

Bottlenecks and broomsticks: the molecular evolution of

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Molecular Tools for Typing and Branding the Tubercle Bacillus. <i>Current Molecular Medicine</i> , 2007, 7, 309-317.	0.6	12
2	Genomics and the evolution, pathogenesis, and diagnosis of tuberculosis. <i>Journal of Clinical Investigation</i> , 2007, 117, 1738-1745.	3.9	69
3	Global phylogeography of <i>Mycobacterium tuberculosis</i> and implications for tuberculosis product development. <i>Lancet Infectious Diseases</i> , The, 2007, 7, 328-337.	4.6	634
4	Human Benefits of Animal Interventions for Zoonosis Control. <i>Emerging Infectious Diseases</i> , 2007, 13, 527-531.	2.0	205
5	Evolution of two distinct phylogenetic lineages of the emerging human pathogen <i>Mycobacterium ulcerans</i> . <i>BMC Evolutionary Biology</i> , 2007, 7, 177.	3.2	81
6	Molecular characterisation of <i>Mycobacterium bovis</i> isolated from cattle slaughtered at the Bamako abattoir in Mali. <i>BMC Veterinary Research</i> , 2008, 4, 26.	0.7	62
7	Evolution, Population Structure, and Phylogeography of Genetically Monomorphic Bacterial Pathogens. <i>Annual Review of Microbiology</i> , 2008, 62, 53-70.	2.9	402
8	Microbial diversity and the genetic nature of microbial species. <i>Nature Reviews Microbiology</i> , 2008, 6, 431-440.	13.6	521
9	High <i>Mycobacterium bovis</i> genetic diversity in a low prevalence setting. <i>Veterinary Microbiology</i> , 2008, 126, 151-159.	0.8	68
10	Spoligotype diversity of <i>Mycobacterium bovis</i> and <i>Mycobacterium caprae</i> animal isolates. <i>Veterinary Microbiology</i> , 2008, 130, 415-421.	0.8	93
11	Construction of a severely attenuated mutant of <i>Mycobacterium tuberculosis</i> for reducing risk to laboratory workers. <i>Tuberculosis</i> , 2008, 88, 375-381.	0.8	10
12	IS <i>6110</i> , a <i>Mycobacterium tuberculosis</i> Complex-Specific Insertion Sequence, Is Also Present in the Genome of <i>Mycobacterium smegmatis</i> , Suggestive of Lateral Gene Transfer among Mycobacterial Species. <i>Journal of Bacteriology</i> , 2008, 190, 3408-3410.	1.0	76
13	Functional analysis of a clonal deletion in an epidemic strain of <i>Mycobacterium bovis</i> reveals a role in lipid metabolism. <i>Microbiology (United Kingdom)</i> , 2008, 154, 3731-3742.	0.7	12
14	High Functional Diversity in <i>Mycobacterium tuberculosis</i> Driven by Genetic Drift and Human Demography. <i>PLoS Biology</i> , 2008, 6, e311.	2.6	507
15	Estimates for local and movement-based transmission of bovine tuberculosis in British cattle. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 1001-1005.	1.2	110
16	Human and canine pulmonary <i>Mycobacterium bovis</i> infection in the same household: re-emergence of an old zoonotic threat?. <i>Thorax</i> , 2008, 64, 89-91.	2.7	41
17	<i>Mycobacterium bovis</i> Infection in Holstein Friesian Cattle, Iran. <i>Emerging Infectious Diseases</i> , 2008, 14, 1919-1921.	2.0	19
18	Differential Gene Repertoire in <i>Mycobacterium ulcerans</i> Identifies Candidate Genes for Patho-Adaptation. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e353.	1.3	13

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19	Bayesian Receiver Operating Characteristic Estimation of Multiple Tests for Diagnosis of Bovine Tuberculosis in Chadian Cattle. <i>PLoS ONE</i> , 2009, 4, e8215.	1.1	32
20	Large Sequence Polymorphisms Unveil the Phylogenetic Relationship of Environmental and Pathogenic <i>Mycobacterium</i> Related to <i>Mycobacterium ulcerans</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 5667-5675.	1.4	30
21	<i>Mycobacterium microti</i> : More Diverse than Previously Thought. <i>Journal of Clinical Microbiology</i> , 2009, 47, 2551-2559.	1.8	72
22	A Comprehensive Survey of Single Nucleotide Polymorphisms (SNPs) across <i>Mycobacterium bovis</i> Strains and <i>M. bovis</i> BCG Vaccine Strains Refines the Genealogy and Defines a Minimal Set of SNPs That Separate Virulent <i>M. bovis</i> Strains and <i>M. bovis</i> BCG Strains. <i>Infection and Immunity</i> , 2009, 77, 2230-2238.	1.0	67
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25	Outbreak of tuberculosis caused by <i>Mycobacterium bovis</i> in golden Guernsey goats in Great Britain. <i>Veterinary Record</i> , 2009, 165, 335-342.	0.2	65
26	African 1, an Epidemiologically Important Clonal Complex of <i>Mycobacterium bovis</i> Dominant in Mali, Nigeria, Cameroon, and Chad. <i>Journal of Bacteriology</i> , 2009, 191, 1951-1960.	1.0	125
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38	High spoligotype diversity within a <i>Mycobacterium bovis</i> population: Clues to understanding the demography of the pathogen in Europe. <i>Veterinary Microbiology</i> , 2010, 141, 89-95.	0.8	94
39	<i>Mycobacterium bovis</i> at the animal-human interface: A problem, or not?. <i>Veterinary Microbiology</i> , 2010, 140, 371-381.	0.8	248
40	Identification of <i>Mycobacterium tuberculosis</i> clinical isolates in Bangladesh by a species distinguishable multiplex PCR. <i>BMC Infectious Diseases</i> , 2010, 10, 118.	1.3	30

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50	Bovine tuberculosis: the genetic basis of host susceptibility. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 2737-2745.	1.2	83
51	Evolution and Population Structure of <i>Salmonella enterica</i> Serovar Newport. <i>Journal of Bacteriology</i> , 2010, 192, 6465-6476.	1.0	109
52	Evaluation of Mycobacterial Interspersed Repetitive-Unit-Variable-Number Tandem-Repeat Analysis and Spoligotyping for Genotyping of <i>Mycobacterium bovis</i> Isolates and a Comparison with Restriction Fragment Length Polymorphism Typing. <i>Journal of Clinical Microbiology</i> , 2010, 48, 4541-4545.	1.8	32
53	<i>Mycobacterium bovis</i> genotypes in Northern Ireland: herd-level surveillance (2003 to 2008). <i>Veterinary Record</i> , 2010, 167, 684-689.	0.2	34
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55	Fine-Scale Distribution Patterns of <i>Synechococcus</i> Ecological Diversity in Microbial Mats of Mushroom Spring, Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7689-7697.	1.4	72
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59	A species concept for bacteria based on adaptive divergence. <i>Trends in Microbiology</i> , 2011, 19, 1-7.	3.5	79

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61	Genotype and Geography. , 2011, , 43-58.		2
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71	African 2, a Clonal Complex of <i>Mycobacterium bovis</i> Epidemiologically Important in East Africa. <i>Journal of Bacteriology</i> , 2011, 193, 670-678.	1.0	96
72	Limitations of Spoligotyping and Variable-Number Tandem-Repeat Typing for Molecular Tracing of <i>Mycobacterium bovis</i> in a High-Diversity Setting. <i>Journal of Clinical Microbiology</i> , 2011, 49, 3361-3364.	1.8	42
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74	The Impact of Recombination on dN/dS within Recently Emerged Bacterial Clones. <i>PLoS Pathogens</i> , 2011, 7, e1002129.	2.1	105
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83	Spoligotyping and variable number tandem repeat analysis of Mycobacterium bovis isolates from cattle in Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2012, 107, 64-73.	0.8	28
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98	The phylogeny and population structure of <i>Mycobacterium bovis</i> in the British Isles. <i>Infection, Genetics and Evolution</i> , 2013, 20, 8-15.	1.0	25
99	Phenotypic and genetic parameters of antibody and delayed-type hypersensitivity responses of lactating Holstein cows. <i>Veterinary Immunology and Immunopathology</i> , 2013, 154, 83-92.	0.5	21
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112	Differences in Primary Sites of Infection between Zoonotic and Human Tuberculosis: Results from a Worldwide Systematic Review. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2399.	1.3	45
113	The Role of Selection in Shaping Diversity of Natural <i>M. tuberculosis</i> Populations. <i>PLoS Pathogens</i> , 2013, 9, e1003543.	2.1	138
114	Coalition Culls and Zoonotic Ontologies. <i>Environment and Planning A</i> , 2013, 45, 1372-1386.	2.1	8
115	Isolation and molecular characterization of non tuberculosis mycobacteria from skin positive reactors and pathological lesions of cattle at Bako, Western Ethiopia. <i>African Journal of Microbiology Research</i> , 2013, 7, 2190-2197.	0.4	2

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117	Standing of nucleic acid testing strategies in veterinary diagnosis laboratories to uncover Mycobacterium tuberculosis complex members. <i>Frontiers in Molecular Biosciences</i> , 2014, 1, 16.	1.6	13
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126	Relaxed Selection Drives a Noisy Noncoding Transcriptome in Members of the Mycobacterium tuberculosis Complex. <i>MBio</i> , 2014, 5, e01169-14.	1.8	20
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134	Sources of bovine tuberculosis in the United States. <i>Infection, Genetics and Evolution</i> , 2014, 28, 137-143.	1.0	26

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141	Genomic Heterogeneity and Ecological Speciation within One Subspecies of <i>Bacillus subtilis</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 4842-4853.	1.4	44
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147	The molecular dimension of microbial species: 1. Ecological distinctions among, and homogeneity within, putative ecotypes of <i>Synechococcus</i> inhabiting the cyanobacterial mat of Mushroom Spring, Yellowstone National Park. <i>Frontiers in Microbiology</i> , 2015, 6, 590.	1.5	49
148	Molecular diagnosis of bovine tuberculosis in bovine and human samples: implications for zoonosis. <i>Future Microbiology</i> , 2015, 10, 527-535.	1.0	12
149	Genetic Evolution of <i>Mycobacterium bovis</i> Causing Tuberculosis in Livestock and Wildlife in France since 1978. <i>PLoS ONE</i> , 2015, 10, e0117103.	1.1	85
150	Microbiome Ecosystem Ecology: Unseen Majority in an Anthropogenic Ecosystem. <i>SpringerBriefs in Ecology</i> , 2015, , 1-11.	0.2	3
151	Gene Loss Dominates As a Source of Genetic Variation within Clonal Pathogenic Bacterial Species. <i>Genome Biology and Evolution</i> , 2015, 7, 2173-2187.	1.1	69
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154	<i>Mycobacterium bovis</i> Infection of Cattle and White-Tailed Deer: Translational Research of Relevance to Human Tuberculosis. <i>ILAR Journal</i> , 2015, 56, 26-43.	1.8	36
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