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major or sole pathogen infecting a joint, the duration of treatment should be similar to that used for arthritis caused by aerobic bacteria (Chap. 135).

Although not every anaerobe needs to be covered with pathogendirected therapy in most polymicrobial infections, several studies of Bacteroides bacteremia have clearly demonstrated that patients receiving effective therapy have lower mortality rates and more rapid sterilization of blood cultures than patients receiving ineffec tive therapy. FAILURE OF THERAPY Anaerobic infections that fail to respond to treatment or that relapse should be reassessed. Potential causes include an uncontrolled source of infection (e.g., ongoing intestinal leak into the perito neum), superinfection with a new organism, and/or antibiotic fail ure. Additional imaging may be useful to discern whether surgical drainage or debridement is warranted. Obtaining additional culture specimens will help identify whether an organism resistant to the antibiotics being used is present. Strong consideration should be given to obtaining susceptibility profiles for the isolates. ■ ■FURTHER READING Cooley L, Teng J: Anaerobic resistance: Should we be worried? Curr Opin Infect Dis 32:523, 2019. Debreuil LJ: Fifty years devoted to anaerobes: Historical, lessons, and highlights. Eur J Clin Microbiol Infect Dis 43:1, 2024. Finegold SM: Anaerobes: Problems and controversies in bacteriology, infections, and susceptibility testing. Rev Infect Dis 12:S223, 1990. Reissier S et al: Recent trends in antimicrobial resistance among PART 5 Infectious Diseases anaerobic clinical isolates. Microorganisms 11:1474, 2023. Styrt B, Gorbach SL: Recent developments in the understanding of the pathogenesis and treatment of anaerobic infections (2). N Engl J Med 321:240, 1989. Wexler HM: Bacteroides: The good, the bad, and the nitty-gritty. Clin Microbiol Rev 20:593, 2007. Section 8 Mycobacterial Diseases Mario C. B. Raviglione, Andrea Gori

Tuberculosis Tuberculosis (TB), which is caused by bacteria of the Mycobacterium tuberculosis complex, is one of the oldest diseases known to affect humans. In 2023, after being replaced by COVID-19 during the three previous years, TB probably returned to be the top cause of infectious death from a single infectious agent. Population genomic studies suggest that M. tuberculosis may have emerged ~70,000 years ago in Africa and subsequently disseminated along with anatomi cally modern humans, expanding globally during the Neolithic Age as human density started to increase. This disease most often affects the lungs, although other organs are involved in up to one-third of cases. If properly treated, TB caused by drug-susceptible strains is curable in the vast majority of cases. If untreated, the disease may be fatal in more than 70% of people. Transmission

usually takes place through the airborne spread of droplet nuclei produced by patients with infectious pulmonary TB. Through pharmacologic prophylaxis, the development of the disease can be prevented in those who have contracted TB infection.

ETIOLOGIC AGENT Mycobacteria belong to the family Mycobacteriaceae and the order Actinomycetales. Of the pathogenic species belonging to the M. tuber culosis complex, which comprises eight distinct subgroups, the most common and important agent of human disease by far is M. tuberculosis (sensu stricto). A closely related organism isolated from cases in West, Central, and East Africa is M. africanum. The complex includes some zoonotic members, such as M. bovis (the bovine tubercle bacillus— characteristically resistant to pyrazinamide, once an important cause of TB transmitted by unpasteurized milk, and currently responsible for 140,000 human cases worldwide in 2020, half of them in Africa) and M. caprae (related to M. bovis). In addition, other organisms that have been reported rarely as causing TB include M. pinnipedii (a bacillus infecting seals and sea lions in the southern hemisphere and recently isolated from humans), M. mungi (isolated from banded mongooses in southern Africa), M. orygis (described in oryxes and other Bovidae in Africa and Asia and a potential cause of infection in humans), and

M. microti (the “vole” bacillus, a less virulent organism). Finally, M. canetti is a rare isolate from East African cases that produces unusual smooth colonies on solid media and is considered closely related to a supposed progenitor type. There is no known environmen tal reservoir for any of these organisms. M. tuberculosis is a rod-shaped, non-spore-forming, thin aero bic bacterium measuring 0.5 µm by 3 µm. Mycobacteria, including M. tuberculosis, are often neutral on Gram staining. However, once stained, the bacilli cannot be decolorized by acid alcohol; this charac teristic justifies their classification as acid-fast bacilli (AFB; Fig. 183-1). Acid fastness is due mainly to the organisms’ high content of mycolic acids, long-chain cross-linked fatty acids, and other cell-wall lipids. Microorganisms other than mycobacteria that display some acid fast ness include species of Nocardia and Rhodococcus, Legionella micdadei, and the protozoa Isospora and Cryptosporidium. In the mycobacterial cell wall, lipids (e.g., mycolic acids) are linked to underlying ara binogalactan and peptidoglycan. This structure results in very low FIGURE 183-1 Acid-fast bacillus smear showing M. tuberculosis bacilli. (Courtesy of the Centers for Disease Control and Prevention, Atlanta.)

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