Abstract

Mycobacterium abscessus complex (MABSC), a rapidly growing nontuberculous mycobacterium, is an emerging global pathogen due to its increasing prevalence and intrinsic multidrug resistance. This study characterized 48 clinical MABSC isolates from King Chulalongkorn Memorial Hospital, Bangkok, Thailand, focusing on subspecies distribution, colony morphotypes, antimicrobial susceptibility, biofilm formation, and genetic determinants. *M. abscessus* subsp. *abscessus* (MAB) was the most common (58.3%), followed by *M. abscessus* subsp. *massiliense* (MMA) (43.8%). Smooth morphotypes predominated (68.8%), especially in MMA (81%). All MMA isolates were susceptible to clarithromycin and amikacin, whereas 96.3% of MAB isolates were clarithromycin-resistant, with 33.3% showing inducible resistance by day 14. Amikacin susceptibility in MAB was 63%. Whole-genome sequencing revealed A1408G mutations in the *rrs* gene (amikacin resistance) and mutations at A2058, A2059, and A2080 in the *rrl* gene (clarithromycin resistance). All clarithromycin-resistant MAB isolates carried a functional *erm(41)* gene (T28), while all MMA had a truncated, nonfunctional variant. Biofilm formation was detected in 79.2% of isolates, with significantly higher production in MAB ($p < 0.05$), though no significant difference was observed between morphotypes ($p = 0.63$). Rough isolates harbored disruptive mutations in *mps1* and *mps2*, key genes in glycopeptidolipid biosynthesis. These findings emphasize the importance of subspecies-level identification and genetic resistance profiling to inform appropriate therapeutic strategies against MABSC infections.

Keywords: *Mycobacterium abscessus complex*, *drug resistance, biofilm*