SPECIES-SPECIFIC IDENTIFICATION OF MYCOBACTERIA DIRECTLY FROM BACTEC MGIT 960 SYSTEM TUBES USING COMMERCIAL INNO-LIPA MYCOBACTERIA V2 AND DNA ACCUPROBE ASSAYS

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Purpose of the study: Specific identification of mycobacteria is of clinical relevance since treatment varies according to the species causing infection. This study evaluated INNO-LiPA MYCOBACTERIA v2 (LiPA) and AccuProbe assays for species-specific identification of mycobacterial isolates in Kuwait directly from MGIT 960 system tubes.

Methods: Clinical specimens (n=113) cultured and flagged positive for mycobacterial growth by MGIT 960 system were evaluated. The LiPA and AccuProbe assays were performed and interpreted according to the manufacturer's instructions. The results were validated by DNA sequencing of 16S-23S internal transcribed spacer region (ITSR).

Results: Each of the 113 tubes grew only one *Mycobacterium* species. Both AccuProbe and LiPA identified 80 isolates as *Mycobacterium tuberculosis* complex (MTC) members and ITSR sequences of 12 randomly selected isolates were concordant. AccuProbe assay identified 33 isolates as non-tuberculous mycobacteria (NTM) with species-specific identification of 14 isolates. ITSR sequences were concordant with species-specific identification of 12 of 14 isolates and with the NTM status of the remaining isolates. The LiPA identified 28 isolates as NTM with species-specific identification of 25 isolates while no result was obtained for 5 isolates (no amplicons in LiPA). The ITSR sequencing confirmed specific identification by LiPA for 24 of 25 isolates and NTM status of the remaining isolates. Further, 4 and 1 of 5 isolates yielding no result in LiPA were identified as *M. kansasii* and *M. chimaera*, respectively.

Conclusions: All the MTC isolates were correctly identified by LiPA and AccuProbe assays. Although, AccuProbe assay correctly identified only some (12 of 33) while LiPA identified most (24 of 33) NTM isolates to the species level, 4 *M. kansasii* isolates correctly identified by AccuProbe assay were not even detected by LiPA indicating sequence variations in LiPA target region in some *M. kansasii* strains in Kuwait.

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