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Paper Poster Session

Pathology, diversity and clinical outcome in TB

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

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Background: 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 non-tuberculous mycobacteria (NTM) species.

Material/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 (SITVIT WEB, 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).

Results: Of 177 strains analysed by spoligotyping, the patterns obtained for three strains suggested the presence of mixed lineages. Among the 174 remaining strains, a total of 17 clusters, with 2 to 82 strains each, were obtained. According to the international database, 88 (50.6%) strains belonged to the Beijing lineage; 36 (20.6%) to the T family; 18 (10.3%) to LAM; 15 (8.6%) to Haarlem; and the remaining 15 (8.6%) strains had unknown spoligotypes. Regarding the 13 NTM strains, two strains were not mycobacteria, being one identified as *Rhodococcus equi* by MALDI-TOF, six strains were identified as *Mycobacterium* genus, three strains as *M. fortuitum-M.peregrinum* complex, one strain as *M. kansasii*, and one strain as a mix of *M. tuberculosis* complex and *M. fortuitum-M.peregrinum* complex. For the seven strains for which a species was not assigned, identification by MALDI-TOF will be optimized.

Conclusions: The predominant *M. tuberculosis* lineage in Odessa Regional Tuberculosis Hospital during the six-month study period is Beijing, which is characterized by a high transmissibility and association to drug resistance. In addition, the uncommon NTM species isolated raises concern about the alternative diagnosis like NTM or other actinomycetales that may be misdiagnosed as TB.