

AUTHORS' CORRECTIONS

Necessity of Quality-Controlled 16S rRNA Gene Sequence Databases: Identifying Nontuberculous *Mycobacterium* Species

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Volume 39, no. 10, p. 3637–3648, 2001. The near-complete 16S rRNA gene sequence was determined for three strains of *Mycobacterium flavescens*, ATCC 14474^T, ATCC 23008, and ATCC 23033. Based on our initial sequencing results, it was determined that *M. flavescens* ATCC 14474^T and ATCC 23008 had 100% sequence identity with “*Mycobacterium acapulcensis*” ATCC 14473, while ATCC 23033 had a unique sequence, which was closest to that of *Mycobacterium novocastrense* DSM 44203^T. The strains sequenced had been stocked in 1994. All three isolates were reordered from the American Type Culture Collection in December 2001, and their 16S rRNA gene sequences were reevaluated. The results revealed the following (identity values given hereafter were obtained by using the RIDOM database [<http://www.ridom.de>]). First, ATCC 14474^T corresponds, with 100% sequence identity, to ATCC 14474^T. This sequence of this strain also corresponds to that of *M. flavescens* ATCC 14474^T from GenBank (accession no. X52932), with the exception of a few Ns. Second, ATCC 23008 has a unique sequence, closest to that of “*M. acapulcensis*,” with a (corrected) identity of 98.61%. Third, ATCC 23033 has a sequence identical to that initially determined for the same strain. It is closest to that of *M. novocastrense*, with a (corrected) identity of 98.95%. These results do not impact the analyses of the other type strains of *Mycobacterium* spp. in our study, as it was confirmed that the previously obtained sequences of those strains correspond (with 100% sequence identity) to the sequences of the same type strains in the RIDOM database.

Evaluation of Use of Epstein-Barr Viral Load in Patients after Allogeneic Stem Cell Transplantation To Diagnose and Monitor Posttransplant Lymphoproliferative Disease

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