Epidemiology

PO - (8408) - DETECTION OF EXTENSIVELY DRUG RESISTANT TUBERCULOSIS AMONG MULTI-DRUG RESISTANT MYCOBACTERIUM TUBERCULOSIS CLINICAL ISOLATES IN BOTSWANA

Mogashoa, Tuelo (Botswana)1,2; Mupfumi, Lucy (Botswana)1,2; Iketleng, Thato (Botswana)2,3; Melamu, Pinkie (Botswana)2; Kelentse, Nametso (Botswana)2; Zetola, Nicola (Botswana)2; Mokomane, Margaret (Botswana)2; Letsibogo, Letsibogo (Botswana)2; Streicher, Elizabeth Maria (South Africa)6; Ley, Serej (South Africa)6; Kasvosve, Ishmael (Botswana)1; Moyo, Sikhulile (Botswana)1,2,7; Warren, Robin (South Africa)2; Gaseitsiwe, Simani (Botswana)2,7

1 - Department of Medical Laboratory Sciences, University of Botswana, Gaborone, Botswana, 2 - Botswana Harvard AIDS Institute Partnership, Gaborone, Botswana; 3 - College of Health Sciences, School of Laboratory Medicine and Medical Sciences, University of KwaZulu-Natal, Durban, South Africa; 4 - Botswana Upenn Partnership, Gaborone Botswana; 5 - National Tuberculosis Reference Laboratory, Ministry of Health and Wellness, Gaborone, Botswana; 6 - DST/NRF Centre of Excellence in Biomedical Tuberculosis Research/South African Medical Research Council Centre for Tuberculosis Research, Division of Molecular Biology and Human Genetics, Faculty of Medicine and Health Sciences, Stellenbosch University, Cape Town, South Africa; 7 - Harvard T.H. Chan School of Public Health, Boston, Massachusetts, USA

Background: The emergence and transmission of multi-drug resistant (MDR) and extensively drug-resistant (XDR) Mycobacterium tuberculosis (M.tuberculosis) strains is a serious threat to tuberculosis control in Botswana. Early detection of drug-resistant isolates is critical to ensure optimal treatment and thereby improve treatment outcomes. The objective of this study was to determine the extent of second-line drug resistance among drug-resistant M.tuberculosis isolates from Botswana.

Methods: A total of 60 drug-resistant M.tuberculosis isolates received at Botswana National Tuberculosis Reference Laboratory between 2012 and 2013 were analyzed. DNA was extracted from BD Mycobacterial Growth Indicator Tubes (MGIT) using GenoLyse DNA isolation kit® (Hain Lifescience). Spoligotyping was done using a commercially available spoligotyping kit (Isogen Bioscience). The spoligotype patterns were compared with existing patterns in the SITVIT2 Web database. GenoType MTBDRsl assay (Hain Lifescience) was used for second-line drug susceptibility testing (DST). Fisher’s exact test was used to test for association between drug resistance patterns and HIV status, lineage and geographical location.

Results: Seventeen distinct spoligotype patterns were detected amongst the 60 drug-resistant isolates. The most predominant lineages were Euro-American (58.3%), East Asian (25%) and Indo-Oceanic (15%). Fifty (83.3%) were MDR, 7 (11.7%) were resistant to fluoroquinolones (Pre-XDR) whereas 3 (5%) were resistant to both fluoroquinolones and second-line injectable drugs (XDR). Drug resistance profiles were significantly associated with M.tuberculosis lineage (p=0.001). There was no association between drug resistance profile and HIV status (p=0.057) and geographical location (p=0.372).

Conclusions: This study highlights the importance of including second-line drug susceptibility testing in a testing algorithm in Botswana. The detection of XDR isolates among MDR-TB isolates highlights the ongoing evolution of resistance and the need for strengthened treatment regimens to improve treatment outcomes and to prevent the spread of these highly resistant strains. Second-line testing will be essential if the 9-month MDR regimen is used in Botswana.