

Although most CAP cases are caused by relatively few pathogens, an accurate determination of their prevalence is difficult because laboratory testing methods are often insensitive and indirect (**Table 126-1**). Separation of potential agents into “typical” bacterial pathogens and “atypical” organisms may be helpful. The former group includes *S. pneumoniae*, *Haemophilus influenzae*, and, in selected patients, *S. aureus* and gram-negative bacilli such as *Klebsiella pneumoniae* and *P. aeruginosa*. The “atypical” organisms include *Mycoplasma pneumoniae*, *Chlamydia pneumoniae*, and *Legionella* species as well as respiratory viruses such as influenza virus, adenoviruses, human metapneumoviruses, respiratory syncytial virus, and coronaviruses. With the increasing use of pneumococcal vaccine, the incidence of pneumococcal pneumonia is decreasing. Cases due to *M. pneumoniae* and *C. pneumoniae*, however, appear to be increasing, especially among young adults. Viruses are recognized as increasingly important in pneumonia, and polymerase chain reaction (PCR)–based testing indicates their presence in the respiratory tract of 20–30% of healthy adults and in the same percentage of pneumonia patients, including those who are severely ill. The most common are influenza, parainfluenza, and respiratory syncytial viruses. Whether they are true etiologic pathogens, co-pathogens, or simply colonizers cannot always be determined. Atypical organisms cannot be cultured on standard media or seen on Gram’s stain, but their frequency and importance have significant implications for therapy. They are intrinsically resistant to all β -lactams and require treatment with a macrolide, a fluoroquinolone, or a tetracycline. In the 10–15% of CAP cases that are polymicrobial, the etiology usually includes a combination of typical and atypical pathogens.

TABLE 126-1 Microbial Causes of Community-Acquired Pneumonia, by Site of Care