

A

An Atlas of Viral Adaptation

A comparison of adaptive evolution across a panel of human pathogenic viruses.

Method

Order of viruses

Y-axis units

Viruses to Plot

B

Adaptive Evolution of Coronavirus 229E

Accompanied by the [Nobayan 229E_Scots](#) phylogeny.

Method

Y-axis units

C

Genotype at S1 site 343

Date

Figure S1: Screenshots of the interactive website presenting the results in this manuscript, related to Figure 3 and 4. A) Screenshot of the main page, accessed at <https://blab.github.io/atlas-of-viral-adaptation/>. Buttons allow the user to toggle the method used to calculate rate of adaptation (update outgroup or constant outgroup), how the viruses are ordered in the plot (by rate or by viral family), the units the rate is displayed in (per year or per codon per year), and which viruses shown on the plot. Hovering over any of the points will display more information about that virus. Clicking on any point will redirect the user to a virus-specific page that shows rates of adaptation across the genome of that virus. B) Screenshot of the coronavirus 229E page. C) Screenshot of the 229E Nextstrain phylogeny that is paired with the analysis and can accessed from the virus-specific page. In this example, the phylogeny is colored by the genotype at amino acid 343, a residue which has experienced multiple fixation events.

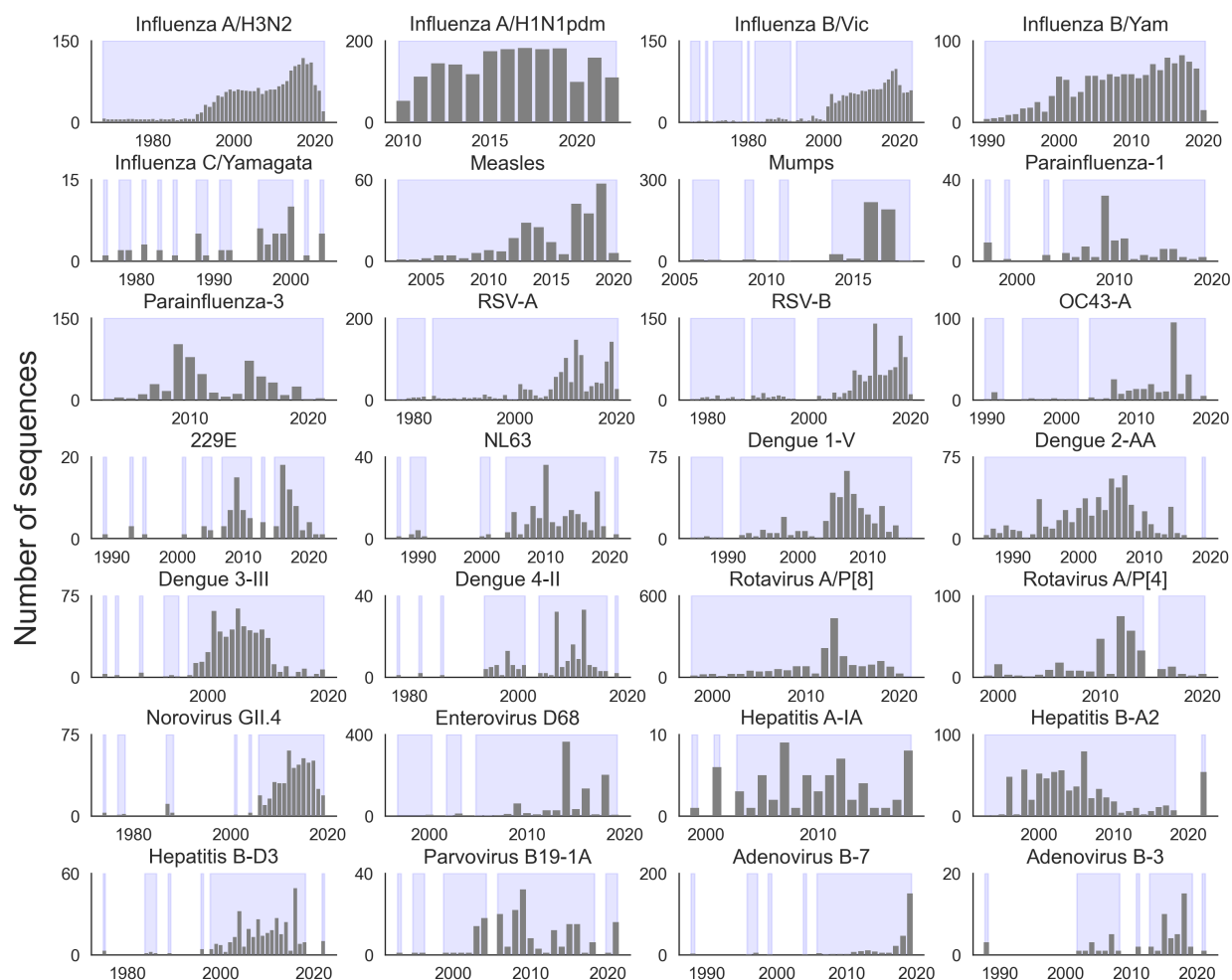


Figure S2: Count of sequences per year for each virus in the panel, related to STAR Methods. The number of receptor-binding gene sequences per year is shown for each virus. Because some years have one or a few sampled sequences and others have hundreds, we have highlighted each year with at least one sequence in blue to better show the distribution of samples over time.

Virus	RB	Polymerase	Surface	Non-Surface
Influenza A/H3N2	HA1	PB1	HA2, NA	NP, PA, PB2
Influenza A/H1N1pdm	HA1	PB1	HA2, NA	NP, PA, PB2
Influenza B/Vic	HA1	PB1	HA2, NA	NP, PA, PB2
Influenza B/Yam	HA1	PB1	HA2, NA	NP, PA, PB2
Influenza C/Yamagata	HEF1	PB1	HEF2	NP, PB2, P3, M, NS
RSV-B	G	L	F, SH	NS1, NS2, N, P, M
RSV-A	G	L	F, SH	NS1, NS2, N, P, M
Parainfluenza-1	HN	L	F	N, P, C, M
Measles	H	L	F	N, P, V, C, M
Mumps	HN	L	F, SH	NC, V, I, M
Parainfluenza-3	HN	L	F	N, P, C, M
Dengue 2-AA	E	NS5		C, M, NS1, NS2A, NS2B, NS3, NS4A, NS4B
Dengue 4-II	E	NS5		C, M, NS1, NS2A, NS2B, NS3, NS4A, NS4B
Dengue 3-III	E	NS5		C, M, NS1, NS2A, NS2B, NS3, NS4A, NS4B
Dengue 1-V	E	NS5		C, M, NS1, NS2A, NS2B, NS3, NS4A, NS4B
OC43-A	S1	RdRp	S2, HE	Orflab, E, M, N
229E	S1	RdRp	S2	Orflab, Protein 4A, Protein 4B, E, M, N
NL63	S1	RdRp	S2	Orflab, Protein 3, E, M, N
Rotavirus A/P[8]	VP4 (P)	R (VP1)	VP7 (G)	VP2, VP3, VP6, NSP1, NSP2, NSP3, NSP4
Rotavirus A/P[4]	VP4 (P)	R (VP1)	VP7 (G)	VP2, VP3, VP6, NSP1, NSP2, NSP3, NSP4
Norovirus GII.4	VP1	RdRp		p48, NTPase, p22, Vpg, 3CL-pro, VP2
Enterovirus D68	VP1	3D	VP2, VP3	VP4, 2A, 2B, 2C, 3A, 3B, 3C
Hepatitis A-IA	VP1	3D	VP2, VP3	VP4, 2A, 2B, 2C, 3A, 3B, 3C
Hepatitis B-A2	Large	Polymerase		Middle, Small, X, Core
Hepatitis B-D3	Large	Polymerase		Middle, Small, X, Core
Parvovirus B19-1A	VP1		VP2	NS, U7.5kDa, X, U11kDa
Adenovirus B-7	Fiber	Pol		E1A, E1B.55K, IVa2, pTp, pI-IIA, Penton, Hexon, Protease, 100K
Adenovirus B-3	Fiber	Pol		E1A, E1B.55K, IVa2, pTp, pI-IIA, Penton, Hexon, Protease, 100K

Table S1: Genes analyzed in this manuscript, for each virus, related to STAR Methods. For each virus, the receptor-binding (RB) and polymerase genes are listed, along with all other surface (but not receptor-binding) and non-surface (but not polymerase) genes that were analyzed in this study.