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 make 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.

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 our 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.

REFERENCES


Enrico Tortoli*
Regional Mycobacteria Reference Center
Microbiology and Virology Laboratory
Careggi Hospital
Piastra dei Servizi
Viale Morgagni 85
50134 Florence, Italy
*Phone: 39 055 4279199
Fax: 39 055 4279830
E-mail: e.tortoli@libero.it

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Philip Suffys*
Laboratory of Molecular Biology and Diagnosis of Infectious Diseases
Oswaldo Cruz Foundation, Fiocruz
Avenida Brasil 4365, Manguinhos 21045-900
Rio de Janeiro, Brazil
*Phone: 55 21 25984289
Fax: 55 21 22709997
E-mail: psuffys@ioc.fiocruz.br