

Spoligotypes of *Mycobacterium tuberculosis* isolated from tuberculosis patients in Odessa, Ukraine

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Introduction and Purpose

In Ukraine, tuberculosis (TB), TB/HIV co-infection, and quick propagation of multidrug-resistant (MDR) TB have been a cause of high morbidity and mortality for the last two decades.

One of the most affected parts of Ukraine is the Odessa region with a population of almost 2.5 million people.

Little is known about recent dynamics of *Mycobacterium tuberculosis* strains in this area.



To better understand the epidemiologic situation, we aimed to determine the predominant lineages of *M. tuberculosis* complex and to identify the nontuberculous mycobacteria (NTM) species.

Methods

A total of 190 strains were isolated in BACTEC MGIT960 and/or Löwenstein-Jensen during January-July 2015 from smear positive subjects admitted to the Odessa Regional Tuberculosis Hospital.

Among these isolates, 177 strains were genotyped by standard spoligotyping, and patterns obtained were compared with those in the international spoligotyping database (SITVITWEB, Institut Pasteur de Guadeloupe).

In addition, species identification was performed for the 13 remaining strains suspected to be NTM by the line probe assay Innolipa Mycobacteria v2 (Fujirebio Europe, Belgium).

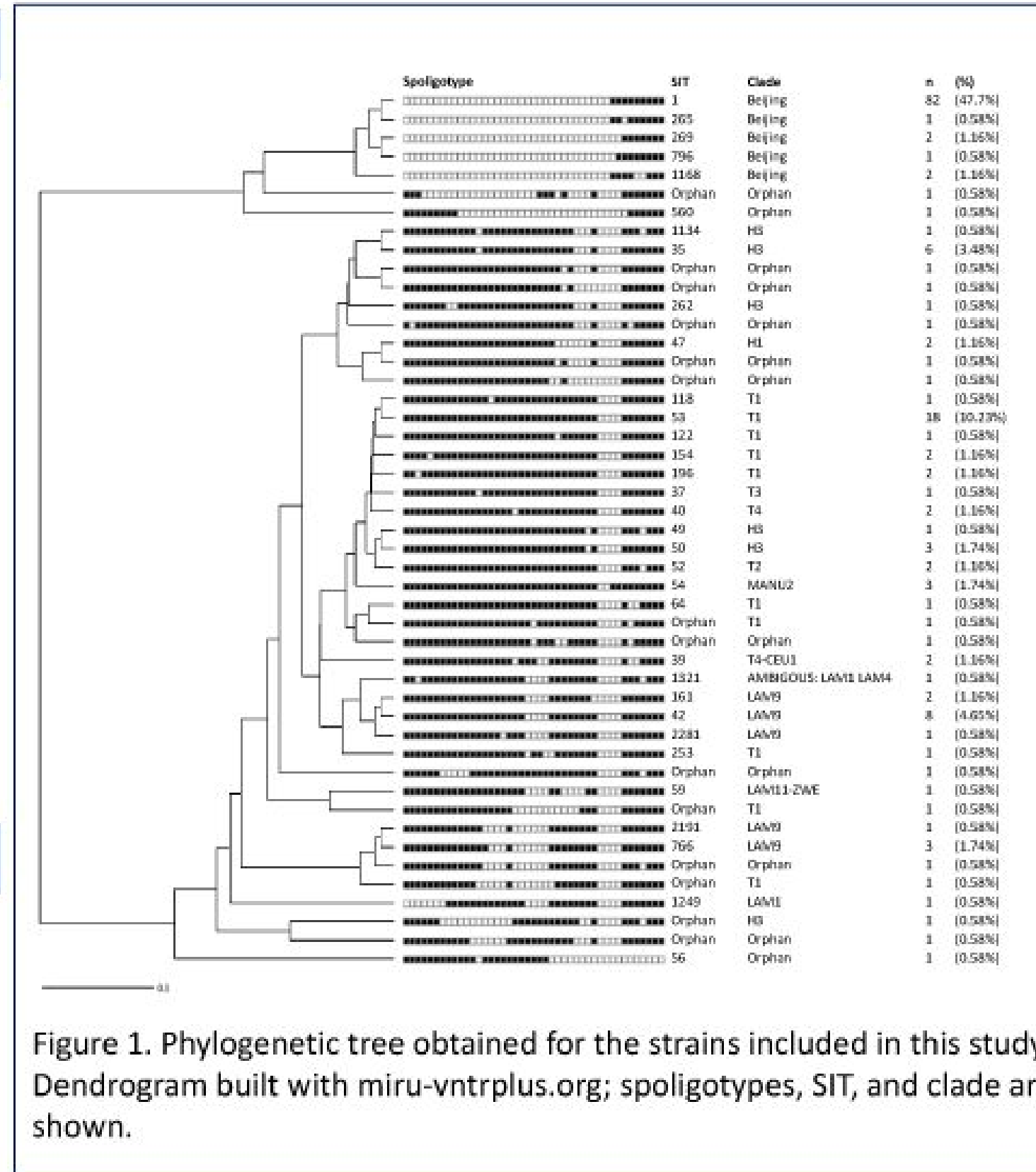


Figure 1. Phylogenetic tree obtained for the strains included in this study. Dendrogram built with miru-vnrplus.org; spoligotypes, SIT, and clade are shown.

Results

Of 177 strains analysed by spoligotyping, the patterns obtained for three strains suggested the presence of mixed lineages and no result was obtained for two strains.

Among the 172 remaining strains, a total of 17 clusters, with 2 to 82 strains each, were obtained (Figure 1).

Distribution of families according to SITVITWEB was the following (Figure 1):

- 88 (51.2%) Beijing
- 36 (20.9%) T;
- 18 (10.5%) LAM;
- 15 (8.7%) Haarlem;
- 3 (1.7%) MANU2;
- 12 (7.0%) with unknown spoligotypes.

Species identification of the 13 suspected NTM strains was the following:

- Mycobacterium* genus - 6 strains
- M. fortuitum*-*M.peregrinum* complex - 3 strains
- M. kansasii* - 1 strain
- A mix of *M. tuberculosis* complex & *M. fortuitum*-*M.peregrinum* complex - 1 strain

Two isolates were not mycobacteria. One of them was identified by MALDI-TOF as *Rhodococcus equi* and the other one remains unknown.

Conclusions

The predominant *M. tuberculosis* lineage in Odessa Regional Tuberculosis Hospital during the six-month study period was Beijing, which is characterized by a high transmissibility and association to drug resistance.

In addition, the uncommon NTM species isolated, raise concern about the alternative diagnosis like NTM or other actinomycetales that may be misdiagnosed as TB.