800. Drug-Resistant TB: An Experience From Qatar
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Background. Drug-resistant tuberculosis (DR-TB) is an important issue for public health. This study was conducted to evaluate the characteristics, treatment outcome, and risk factors associated with 223 DR-TB cases in the State of Qatar.

Methods. A descriptive records-based retrospective study was conducted on patients registered at Communicable Disease Centre (CDC), Qatar to all consecutive microbiologically confirmed tuberculosis cases for the period January 2010–March 2015. Demographic and clinical data extracted included: patient’s age, sex, and country of origin; disease (pulmonary or extra-pulmonary); presence of comorbidities, HIV/AIDS status, previous chemotherapy and/or previous treatment for TB, and anti-TB drug resistance the resistance pattern of isolated mycobacteria. The sputum culture conversion rate and treatment outcome was assessed for the patient who completed their treatment in Qatar.

Results. Of 330 patients with positive M. tuberculosis culture were analyzed; 223 (6.7%) were resistant to one or more first-line drugs, to isoniazid in 3.1% (n = 102), streptomycin in 1.2% (n = 41), rifampicin in 0.2% (n = 6), ethambutol in 0.15% (n = 3), and multi-drug resistance in 1.2% (n = 38) of patients. Among the resistant TB patients, more common demographic characteristics were former resident of Indian subcontinent (64.1%). A history of anti-TB treatment was not a risk factor with drug resistance in our cohort. Only 111 (49.7%) patients were tested for HIV antibodies and the results were all negative. There was significant correlation between the type of drug resistance the resistance pattern of isolated mycobacteria. The sputum culture conversion rate and treatment outcome was assessed for the patient who completed their treatment in Qatar.

Conclusions. A total of 35 strains from Beira Mozambique were evaluated with genotypic tests (Genotype MTBDRPlus1, and MTBDRB2); phenotypic (MGIT-SIRE1), and DST. All isolates resistant to isoniazid (H) or rifampicin (R) or both were submitted to WGS. Illumina HiSEQ 2000 and analyzed with TB profiler database and phylogenetic tree was done using FIGTREE tool. This was a descriptive cross-sectional study.

Results. WGS shown that strains analyzed, belongs to three of six major lineages, with Lineage 4: 25(71.4%), Lineage 1: 5(14.3%); and Lineage 2 Beijing family: 5(14.3%). All pre-XDR strains 3(8.6%) were from lineage 4.3. By WGS, all 35 strains had any mutations conferring DR-TB while in one strain, mutation was not shown by genotypic neither phenotypic DST. Compared with genotypic tests, WGS had best performance in showing mutation conferring resistance to ethambutol 12/35 (34.3%) and 7/35 (20%).

Conclusion. The DR-TB disease in Beira Mozambique is mainly caused by M. tuberculosis strains of Lineage 4, sub-lineage although lineage 1 and 2 are also present. WGS shows underline mutations causing DR-TB which are not detected by genotypic and phenotypic DST.

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