

Supplementary online material

Russian 'successful' clone B0/W148 of *Mycobacterium tuberculosis* Beijing genotype: multiplex PCR method for rapid detection and global screening

Igor Mokrousov*, Olga Narvskaya, Anna Vyazovaya, Tatiana Otten, Wei-Wei Jiao, Lia Lima Gomes, Philip N. Suffys, A-Dong Shen, and Boris Vishnevsky

Table S1: Characteristics of the studied *M. tuberculosis* DNA collections.

Genotype	Russia, St. Petersburg (n=134)	Russia, Karelia (n=68)	Russia, Pskov (n=70)	Belorussia (n=106)	China (n=55)	Vietnam (n=72)	Brazil (n=11)	TOTAL (n=516)
Beijing, IS6110-RFLP and spoligotyped*	48 (10)	43 (10)		80 (42)	45		11	227
Beijing, spoligotyped only*	49 (18**)		39 (7**)			37		125
Other families, spoligotyped	37	25	31	26	10	35		164
LAM	15	10	11	12	1	1		50
T	9	6	6	7	8	4		40
EAI						24		24
Haarlem	8	3	7	2		2		22
Ural		2	4	2				8
Manu2		1	1	2		1		5
X	1			1				2
S			1					1
Clade unknown	4	3	1		1	3		12

* For Beijing strains, in brackets: B0/W148-cluster, based on IS6110-RFLP analysis.

** As detected in this study by multiplex PCR assay.

Spoligoprofiles were assigned to phylogenetic families using SITVITWEB (http://www.pasteur-guadeloupe.fr:8081/SITVIT_ONLINE) and SPOTCLUST (http://tbinsight.cs.rpi.edu/run_spotclust.html) online tools.