Supporting Information for: Evolutionary dynamics of viral escape under antibody stress: A biophysical model

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1. Experimentally observed mutation rates and burst size of some RNA viruses

Group	Virus	Genome size (kb)	μ_n	μ_g	M
ssRNA(+)	Tobacco mosaic virus	6.40	$8.7x10^{-6}$	0.056	n.a.
	Human rhinovirus 14	7.13	$6.9x10^{-5}$	0.49	n.a.
	Poliovirus 1	7.44	$9.0x10^{-5}$	0.67	1694
	Tobacco etch virus	9.49	$1.2x10^{-5}$	0.11	1555
	Hepatitis C virus	9.65	$1.2x10^{-4}$	1.2	n.a.
	Murine hepatitis virus	31.4	$3.5x10^{-6}$	0.11	650
ssRNA(-)	Vesicular stomatitis virus	11.2	$3.5x10^{-5}$	0.39	1250
	Influenza A virus	13.6	$2.3x10^{-5}$	0.31	50
	Influenza B virus	14.5	$1.7x10^{-6}$	0.024	n.a.

Table S1. Experimentally observed mutation rates and burst size (M) of some RNA viruses (from ref. (22)). μ_n is the mutation rate per nucleotide, μ_g is the mutation rate per genome ($\mu_g=\mu_n$*genome size). n.a.=not available.

2. Influence of biophysical parameters on the fitness function.

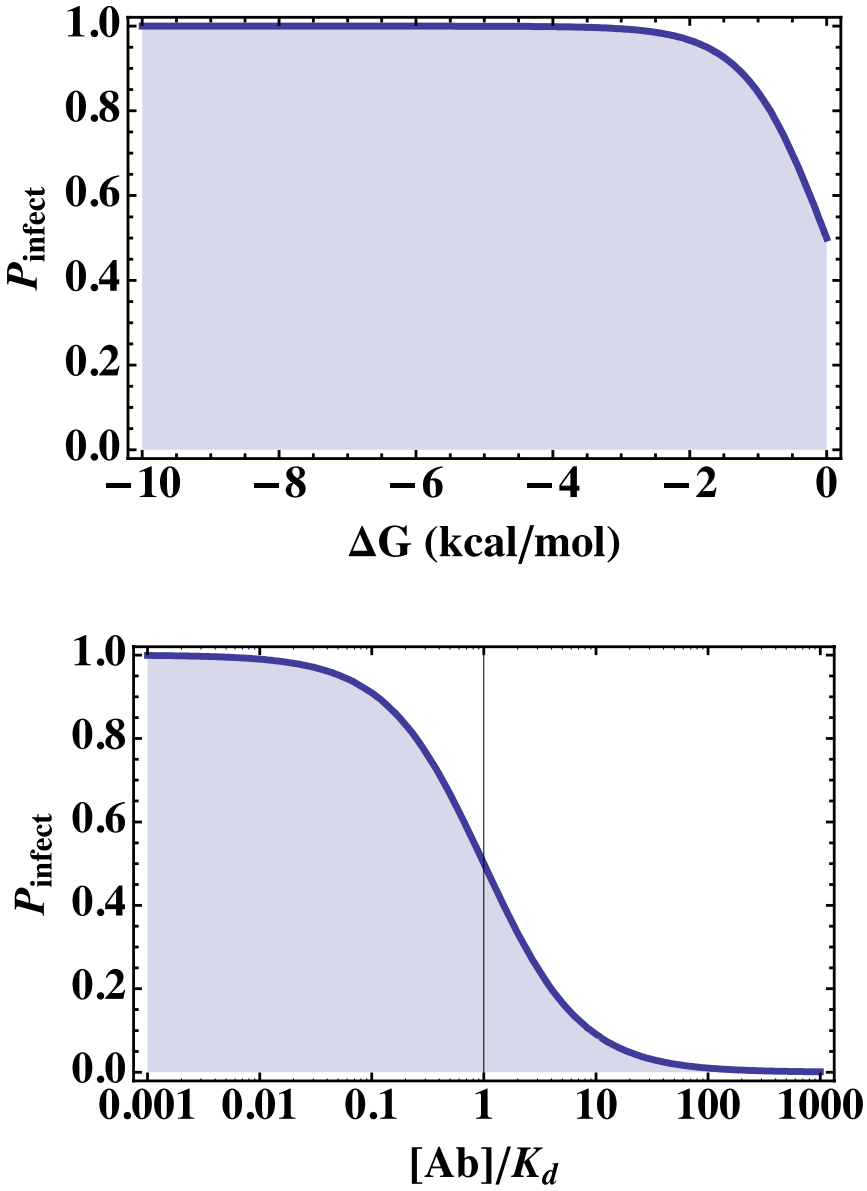


Figure S1. Influence of biophysical parameters ΔG and K_d on $P_{inf.}$.

3. Trajectory of evolution

Shown in Figure S2 is a typical evolutionary trajectory using the biophysics-based population dynamics model. This specific trajectory used a single protein of 208 amino acids, a mutation rate per nucleotide of $\mu_n=10^{-2}$ ($\mu_{genome}=7.56$) and a burst size of $M=100$. Starting with 10^5 viral particles and no external pressure (that is, $[Ab]=0$), the viral count first increases and quickly equilibrates to the viral count dictated by mutation-selection balance. Antibody is then "added" at passage 101, the viral count collapses but eventually increases after finding a beneficial mutation that allows escape from the antibody. The population count at the new steady state with antibody pressure is lower than that without antibody.

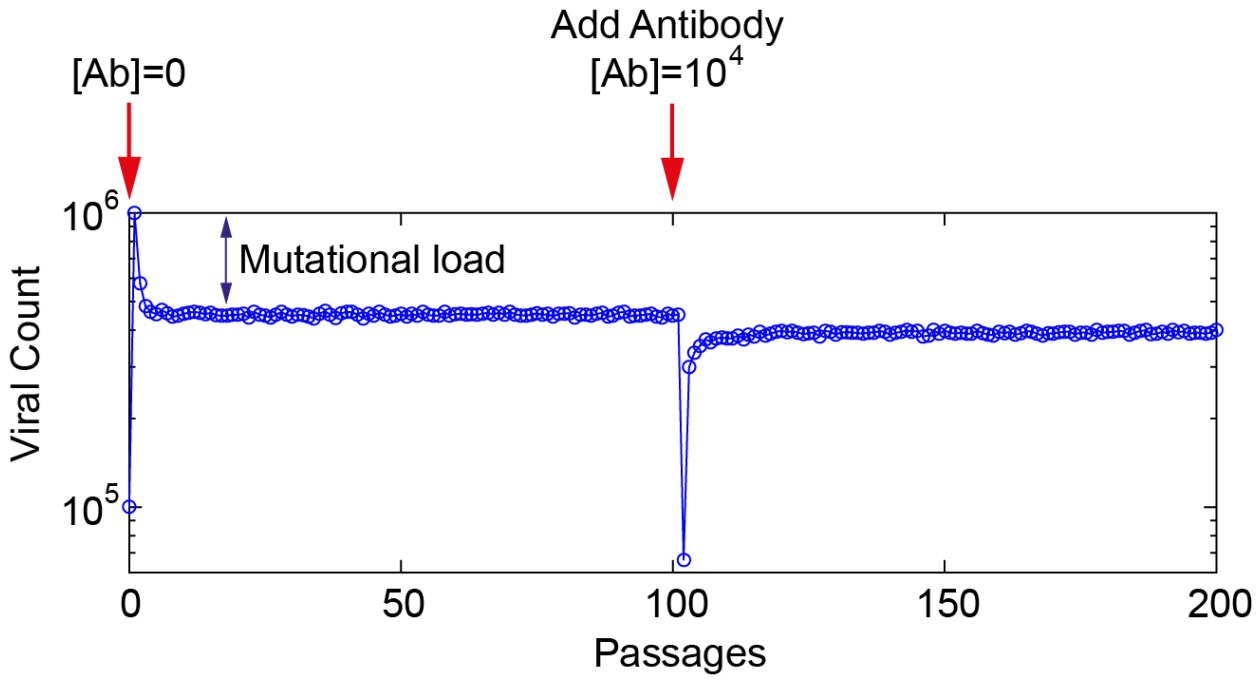
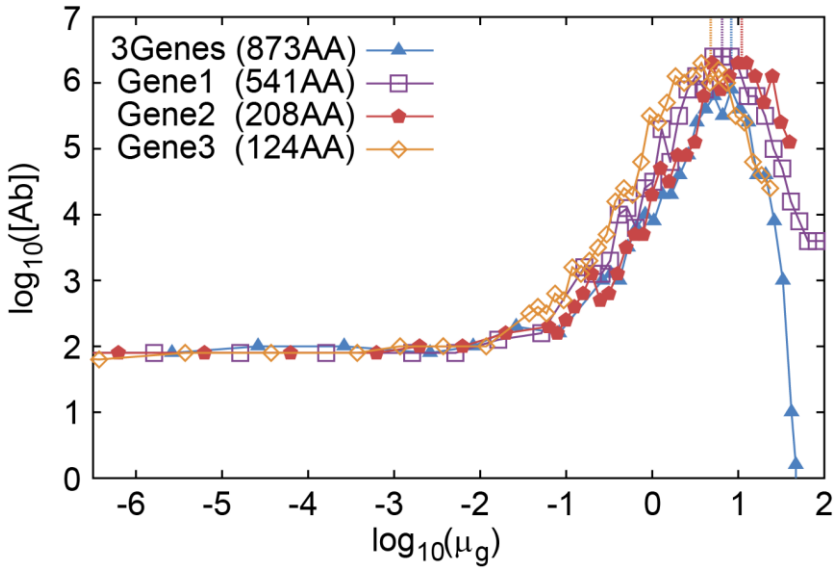


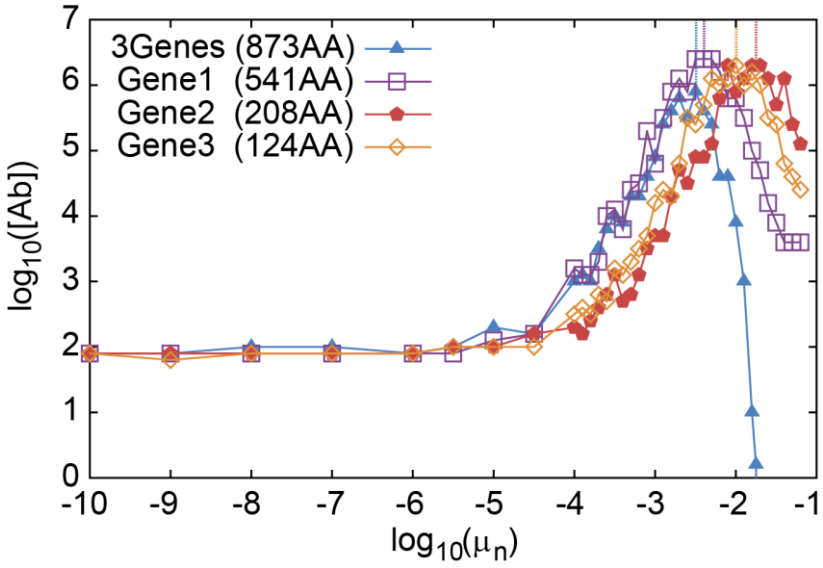
Figure S2. Viral population dynamics.

4. Influence of the genome size

The optimal mutation rate does not strongly depend on per genome mutation rate (Figure S3-a). However, when the phase diagrams are plotted with respect to the mutation rate per genome (Figure S3-b), a trend appears: the longer the genome, the lower the optimal mutation rate per nucleotide.



(a) Influence of the genome size with respect to the mutation rate per genome



(b) Influence of the genome size with respect to the mutation rate per nucleotide

Figure S3. Influence of the genome size (the optimal mutations rates are marked with vertical lines at the top of each curve).

5. Influence of the burst size

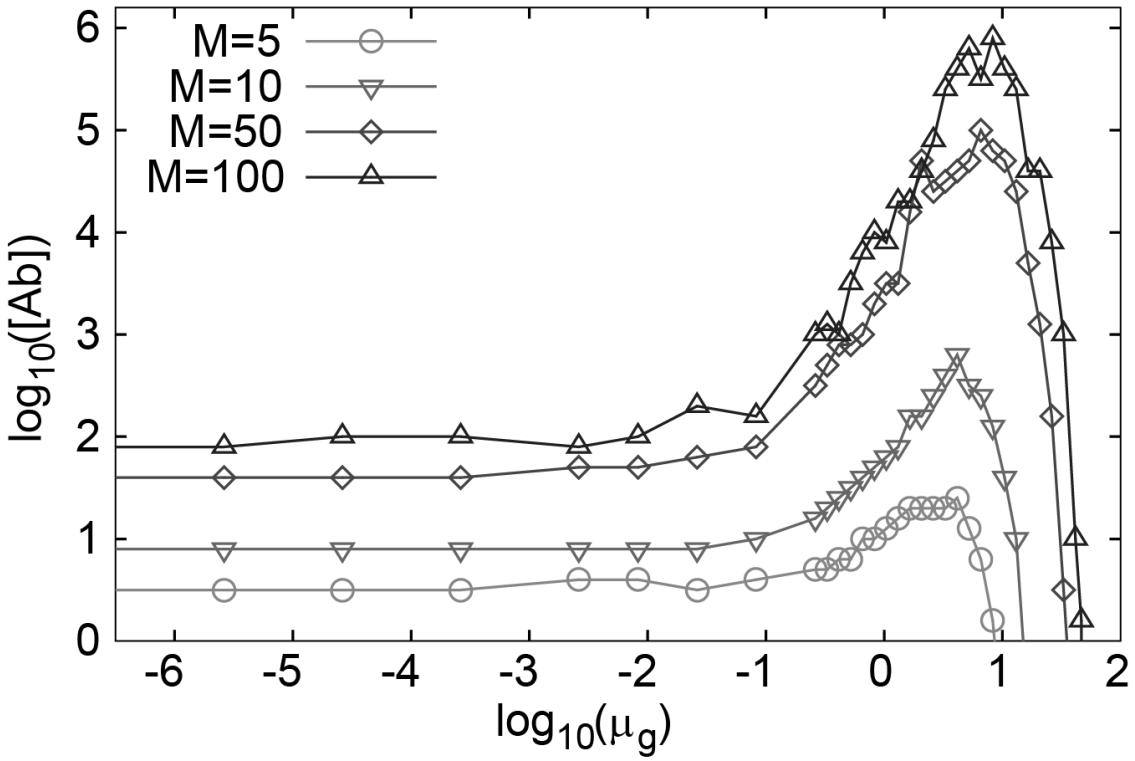


Figure S4. Influence of the burst size (M) on the phase diagram.