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Identification of Mycobacteria by Using INNO LiPA

I have read with interest the recent paper of Suffys et al. (1) concerning the identification of 157 mycobacterium strains by using the INNO LiPA Mycobacteria (LiPA) assay. The same journal had published, 1 year ago, a similar paper, which I coauthored, on 238 strains (2), the results of which are now substantially confirmed. I feel, however, that Suffys et al. did not take it into due account; in fact, they quote it cursorily on two occasions and inappropriately.

In the first case, the authors state that their results are in contrast with ours as their *Mycobacterium abscessus* strains reacted with LiPA probes MCH-1 and MCH-2 and as all of their *Mycobacterium kansasii* strains that were MKA-1-positive belonged to PCR restriction enzyme analysis (PRA) group I.

I do not think, on the contrary, that there is any contrast; in fact, as the LiPA system does not make any distinction between *Mycobacterium chelonae* and *M. abscessus*, we behaved likewise. Consequently, the fact that among our *M. chelonae* sensu lato strains there were strains reacting with all of the MCH LiPA probes does not imply that *M. chelonae* sensu stricto strains reacted with MCH-2 and all the more so since no strain labeled as *M. abscessus* was present in our panel. Furthermore, regarding *M. kansasii*, our paper did not made any mention of PRA; it compared the results of LiPA with those of the widely used AccuProbe assay and highlighted an interesting correlation between the reactivity of the first- and second-generation AccuProbe assays and the different *M. kansasii*-specific LiPA probes.

In the second case, the authors do not seem to realize that our discrepant case, a strain identified as *Mycobacterium avium* complex (MAC) intermediate with LiPA and as *Mycobacterium intracellulare* with the AccuProbe assay, fits exactly with their two strains, MAC intermediate with LiPA and *M. intracellulare* PRA group I.

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Author's Reply

We took into account the publication of Tortoli et al. (2) published in the March issue of 2001 but did not comment on it in an extensive way because at that time our study (1) was in its final phase of preparation. We do apologize, however, for a somewhat inaccurate definition of the difference between their study and ours, consisting mainly of more genetic variability in the strains of *M. chelonae* and *M. kansasii* in the Tortoli study. While their strains of *M. kansasii* hybridized to either MKA-1 (*M. kansasii* group I), MKA-2 (*M. kansasii* group II), or MKA-3 (*M. kansasii* groups III, IV, and V) and their strains of *M. chelonae* hybridized to MCH-1 (*M. chelonae* groups I, II, III, and IV) and either MCH-2 (*M. chelonae* group III, including *M. chelonae* subsp. *chelonae* and *M. chelonae* subsp. *abscessus*) or MCH-3 (*M. chelonae* group I), our strains of *M. kansasii* all reacted with MKA-1 and our strains of *M. chelonae* all reacted with MCH-1 and MCH-2 (all were indeed *M. abscessus*). The difference, therefore, concerns genetic variability of the strains of these species and not results upon comparison of LiPA and other identification procedures. We agree that the strain described by Tortoli et al. as discrepant (it reacted with *M. avium-M. intracellulare-Mycobacterium scrofulaceum* [MAIS] only on LiPA but was *M. intracellulare* with the AccuProbe assay) was indeed observed twice in our study (MAIS only on LiPA and *M. intracellulare* with PRA), but whether the result between the assays should be considered discrepant is a matter of discussion. The hybridization target of LiPA is ITS, that of the AccuProbe assay is 16S, and that of PRA is *hsp65*; a better relation between the use of different genetic targets for taxonomic definition of strains belonging to the MAIS complex should be established.

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