Conference Programme and Abstracts

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Mycobacterium avium Complex (MAC) has been isolated from the lesions of patients with tuberculosis (TB). The presence of MAC in TB lesions suggests a potential role of these bacteria in the pathogenesis of TB. The aim of this study was to investigate the prevalence and distribution of MAC in TB lesions using molecular methods.

Materials and Methods: A total of 50 TB lesions from different patients were collected and subjected to molecular analysis. The lesions were fixed in 10% formalin and embedded in paraffin. Sections of 5 μm were cut and stained with hematoxylin and eosin (H&E) for histopathological examination. DNA was extracted from the paraffin-embedded sections using the QIAamp DNA FFPE Tissue Kit (Qiagen, Germany). The extracted DNA was used for PCR amplification of the 16S rRNA gene using the primer pair 16Sf/16Sr. The amplified products were subjected to sequencing using the Sanger method.

Results: The molecular analysis revealed the presence of Mycobacterium avium Complex (MAC) in 10% of the TB lesions examined. The highest prevalence of MAC was observed in the lymph nodes (20%) followed by the lungs (5%). MAC was not detected in the bone, skin, or cerebrospinal fluid samples.

Conclusion: The presence of Mycobacterium avium Complex (MAC) in TB lesions suggests a potential role of these bacteria in the pathogenesis of TB. Further studies are needed to investigate the role of Mycobacterium avium Complex (MAC) in the pathogenesis of TB.