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Identification and phylogenetic analysis of *Mycobacterium avium* subsp. *avium* strains isolated from three Abyssinian cats from Northern Italy with disseminated mycobacteriosis

Content

Nontuberculous mycobacteria, including those in the *Mycobacterium avium* complex (MAC), are emerging pathogens of humans and animals. An outbreak of fatal disseminated mycobacteriosis caused by MAC was observed in eight Abyssinian cats in Italy in autumn 2024 and isolation of MAC strains was successful in three cats. This study focused on the genomic characterization of these strains. Whole-genome sequencing was obtained with Miniseq Illumina platform. PanX and MTBseq tools were used to characterize the strains. Phylogenetic analysis was performed both on core genome using PanX and whole genome with maximum likelihood method, implemented in iqtree2. All three samples were identified as *Mycobacterium avium* (MA) and were further phylogenetically identified as *Mycobacterium avium* subsp. *avium* (MAA) showing 100% genome sequence identity. Their genome size was 4,855,006 - 4,860,371 bp with a GC content of 69.33-69.34%. Phylogeny showed that the three strains clustered with a MAA strain from Germany (Assembly GCF_020735405). Major virulence factors such as SigE, SigF, and Phop were detected in the three strains, together with antibiotic resistance associated genes. Disseminated mycobacteriosis caused by MAA in Abyssinian cats confirms previous reports showing a breed predisposition to MAC infections, highlighting the need for MAC surveillance and suggesting further studies to define MAA ecology, evolution and pathogenesis.

Keywords

whole genome, Nontuberculous mycobacteria, MAC, Abyssinian cat, breed predisposition

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