

# Insights on the Emergence of *Mycobacterium tuberculosis* *Mycobacterium kansasii*

Genome Biology and Evolution

7, 856-870

DOI: [10.1093/gbe/evv035](https://doi.org/10.1093/gbe/evv035)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Draft Genome Sequence of <i>Mycobacterium arupense</i> Strain GUC1. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
2	Population genomics of <i>Mycobacterium tuberculosis</i> in the Inuit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13609-13614.	3.3	77
3	Smooth Tubercle Bacilli: Neglected Opportunistic Tropical Pathogens. <i>Frontiers in Public Health</i> , 2015, 3, 283.	1.3	24
4	Perspectives on mycobacterial vacuole-to-cytosol translocation: the importance of cytosolic access. <i>Cellular Microbiology</i> , 2016, 18, 1070-1077.	1.1	26
5	The distinct fate of smooth and rough <i>Mycobacterium abscessus</i> variants inside macrophages. <i>Open Biology</i> , 2016, 6, 160185.	1.5	132
6	Does Choice Matter? Reference-Based Alignment for Molecular Epidemiology of Tuberculosis. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1891-1895.	1.8	25
7	ESX secretion systems: mycobacterial evolution to counter host immunity. <i>Nature Reviews Microbiology</i> , 2016, 14, 677-691.	13.6	306
8	Treatment of Non-Tuberculous Mycobacterial Lung Disease. <i>Current Treatment Options in Infectious Diseases</i> , 2016, 8, 275-296.	0.8	46
9	Evolution of <i>Mycobacterium tuberculosis</i> : New Insights into Pathogenicity and Drug Resistance. <i>Microbiology Spectrum</i> , 2016, 4, .	1.2	17
10	Controlled fire use in early humans might have triggered the evolutionary emergence of tuberculosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9051-9056.	3.3	36
11	Tuberculosis. <i>Nature Reviews Disease Primers</i> , 2016, 2, 16076.	18.1	830
12	<i>pks5</i> -recombination-mediated surface remodelling in <i>Mycobacterium tuberculosis</i> emergence. <i>Nature Microbiology</i> , 2016, 1, 15019.	5.9	81
13	Mycobacterial Pan-Genome Analysis Suggests Important Role of Plasmids in the Radiation of Type VII Secretion Systems. <i>Genome Biology and Evolution</i> , 2016, 8, 387-402.	1.1	81
14	Complications in the study of ancient tuberculosis: Presence of environmental bacteria in human archaeological remains. <i>Journal of Archaeological Science</i> , 2016, 68, 5-11.	1.2	16
15	ESX-1 and phthiocerol dimycocerosates of <i>Mycobacterium tuberculosis</i> act in concert to cause phagosomal rupture and host cell apoptosis. <i>Cellular Microbiology</i> , 2017, 19, e12726.	1.1	174
16	The role of hydrophobicity in tuberculosis evolution and pathogenicity. <i>Scientific Reports</i> , 2017, 7, 1315.	1.6	75
17	Genomic characterization of Nontuberculous Mycobacteria. <i>Scientific Reports</i> , 2017, 7, 45258.	1.6	176
18	Recombinant BCG Expressing ESX-1 of <i>Mycobacterium marinum</i> Combines Low Virulence with Cytosolic Immune Signaling and Improved TB Protection. <i>Cell Reports</i> , 2017, 18, 2752-2765.	2.9	98

#	ARTICLE	IF	CITATIONS
19	Ready Experimental Translocation of <i>Mycobacterium canettii</i> Yields Pulmonary Tuberculosis. <i>Infection and Immunity</i> , 2017, 85, .	1.0	12
20	The Nature and Evolution of Genomic Diversity in the <i>Mycobacterium tuberculosis</i> Complex. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 1-26.	0.8	52
22	Discovery of the type VII ESX secretion needle?. <i>Molecular Microbiology</i> , 2017, 103, 7-12.	1.2	30
23	Evolution of <i>Mycobacterium tuberculosis</i> : New Insights into Pathogenicity and Drug Resistance. , 0, , 495-515.		3
24	Toxin-antitoxin systems and regulatory mechanisms in <i>Mycobacterium tuberculosis</i> . <i>Pathogens and Disease</i> , 2018, 76, .	0.8	76
25	Ecology and evolution of <i>Mycobacterium tuberculosis</i> . <i>Nature Reviews Microbiology</i> , 2018, 16, 202-213.	13.6	414
26	Impact of Genomics on Clarifying the Evolutionary Relationships amongst <i>Mycobacteria</i> : Identification of Molecular Signatures Specific for the Tuberculosis-Complex of Bacteria with Potential Applications for Novel Diagnostics and Therapeutics. <i>High-Throughput</i> , 2018, 7, 31.	4.4	7
27	Whole genome sequence of <i>Mycobacterium kansasii</i> isolates of the genotype 1 from Brazilian patients with pulmonary disease demonstrates considerable heterogeneity. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2018, 113, e180085.	0.8	7
28	Phylogenomics and Comparative Genomic Studies Robustly Support Division of the Genus <i>Mycobacterium</i> into an Emended Genus <i>Mycobacterium</i> and Four Novel Genera. <i>Frontiers in Microbiology</i> , 2018, 9, 67.	1.5	878
29	Extensive genomic diversity among <i>Mycobacterium marinum</i> strains revealed by whole genome sequencing. <i>Scientific Reports</i> , 2018, 8, 12040.	1.6	25
30	Shared Pathogenomic Patterns Characterize a New Phylotype, Revealing Transition toward Host-Adaptation Long before Speciation of <i>Mycobacterium tuberculosis</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 2420-2438.	1.1	29
31	Protein Export into and across the Atypical Diderm Cell Envelope of <i>Mycobacteria</i> . <i>Microbiology Spectrum</i> , 2019, 7, .	1.2	13
32	<i>Mycobacterium tuberculosis</i> infection of host cells in space and time. <i>FEMS Microbiology Reviews</i> , 2019, 43, 341-361.	3.9	234
33	<i>Mycobacterial</i> Evolution Intersects With Host Tolerance. <i>Frontiers in Immunology</i> , 2019, 10, 528.	2.2	29
34	Protein Export into and across the Atypical Diderm Cell Envelope of <i>Mycobacteria</i> . , 2019, , 1129-1153.		1
35	Update on the virulence factors of the obligate pathogen <i>Mycobacterium tuberculosis</i> and related tuberculosis-causing <i>mycobacteria</i> . <i>Infection, Genetics and Evolution</i> , 2019, 72, 67-77.	1.0	16
36	Nontuberculous <i>mycobacteria</i> : Insights on taxonomy and evolution. <i>Infection, Genetics and Evolution</i> , 2019, 72, 159-168.	1.0	46
38	CAPRIB: a user-friendly tool to study amino acid changes and selection for the exploration of intra-genus evolution. <i>BMC Genomics</i> , 2020, 21, 832.	1.2	2

#	ARTICLE	IF	CITATIONS
39	A sister lineage of the <i>Mycobacterium tuberculosis</i> complex discovered in the African Great Lakes region. <i>Nature Communications</i> , 2020, 11, 2917.	5.8	136
40	Transposon mutagenesis in <i>Mycobacterium kansasii</i> links a small RNA gene to colony morphology and biofilm formation and identifies 9,885 intragenic insertions that do not compromise colony outgrowth. <i>MicrobiologyOpen</i> , 2020, 9, e988.	1.2	13
41	The Many Hosts of <i>Mycobacteria</i> 8 (MHM8): A conference report. <i>Tuberculosis</i> , 2020, 121, 101914.	0.8	6
42	TbD1 deletion as a driver of the evolutionary success of modern epidemic <i>Mycobacterium tuberculosis</i> lineages. <i>Nature Communications</i> , 2020, 11, 684.	5.8	68
43	Comparative Genomic and Transcriptomic Analyses of <i>Mycobacterium kansasii</i> Subtypes Provide New Insights Into Their Pathogenicity and Taxonomy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 122.	1.8	10
44	Large Extracellular Cord Formation in a Zebrafish Model of <i>Mycobacterium kansasii</i> Infection. <i>Journal of Infectious Diseases</i> , 2020, 222, 1046-1050.	1.9	13
45	Pathogenic Determinants of the <i>Mycobacterium kansasii</i> Complex: An Unsuspected Role for Distributive Conjugal Transfer. <i>Microorganisms</i> , 2021, 9, 348.	1.6	5
46	Population genomics provides insights into the evolution and adaptation to humans of the waterborne pathogen <i>Mycobacterium kansasii</i> . <i>Nature Communications</i> , 2021, 12, 2491.	5.8	20
47	Control of Toxin-Antitoxin Systems by Proteases in <i>Mycobacterium Tuberculosis</i> . <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 691399.	1.6	14
48	Insights into the ancestry evolution of the <i>Mycobacterium tuberculosis</i> complex from analysis of <i>Mycobacterium riyadhense</i> . <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab070.	1.5	3
49	Conserved and specialized functions of Type VII secretion systems in non-tuberculous mycobacteria. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	14
50	A Murine Model of <i>Mycobacterium kansasii</i> Infection Reproducing Necrotic Lung Pathology Reveals Considerable Heterogeneity in Virulence of Clinical Isolates. <i>Frontiers in Microbiology</i> , 2021, 12, 718477.	1.5	1
51	Comprehensive profiling of functional attributes, virulence potential and evolutionary dynamics in mycobacterial secretomes. <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 5.	1.7	4
52	Crystal structure of a hemerythrin-like protein from <i>Mycobacterium kansasii</i> and homology model of the orthologous Rv2633c protein of <i>M. tuberculosis</i> . <i>Biochemical Journal</i> , 2020, 477, 567-581.	1.7	8
53	<i>Mycobacterium stellerae</i> sp. nov., a rapidly growing scotochromogenic strain isolated from <i>Stellera chamaejasme</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3465-3471.	0.8	14
56	Heterologous Production of 1-Tubercosinyladenosine in <i>Mycobacterium kansasii</i> Models Pathoevolution towards the Transcellular Lifestyle of <i>Mycobacterium tuberculosis</i> . <i>MBio</i> , 2020, 11, .	1.8	9
57	Mycobacterial virulence: impact on immunogenicity and vaccine research. <i>F1000Research</i> , 2019, 8, 2025.	0.8	15
58	16S-23S Internal Transcribed Spacer Region PCR and Sequencer-Based Capillary Gel Electrophoresis has Potential as an Alternative to High Performance Liquid Chromatography for Identification of Slowly Growing Nontuberculous Mycobacteria. <i>PLoS ONE</i> , 2016, 11, e0164138.	1.1	4

#	ARTICLE	IF	CITATIONS
59	Activity of N-Phenylpiperazine Derivatives Against Bacterial and Fungal Pathogens. <i>Current Protein and Peptide Science</i> , 2019, 20, 1119-1129.	0.7	4
69	Evaluation of <i>Mycobacterium kansasii</i> Extracellular Vesicles Role in BALB/c Mice Immune Modulatory. <i>International Journal of Mycobacteriology</i> , 2020, 9, 58-61.	0.3	0
70	Macrophage: A Cell With Many Faces and Functions in Tuberculosis. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	35
72	The Other Nontuberculous Mycobacteria. <i>Chest</i> , 2023, 163, 281-291.	0.4	5
73	<i>Galleria mellonella</i> “intracellular bacteria pathogen infection models: the ins and outs. <i>FEMS Microbiology Reviews</i> , 2023, 47, .	3.9	12