PSEUDOMONAS AERUGINOSA

EPIDEMIOLOGY

P. aeruginosa is found in most moist environments. Soil, plants, vegetables, tap water, and countertops are all potential reservoirs for this microbe, as it has simple nutritional needs. Given the ubiquity of *P. aeruginosa*, simple contact with the organism is not sufficient for colonization or infection. Clinical and experimental observations suggest that *P. aeruginosa* infection often occurs concomitantly with host defense compromise, mucosal trauma, physiologic derangement, and antibiotic-mediated suppression of normal flora. Thus, it comes as no surprise that the majority of *P. aeruginosa* infections occur in intensive care units (ICUs), where these factors frequently converge. The organism is initially acquired from environmental sources, but patient-to-patient spread also occurs in clinics and families.

In the past, burned patients appeared to be unusually susceptible to *P. aeruginosa*. For example, in 1959–1963, *Pseudomonas* burn-wound sepsis was the principal cause of death in 60% of burned patients dying at the U.S. Army Institute of Surgical Research. For reasons that are unclear, *P. aeruginosa* infection in burns is no longer the major problem that it was during the 1950s and 1960s. Similarly, in the 1960s, *P. aeruginosa* appeared as a common pathogen in patients receiving cytotoxic chemotherapy at many institutions in the United States, but it subsequently diminished in importance. Despite this subsidence, *P. aeruginosa* remains one of the most feared pathogens in this population because of its high attributable mortality rate.

In some parts of Asia and Latin America, *P. aeruginosa* continues to be the most common cause of gram-negative bacteremia in neutropenic patients.

In contrast to the trends for burned patients and neutropenic patients in the United States, the incidence of *P. aeruginosa* infections among patients with CF has not changed. *P. aeruginosa* remains the most common contributing factor to respiratory failure in CF and is responsible for the majority of deaths among CF patients.

LABORATORY FEATURES

P. aeruginosa is a nonfastidious, motile, gram-negative rod that grows on most common laboratory media, including blood and MacConkey agars. It is easily identified in the laboratory on primary-isolation agar plates by pigment production that confers a yellow to dark green or even bluish appearance. Colonies have a shiny "gun-metal" appearance and a characteristic fruity odor. Two of the identifying biochemical characteristics of *P. aeruginosa* are an inability to ferment lactose on MacConkey agar and a positive reaction in the oxidase test. Most strains are identified on the basis of these readily detectable laboratory features even before extensive biochemical testing is done. Some isolates from CF patients are easily identified by their mucoid appearance, which is due to the production of large amounts of the mucoid exopolysaccharide or alginate.

PATHOGENESIS

Unraveling the mechanisms that underlie disease caused by *P. aeruginosa* has proved challenging. Of the common gram-negative bacteria, no other species produces such a large number of putative virulence factors (Table 189-1). Yet *P. aeruginosa* rarely initiates an infectious process in the absence of host injury or compromise, and few of its putative virulence factors have been shown definitively to be involved in disease in humans. Despite its metabolic versatility and possession of multiple colonizing factors, *P. aeruginosa* exhibits no competitive advantage over enteric bacteria in the human gut; neither is it a normal inhabitant of the human gastrointestinal tract, despite the host's continuous environmental exposure to the organism.

Virulence Attributes Involved in Acute *P. aeruginosa* Infections • ***MOTILITY AND COLONIZATION*** A general tenet of bacterial pathogenesis is that most bacteria must adhere to surfaces or colonize a host niche in order to initiate disease. Most pathogens examined thus far possess adherence factors called *adhesins*. *P. aeruginosa* is no exception. Among its many adhesins are its pili, which demonstrate adhesive properties for a variety of cells and adhere best to injured cell surfaces. In the organism's flagellum, the flagellin molecule binds to cells, and the flagellar cap attaches to mucins through the recognition of glycan chains. Other *P. aeruginosa* adhesins include the outer core of the lipopolysaccharide (LPS) molecule, which binds to the cystic fibrosis transmembrane conductance regulator (CFTR) and aids in internalization of the organism, and the alginate coat of mucoid strains, which enhances adhesion to cells and mucins. In addition, membrane proteins and lectins have been proposed as colonization factors. The deletion of any given adhesin is not sufficient to abrogate the ability of *P. aeruginosa* to colonize surfaces. Motility is important in host invasion via mucosal surfaces in some animal models; however, nonmotile strains are not uniformly avirulent.

TABLE 189-1 MAIN PUTATIVE VIRULENCE FACTORS OF *PSEUDOMONAS AERUGINOSA*

Substance/Organelle	Function	Virulence in Animal Disease
Pili	Adhesion to cells	?
Flagella	Adhesion, motility, inflammation	Yes
Lipopolysaccharide	Antiphagocytic activity, inflammation	Yes
Type III secretion system	Toxic activity (ExoU, ExoS)	Yes
Type II secretion system	Toxic activity	Yes
Proteases	Proteolytic activity	?
Phospholipases	Cytotoxicity	?
Exotoxin A	Cytotoxicity	?

EVASION OF HOST DEFENSES The transition from bacterial colonization to disease requires the evasion of host defenses followed by invasion of the microorganism. *P. aeruginosa* appears to be well equipped for evasion. Attached bacteria inject four known toxins (ExoS or ExoU, ExoT, and ExoY) via a type III secretion system that allows the bacteria to evade phagocytic cells either by direct cytotoxicity or by inhibition of phagocytosis. Mutants with defects in this system fail to disseminate in some animal models of infection. The type II secretion system as a whole secretes toxins that can kill animals, and some of its secreted toxins, such as exotoxin A, have the potential to kill phagocytic cells. Multiple proteases secreted by this system may degrade host effector molecules, such as cytokines and chemokines, that are released in response to infection. Thus this system may also contribute to host evasion.

TISSUE INJURY Among gram-negative bacteria, *P. aeruginosa* probably produces the largest number of substances that are toxic to cells and thus may injure tissues. The toxins secreted by its type III secretion system are capable of tissue injury. However, their delivery requires the adherence of the organism to cells. Thus, the effects of these toxins are likely to be local or to depend on the presence of vast numbers of bacteria. On the other hand, diffusible toxins, secreted by the organism's type II secretion system, can act freely wherever they come into contact with cells. Possible effectors include exotoxin A, four different proteases, and at least two phospholipases; in addition to these secreted toxins, rhamnolipids, pyocyanin, and hydrocyanic acid are produced by *P. aeruginosa* and are all capable of inducing host injury.

INFLAMMATORY COMPONENTS The inflammatory components of *P. aeruginosa*—e.g., the inflammatory responses to the lipid A component of LPSs and to flagellin, mediated through the Toll-like receptor (TLR) system (principally TLR4 and TLR5)—have been thought to represent important factors in disease causation. Although these inflammatory responses are required for successful defense against *P. aeruginosa* (i.e., in their absence, animals are defenseless against *P. aeruginosa* infection), florid responses are likely to result in disease. When the sepsis syndrome and septic shock develop in *P. aeruginosa* infection, they are probably the result of the host response to one or both of these substances, but injury to the lung by *Pseudomonas* toxins may also result in sepsis syndromes, possibly by causing cell death and the release of cellular components (e.g., heat-shock proteins) that may activate the TLR or another proinflammatory system.