The true international epidemiology of infections due to NTM is hard to determine because the isolation of these organisms often is not reported and speciation often is not performed for *M. tuberculosis* and NTM. The increasing ease of identification and speciation of these organisms is likely to have a major impact on the description of their international epidemiology in the next few years.

PATHOBIOLOGY

Because exposure to NTM is essentially universal and disease is rare, it can be assumed that normal host defenses against these organisms must be strong and that otherwise healthy individuals in whom significant disease develops are highly likely to have specific susceptibility factors that permit NTM to become established, multiply, and cause disease. At the advent of HIV infection, CD4+ T lymphocytes were recognized as key effector cells against NTM; the development of disseminated MAC disease was highly correlated with a decline in CD4+ T lymphocyte numbers. Such a decrease has also been implicated in disseminated MAC infection in patients with idiopathic CD4+ T lymphocytopenia. Potent inhibitors of tumor necrosis factor α (TNF-α), such as infliximab, adalimumab, certolizumab, golimumab, and etanercept, can neutralize this critical cytokine. The occasional result is severe mycobacterial or fungal infection; these associations indicate that TNF-α is a crucial element in mycobacterial control. However, in cases without the above risk factors, much of the genetic basis of susceptibility to disseminated infection with NTM is accounted for by specific mutations in the interferon γ (IFN-γ)/interleukin 12 (IL-12) synthesis and response pathways.

Mycobacteria are typically phagocytosed by macrophages, which respond with the production of IL-12, a heterodimer composed of IL-12p35 and IL-12p40 moieties that together make up IL-12p70. IL-12 activates T lymphocytes and natural killer cells through binding to its receptor (composed of IL-12Rβ1 and IL-12Rβ2/IL-23R), with consequent phosphorylation of STAT4. IL-12 stimulation of STAT4 leads to secretion of IFN-γ, which activates neutrophils and macrophages to produce reactive oxidants, to increase expression of the major histocompatibility complex and Fc receptors, and to concentrate certain antibiotics intracellularly. Signaling by IFN-γ through its receptor (composed of IFN-γR1 and IFN-γR2) leads to phosphorylation of STAT1, which in turn regulates IFN-γ-responsive genes, such as those coding for IL-12 and TNF-α. TNF-α signals through its own receptor via a downstream complex containing the nuclear factor κB (NF-κB) essential modulator (NEMO). Therefore, the positive feedback loop between IFN-γ and IL-12/IL-23 drives the immune response to mycobacteria and other intracellular infections. These genes are known to be the critical ones in the pathway of mycobacterial control: specific Mendelian mutations have been identified in *IFN-γR1, IFN-γR2, STAT1, GATA2, ISG15, IRF8, IL-12A, IL-12Rβ1, IL-12Rβ2, CYBB*, and *NEMO* **(Fig. 204-1)**. Despite the identification of genes associated with disseminated disease, only ~70% of cases of disseminated nontuberculous mycobacterial infections that are not associated with HIV infection have a genetic diagnosis; the implication is that more mycobacterial susceptibility genes and pathways remain to be identified.

In contrast to the recognized genes and mechanisms associated with disseminated nontuberculous mycobacterial infection, the best-recognized underlying condition for pulmonary infection with NTM is bronchiectasis **(Chap. 312)**. Most of the well-characterized forms of bronchiectasis, including cystic fibrosis, primary ciliary dyskinesia, STAT3-deficient hyper-IgE syndrome, and idiopathic bronchiectasis, have high rates of association with nontuberculous mycobacterial infection. The precise mechanism by which bronchiectasis predisposes to locally destructive but not systemic involvement is unknown.

Unlike disseminated or pulmonary infection, "hot-tub lung" represents pulmonary hypersensitivity to NTM—most commonly MAC organisms—growing in underchlorinated, often indoor hot tubs.

CLINICAL MANIFESTATIONS

Disseminated Disease Disseminated MAC or *M. kansasii* infections in patients with advanced HIV infection are now uncommon in North America because of effective antimycobacterial prophylaxis and improved treatment of HIV infection. When such mycobacterial disease was common, the portal of entry was the bowel, with spread to bone marrow and the bloodstream. Surprisingly, disseminated infections with rapidly growing NTM (e.g., *M. abscessus, M. fortuitum*) are very rare in HIV-infected patients, even those with very advanced HIV infection. Because these organisms are of low intrinsic virulence and disseminate only in conjunction with impaired immunity, disseminated disease can be indolent and progressive over weeks to months. Typical manifestations of malaise, fever, and weight loss are often accompanied by organomegaly, lymphadenopathy, and anemia. Because special cultures or stains are required to identify the organisms, the most critical step in diagnosis is to suspect infection with NTM. Blood cultures may be negative, but involved organs typically have significant organism burdens, sometimes with a grossly impaired granulomatous response. In a child, disseminated involvement (i.e., involvement of two or more organs) without an underlying iatrogenic cause should prompt an investigation of the IFN-γ/IL-12 pathway. Recessive mutations in *IFN-γR1* and *IFN-γR2* typically lead to severe infection with NTM. In contrast, dominant negative mutations in *IFN-γR1*, which lead to overaccumulation of a defective interfering mutant receptor on the cell surface, inhibit normal IFN-γ signaling and thus lead to nontuberculous mycobacterial osteomyelitis. Dominant negative mutations in *STAT1* and recessive mutations in *IL-12Rβ1* can produce variable phenotypes consistent with their residual capacities for IFN-γ synthesis and response. Male patients who have disseminated nontuberculous mycobacterial infections along with conical, peg, or missing teeth and an abnormal hair pattern should be evaluated for defects in the pathway

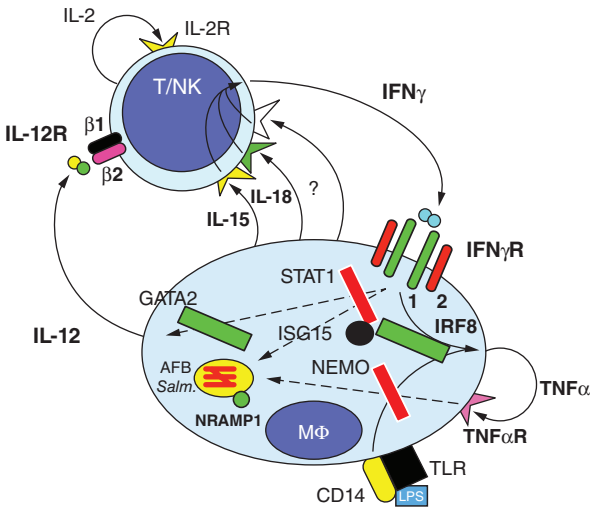

FIGURE 204-1 Cytokine interactions of infected macrophages (Mϕ) with T and natural killer (NK) lymphocytes. Infection of macrophages by mycobacteria (AFB) leads to the release of heterodimeric interleukin 12 (IL-12). IL-12 acts on its receptor complex (IL-12R), with consequent STAT4 activation and production of homodimeric interferon γ (IFNγ). Through its receptor (IFNγR), IFNγ activates STAT1, stimulating the production of tumor necrosis factor α (TNFα) and leading to the killing of intracellular organisms such as mycobacteria, salmonellae (Salm), and some fungi. Homotrimeric TNFα acts through its receptor (TNFαR) and requires nuclear factor κB essential modulator (NEMO) to activate nuclear factor κB, which also contributes to the killing of intracellular bacteria. Both IFNγ and TNFα lead to upregulation of IL-12. TNFα-blocking antibodies work either by blocking the ligand (infliximab, adalimumab, certolizumab, golimumab) or by providing soluble receptor (etanercept). Mutations in *IFNγR1, IFNγR2, IL-12p40, IL-12Rβ1, IL-12Rβ2, STAT1, GATA2, ISG15, IRF8, CYBB,* and *NEMO* have been associated with a predisposition to mycobacterial infections. Other cytokines, such as IL-15 and IL-18, also contribute to IFNγ production. Signaling through the Toll-like receptor (TLR) complex and CD14 also upregulates TNFα production. LPS, lipopolysaccharide; NRAMP1, natural resistance-associated macrophage protein 1.