
***Mycobacterium avium* Complex in Domestic and Wild Animals**

Ana Cláudia Coelho, Maria de Lurdes Pinto,
Ana Matos, Manuela Matos and
Maria dos Anjos Pires

Additional information is available at the end of the chapter

<http://dx.doi.org/10.5772/54323>

1. Introduction

Mycobacteria from the *Mycobacterium avium* complex (MAC) cause a variety of diseases including tuberculosis-like disease in humans and birds, disseminated infections in AIDS patients and otherwise immunocompromised patients, lymphadenitis in humans and mammals and paratuberculosis in ruminants. *M. avium* subsp. *paratuberculosis* (*Map*) is the etiologic agent of Johne's disease in cattle and it has been identified in human patients with Crohn's disease. The MAC comprises slow growing mycobacteria that are ubiquitous in the environment (soil and water), and have a wide source range, causing disease in various domestic and wild mammals and birds [1].

The aim of this study was to discuss the classification and biology, epidemiology, clinical signs, pathology, diagnostic techniques, and public health concerns in *Mycobacterium avium* complex in domestic and wild animals.

2. Classification and biology of *Mycobacterium avium* complex

The phylum Actinobacteria is large and very complex; it contains one class (Actinobacteria), five subclasses, six orders, 14 suborders, and 40 families. The orders, suborders, and families are defined based on 16S rRNA sequences and distinctive signature nucleotides. The suborder Corynebacterineae contains seven families with several well-known genera. Three of the most important genera are *Corynebacterium*, *Mycobacterium*, and *Nocardia* [2].