

Table S1. Description of *M. tuberculosis* clinical isolates resistant to antituberculosis drugs

Drug-resistant <i>M. tuberculosis</i> clinical isolates	n (%)
<i>Monoresistant isolates (resistant only to one anti-TB drug):</i>	49 (16.3%)
resistant only to RMP*	6 (2%)
resistant only to INH*	14 (4.7%)
resistant only to EMB*	7 (2.3%)
resistant only to SM*	22 (7.3%)
<i>Multidrug resistant isolates (resistant at least to RMP and INH):</i>	157 (52.3%)
resistant to RMP+INH	13 (4.3%)
resistant to RMP+INH+EMB	3 (1%)
resistant to RMP+INH+SM	30 (10%)
resistant to RMP+INH+EMB+SM	111 (37%)
<i>Polyresistant isolates (resistant at least to two or more antibiotics except RMP+INH combination):</i>	94 (31.3%)
resistant to INH+EMB	4 (1.33%)
resistant to INH+SM	25 (8.32%)
resistant to INH+EMB+SM	28 (9.32%)
resistant to RMP+EMB	1 (0.33%)
resistant to RMP+SM	10 (3.32%)
resistant to RMP+EMB+SM	1 (0.33%)
resistant to EMB+SM	25 (8.32%)
<i>Total:</i>	300 (100%)

*RMP – rifampicin; INH – isoniazid; EMB – ethambutol; SM – streptomycin.

Table S2. Sequences of primers used in AS-RT-PCR to determine resistance in the analyzed *M. tuberculosis* genes

Genetic locus	Codon	Primer name	Nucleotide sequence (5'-3')
<i>katG</i>	315	Mt315F	GTAAGGACGCGATCACCAC
		Wt315F	GTAAGGACGCGATCACCAG
		315R	GAAACTGTTGTCCCATTTTCG
<i>rpoB</i>	531	Mt531F	CACAAGCGCCGACTGTT
		Wt531F	CACAAGCGCCGACTGTC
		531R	GGCACGCTCACGTGACAGAC