38th

Annual Congress
of the European Society
of Mycobacteriology

ESM

25th – 28th June 2017
Šibenik, Croatia

Scientific Program including Abstracts

type and S family.
Conclusion: The observation obtained using spoligotyping from the Sudanese patients reflects in comparison to the global distribution highly diverse clades circulating in the country. In general the study could not detect any major differences between MDR and non-MDR isolates within the clade types.

P 145

Investigation of Pyrazinamide Resistance in Drug Resistant Mycobacterium tuberculosis complex in Turkey

Didem Özgür[1], Mahmut Ulger[1], Begum Kayar[2], Seda Tezcan Ulger[1], Leyla Ersoy[1], Gönül Aslan[1], Fatih Köksal[2]
[1]Faculty of Medicine, Department of Medical Microbiology, Mersin University, Turkey
[2]Tropical Disease Research and Application Center, Cukurova University, Adana, Turkey

Objective: Rifampicin (RIF), isoniazid (INH), pyrazinamide (PZA) and ethambutol (EMB) are the first-line drugs in the treatment regimen of TB which remains an important global health problem. Considering the unique ability of PZA to eradicate persistent bacilli and decrease the treatment process from 9–12 months to 6 months, it's obvious the PZA forms a critical cornerstone of this regimen. The aim of the present study was to determine the incidence of PZA resistance in drug resistant M. tuberculosis complex (MTC) isolates in our region.
Materials and Methods: A total of 57 MTC isolates resistant to at least one of the RIF, INH, EMB and streptomycin (SM) anti-TB drugs, which were isolated in the Mycobacteriology Laboratory of Medical Microbiology, Department of Mersin University, Faculty of Medicine included in this study. PZA sensitivities were determined with using the BACTEC MGIT 960 sensitivity test method (accepted as standard method by CLSI). The susceptibility test was performed using the BD MGIT 960 PZA Kit, PZA Medium (Becton Dickinson, Sparks, MD) and the critical concentration of 100.0 µg/ml PZA according to the manufacturer recommendation. İdentification of MTC isolates were determined by spoligotyping. M. tuberculosis H37Rv (PZA sensitive) and M. bovis BCG (PZA resistant laboratory isolate) were used as the control strains in the study.
Results: Of the 57 MTC isolate, PZA resistance was determined in 6 (10,5%) isolate. One of the PZA resistant isolate was identified as M. bovis BCG by spoligotyping. PZA resistance was detected in 5 isolates (2 isolates with EMB, 2 isolates with INH and 1 isolate with SM). In Additionally, PZA with INH and EMB resistance was detected in the M. bovis BCG strain. PZA resistance was not detected in MDR-TB isolates.
Conclusion: In our country, because of the PZA resistance was not routinely tested in tuberculosis laboratories, the data of PZA resistance rate is not known exactly. Therefore, a nationwide sensitivity test policy can be developed for determining the PZA resistance rates with the increase of further similar researches.

P 152

First study of the nationwide population structure of the Mycobacterium tuberculosis complex in Benin

C. N'Dira Sanoussi[1], Dissou Affolabi[2], Mathieu Odoun[2], Karamatou Arekpa[2], Sabine Houéto[2], Ousman Bodi[2], Séverin Anagonou[2], Leen Rigouts[3], Bouke De Jong[4]
[1]National Reference Laboratory for Mycobacteria, Cotonou, Benin; Institute of Tropical Medicine, Antwerp, Belgium
[2]National Reference Laboratory for Mycobacteria, Cotonou, Benin
[3]Institute of Tropical Medicine, Faculty of Pharmaceutical, Biomedical and Veterinary Sciences, University of Antwerp, Belgium
[4]Institute of Tropical Medicine, Antwerp, Belgium

Background: Genotypic diversity studies are important for deeper understanding of circulating *M. tuberculosis* complex (MTBc) strains in a population. To date, no study has investigated the nationwide population structure of the MTBc in new tuberculosis (TB) patients in Benin.
Methods: Smear-positive sputa were collected from a representative sample of new TB patients from all regions in Benin, through a prospective nationwide surveillance. The next four new TB patients diagnosed after a retreatment patient were included. DNA was extracted from the sputa using the Maxwell DNA Tissue Purification kit, after a digestion with proteinase K. Spoligotyping was performed using standard methods. The TB lineage database was used for lineage assignment, and SITVIT web database for SIT-type assignment.
Results: From 240 patient's sputa from all regions of Benin, the majority (56%) came from Atlantique/Littoral. A spoligotype pattern was available for 234 (98%) of the specimens.
Nationwide, Lineage (L) 4 (Euro-american) strains were the most prevalent (47.9%, 112) followed by L5 (*M. africanum* West African 1) (73, 31.2%), L6 (*M. africanum* West African 2) (21, 9%), L2 (East-Asian Beijing) (12, 5.1%), L1 (Indo-oceanic) (12, 5.1%,), and L3 (East African Indian) (1, 0.4%). Three *M. bovis* strains (1.3%) were also detected. The prevalence of *M. africanum* L5 and L6 combined was 40.2%.