

## Abstract

Our understanding of the sources of *Mycobacterium avium* infection is partially based on genotypic matching of pathogen isolates from cases and environmental sources. These approaches assume that genotypic identity is rare in isolates from unlinked cases or sources. To test this assumption, a high-resolution PCR-based genotyping approach, LSP-MVR, was selected and used to analyze clinical and environmental isolates of *M. avium* from geographically diverse sources. Among 127 clinical isolates from seven locations in North America, South America, and Europe, 42 genotypes were observed. Twelve of these genotypes were seen in isolates from apparently unlinked patients in two or more geographic locations. Six of the twelve were also observed in environmental isolates. A subset of these isolates was further analyzed by alternative strain genotyping methods, PFGE and MIRU-VNTR, which confirmed the existence of geographically dispersed strain genotypes. These results suggest that caution should be exercised in interpreting high-resolution genotypic matches as evidence for an acquisition event.