

Supporting Information

Relevance of host cell surface glycan structure for cell specificity of influenza A viruses

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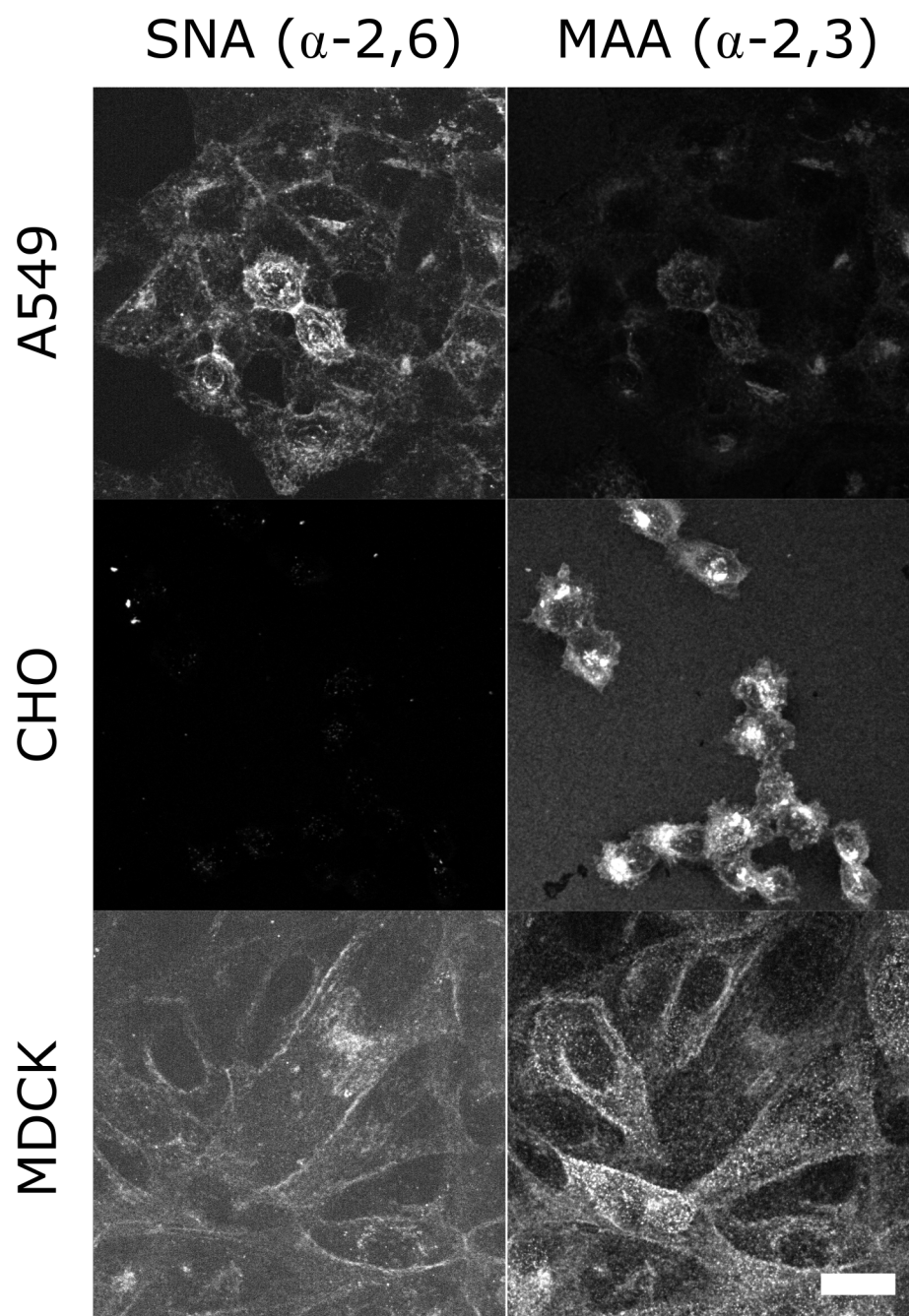
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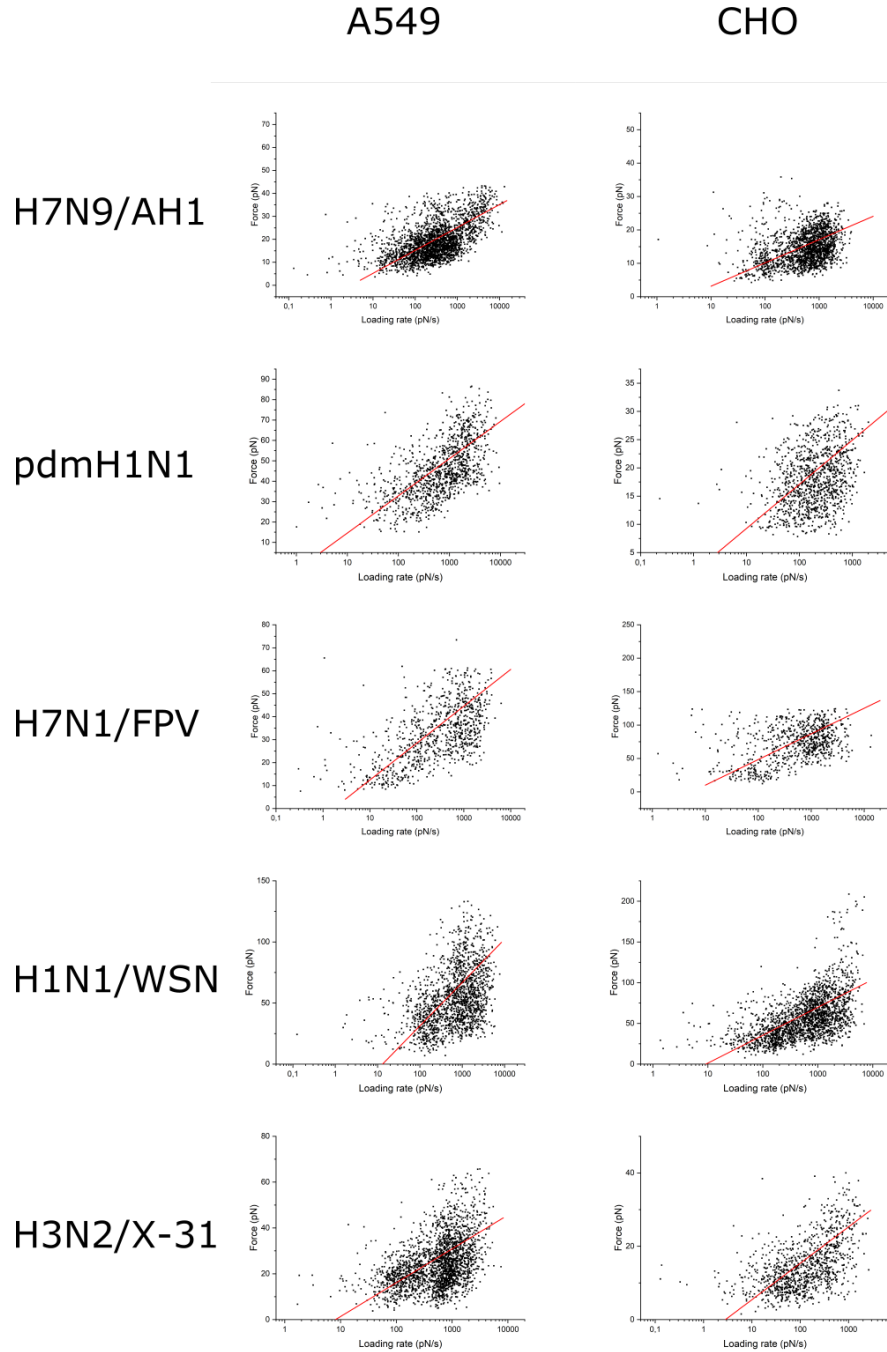
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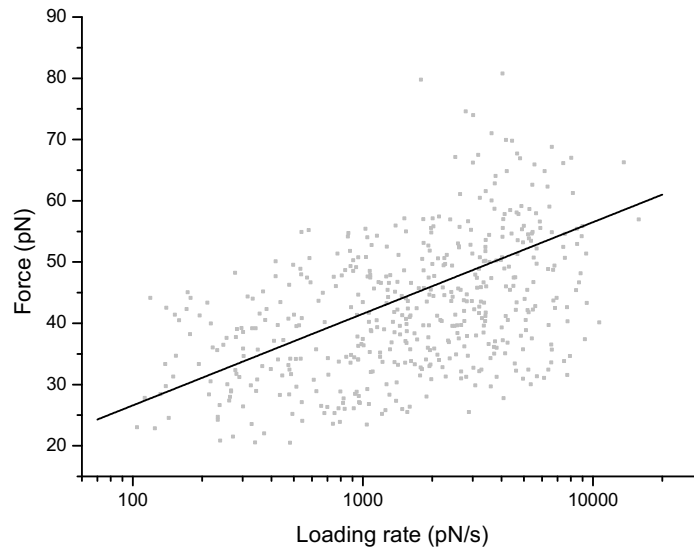
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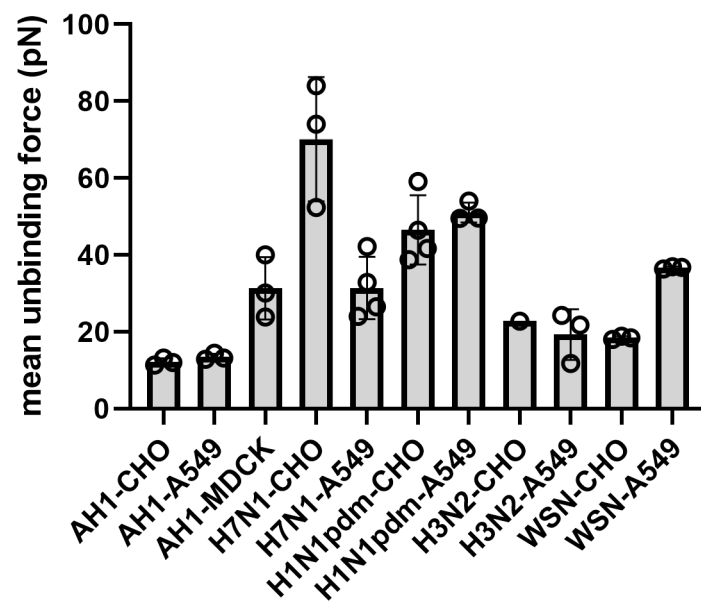
Supplementary Figure S1. Surface sialic acid characterization by fluorescence confocal microscopy. MDCK, CHO, and A549 cells were washed with PBS and fixed with PFA for 20 min at room temperature. The cells were incubated with SNA-FITC (10 μ g/ml) and MAA-Alexa647 (50 μ g/ml) for 20 min, washed with PBS and imaged by confocal microscopy.



Supplementary Figure S2. Overview showing force vs. loading rate scatter plots for all virus-cell combinations. Scatter plots showing unbinding force F plotted against the loading rate r of every individual force curve. From those data, the values for k_{off} and x_u were determined (Table 2). For each virus-cell combination, we measured between 12-15 cells.



Supplementary Figure S3. SVFS dynamic force spectra of H7N9 AH1 interacting with single receptors on living MDCK cells. Scatter plot showing unbinding force F plotted against the loading rate r of every individual force curve. From those data, the values for k_{off} and x_u were determined to be $0.256 \pm 0.00169 \text{ s}^{-1}$ and $6.160 \pm 0.0146 \text{ \AA}$ (mean \pm SD), respectively. We measured between 12-15 cells.



Supplementary Figure S4. Comparison of the mean unbinding force at pulling velocity 4 $\mu\text{m}/\text{sec}$. Each point represents one cell of the shown virus-cell interaction pair. Shown are mean \pm SD, $n=3$.

Supplementary Table S1. Comparison of SVFS results obtained by using two different fitting approaches. Loading rates LR can either be obtained by using the mean effective spring constant $\langle k_{eff} \rangle$ for each pulling velocity v ($LR = v \cdot k_{eff}$) or, using a more adapted approach reported previously and now used in this study, calculated for each individual force-distance curve. Each fitting approach results in slightly different fitting parameters. Dissociation rate k_{off} , separation from the energy barrier x_u , and average bond lifetime τ_{off} obtained by fitting the SVFS data to a single energy barrier binding model.

New Analysis, MLE from force vs. loading rate scatter plots (mean \pm SD)

Virus	Cell	k_off (1/s)	x_beta (A)		tau (s)		
H1N1_WSN	A549	0.851	0.0525	2.67	0.0445	1.1751	0.0725
H1N1_WSN	CHO	0.62	0.0355	2.77	0.0397	1.6129	0.0924
H3N2_X31	A549	1.27	0.0704	6.42	0.0897	0.7874	0.0436
H3N2_X31	CHO	0.66	0.0472	9.54	0.183	1.5152	0.1084
H3N2_X31	MDCK	1.61	0.141	9.11	0.198	0.6211	0.0544

Old Analysis, fit with grouped loading rates, (mean \pm SD)

Virus	Cell	k_off (1/s)	x_beta (A)		tau (s)		
H1N1_WSN	A549	1.22	0.32	1.8	0.3	0.8197	0.2150
H1N1_WSN	CHO	1.16	0.13	2.4	0.3	0.8621	0.0966
H3N2_X31	A549	0.64	0.52	4.2	4.1	1.5625	1.2695
H3N2_X31	CHO	0.18	0.17	26.1	31.1	5.5556	5.2469
H3N2_X31	MDCK	0.45	0.35	8.4	7.9	2.2222	1.7284