

PA-062 **DISCORDANT RESULTS BETWEEN GENOTYPIC ASSAYS (XPert MTB/RIF AND HAIN MTBDRPLUS) AND BACTEC MGIT 960 SYSTEM FOR DETECTION OF RIFAMPICIN-RESISTANT MYCOBACTERIUM TUBERCULOSIS ISOLATES IN ZAMBIA**

Winnie Mwanza,¹ Deborah Milimo,² Maureen Moyo,² Nkatya Kasese,² Maina Cheeba-Lengwe,² Stembiso Munkondya,² Helen Ayles,² Petra De Haas,³ Monde Muyoyeta¹. ¹CIDRZ, Zambia; ²ZAMBART, Zambia; ³KNCV Tuberculosis Foundation, The Netherlands

10.1136/bmjgh-2016-000260.95

Background Combination of genotypic assays (Xpert MTB/RIF and MTBDRplus (LiPA) would be a powerful tool to shorten the time for diagnosis of MDR tuberculosis (TB). However, the algorithm used for these assays in Zambia has not yet been implemented and the most widely used drug susceptibility testing (DST) method remains MGIT DST. Missed rifampicin resistance on the MGIT 960 system has been reported by several studies due to silent *rpoB* gene mutations. We report comparative observations made on the performance of Xpert, LiPA and MGIT DST methods for detection of rifampicin resistance (RR) at the ZAMBART Central Laboratory (ZCL).

Methods Specimens were collected from consecutive patients with Xpert rifampicin resistance positive (RR+) or rifampicin resistance indeterminate (RRI) results at peripheral site laboratories for further testing at the ZCL. Each sample was tested using Xpert, LiPA and MGIT culture/DST.

Results 30 patient samples were received and 17 were RR+, 8 were rifampicin-sensitive (RR-) and 5 were TB-negative by Xpert. All 17 RR+ on Xpert were RR+ on LiPA and all 8 Xpert RR- were sensitive on LiPA giving a 100% concordance for diagnosis of RR. Three isolates that were rifampicin sensitive by the MGIT system (Gold standard) were RR+ by both genotypic tests. Genotypic tests showed evidence of mutation in the codon 526 region of the *rpoB* gene for all the three isolates with discordant RR MGIT DST results. Xpert positive predictive value for Multidrug Resistance (MDR) TB was 62.5% and 81.2% compared to MGIT DST and LiPA, respectively.

Conclusions There is need for Zambia to perform a full classification of *rpoB* mutations to determine the prevalence of silent mutations. This will optimise national guidelines for diagnosis of RR- and MDR-TB.