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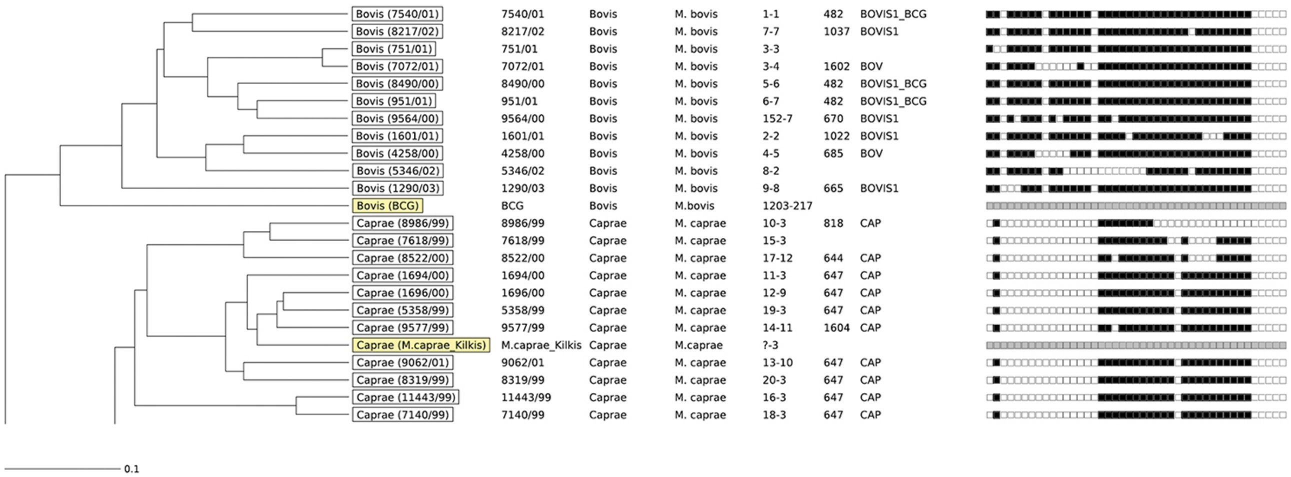
Occupational Exposure to Zoonotic Tuberculosis Caused by *Mycobacterium caprae*, Northern Greece, 2019

Appendix



Bovis (7540/01)	7540/01	Bovis	M. bovis	1-1	482	BOVIS1_BCG
Bovis (8217/02)	8217/02	Bovis	M. bovis	7-7	1037	BOVIS1
Bovis (751/01)	751/01	Bovis	M. bovis	3-3		
Bovis (7072/01)	7072/01	Bovis	M. bovis	3-4	1602	BOV
Bovis (8490/00)	8490/00	Bovis	M. bovis	5-6	482	BOVIS1_BCG
Bovis (951/01)	951/01	Bovis	M. bovis	6-7	482	BOVIS1_BCG
Bovis (9564/00)	9564/00	Bovis	M. bovis	152-7	670	BOVIS1
Bovis (1601/01)	1601/01	Bovis	M. bovis	2-2	1022	BOVIS1
Bovis (4258/00)	4258/00	Bovis	M. bovis	4-5	685	BOV
Bovis (5346/02)	5346/02	Bovis	M. bovis	8-2		
Bovis (1290/03)	1290/03	Bovis	M. bovis	9-8	665	BOVIS1
Bovis (BCG)	BCG	Bovis	M.bovis	1203-217		
Caprae (8986/99)	8986/99	Caprae	M. caprae	10-3	818	CAP
Caprae (7618/99)	7618/99	Caprae	M. caprae	15-3		
Caprae (8522/00)	8522/00	Caprae	M. caprae	17-12	644	CAP
Caprae (1694/00)	1694/00	Caprae	M. caprae	11-3	647	CAP
Caprae (1696/00)	1696/00	Caprae	M. caprae	12-9	647	CAP
Caprae (5358/99)	5358/99	Caprae	M. caprae	19-3	647	CAP
Caprae (9577/99)	9577/99	Caprae	M. caprae	14-11	1604	CAP
Caprae (M.caprae_Kilkis)	M.caprae_Kilkis	Caprae	M.caprae	?-3		
Caprae (9062/01)	9062/01	Caprae	M. caprae	13-10	647	CAP
Caprae (8319/99)	8319/99	Caprae	M. caprae	20-3	647	CAP
Caprae (11443/99)	11443/99	Caprae	M. caprae	16-3	647	CAP
Caprae (7140/99)	7140/99	Caprae	M. caprae	18-3	647	CAP

Appendix Figure. Phylogenic tree of a *Mycobacterium caprae* isolate from a 65-year-old goat breeder from Kilkis, northern Greece (M.caprae_Kilkis: MIRU-VNTR 24-loci pattern 255326322553434243231432). The tree was calculated and drawn by using the UPGMA method and utilizing the MIRU-VNTRplus database reference strains (*1*). VNTR patterns were first searched against the MIRU-VNTRplus database using a default stringent distance cut-off of 0.17, which corresponds to a tolerance of ≤4 locus differences. Since no match was detected after the initial best-match analysis, a tree-based identification was used. Species, Lineage, MLVA MtbC15-9, SpolDB4 Type, and Spoligo pattern information has been included. The patient's isolate shows tight genetic clustering with *M. caprae* reference strains that dominate in central and eastern Europe (spoligotypes lacking spacers 1, 3 to 16, 28, and 39 to 43, BOV_4-CAPRAE, SIT647, SB0418). A clear genetic separation from the Iberian isolates, mainly characterized by the additional absence of spacers 30-33 (BOV-CAPRAE, SIT644/SB0157) has been demonstrated. The *M. bovis* BCG control is also depicted. Scale bar represents 10% sequence divergence. BCG, Bacillus Calmette–Guérin; MLVA, Multiple-locus variable-number tandem repeat analysis; VNTR, variable number of tandem DNA repeats

Reference

1. Allix-Béguec C, Harmsen D, Weniger T, Supply P, Niemann S. Evaluation and strategy for use of MIRU-VNTRplus, a multifunctional database for online analysis of genotyping data and phylogenetic identification of *Mycobacterium tuberculosis* complex isolates. J Clin Microbiol. 2008;46:2692–9. PubMed https://doi.org/10.1128/JCM.00540-08