CLINICAL MICROBIOLOGY

New Process for the Identification of Non-Tuberculous Mycobacteria (NTM)

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The Clinical Microbiology Laboratory has implemented a new process for the identification of isolates of NTM. Previously, our identification algorithm first ruled out *Mycobacterium tuberculosis* (by an antigen test or DNA probe) on all positive mycobacterial cultures. The culture was then tested by DNA probe(s) for *Mycobacterium avium* complex and *Mycobacterium gordonae* as needed, based on the growth and smear results. Any culture that was not identified by these tests was then sent to the National Microbiology Laboratory (NML) for identification.

Until recently, AccuProbe™s (DNA probes) were used in the majority of North American mycobacteriology laboratories; however, they have been discontinued for *Mycobacterium* spp., as well as fungi, by the sole company that produced them.

As a result, we have validated a Mycobacteria-specific extraction process to identify Mycobacteria by MALDI-ToF. The MALDI-ToF protocol enables us to identify a significantly greater number of species in-house, without sending out cultures and waiting for the NML identification. This change will significantly improve our time to identification, particularly for rapidly-growing mycobacteria. However, the MALDI-ToF protocol only works from growth on solid media (agar) and not liquid media (broth). The DNA probe tests were able to be conducted on liquid media. As a result, cultures that will ultimately be identified as *M. avium* complex (and *M. gordonae*) will first be reported as NTM, after *M. tuberculosis* has been ruled out, and will not be updated to *M. avium* complex (or *M. gordonae*) until the solid media subculture grows for MALDI-ToF identification (approximately 1 week).

Contact Information:
Dr. Heather Adam, Clinical Microbiologist, Clinical Microbiology, Shared Health, 204-787-8678.
HAdam@sharedhealthmb.ca
Dr. James Karlowsky, Medical Director, Clinical Microbiology, Shared Health, 204-237-2105,
jkarlowsky@sharedhealthmb.ca
Joelle Carlson, Technical Director, Clinical Microbiology, Shared Health 204-237-2073,
jcarlson@sharedhealthmb.ca