

Supplementary Table 1: Mutations detected among the seven isolates over 20 years compared to 41

Locus_tag	Gene	Position	Change type	SNP call								Observed read coverage and composition across each position							Comments		
				41-1991	323-1992	682-1993	1087-1995	2573-2002	2855-2003	4891-2010	5288-2011	41-1991	323-1992	682-1993	1087-1995	2573-2002	2855-2003	4891-2010		5288-2011	
Rv0486	mshA	576461-63	deletion	GCG	-	-	-	-	-	-	-	GCGx216	x130 Gx5	-x17 Gx1	-x27 Gx1	-x58 Gx2	-x16 Gx1	-x83 Gx4	-x13	In-frame deletion, codon 372 of MshA, D-inositol 3-phosphate glycosyltransferase	
		755289*	insertion	-	A	-	-	-	-	-	-	-	x217	Ax104 -x19	-x25	-x29 Ax1	-x67	-x18 Ax1	-x90		-x11
		755294-96*	substitution	TCG	CGA	TCG	TCG	TCG	TCG	TCG	TCG	TCG	TCGx215 Cx2	CGAx106 TCGx19	TCGx25	TCGx28 Cx1	TCGx67	TCGx18 Cx1	TCGx88 Cx1		TCGx11
Rv1386		755302*	deletion	T	-	T	T	T	T	T	T	Tx218 Ax3	-x105 Tx22	Tx26	Tx27 -x1	Tx72	Tx14 -x1	Tx88 -x5	Tx11	Intergenic, -9 'A' substitution within possible RBS for PE family protein, PE15	
		1561455	substitution	G	G	G	G	G	G	G	A	Gx161	Gx77	Gx19	Gx18	Gx77	Gx12	Gx121	Ax11		
Rv1819c	bacA	2063079	insertion	-	-	-	-	C	C	C	C	-x173	-x135	-x38	-x37 Cx2	Cx101 -x2	Cx33	Cx125 -x5	Cx10	Frame shift, 'G' insertion in bacA, vitamin B12 transport ATP-binding protein, BacA	
Rv2043c	pncA	2289151	substitution	T	A	A	A	A	A	A	A	Tx218 Ax1	Ax137	Ax37	Ax51	Ax132	Ax37	Ax147	Ax12	Amino acid substitution in pyrazinamidase/nicotinamidase PncA (I31F)	
		2368904	insertion	-	-	-	CGG/-	-	-	-	-	-x275	-x252	-x28 CGGx8	CGGx51 -x15	-x218	-x32	-x177	-x1	Intergenic, non-persisting mutation	
		2584951	substitution	C	C	C	C	C	C	C	G	Cx237	Cx187	Cx38	Cx36	Cx80 Gx1	Cx23	Cx144 Ax1	Gx20	Intergenic	
Rv2326c		2597976	insertion	-	-	-	-	-	G	-/G	G	-x166	-x97	-x36	-x32	-x80 Gx9	Gx13	-x46 Gx37	Gx9 -x1	Frame shift, 'C' insertion, ABC transporter ATP-binding protein	
		2610704	substitution	G	A	G	G	G	G	G	G	Gx239	Ax222 Gx70	Gx71	Gx68	Gx201	Gx63	Gx174 Ax1	Gx12	Intergenic, non-persisting mutation	
Rv2428	ahpC	2726149	substitution	T	T	T	T	T	C	T/C	C	Tx279	Tx218	Tx59	Tx82	Tx128 Cx11	Cx44	Tx87 Cx81	Cx18	Intergenic, ahpC -44 T->C substitution in oxyR-ahpC region	
Rv3033		3393491	substitution	A	A	A/G	A/G	G	G	G	G	Ax180 Gx2	Ax123 Cx1	Ax23 Gx8	Ax36 Gx3	Gx121 Tx1	Gx27 Ax1	Gx111	Gx16	Amino acid substitution in hypothetical protein (S38G)	
Rv3200c		3573526	substitution	C	C	C/T	T	C	C	C	C	Cx163	Cx109	Cx24 Tx10	Tx28 Cx5	Cx79	Cx27	Cx102	Cx13	Synonymous, non-persisting mutation, transmembrane cation transporter	
Rv3340	metC	3726078	insertion	-	-	-	-	-	GA	-/GA	GA	-x235	-x159	-x40	-x44	-x91	Gx26	-x84 Gx12	Gx11	Intergenic, metC -49 'GA' insertion, methionine biosynthesis enzyme MetC	
Rv3854	ethA	4327133	deletion	T	T	T/-	T/-	-	-	-	-	Tx217	Tx173	Tx31 -x11	Tx38 -x7	-x136 Gx1	-x49	-x164	-x10 Tx1	Frameshift, 'A' deletion, monooxygenase EthA	
Rv3854	ethA	4327169	substitution	T	T/G	T/G	T/G	T	T	T	T	Tx225	Tx136 Gx33	Gx37 Tx13	Gx33 Tx6	Tx140 Gx1	Tx50	Tx164 Gx1	Tx9	Amino acid substitution in monooxygenase EthA (H102P)	
		4403459	substitution	C	C	C	A/C	C	C	C	C	Cx270	Gx240 Ax1	Cx68 Ax1	Ax82 Cx13	Cx183 Ax2	Cx54 Ax1	Cx183	Cx9	Intergenic, non-persisting mutation	
Rv3919c	gidB	4407928	substitution	T	T	T	T	T	T	G	T	G	Tx273	Tx211 Cx1	Tx49	Tx68	Tx168	Gx61 Tx3	Tx225 Cx1	Gx6	Amino acid substitution in rRNA small subunit methyltransferase, GidB (E92A)

Notes: Bases highlighted in red type face and bold border indicates persisting mutation; "A/C" notation indicates ambiguous base call at that position; "-" indicates deletion; "*" indicates cluster counted as a single mutation event