organism was identified biochemically (i.e., by the niacin and nitrate production test) as *M. abscessus*.

The genomic DNA from the culture of mycobacterial isolates was extracted by standardized protocol (6) and subjected to PCR-restriction enzyme pattern analysis (PRA) (2). Primers TB11 (5'-ACC AAC GAT GGG GTG TGT CCA T) and TB12 (5'-CTT GTC GAA CCG CAT ACC CT) amplified a 439-bp fragment between positions 398 and 836 of the published gene sequence for 65-kDa heat shock protein (3). The PCR products were then digested separately by using restriction enzymes *Bst* EII and *Hae*III. The digests were fractionated on nondenaturing 10% polyacrylamide gel. The *Bst* EII pattern generated during PRA yielded two 235/210-bp bands similar to the patterns attributed to *M. chelonae* subsp. *abscessus* (2). The patterns displayed on *Hae*III digestion had distinctive 150/60-bp bands that were once again similar to the pattern attributed to *M. chelonae* subsp. *abscessus* (2). PRA results confirmed that the isolates were *M. abscessus*. The source of the outbreak was traced to the tap water in the operating room and to a defective autoclaving process (the result of a leaking vacuum pump and faulty pressure gauge in the autoclave).

This report highlights the role of rapidly growing mycobacteria in a water-related nosocomial outbreak. The PCR-PRA method promises to be a very rapid, economical, and universal system of identifying mycobacteria to the species level. This technique does not require hybridization to a panel of species-specific probes, which is a limitation of other PCR-based and hybridization methods for differentiating mycobacterial species. This method has the potential to be a useful diagnostic as well as epidemiologic marker for typing isolates of most mycobacteria during institutional outbreaks.

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Erratum Vol. 6, No. 4

In the letter "First Report of Human Granulocytic Ehrlichiosis from Southern Europe (Spain)," by José Oteo et al., there are two citation errors on p. 431, column 2. The correct citations follow.

First paragraph, second sentence: "We used a set of primers based on the published sequence of the 16s rRNA of *E. phagocytophila* (E1: 5'-GGC ATG TAG GCG GTT CGC TAA GTT-3' and E2: 5'-CCC CAC ATT CAG CAC TCA TCG TTT A-3' (10)."

Second paragraph, second sentence: "The prevalence of *E. phagocytophila* genogroup in the tick *Ixodes ricinus* is high (24.1% of nymphs, determined by PCR) in La Rioja, and evidence of HGE infection in patients at risk has been reported (11)."

We regret any confusion this error may have caused.