

**P0986 Isolation profile of *Mycobacteraceae* in Japan, 2014-2015**

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**Background:** The incidence (per 100,000) of non-tuberculosis mycobacteria (NTM) infections is reported as 14.7 in 2014 (Namkoong H. EID 191;2015:A5268). Family Mycobacteraceae holds 198 species as of Nov. 2018. In Japan, we have been using the DNA-DNA hybridisation kit (DDH, Kyokuto Pharmaceuticals<sup>®</sup>) which identifies 18 mycobacterial species since early 1990s. In recent years, many uncommon NTMs are misidentified or unidentifiable, and our species identification methods is now in transition to mass spectrometry (MS). The reliable species profile of Mycobacteraceae in our practical clinical setting will be useful for the management of the patients infected by the species in Mycobacteriaceae other than *Mycobacterium tuberculosis* and *leprae* (SMOTL).

**Materials/methods:** A total of 27,392 SMOTLs in 32,841 Mycobacteraceae were identified using DDH from dominant four private laboratories over Japan in 2014. We sequentially collected DDH-identified 432 isolates (15 species except for *Mycobacterium tuberculosis/avium/intracellulare*) and 200 unidentified isolates in 2015, and identified those species with VITEK MS KB v3.0 (BioMérieux) and 16S rRNA, *rpoB* and *hsp65* sequencing.

**Results:** Using DDH, the major SMOTLs isolated were *M. avium complex* (67%), *Mycobacterium gordonae* (7.9%), *Mycobacteroides abscessus* (6.6%), *Mycobacterium kansasii* (4.6%) from the dominant isolates, and the unidentified SMOTLs were 7.1%. DDH identified 85.2% (368/432 isolates) of 15 species correctly compared to MS and sequencing methods. The unidentified 200 SMOTLs with DDH were identified as *Mycobacterium lentiflavum* (15.5%), *Mycolicibacterium mucogenicum* (10%), *Mycobacterium asiaticum* (6.5%) and other species to date. Especially, 94.9% (56/59) of *Mycolicibacter terrae*, *Mycolicibacter nonchromogenicus* and *Mycolicibacillus trivialis* by DDH were identified as *Mycolicibacter kumamotonensis* (54.2%, 32/59), *Mycolicibacter virginienensis* (16.9%) and others.

**Conclusions:** Many uncommon SMOTLs were identified in Japan. Among the unidentified SMOTLs with DDH, *M. lentiflavum* (1.1%, the eighth) was the top, followed by *M. mucogenicum* (0.73%, the ninth) and *M. kumamotonensis* (0.66%, the eleventh). MALDI-TOF MS will be the powerful alternative of genome DNA-DNA hybridization.

