IDENTIFICATION OF VIRULENCE MARKERS OF MYCOBACTERIUM ABSCESSUS FOR INTRACELLULAR REPLICATION IN PHAGOCYTES

What differentiates Mycobacterium abscessus from other saprophytic mycobacteria is the ability to resist phagocytosis by human macrophages and the ability to multiply inside such cells. Fabienne Mishguich explains us how and why.

These virulence traits render M. abscessus pathogenic, especially in vulnerable hosts with underlying structural lung disease, such as cystic fibrosis, bronchiectasis or tuberculosis. How patients become infected with M. abscessus remains unclear. Unlike many mycobacteria, M. abscessus is not found in the environment but might reside inside amoebae, environmental phagocytes that represent a potential reservoir for M. abscessus. Indeed, M. abscessus is resistant to amoebal phagocytosis and the intra-amoeba life seems to increase M. abscessus virulence in an experimental model of infection. However, little is known about M. abscessus virulence in itself. To decipher the

genes conferring an advantage to M. abscessus intracellular life, a screening of a M. abscessus transposon mutant library was developed. In parallel, a method of RNA extraction from intracellular Mycobacteria after co-culture with amoebae was developed. This method was validated and allowed the sequencing of whole M. abscessus transcriptomes inside the cells; providing, for the first time, a global view on M. abscessus adaptation to intracellular life. Both approaches give us an insight into M. abscessus virulence factors that enable M. abscessus to colonize the airways in humans.

INFORMATIONS COMPLÉMENTAIRES

More information: https://www.jove.com/video/57766/identification-virulence-markers-mycobacterium-abscessus-for