

Supplementary material

Table S1. Sequences of *Mycobacterium. sp.* isolates included in the analysis

Isolate	Reference	GenBank accession number
<i>M. africanum</i> 4141_04	(2)	SRX007726
<i>M. africanum</i> 533604	(3)	ERS153831
<i>M. africanum</i> 541504	(3)	ERR031459
<i>M. africanum</i> 544404	(2)	SRX007725
<i>M. africanum</i> 823602	(3)	ERS153832
<i>M. africanum</i> L5 (MAFL5)	(2)	SRX007724
<i>M. africanum</i> L60981	(2)	SRX007722
<i>M. africanum</i> N0091	(3)	ERR031479
<i>M. africanum</i> N0092	(3)	ERR031480
<i>M. africanum</i> N0115	(3)	ERR031484
<i>M. bovis</i> (ravenel)	SRA EBI Animal	SRR022532
<i>M. bovis</i> 05-9937_Herd B-1	(4)	SRR1791979
<i>M. bovis</i> 06-1534_Herd E-1-LNABD	(4)	SRR1791997
<i>M. bovis</i> 06-3639_Deer 2-Carcass	(4)	SRR1792009
<i>M. bovis</i> 07-7693_Deer 12	(4)	SRR1792076
<i>M. bovis</i> 08-2629_Herd J-1-LNTHX	(4)	SRR1792114
<i>M. bovis</i> 08-2629_Herd J-1-LNTHX	(4)	SRR1792144
<i>M. bovis</i> 09-3405_Herd L-7	(4)	SRR1792179
<i>M. bovis</i> 1067(2)	(5)	ERS1534750
<i>M. bovis</i> 1081(1)	(5)	ERS1534751
<i>M. bovis</i> 1121_T17	PRJEB2088 [#]	ERR016864
<i>M. bovis</i> 1199 B(19)	(5)	ERS1534764
<i>M. bovis</i> 12-5090_TX_Beef_12-A_2LNHD THX	(4)	SRR1792338
<i>M. bovis</i> 13-3990_ND_Beef_13-A_1	(4)	SRR1792429
<i>M. bovis</i> 1307_T35	PRJEB2088 [#]	ERR016866
<i>M. bovis</i> 1457(4)	(5)	ERS1534752
<i>M. bovis</i> 1474	(5)	ERS1534748
<i>M. bovis</i> 150(3)	(5)	ERS1534753
<i>M. bovis</i> 1531(10)	(5)	ERS1534754
<i>M. bovis</i> 1595-F(24)	(5)	ERS1534763
<i>M. bovis</i> 1771	(5)	ERS1534749
<i>M. bovis</i> 1865(A)	(5)	ERS1534755
<i>M. bovis</i> 2122_PDIMneg	PRJEB2088 [#]	ERR016868
<i>M. bovis</i> 2122_PDIMpos	PRJEB2088 [#]	ERR016867
<i>M. bovis</i> 2451_T25	PRJEB2088 [#]	ERR016865
<i>M. bovis</i> 2837(33)	(5)	ERS1534756
<i>M. bovis</i> 3912 (B)	(5)	ERS1534757
<i>M. bovis</i> 440(5)	(5)	ERS1534758
<i>M. bovis</i> 659(A)	(5)	ERS1534759
<i>M. bovis</i> 734(16)	(5)	ERS1534760
<i>M. bovis</i> 747(11)	(5)	ERS1534761
<i>M. bovis</i> 9969-1	(5)	ERS1534762
<i>M. bovis</i> AgR1-sc-1882022	PRJEB5830 ^{\$}	ERR564260
<i>M. bovis</i> AgR2-sc-1882023	PRJEB5830 ^{\$}	ERR564261
<i>M. bovis</i> AgR3-sc-1882024	PRJEB5830 ^{\$}	ERR564262
<i>M. bovis</i> AN5	PRJEB2088 [#]	ERR016863

<i>M. bovis</i> AN5R	PRJEB2088#	ERR032134
<i>M. bovis</i> BT-70250	(6)	SRR1657070
<i>M. bovis</i> BT-81069	(6)	SRR1657101
<i>M. bovis</i> c_0112	(6)	SRR1657059
<i>M. bovis</i> c_0254	(6)	SRR1657056
<i>M. bovis</i> c_1235	(6)	SRR1657057
<i>M. bovis</i> c_4875	(6)	SRR1657061
<i>M. bovis</i> c_5375	(6)	SRR1657063
<i>M. bovis</i> c_6256	(6)	SRR1657065
<i>M. bovis</i> c_6347	(6)	SRR1657068
<i>M. bovis</i> Case 11 (HiP4)	This study	ERS4828926
<i>M. bovis</i> Case 12.1 (HiP5)	This study	ERS4828927
<i>M. bovis</i> Case 12.2 (HiP5)	This study	ERS4828928
<i>M. bovis</i> Case 4 (LVS2016-05-008)	This study	ERS4828924
<i>M. bovis</i> Case 5 (LVS2016-05-010)	This study	ERS4828925
<i>M. bovis</i> H2	(7)	ERR841904
<i>M. bovis</i> MbURU-001	(1)	LFGY01000000
<i>M. bovis</i> RK01	(8)	ERR125598
<i>M. bovis</i> RK06	(7)	ERR125603
<i>M. bovis</i> RK08	(8)	ERR125605
<i>M. bovis</i> RK12	(8)	ERR125608
<i>M. bovis</i> RK124	(7)	ERR841877
<i>M. bovis</i> RK125	(7)	ERR841874
<i>M. bovis</i> RK16	(8)	ERR125612
<i>M. bovis</i> RK17	(7)	ERR125613
<i>M. bovis</i> RK22	(8)	ERR125618
<i>M. bovis</i> RK25	(8)	ERR125621
<i>M. bovis</i> RK29	(8)	ERR125625
<i>M. bovis</i> RK30	(8)	ERR125626
<i>M. bovis</i> RK31	(8)	ERR125627
<i>M. bovis</i> RK32	(8)	ERR125628
<i>M. bovis</i> RK39	(7)	ERR841793
<i>M. bovis</i> RK72	(7)	ERR841815
<i>M. bovis</i> T17R	PRJEB2088#	ERR016861
<i>M. bovis</i> T25R	PRJEB2088#	ERR032132
<i>M. bovis</i> T35R	PRJEB2088#	ERR032133
<i>M. canetti</i>	(2)	ERR266107
<i>M. caprae</i> D028	(9)	SRR650227
<i>M. caprae</i> D102	(9)	SRR650226
<i>M. caprae</i> RW044	(9)	SRR650219
<i>M. caprae</i> RW079	(9)	SRR650221
<i>M. orygis</i>	SRA EBI Animal	ERR015582
<i>M. pinnipedii</i> 7011	(9)	SRR1239340
<i>M. pinnipedii</i> 7739	(9)	SRR1239341
<i>M. pinnipedii</i> G01222	(9)	SRR1239336
<i>M. pinnipedii</i> G01491	(9)	SRR1239337
<i>M. pinnipedii</i> G01492	(9)	SRR1239338
<i>M. pinnipedii</i> G01498	(9)	SRR1239339
<i>M. suricattae</i>	(10)	ERR970409
<i>M. tuberculosis</i> K37	(2)	SRR006918
<i>M. tuberculosis</i> 00_1695	(2)	SRR022870
<i>M. tuberculosis</i> 256	(11)	ERR181435
<i>M. tuberculosis</i> 4783_04	(2)	SRX007723
<i>M. tuberculosis</i> 91_0079	(2)	SRR022874
<i>M. tuberculosis</i> 95_0545	(2)	SRX007721

<i>M. tuberculosis</i> 98_1833	(2)	SRR022872
<i>M. tuberculosis</i> GM_1503	(2)	SRX012272
<i>M. tuberculosis</i> H37Rv	(3)	ERR150045
<i>M. tuberculosis</i> K21	(2)	SRR006916
<i>M. tuberculosis</i> K49	(2)	SRR006917
<i>M. tuberculosis</i> K67	(2)	SRR006919
<i>M. tuberculosis</i> K93	(2)	SRR006920
<i>M. tuberculosis</i> M4100A	(2)	SRR022873
<i>M. tuberculosis</i> T17	(2)	SRX005394
<i>M. tuberculosis</i> T67	(2)	SRR022869
<i>M. tuberculosis</i> T85	(2)	SRR014814
<i>M. tuberculosis</i> T92	(2)	SRX003589

1. Lasserre M, Berná L, Greif G, Díaz-Viraqué F, Iraola G, Naya H, et al. Whole-Genome Sequences of *Mycobacterium bovis* Strain MbURU-001, Isolated from Fresh Bovine Infected Samples. *Genome Announc* [Internet]. 2015 Nov 5 [cited 2020 Jun 11];3(6). Available from: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4645193/>
2. Comas I, Chakravarti J, Small PM, Galagan J, Niemann S, Kremer K, et al. Human T cell epitopes of *Mycobacterium tuberculosis* are evolutionarily hyperconserved. *Nat Genet*. 2010 Jun;42(6):498–503.
3. Coscolla M, Lewin A, Metzger S, Maetz-Renning K, Calvignac-Spencer S, Nitsche A, et al. Novel *Mycobacterium tuberculosis* Complex Isolate from a Wild Chimpanzee. *Emerg Infect Dis*. 2013 Jun;19(6):969–76.
4. Glaser L, Carstensen M, Shaw S, Robbe-Austerman S, Wunschmann A, Grear D, et al. Descriptive Epidemiology and Whole Genome Sequencing Analysis for an Outbreak of Bovine Tuberculosis in Beef Cattle and White-Tailed Deer in Northwestern Minnesota. *PLOS ONE*. 2016 Jan 19;11(1):e0145735.
5. Dippenaar A, Parsons SDC, Miller MA, Hlokwe T, Gey van Pittius NC, Adroub SA, et al. Progenitor strain introduction of *Mycobacterium bovis* at the wildlife-livestock interface can lead to clonal expansion of the disease in a single ecosystem. *Infect Genet Evol*. 2017 Jul 1;51:235–8.
6. Acosta F, Chernyaeva E, Mendoza L, Sambrano D, Correa R, Rotkevich M, et al. *Mycobacterium bovis* in Panama, 2013 - Volume 21, Number 6—June 2015 - *Emerging Infectious Diseases*

journal - CDC. [cited 2020 Jun 11]; Available from:

https://wwwnc.cdc.gov/eid/article/21/6/14-1821_article

7. Trewby H, Wright D, Breadon EL, Lycett SJ, Mallon TR, McCormick C, et al. Use of bacterial whole-genome sequencing to investigate local persistence and spread in bovine tuberculosis. *Epidemics*. 2016 Mar;14:26–35.
8. Biek R, O'Hare A, Wright D, Mallon T, McCormick C, Orton RJ, et al. Whole genome sequencing reveals local transmission patterns of *Mycobacterium bovis* in sympatric cattle and badger populations. *PLoS Pathog*. 2012;8(11):e1003008.
9. Bos KI, Harkins KM, Herbig A, Coscolla M, Weber N, Comas I, et al. Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. *Nature*. 2014 Oct 23;514(7523):494–7.
10. Dippenaar A, Parsons SDC, Sampson SL, van der Merwe RG, Drewe JA, Abdallah AM, et al. Whole genome sequence analysis of *Mycobacterium suricattae*. *Tuberculosis*. 2015 Dec 1;95(6):682–8.
11. Blouin Y, Hauck Y, Soler C, Fabre M, Vong R, Dehan C, et al. Significance of the Identification in the Horn of Africa of an Exceptionally Deep Branching *Mycobacterium tuberculosis* Clade. *PLOS ONE*. 2012 Dec 27;7(12):e52841.

PRJEB2088[#]Sanger Institute: Discovery of sequence diversity in *Mycobacterium bovis*. URL:

<http://www.sanger.ac.uk/resources/downloads/bacteria/mycobacterium.html>

PRJEB5830[§]: *Mycobacterium bovis* study on samples from New Zealand, URL:

<http://www.sanger.ac.uk/resources/downloads/bacteria/mycobacterium.html>