Seminar

Title: Genomic characterization and drug susceptibility profiles of *Mycobacterium kansasii*: Insights from whole-genome sequencing studies in Asia

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Abstract

Mycobacterium kansasii is an important nontuberculous mycobacterium associated with both pulmonary and extrapulmonary diseases. Whole-genome sequencing (WGS) has significantly advanced our understanding of its genetic diversity, subtype distribution, and drug resistance mechanisms. Recent studies conducted in China and India have yielded valuable insights into the epidemiology and antimicrobial susceptibility of *M. kansasii* across Asia.

In China, 153 clinical isolates underwent WGS and broth microdilution susceptibility testing. All isolates were classified as subtype I and grouped into three genomic clusters comprising 141 distinct genotypes. Rifabutin (100% susceptible) and clarithromycin (99.35% susceptible) showed the highest antimicrobial activity, followed by amikacin and linezolid. Notably, rifampin resistance was observed in 22.22% of isolates. Several novel anti-tuberculosis agents, including bedaquiline, sutezolid, delamanid, and clofazimine, exhibited very low minimum inhibitory concentrations (MICs), indicating promising therapeutic potential. The Indian study analyzed 12 isolates through WGS, confirming all as subtype I. Mutations in drug resistance-associated loci were identified; however, their clinical relevance remains unclear due to the limited dataset.

Overall, these findings emphasize the predominance of *M. kansasii* subtype I throughout Asia and highlight the need for integrated genomic and phenotypic approaches to improve treatment strategies and guide the clinical use of both established and novel therapeutics.

Reference

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