

(47.6% and 52.4% respectively). Genotype 2 was detected only in one intravenous drug addict, while genotype 4 characteristic for European immigrants from African countries was not detected in any patient, as well as genotypes 5 and 6.

Conclusion: Dominant presence of HCV genotype 3 in intravenous drug addicts in north-western Croatia may be result of group homogeneity and younger age, while prisoners were less homogeneous group with different risk factors, in addition of drug addiction.

<http://dx.doi.org/10.1016/j.ijid.2014.03.1229>

Type: Poster Presentation

Final Abstract Number: 60.013

Session: *Epidemiology and Public Health III*

Date: Saturday, April 5, 2014

Time: 12:45-14:15

Room: Ballroom

Phenotypic and genotypic assessment of mycobacteria isolates in north east Ethiopia



M.M. Temesgen^{1,*}, S. Habtemariam², A. Aseffa³, E. Gadisa³

¹ Addis Ababa University, Dessie, Ethiopia

² Addis Ababa University, Addis Ababa, Ethiopia

³ Armauer Hansen Research Institute, Addis Ababa, Ethiopia

Background: Ethiopia is one of the countries with high incidence and prevalence of TB and multidrug resistance TB (MDR TB). Ability of *Mycobacterium tuberculosis* (*M. tuberculosis*) to spread or to resist drugs varies from strain to strain and various strains have different geographical distributions however this information is inadequate in Ethiopia. So the objective of this study is to identify the species and strains of *Mycobacteria* isolates causing pulmonary TB, to assess drug susceptibility pattern and risk factors in and around Dessie, north east Ethiopia.

Methods & Materials: A cross-sectional study was conducted between October 1 to September 30/2013 and Spoligotyping, RD9 deletion typing and proportion method drug susceptibility test using Middle Brook 7H10 was done.

Results: A total of 92 smear positive pulmonary tuberculosis patients were enrolled. The mean age was 28.29 years. Children less than 18 years of age comprise 7.6% (n=7). In this study 82.7% (n=62) of the isolates were sensitive to all first line drugs. Resistance to any of the four first line drugs tested was 17.3% (n=13). A high frequency resistance was observed in isonized, 12%, (n=9). Resistance to any of the first line anti-tuberculosis drugs was not associated with HIV status, sex and history of previous TB treatment but it was significantly associated with age, high between 31–35 years of age ($p=0.025$). No MDR TB identified. With respect to their Spoligotype pattern, the most frequent families were T family (T1, 36% (n=27), T3, 10.7% (n=8), CAS, 21.3% (n=16), Haarlem3, 8% (n=6), family 36, 8% (n=6) and there was no Beijing family. Euro-American lineage comprised 48 (64%) but the lineage of 15 (20%) isolates were not found in the spotclust database, the remaining 12 (16%) were grouped into indo-oceanic lineage.

Conclusion: High proportion resistance to any of the first line anti tuberculosis drugs was observed in this study. This may be a potential source in the emergence of MDR TB. The dominant strain

circulating in the area belongs to the modern lineages which may indicate recent transmission.

<http://dx.doi.org/10.1016/j.ijid.2014.03.1230>

Type: Poster Presentation

Final Abstract Number: 60.014

Session: *Epidemiology and Public Health III*

Date: Saturday, April 5, 2014

Time: 12:45-14:15

Room: Ballroom

Tick identification in Northwestern Kazakhstan using morphological and molecular characteristics



A. Andryushchenko^{1,*}, T. Ayazbayev¹, A. Richards², S. Pisarcik³

¹ Uralsk Anti-Plague Station, Uralsk, Kazakhstan

² Viral and Rickettsial Diseases Department Naval Medical Research Center, MD 20910-7500 USA, Silver Spring, MD, USA

³ USAMRIID, Frederick, MD, USA

Background: Ticks are a diverse group of arachnids that are found throughout the world in varying climate zones, terrain, and environments. The study of these ectoparasites is important due to the fact that they are known to vector Especially Dangerous Pathogens (EDPs) such as: *Tick Borne Encephalitis*, *Crimson Congo Hemorrhagic Fever*, *Rickettsia* and *Tularemia*, all of which are found in the Northwest region of Kazakhstan. These EDPs are known to cause disease ranging from mild to life-threatening and have the potential to cause sporadic or unpredictable outbreaks. In this study molecular methods, tick genus specific qPCR assays and tick species-specific sequencing procedures were tested.

Methods & Materials: Collection of adult ticks was conducted in the spring and summer of 2012 and 2013 in the seven administrative regions of the West Kazakhstan oblast. Ticks were collected via flagging and collection from animals and humans. All ectoparasites were divided into pools based on the tick species, location, and method of collection. The pools of ticks were homogenized and processed for DNA via Qiagen Viral RNA extraction kits. Genus specific molecular PCR assays were used to test the sensitivity and cross reactivity for *Dermacentor*, *Hyalomma*, *Rhipicephalus*, and *Ixodes* ticks.

Results: In total 2,232 ticks were collected and identified according to morphological characteristics. Four tick genera were identified *Dermacentor* (n=2,097), *Hyalomma* (n=4), *Rhipicephalus* (n=126), and *Ixodes* (n=5).

Conclusion: To date, most ectoparasites are identified by morphological characteristics; this method, although convenient when in the field, can prove to be difficult and sometimes unreliable when the specimens are immature or damaged. This study used molecular methods such as qPCR and tick species-specific sequencing procedures were tested and identified four tick genera. These results help in understanding the specific tick species found in the regions of Kazakhstan and will assist in the prevention and preparation for potential risk of infectious disease outbreaks.

<http://dx.doi.org/10.1016/j.ijid.2014.03.1231>