

Whole-genome sequencing for prediction of Mycobacterium tuberculosis susceptibility and resistance: a retrospective cohort study

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Pathogens: Wantedâ€”Dead or Alive. <i>Microbe Magazine</i> , 2015, 10, 513-520.	0.4	2
2	A Collaborative Approach for â€œReSeq-ingâ€•Mycobacterium tuberculosis Drug Resistance: Convergence for Drug and Diagnostic Developers. <i>EBioMedicine</i> , 2015, 2, 1262-1265.	2.7	15
3	Genome sequence comparisons of serial multi-drug-resistant Mycobacterium tuberculosis isolates over 21 years of infection in a single patient. <i>Microbial Genomics</i> , 2015, 1, e000037.	1.0	15
4	Clinical implications of the global multidrug-resistant tuberculosis epidemic. <i>Clinical Medicine</i> , 2015, 15, s37-s42.	0.8	16
5	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. <i>Nature Communications</i> , 2015, 6, 10063.	5.8	479
6	Clinical value of whole-genome sequencing of Mycobacterium tuberculosis. <i>Lancet Infectious Diseases, The</i> , 2015, 15, 1077-1090.	4.6	57
7	Towards genomic prediction of drug resistance in tuberculosis. <i>Lancet Infectious Diseases, The</i> , 2015, 15, 1124-1125.	4.6	9
8	Treatment of Tuberculosis. <i>New England Journal of Medicine</i> , 2015, 373, 2149-2160.	13.9	290
9	Molecular Typing of Mycobacterium tuberculosis Strains: A Fundamental Tool for Tuberculosis Control and Elimination. <i>Gastroenterology Insights</i> , 2016, 8, 6567.	0.7	19
10	Whole-genome Sequencing for Surveillance of Invasive Pneumococcal Diseases in Ontario, Canada: Rapid Prediction of Genotype, Antibiotic Resistance and Characterization of Emerging Serotype 22F. <i>Frontiers in Microbiology</i> , 2016, 7, 2099.	1.5	7
11	Whole genome sequencing reveals mycobacterial microevolution among concurrent isolates from sputum and blood in HIV infected TB patients. <i>BMC Infectious Diseases</i> , 2016, 16, 371.	1.3	11
12	Discordance across Phenotypic and Molecular Methods for Drug Susceptibility Testing of Drug-Resistant Mycobacterium tuberculosis Isolates in a Low TB Incidence Country. <i>PLoS ONE</i> , 2016, 11, e0153563.	1.1	55
13	Tuberculosis 2015: Burden, Challenges and Strategy for Control and Elimination. <i>Gastroenterology Insights</i> , 2016, 8, 6570.	0.7	175
14	Personalizing therapy for multidrug resistant TB: the potential of Rapid Whole Genome Sequencing. <i>Expert Review of Anti-Infective Therapy</i> , 2016, 14, 1-3.	2.0	3
15	Tuberculosis Diagnostics: State of the Art and Future Directions. <i>Microbiology Spectrum</i> , 2016, 4, .	1.2	87
16	Unexpected high prevalence of resistance-associated <i>Rv0678</i> variants in MDR-TB patients without documented prior use of clofazimine or bedaquiline. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, dkw502.	1.3	134
17	Diagnosing tuberculosis in the 21st century â€“ Dawn of a genomics revolution?. <i>International Journal of Mycobacteriology</i> , 2016, 5, 384-391.	0.3	22
18	Clinical implications of the global multidrug-resistant tuberculosis epidemic. <i>Clinical Medicine</i> , 2016, 16, 565-570.	0.8	2

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19	Antimicrobial Resistance Prediction in PATRIC and RAST. <i>Scientific Reports</i> , 2016, 6, 27930.	1.6	179
20	Occupational Tuberculosis despite Minimal Nosocomial Contact in a Health Care Worker Undergoing Treatment with a Tumor Necrosis Factor Inhibitor. <i>Annals of the American Thoracic Society</i> , 2016, 13, 2275-2277.	1.5	3
21	Whole genome sequencing to complement tuberculosis drug resistance surveys in Uganda. <i>Infection, Genetics and Evolution</i> , 2016, 40, 8-16.	1.0	28
23	Diagnosis of active tuberculosis disease: From microscopy to molecular techniques. <i>Journal of Clinical Tuberculosis and Other Mycobacterial Diseases</i> , 2016, 4, 33-43.	0.6	97
25	Standard Genotyping Overestimates Transmission of <i>Mycobacterium tuberculosis</i> among Immigrants in a Low-Incidence Country. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1862-1870.	1.8	94
26	The implications of whole-genome sequencing in the control of tuberculosis. <i>Therapeutic Advances in Infectious Disease</i> , 2016, 3, 47-62.	1.1	28
27	Clinical use of whole genome sequencing for <i>Mycobacterium tuberculosis</i> . <i>BMC Medicine</i> , 2016, 14, 46.	2.3	91
28	GenoType <sup>®</sup> MTBDR <sub>sl</sub> assay for resistance to second-line anti-tuberculosis drugs. <i>The Cochrane Library</i> , 2016, 2016, CD010705.	1.5	42
29	Drug-resistant tuberculosis among previously treated patients in Yangon, Myanmar. <i>International Journal of Mycobacteriology</i> , 2016, 5, 366-367.	0.3	2
30	Recent developments in genomics, bioinformatics and drug discovery to combat emerging drug-resistant tuberculosis. <i>Tuberculosis</i> , 2016, 101, 31-40.	0.8	19
31	Multidrug-Resistant Tuberculosis in Children: Recent Developments in Diagnosis, Treatment and Prevention. <i>Current Pediatrics Reports</i> , 2016, 4, 53-62.	1.7	4
32	Evolution of <i>Mycobacterium tuberculosis</i> : New Insights into Pathogenicity and Drug Resistance. <i>Microbiology Spectrum</i> , 2016, 4, .	1.2	17
33	Use of bacterial whole-genome sequencing to understand and improve the management of invasive <i>Staphylococcus aureus</i> infections. <i>Expert Review of Anti-Infective Therapy</i> , 2016, 14, 1023-1036.	2.0	16
34	Whole-genome sequencing of multidrug-resistant <i>Mycobacterium tuberculosis</i> isolates from Myanmar. <i>Journal of Global Antimicrobial Resistance</i> , 2016, 6, 113-117.	0.9	28
35	First Evaluation of GenoType MTBDR <sub>plus</sub> 2.0 Performed Directly on Respiratory Specimens in Central America. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2498-2502.	1.8	8
36	Extensively drug-resistant tuberculosis in long-term travellers. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 642-643.	4.6	2
38	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016, 1, 16041.	5.9	247
39	Tuberculosis. <i>Nature Reviews Disease Primers</i> , 2016, 2, 16076.	18.1	830

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41	Reply: Call for Regular Susceptibility Testing of Bedaquiline and Delamanid. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 1171-1172.	2.5	5
42	Personalized Medicine for Chronic Respiratory Infectious Diseases: Tuberculosis, Nontuberculous Mycobacterial Pulmonary Diseases, and Chronic Pulmonary Aspergillosis. <i>Respiration</i> , 2016, 92, 199-214.	1.2	18
43	Can routine genetic testing help to end TB transmission?. <i>Thorax</i> , 2016, 71, 681-682.	2.7	1
44	Genomic epidemiology of Lineage 4 <i>Mycobacterium tuberculosis</i> subpopulations in New York City and New Jersey, 1999-2009. <i>BMC Genomics</i> , 2016, 17, 947.	1.2	13
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51	Capsular Typing Method for <i>Streptococcus agalactiae</i> Using Whole-Genome Sequence Data. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1388-1390.	1.8	35
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54	Simultaneous drug resistance detection and genotyping of <i>Mycobacterium tuberculosis</i> using a low-density hydrogel microarray. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 1520-1531.	1.3	27
55	The changing landscape in drug resistant-tuberculosis: an analysis of recent advances. <i>Expert Review of Respiratory Medicine</i> , 2016, 10, 603-606.	1.0	5
56	Current status and opportunities for therapeutic drug monitoring in the treatment of tuberculosis. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2016, 12, 509-521.	1.5	62
57	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> for detection of recent transmission and tracing outbreaks: A systematic review. <i>Tuberculosis</i> , 2016, 98, 77-85.	0.8	108
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60	FIND Tuberculosis Strain Bank: a Resource for Researchers and Developers Working on Tests To Detect <i>Mycobacterium tuberculosis</i> and Related Drug Resistance. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1066-1073.	1.8	21
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62	Some Synonymous and Nonsynonymous <i>gyrA</i> Mutations in <i>Mycobacterium tuberculosis</i> Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR Assays. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	29
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64	Same-Day Diagnostic and Surveillance Data for Tuberculosis via Whole-Genome Sequencing of Direct Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1285-1298.	1.8	315
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66	<i>Mycobacterium tuberculosis</i> resistance prediction and lineage classification from genome sequencing: comparison of automated analysis tools. <i>Scientific Reports</i> , 2017, 7, 46327.	1.6	82
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74	First 2 Extensively Drug-Resistant Tuberculosis Cases From Myanmar Treated With Bedaquiline. <i>Clinical Infectious Diseases</i> , 2017, 65, 531-532.	2.9	5
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78	The epidemiology, pathogenesis, transmission, diagnosis, and management of multidrug-resistant, extensively drug-resistant, and incurable tuberculosis. <i>Lancet Respiratory Medicine</i> , 2017, 5, 291-360.	5.2	459
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80	Real-Time Sequencing of <i>Mycobacterium tuberculosis</i> : Are We There Yet?. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1249-1254.	1.8	38
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82	Whole-Transcriptome and -Genome Analysis of Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Clinical Isolates Identifies Downregulation of <i>ethA</i> as a Mechanism of Ethionamide Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	32
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84	Machine learning: novel bioinformatics approaches for combating antimicrobial resistance. <i>Current Opinion in Infectious Diseases</i> , 2017, 30, 511-517.	1.3	55
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120	Accuracy of whole genome sequencing versus phenotypic (MGIT) and commercial molecular tests for detection of drug-resistant <i>Mycobacterium tuberculosis</i> isolated from patients in Brazil and Mozambique. <i>Tuberculosis</i> , 2018, 110, 59-67.	0.8	26
121	Optimal Management of Drug-Resistant Tuberculosis and Human Immunodeficiency Virus: an Update. <i>Current Treatment Options in Infectious Diseases</i> , 2018, 10, 90-106.	0.8	0
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152	Machine learning and structural analysis of <i>Mycobacterium tuberculosis</i> pan-genome identifies genetic signatures of antibiotic resistance. <i>Nature Communications</i> , 2018, 9, 4306.	5.8	126

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