is cast onto a light-colored, textured surface. The shadow is positioned on the right side of the frame, with the hand raised near the forehead. The background is a light gray, mottled texture.

Pathogen +/-
Commensal +/-
Mutualist +/+

Epidemiology terms (CDC)

Epidemiology- the branch of medicine that deals with the incidence, distribution and possible control of diseases and other factors relating to health.

Epidemic-the occurrence of more cases of *a specific* disease than expected in a given area or among a specific group of people over a particular period of time.

Outbreak- synonymous with epidemic. Alternatively, a localized as opposed to generalized epidemic.

Endemic-the constant presence of a disease or infectious agent within a given geographic area or population group; may also refer to the usual prevalence of a given disease within such area or group.

Pandemic=WHO alert status phase 6; an epidemic occurring over a very wide area (several countries or continents) and usually affecting a large proportion of the population.



Three factors needed for a pandemic to occur

1. A new species/variant must emerge (no pre-existing immunity in most of the host population)
2. Must be pathogenic
3. Must be easily transmissible (via droplets, handshakes etc.)

Ok let's move onto.....

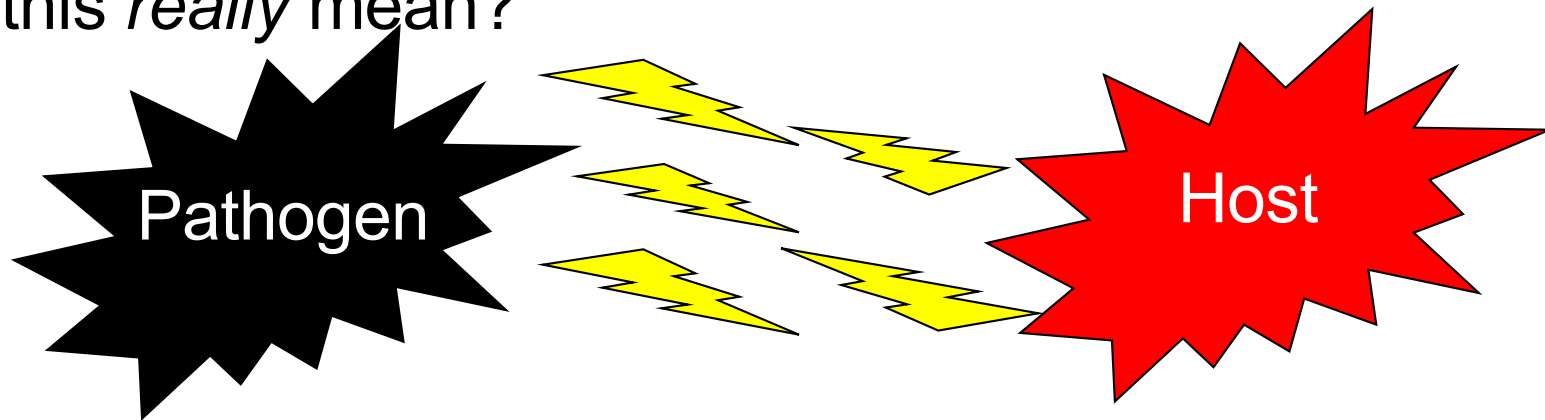
1. Why do pathogen's evolve so fast?
2. What are some of the basic traits that pathogens can evolve?
3. What is virulence, and how does it evolve?

Evolution- ‘Change of life through time’

Why do pathogens evolve so quickly?

The constant arms race between pathogen and host

Pathogens constantly change their genetic makeup to evade host defenses (and vice versa)....what does this *really* mean?



Provides a great example of Red Queen Hypothesis (antagonistic coevolution) !

Evolution- ‘Change of life through time’

Pathogens evolve QUICKLY due to;

1. High population sizes
2. Short generation times
3. High mutation rates

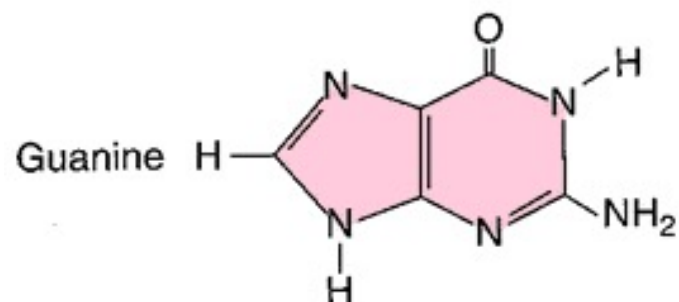
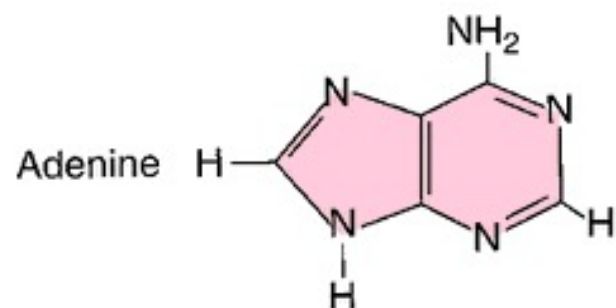
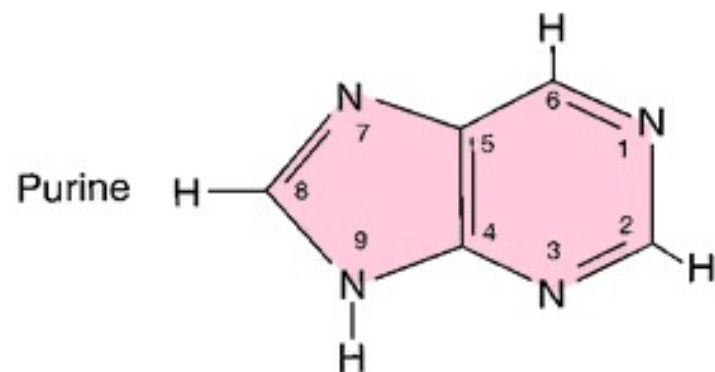
Why is understanding pathogen evolution important, relative to medicine?

Mutations-the raw material of evolutionary change

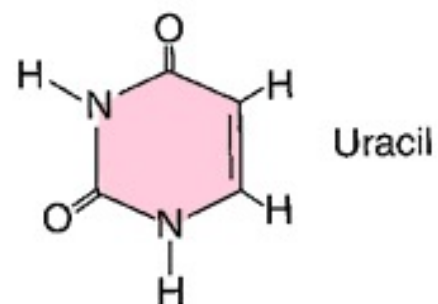
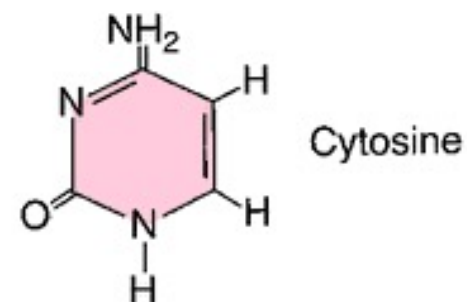
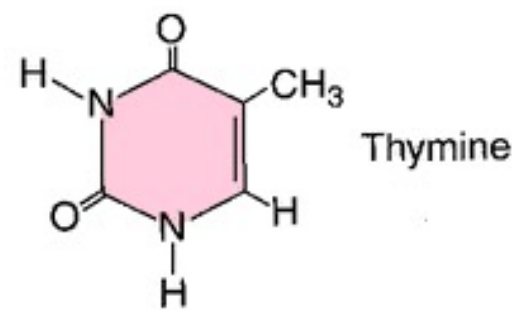
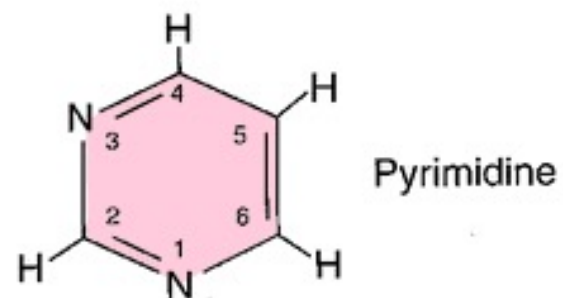
- Changes in running order of bases, give rise to alleles
- Transitions, transversions, indels
- Rates vary tremendously among species (10^{-9} to 10^{-2} mutations/base/yr)
- Caused by faulty replication, spontaneous, exposure to mutagens
- May or may not be inherited
- May or may not affect the protein level (synonymous vs nonsynonymous)

		Position 70								
		↓								
HIV <i>pol</i> allele (1)	A.a.	Glu	Asn	Pro	Thr	Lys	Trp	Lys	Lys	Lys
	DNA	GAA	AAT	CCA	ACT	AAA	TGG	AAA	AAG	AAA
HIV <i>pol</i> allele (2)	A.a.	Glu	Asn	Pro	Thr	Arg	Trp	Lys	Lys	Lys
	DNA	GAA	AAT	CCA	ACT	AGA	TGG	AAA	AAG	AAA

A



B

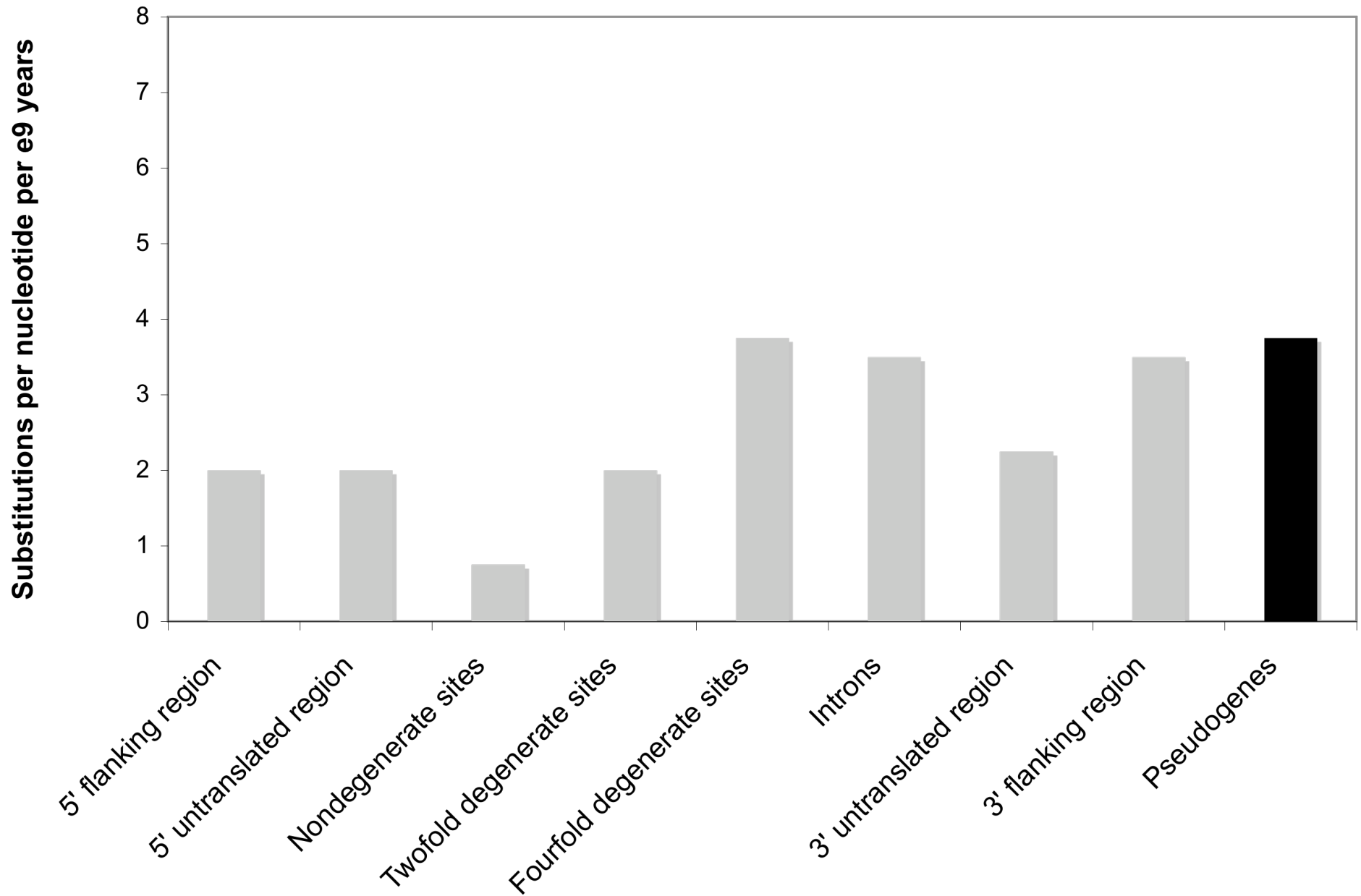


Genetic code

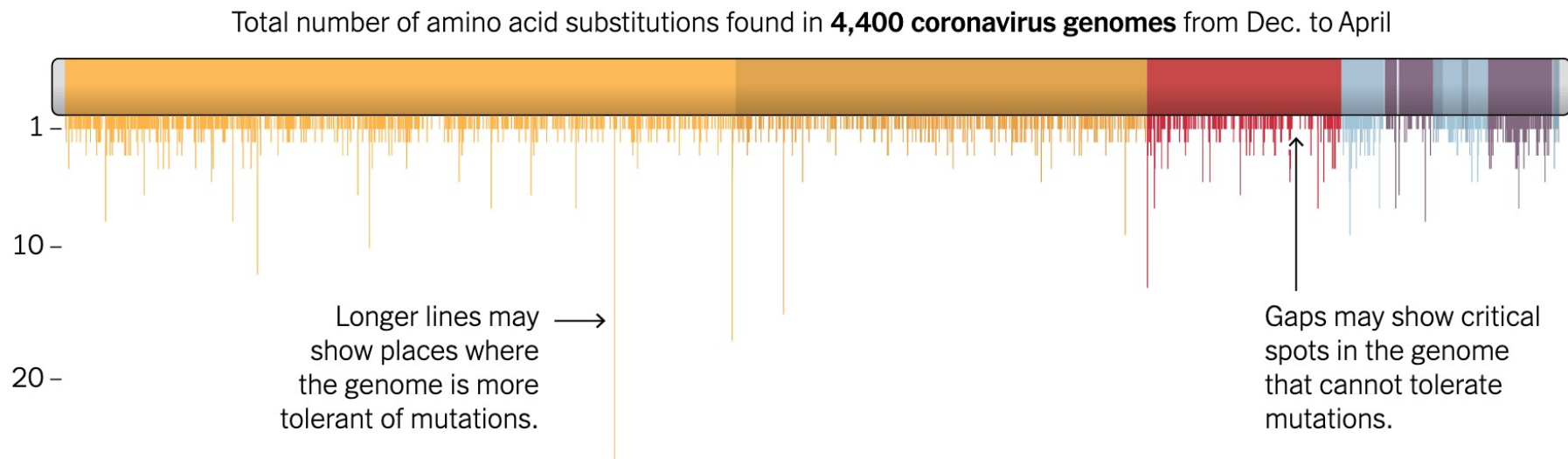
- Each amino acid (a.a.) specified by 3 consecutive, nonoverlapping nt (codons)
- 64 possible codons
- Degenerate
- 1 START codon
- 3 STOP codon (do not encode any a.a.)

		Second base in codon				
		U	C	A	G	
First base in codon	U	Phe Phe Leu Leu	Ser Ser Ser Ser	Tyr Tyr STOP STOP	Cys Cys STOP Trp	U C A G
	C	Leu Leu Leu Leu	Pro Pro Pro Pro	His His Gln Gln	Arg Arg Arg Arg	U C A G
	A	Ile Ile Ile Met	Thr Thr Thr Thr	Asn Asn Lys Lys	Ser Ser Arg Arg	U C A G
	G	Val Val Val Val	Ala Ala Ala Ala	Asp Asp Glu Glu	Gly Gly Gly Gly	U C A G

Different regions of DNA sequence have varying probabilities of mutation



Mutations along the SARS-CoV-2 genome



- Nonsynonymous mutations have stronger natural selection constraints than synonymous mutations, why?
- Do mutations stick around? Purifying versus Diversifying selection.

Do mutations stick around? Depends at the phenotypic level...

Bad-decrease in fitness (high fitness cost) - removed through selection.

Good- increase in fitness (low fitness cost)- retained through selection.

Neutral- (no fitness cost) free from natural selection. These can be fixed through genetic drift.

Genetic drift

- Changes in the frequency of a genetic variant in the population owing to chance alone
- Greater effects in smaller populations

Why?



Modes of selection at the sequence level

Negative (purifying) selection= $d_N < d_S$

Positive (diversifying) selection= $d_N > d_S$

Mutations

- The great majority of sequences show negative or neutral selection.
- Pathogen **antigens** often show +ve selection, as they change to escape host immunity. Some of the best examples of +ve selection involves the evolution of resistance to antibiotics, drugs, and pesticides.
- Other pathogen protein domains low d_N (-ve selection) due to functional or structural constraints and hidden from external recognition.
- Can be used to understand transmission chains

- Why do pathogens differ in virulence (host harm), why the difference in Ebola vs. rhinovirus (common cold)?

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“Transmission and virulence, the yin and yang”
of infectious diseases and pathogen ecology”

Quammen, 2013