

Session: P081 Tuberculosis: populations and patients

**Category: 2a. Tuberculosis and other mycobacterial infections**

25 April 2017, 12:30 - 13:30  
P1649

**VNTR-genotyping results for detecting Mycobacterium families among patients with primary resistant pulmonary tuberculosis in Kharkiv, Ukraine**

Olha Konstantynovska\*<sup>1</sup>

*<sup>1</sup>Kharkiv Medical Academy of Postgraduate Education; Phthisiology, Pulmonology and Family Medicine*

**Background:** In the Ukraine there are approximately 30,000 new cases of tuberculosis (TB) per year. The World Health Organization (WHO) estimates that the incidence of tuberculosis (TB) in the Ukraine is 94 cases per 100,000, while only 70.5 cases per 100,000 in the population have been confirmed. Furthermore, the Ukraine is among five countries with the highest burden of multiple drug-resistance tuberculosis (MRD-TB). The WHO estimates approximately 13,000 new MDR cases in the Ukraine although only 6,878 cases were detected in 2015. MDR TB was found in 22 % new cases of TB and in 56 % of retreated cases in Ukraine (WHO, 2015). The aim of this study was to identify the genotypes of Mycobacterium tuberculosis (MTB) that were isolated from the sputum of patients with primary resistant pulmonary tuberculosis.

**Material/methods:** In 2014-2016, 187 cases of severe primary resistant TB (lung injuring more than 5 segments) were identified in Kharkiv, Ukraine. MTB identification and drug susceptibility testing (DST) were performed as recommended by WHO. VNTR genotyping was done by using sets of primers for amplification of five exact tandem repeats ETR loci (A, B, C, D, E).

**Results:** The variability of each locus was determined by PCR from all 187 strains. There were 6 families of MTB identified: 1) Beijing, 2) Latin American and Mediterranean (LAM), 3) Haarlem, 4) Ural / Uganda1, 5) S, Africanum, and 6) individual genotypes (GIP). The most frequent were: Beijing (63,1%), LAM (14,4 %), S (8,7 %) and Haarlem (11,7%). Other families' profiles and individual genotypes ranged from 0.9 % to 1,2 %, and revealed 20 unique and 12 repeated VNTR-profiles. Among the Beijing family was found a huge cluster with 42435-VNTR profile (95 isolates, 50,8 %). Isolates of Haarlem family were found among patients of elderly and senile age (65 years and older) and each of them had a unique VNTR-profile. Of the cases identified as Beijing, 57.7% were MDR-

TB –and 43,3% were XDR-TB, with 83,5% the of XDR resistance to all first-line TB drugs– Isoniazid, Rifampin, Ethambutol, Pyrazinamide, and almost 43% - to Kanamycin and Ofloxacin.

**Conclusions:** In the Kharkiv region, drug resistant TB is emerging rapidly with 63,1% of all primary resistant MTB strains belonging to the Beijing family. Of the total primary resistant cases, 50,8% were Beijing strains with the VNTR-profile 42435. Further genotypic analysis of MTB strains in different regions of the Ukraine is critical for detection and characterization of MDR and XDR MTB and for effective drug treatment therapy.