

The Infallible Microbial Identification Test: Does It Exist?

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Alby et al. (1) recently reported on errors made by matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS). In their report, the authors clearly show that even this very specific technology is susceptible to mistakes that may have significant clinical consequences if classical microbiological knowledge is disregarded. Careful review of phenotypic results and culture data should always be taken into account is the authors' conclusion. Beyond the fact that if we were to adopt such a methodology, all the advantages of MALDI-TOF MS analyses would evaporate, especially speed and throughput, there is a more fundamental objection to the conclusions brought forward by the authors. It is that all methods currently in use for identification of bacterial species have drawbacks. These may be technical in nature (e.g., mixed cultures or instrument failure), evolutionary (e.g., certain microbial species might have lost certain genes and hence certain phenotypes), due to taxonomic shortcomings (e.g., cryptic species), or due to human error (e.g., misplacement of samples). Most importantly, there is not a single method that functions without inherent faults.

To react more specifically to the analyses presented by Alby et al., it is not entirely surprising that MALDI-TOF MS will be unable to correctly identify bacterial species that are not represented in the affiliated clinical database. The fact that such a species may be wrongly recognized as another species is again due to taxonomic features; in the absence of perfect matches between database-deposited spectra and an experimental spectrum, there may be imperfect matches that still fulfill the clinically validated diagnostic criteria. Of course, database updates could possibly alleviate discordant interpretations. Still, we agree that in such cases, supplementation with classical data could help. But the question is where and how could we find clear indicators that an identification reported by the system is actually incorrect? Further, it is reassuring to see that the misidentifications highlighted by the authors mainly fall in the category where the clinical database is not strong or where species are simply missing. In addition, for bacterial identification using ribosomal sequence analysis, the quality of the database defines the overall quality of the diagnosis (2).

In conclusion, we acknowledge that MALDI-TOF MS technology and the associated databases may fail, on occasion, to correctly identify bacterial isolates, especially if the species concerned are not represented in the database. It is, however, reassuring to see that such mistakes were observed in only 0.5% of all cases, which is significantly below the acceptable error rate of 2% that was previously deemed acceptable for this technology. Finally, the answer to the question posed in the title of this communication is no. In the end, even whole-genome sequencing will demonstrate that bacterial taxonomy is clouded and that sharp definition of what a species really is will remain subject to discussion (3).

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REFERENCES

1. Alby K, Glaser LJ, Edelstein PH. 2015. *Kocuria rhizophila* misidentified as *Corynebacterium jeikeium* and other errors caused by the Vitek MS system call for maintained microbiological competence in the era of matrix-assisted laser desorption ionization–time of flight mass spectrometry. *J Clin Microbiol* 53:360–361. <http://dx.doi.org/10.1128/JCM.02616-14>.
2. Chatellier S, Mugnier N, Allard F, Bonnaud B, Collin V, van Belkum A, Veyrieras JB, Emler S. 2014. Comparison of two approaches for the classification of 16S rRNA gene sequences. *J Med Microbiol* 63(Pt 10):1311–1315. <http://dx.doi.org/10.1099/jmm.0.074377-0>.
3. Vandamme P, Peeters C. 2014. Time to revisit polyphasic taxonomy. *Antonie Van Leeuwenhoek* 106:57–65. <http://dx.doi.org/10.1007/s10482-014-0148-x>.

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