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Mycobacterium tuberculosis/avium complex

Mycobacterium tuberculosis complex (MTBC)

Tuberculosis (TB) is a disease caused by a group of closely related slow growing organisms collectively named the *Mycobacterium tuberculosis* complex (MTBC). These organisms can infect a range of mammals including humans and affect different organs of the body such as lymph nodes, lungs, kidney, brain, larynx and bone. On inhalation, MTBC tubercles may be destroyed by the immune system, may cause an active infection or may become latent in the body, able to reactivate later in life (in ~10%) - therefore creating a reservoir in the human population.

The MTB complex comprises ***M. tuberculosis, M. bovis*, *M.bovis* bacille Calmette-Guérin (BCG), *M. caprae, M. africanum, M. pinnipedii, M. microti, M. orygis, M. mungi*, *M. suricattae*** *(*formerly *M. bovis),* **dassie bacillus, chimpanzee bacillus,** and the rare, smooth-colony-morphology tubercle bacillus named ***M. canettii****.*

The MTBC shares identical MALDI-TOF profiles and 16S rRNA gene sequences, with 99% identity at the nucleotide level for some species. However, despite these similarities, complex members differ significantly in morphology, biochemistry, host spectra, disease patterns in animals, antimicrobial susceptibility testing (AST) data, geographic ranges, and epidemiological patterns. MTBC organisms are slow growing with a generation time of >24 hours in laboratory media, therefore many weeks are needed to identify the organism using culture.

Tuberculosis

M. tuberculosis has killed more than 100 million people over the last century and the current global burden is vast, estimated to infect one-third of the world population. In 2022 an estimated 10.6 million people developed tuberculosis (TB) and 1.3 million died, making it the second leading infectious cause of death after SARS-Cov-2 and Human immuno-deficiency virus (HIV), (World Health Organization, 2023). Most cases are in low- and middle-income countries and cases in the UK are often travel or immigration associated. Pulmonary TB is the commonest presentation; however, TB may also be disseminated (miliary) or found in non-respiratory sites. Disease is often associated with HIV, however there are also social risk factors associated with TB such as imprisonment, alcohol and drug misuse, and homelessness.

The BCG vaccine, which is an attenuated strain of *M. bovis* is offered and administered to high-risk patients and healthcare workers. Treatment of TB and atypical *Mycobacterium* infection is difficult, involving an extensive course of antibiotics which may cause serious side effects.

Mycobacterium avium complex (MAC)

The term *M. avium* complex (MAC) previously referred to only three species, *M. avium, M. intracellulare and M. chimaera*, with three named subspecies of *M. avium: M. avium* subsp*. avium; M. avium* subsp*. paratuberculosis; and M. avium* subsp*. Silvaticum* identified. However, since 2018, recent literature review and phylogenetic analyses have further defined the MAC, with twelve published species now comprising the group, including: ***M. avium, M. intracellulare, M. chimaera, M. colombiense, M. arosiense, M. vulneris, M. bouchedurhonense, M. timonense, M. marseillense, M. yongonense, M. paraintracellulare*** and ***M. lepraemurium*** (van Ingen *et al.,* 2018)**.**

In patients who are immunocompetent, MAC organisms, may invade the bronchial tree, pre-existing areas of bronchiectasis, or old cavities; in susceptible hosts MAC organisms can cause disseminated infection. Infections with *M. avium* may also cause cervical lymphadenitis in young children. These organisms are often present in water supplies and may contaminate specimens. *M. chimaera,* a slow growing non-tuberculosis *Mycobacterium* (NTM) found in the environment has also been implicated in several cases of endocarditis or deep infection following cardiac surgery involving the use of cardiac bypass equipment.

Diagnosis:

Clients may wish to send specimens where organisms of the *Mycobacterium tuberculosis/avium* complex is clinically suspected, where growth has been identified in liquid or *Mycobacterium* specific solid culture, or where acid-fast bacilli have been visualised using acid/alcohol staining techniques. Specimens typically received include lower respiratory samples such as bronchoalveolar lavage (BAL) and sputum, tissues (e.g. lymph nodes, fixed in wax etc.), CSF or culture media where clients suspect they have grown an organism belonging to the *M. tuberculosis* or *M. avium* complex.

Our assay:

At Micropathology Ltd, we use a qualitative, nested, duplex PCR assay to detect *Mycobacterium tuberculosis/avium* complex DNA. UKAS accredited sample types for this assay include: BAL, NPA, sputum, CSF and tissue specimens. Other sample types may be tested and are reported alongside an appropriate caveat stating that the assay is not UKAS accredited for testing such sample types. Turnaround times are stated in the user manual (http://www.micropathology.com/customer-downloads-handbooks.php) with results usually available in practice much sooner than the given time frame. Where there is a delay, we are usually confirming a result and addressing clinical data given with the specimen.

References

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