A putative compensatory mutation and a specific marker exclusively detected in isolates of the European Beijing MDR-TB outbreak strain

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Introduction
European projects on molecular surveillance of MDR-TB detected a cluster of 470 MDR-TB Mycobacterium tuberculosis Beijing genotype isolates, comprising 49.9% of all clustered cases in the EU in the project 2009-2012. All isolates, with identical IS6110 RFLP and 24-loci VNTR profiles, continues to spread in the European region and is responsible for a significant proportion of MDR-TB transmission.

Methods
Forty-eight isolates of the EU cluster were tested in the GenoType MTBDRplus and GenoType MTBDRsl reverse line blot (HAIN, Lifescience, Nehren, Germany) to detect mutations associated with the susceptibility to first- and second-line drugs. For a selection of 8 strains of the MDR-TB cluster and an additional strain with the same typing profiles, but INH mono-resistant, Illumina whole genome-sequencing was performed.

Results
Mutations associated with resistance to rifampicin and isoniazid were identical for 47 of the 48 samples tested; rpoB S531L and katG S315T, respectively. The mutations associated with second-line resistance in a cluster of 470 MDR-TB isolates continued to spread in the European region and is responsible for a significant proportion of MDR-TB transmission.