

# Matters of Size: Genetic Bottlenecks in Virus Infection and Evolution

Annual Review of Virology

2, 161-179

DOI: [10.1146/annurev-virology-100114-055135](https://doi.org/10.1146/annurev-virology-100114-055135)

Citation Report

#	ARTICLE	IF	CITATIONS
1	The Strange Lifestyle of Multipartite Viruses. <i>PLoS Pathogens</i> , 2016, 12, e1005819.	2.1	85
2	Pathogen population bottlenecks and adaptive landscapes: overcoming the barriers to disease emergence. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160727.	1.2	46
3	Genetic variation in fitness within a clonal population of a plant RNA virus. <i>Virus Evolution</i> , 2016, 2, vew006.	2.2	10
4	Collective Infectious Units in Viruses. <i>Trends in Microbiology</i> , 2017, 25, 402-412.	3.5	101
5	Time-Sampled Population Sequencing Reveals the Interplay of Selection and Genetic Drift in Experimental Evolution of <i>Potato Virus Y</i> . <i>Journal of Virology</i> , 2017, 91, .	1.5	24
7	Molecular variation of tomato yellow leaf curl virus in the insect vector <i>Bemisia tabaci</i> . <i>Scientific Reports</i> , 2017, 7, 16427.	1.6	11
8	Evolution of drift robustness in small populations. <i>Nature Communications</i> , 2017, 8, 1012.	5.8	33
9	Predicting virus emergence amid evolutionary noise. <i>Open Biology</i> , 2017, 7, 170189.	1.5	149
10	Diminishing returns of inoculum size on the rate of a plant RNA virus evolution. <i>Europhysics Letters</i> , 2017, 120, 38001.	0.7	2
11	The <i>Operophtera brumata</i> Nucleopolyhedrovirus (OpbuNPV) Represents an Early, Divergent Lineage within Genus <i>Alphabaculovirus</i> . <i>Viruses</i> , 2017, 9, 307.	1.5	20
12	Some properties of the conditioned reconstructed process with Bernoulli sampling. <i>Theoretical Population Biology</i> , 2018, 122, 36-45.	0.5	4
13	Emergency Services of Viral RNAs: Repair and Remodeling. <i>Microbiology and Molecular Biology Reviews</i> , 2018, 82, .	2.9	26
14	Genetic bottlenecks in intraspecies virus transmission. <i>Current Opinion in Virology</i> , 2018, 28, 20-25.	2.6	118
15	A novel framework for inferring parameters of transmission from viral sequence data. <i>PLoS Genetics</i> , 2018, 14, e1007718.	1.5	17
16	Beneficial coinfection can promote within-host viral diversity. <i>Virus Evolution</i> , 2018, 4, vey028.	2.2	29
17	Population bottlenecks in multicomponent viruses: first forays into the uncharted territory of genome-formula drift. <i>Current Opinion in Virology</i> , 2018, 33, 184-190.	2.6	18
18	Influenza Virusâ€™Host Co-evolution. A Predator-Prey Relationship?. <i>Frontiers in Immunology</i> , 2018, 9, 2017.	2.2	18
19	Attenuation of replication by a 29 nucleotide deletion in SARS-coronavirus acquired during the early stages of human-to-human transmission. <i>Scientific Reports</i> , 2018, 8, 15177.	1.6	181

#	ARTICLE	IF	CITATIONS
20	Vector-transmission of plant viruses and constraints imposed by virus-vector interactions. <i>Current Opinion in Virology</i> , 2018, 33, 144-150.	2.6	36
21	Small Bottleneck Size in a Highly Multipartite Virus during a Complete Infection Cycle. <i>Journal of Virology</i> , 2018, 92, .	1.5	26
22	A speed-fidelity trade-off determines the mutation rate and virulence of an RNA virus. <i>PLoS Biology</i> , 2018, 16, e2006459.	2.6	88
23	Impact of genetic drift, selection and accumulation level on virus adaptation to its host plants. <i>Molecular Plant Pathology</i> , 2018, 19, 2575-2589.	2.0	11
24	Stochastic processes constrain the within and between host evolution of influenza virus. <i>ELife</i> , 2018, 7, .	2.8	179
25	Collective properties of viral infectivity. <i>Current Opinion in Virology</i> , 2018, 33, 1-6.	2.6	44
26	Quantitative analysis of the dose-response of white spot syndrome virus in shrimp. <i>Journal of Fish Diseases</i> , 2018, 41, 1733-1744.	0.9	3
27	Discovery of <i>Culex pipiens</i> associated tunisia virus: a new ssRNA(+) virus representing a new insect associated virus family. <i>Virus Evolution</i> , 2018, 4, vex040.	2.2	17
28	Genetic Variation and Biological Activity of Two Closely Related Alphabaculoviruses during Serial Passage in Permissive and Semi-Permissive Heterologous Hosts. <i>Viruses</i> , 2019, 11, 660.	1.5	6
29	Membrane-Associated Enteroviruses Undergo Intercellular Transmission as Pools of Sibling Viral Genomes. <i>Cell Reports</i> , 2019, 29, 714-723.e4.	2.9	28
30	Mutational load causes stochastic evolutionary outcomes in acute RNA viral infection. <i>Virus Evolution</i> , 2019, 5, vez008.	2.2	14
31	Characterization of Mutational Tolerance of a Viral RNA-Protein Interaction. <i>Viruses</i> , 2019, 11, 479.	1.5	1
32	The effect of genetic complementation on the fitness and diversity of viruses spreading as collective infectious units. <i>Virus Research</i> , 2019, 267, 41-48.	1.1	15
33	Virus epidemics, plant-controlled population bottlenecks and the durability of plant resistance. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180263.	1.8	16
34	Social evolution of innate immunity evasion in a virus. <i>Nature Microbiology</i> , 2019, 4, 1006-1013.	5.9	52
35	Detection of Multiple Variants of Grapevine Fanleaf Virus in Single <i>Xiphinema index</i> Nematodes. <i>Viruses</i> , 2019, 11, 1139.	1.5	12
36	On the stability of sequences inserted into viral genomes. <i>Virus Evolution</i> , 2019, 5, vez045.	2.2	41
37	Virus-Host Coevolution with a Focus on Animal and Human DNA Viruses. <i>Journal of Molecular Evolution</i> , 2020, 88, 41-56.	0.8	77

#	ARTICLE	IF	CITATIONS
38	Influenza B Viruses Exhibit Lower Within-Host Diversity than Influenza A Viruses in Human Hosts. <i>Journal of Virology</i> , 2020, 94, .	1.5	46
39	Rapid Dissemination and Monopolization of Viral Populations in Mice Revealed Using a Panel of Barcoded Viruses. <i>Journal of Virology</i> , 2020, 94, .	1.5	14
40	Estimating viral bottleneck sizes for FMDV transmission within and between hosts and implications for the rate of viral evolution. <i>Interface Focus</i> , 2020, 10, 20190066.	1.5	16
41	The Curious Strategy of Multipartite Viruses. <i>Annual Review of Virology</i> , 2020, 7, 203-218.	3.0	34
42	Virions and respiratory droplets in air: Diffusion, drift, and contact with the epithelium. <i>BioSystems</i> , 2020, 198, 104241.	0.9	7
43	Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	203
44	Cooperative nature of viral replication. <i>Science Advances</i> , 2020, 6, .	4.7	19
45	Contribution of Viral Genomic Diversity to Oyster Susceptibility in the Pacific Oyster Mortality Syndrome. <i>Frontiers in Microbiology</i> , 2020, 11, 1579.	1.5	14
46	A new cypovirus from the Japanese peppered moth, <i>Biston robustus</i> . <i>Journal of Invertebrate Pathology</i> , 2020, 174, 107417.	1.5	5
47	SARS-CoV-2 ORF8 and SARS-CoV ORF8ab: Genomic Divergence and Functional Convergence. <i>Pathogens</i> , 2020, 9, 677.	1.2	44
48	Modeling multipartite virus evolution: the genome formula facilitates rapid adaptation to heterogeneous environments. <i>Virus Evolution</i> , 2020, 6, veaa022.	2.2	22
49	Transmission modes affect the population structure of potato virus Y in potato. <i>PLoS Pathogens</i> , 2020, 16, e1008608.	2.1	31
53	Population Bottlenecks and Intra-host Evolution During Human-to-Human Transmission of SARS-CoV-2. <i>Frontiers in Medicine</i> , 2021, 8, 585358.	1.2	28
54	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. <i>Genome Research</i> , 2021, 31, 635-644.	2.4	39
55	Transmission of SARS-CoV-2 in domestic cats imposes a narrow bottleneck. <i>PLoS Pathogens</i> , 2021, 17, e1009373.	2.1	84
56	Quantification of <i>Brucella abortus</i> population structure in a natural host. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	10
58	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	6.0	278
59	Temporal dynamics of SARS-CoV-2 mutation accumulation within and across infected hosts. <i>PLoS Pathogens</i> , 2021, 17, e1009499.	2.1	86

#	ARTICLE	IF	CITATIONS
60	Virus Prevalence and Genetic Diversity Across a Wild Bumblebee Community. <i>Frontiers in Microbiology</i> , 2021, 12, 650747.	1.5	10
62	Retrospective Characterization of the 2006–2007 Swine Vesicular Disease Epidemic in Northern Italy by Whole Genome Sequence Analysis. <i>Viruses</i> , 2021, 13, 1186.	1.5	0
64	Why are viral genomes so fragile? The bottleneck hypothesis. <i>PLoS Computational Biology</i> , 2021, 17, e1009128.	1.5	8
65	SARS-CoV-2: Cross-scale Insights from Ecology and Evolution. <i>Trends in Microbiology</i> , 2021, 29, 593-605.	3.5	12
66	The Social Life of Viruses. <i>Annual Review of Virology</i> , 2021, 8, 183-199.	3.0	25
67	Coalescent models derived from birth–death processes. <i>Theoretical Population Biology</i> , 2021, 142, 1-11.	0.5	3
68	From one to many: The within-host rise of viral variants. <i>PLoS Pathogens</i> , 2021, 17, e1009811.	2.1	9
69	Cross-scale dynamics and the evolutionary emergence of infectious diseases. <i>Virus Evolution</i> , 2021, 7, .	2.2	13
70	Bottleneck, Isolate, Amplify, Select (BIAS) as a mechanistic framework for intracellular population dynamics of positive-sense RNA viruses. <i>Virus Evolution</i> , 2020, 6, veaa086.	2.2	7
71	Quantitative trait loci in pepper control the effective population size of two RNA viruses at inoculation. <i>Journal of General Virology</i> , 2017, 98, 1923-1931.	1.3	10
81	Inferring Transmission Bottleneck Size from Viral Sequence Data Using a Novel Haplotype Reconstruction Method. <i>Journal of Virology</i> , 2020, 94, .	1.5	18
82	The role of spatial structure in the evolution of viral innate immunity evasion: A diffusion-reaction cellular automaton model. <i>PLoS Computational Biology</i> , 2020, 16, e1007656.	1.5	8
83	Opposite Outcomes of the Within-Host Competition between High- and Low-Pathogenic H5N8 Avian Influenza Viruses in Chickens Compared to Ducks. <i>Journal of Virology</i> , 2022, 96, JVI0136621.	1.5	6
90	The evolution of cheating in viruses. <i>Nature Communications</i> , 2021, 12, 6928.	5.8	14
91	Nucleopolyhedrovirus Coocclusion Technology: A New Concept in the Development of Biological Insecticides. <i>Frontiers in Microbiology</i> , 2021, 12, 810026.	1.5	15
93	Limited genomic reconstruction of SARS-CoV-2 transmission history within local epidemiological clusters. <i>Virus Evolution</i> , 2022, 8, veac008.	2.2	10
95	Coocclusion of <i>Helicoverpa armigera</i> Single Nucleopolyhedrovirus (HearSNPV) and <i>Helicoverpa armigera</i> Multiple Nucleopolyhedrovirus (HearMNPV): Pathogenicity and Stability in Homologous and Heterologous Hosts. <i>Viruses</i> , 2022, 14, 687.	1.5	2
96	Natural rodent model of viral transmission reveals biological features of virus population dynamics. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	18

#	ARTICLE	IF	CITATIONS
109	Narrow transmission bottlenecks and limited within-host viral diversity during a SARS-CoV-2 outbreak on a fishing boat. <i>Virus Evolution</i> , 2022, 8, .	2.2	7
110	Empirical estimates of the mutation rate for an alphabaculovirus. <i>PLoS Genetics</i> , 2022, 18, e1009806.	1.5	2
111	Multiple Levels of Triggered Factors and the Obligated Requirement of Cell-to-Cell Movement in the Mutation Repair of Cucumber Mosaic Virus with Defects in the tRNA-like Structure. <i>Biology</i> , 2022, 11, 1051.	1.3	1
112	Deciphering the Tissue Tropism of the RNA Viromes Harbored by Field-Collected <i>Anopheles sinensis</i> and <i>Culex quinquefasciatus</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
113	Challenges and opportunities for plant viruses under a climate change scenario. <i>Advances in Virus Research</i> , 2022, , .	0.9	4
114	Is the Increased Transmissibility of SARS-CoV-2 Variants Driven by within or Outside-Host Processes?. <i>Mathematics</i> , 2022, 10, 3422.	1.1	2
115	A brief view of factors that affect plant virus evolution. <i>Frontiers in Virology</i> , 0, 2, .	0.7	7
116	PrÄhistorische Reflexion 1: HÄrhlenzeit. , 2022, , 175-216.		0
118	Influenza A virus reassortment in mammals gives rise to genetically distinct within-host subpopulations. <i>Nature Communications</i> , 2022, 13, .	5.8	18
119	Evaluating the potential of whole-genome sequencing for tracing transmission routes in experimental infections and natural outbreaks of bovine respiratory syncytial virus. <i>Veterinary Research</i> , 2022, 53, .	1.1	2
120	Rapid transmission and tight bottlenecks constrain the evolution of highly transmissible SARS-CoV-2 variants. <i>Nature Communications</i> , 2023, 14, .	5.8	17
121	Plant Virus Adaptation to New Hosts: A Multi-scale Approach. <i>Current Topics in Microbiology and Immunology</i> , 2023, , 167-196.	0.7	1
122	A Screening for Virus Infections among Wild Eurasian Tundra Reindeer ( <i>Rangifer tarandus tarandus</i> ) in Iceland, 2017Ä2019. <i>Viruses</i> , 2023, 15, 317.	1.5	0
123	Detecting punctuated evolution in SARS-CoV-2 over the first year of the pandemic. <i>Frontiers in Virology</i> , 0, 3, .	0.7	0
124	Developing an appropriate evolutionary baseline model for the study of SARS-CoV-2 patient samples. <i>PLoS Pathogens</i> , 2023, 19, e1011265.	2.1	8
125	The evolution of SARS-CoV-2. <i>Nature Reviews Microbiology</i> , 2023, 21, 361-379.	13.6	239
126	Developing an Appropriate Evolutionary Baseline Model for the Study of Human Cytomegalovirus. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	4