

ANTIBIOTIC RESISTANCE AND TRANSMISSION OF MYCOBACTERIUM ABSCESSUS SUBSPECIES IN CYSTIC FIBROSIS AND NON-CYSTIC FIBROSIS PATIENTS, CZECH REPUBLIC, 2018-2022

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Mycobacterium abscessus complex (*MABC*) is the most prevalent and clinically relevant rapidly growing NTM characterized for its capacity to induce severe pulmonary disease, which can be devastating for individuals with cystic fibrosis (CF). Moreover, the presence of the *MABC* before the transplant may be a contraindication due to concerns for increased morbidity, mortality, and risk of post-transplant transmission.

We retrospectively performed whole genome sequencing (WGS) of all *MABC* (n=25) isolates collected from CF and non-CF patients in Czech Republic during the years 2018 - 2022 to identify possible transmission events and mutations encoding resistance.

Three clusters of genetically similar *MABC* isolates were identified. Patients in two clusters were hospitalized in the same hospital, which indicates rare person-to-person transmission or the same environmental reservoir. Utilizing WGS to evaluate genotypic drug sensitivity to macrolides and aminoglycosides revealed 100% sensitivity and specificity, when compared to the GenoType NTM-DR test. When compared to phenotypic sensitivity testing, the results showed 100% sensitivity and 68.75% specificity for macrolides, and 100% sensitivity and 95.83% specificity for aminoglycosides.

This research emphasizes the capacity of WGS for guiding the treatment of individuals with *MABC* infections.

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