TABLE 201-1 ANAEROBIC HUMAN MICROBIOTA: AN OVERVIEW

Anatomic Site	Total Bacteria[a]	Anaerobic/Aerobic Ratio	Potential Pathogens
Oral cavity			
Saliva	10^8–10^9	1:1	*Fusobacterium nucleatum, Prevotella melaninogenica, Prevotella oralis* group, *Bacteroides ureolyticus* group, *Peptostreptococcus* spp.
Tooth surface	10^{10}–10^{11}	1:1	
Gingival crevices	10^{11}–10^{12}	10^3:1	
Gastrointestinal tract			
Stomach	0–10^5	1:1	*Bacteroides* spp. (principally members of the *B. fragilis* group), *Prevotella* spp., *Clostridium* spp., *Peptostreptococcus* spp.
Jejunum/ileum	10^4–10^7	1:1	
Terminal ileum and colon	10^{11}–10^{12}	10^3:1	
Female genital tract	10^7–10^9	10:1	*Peptostreptococcus* spp., *Bacteroides* spp., *Prevotella bivia*

[a]Per gram or milliliter.

The skin microbiota contains anaerobes as well, the predominant species being *Propionibacterium acnes* and, in lower numbers, other species of propionibacteria and peptostreptococci.

Commensal bacteria in general and commensal anaerobes in particular have been implicated as crucial mediators of physiologic, metabolic, and immunologic functions in the mammalian host. One of the most important roles that anaerobes serve as components of the normal colonic microbiota is the promotion of resistance to colonization; the presence of anaerobic bacteria effectively interferes with colonization by potentially pathogenic bacterial species through the depletion of oxygen and nutrients, the production of enzymes and toxic end products, and the modulation of the host's intestinal innate immune response. For example, *B. thetaiotaomicron* stimulates Paneth cells to produce RegIIIγ, a bactericidal lectin that can result in killing of gram-positive bacteria. The normal colonic microbiota plays an important role in protection against *Clostridium difficile*–associated diarrhea or colitis—a toxin-mediated, potentially life-threatening disease that results when *C. difficile* spores in the colon transform into toxin-producing vegetative forms after antibiotic elimination of critical components of the competing colonic microbiota.

Bacteroides and other intestinal bacteria ferment carbohydrates and produce volatile fatty acids that are reabsorbed and used by the host as an energy source. The anaerobic intestinal microbiota is also responsible for the production of secreted products that promote human health (e.g., vitamin K and bile acids useful in fat absorption and cholesterol regulation).

Moreover, the anaerobic intestinal microbiota influences the development of an intact mucosa and of mucosa-associated lymphoid tissue. Colonization of germ-free mice with a single species, *B. thetaiotaomicron*, affects the expression of various host genes and corrects deficiencies of nutrient uptake, metabolism, angiogenesis, mucosal barrier function, and enteric nervous system development. The symbiosis factor polysaccharide A (PSA) of *B. fragilis* influences the normal development and function of the mammalian immune system and protects mice against colitis in a model of inflammatory bowel disease. It has also been shown that PSA can confer protection both prophylactically and therapeutically, restraining inflammatory processes at an extraintestinal site (the central nervous system [CNS]) and ameliorating disease in a mouse model of multiple sclerosis. Anaerobes can stimulate specific lymphocyte populations of the small and large intestine and can influence immunologic balance (including T_H1/T_H2 balance) as well as the number of T_H17 and regulatory T cells in gut tissues.

Clearly, the gut microbiota confers many benefits, and its dysregulation may play a role in the pathogenesis of diseases characterized by inflammation and aberrant immune responses, such as inflammatory bowel disease, rheumatoid arthritis, multiple sclerosis, asthma, and type 1 diabetes. Furthermore, the gut microbiota has been associated with obesity and metabolic syndrome. An interesting association between certain microbes found in the microbiota and testosterone production has been suggested as well.

ETIOLOGY

Thousands of species of anaerobic bacteria have been identified as components of the complete human microbiota, with each individual colonized by hundreds of these species. Despite the complex array of bacteria in the normal microbiota, relatively few species are isolated commonly from human infections. Anaerobic infections occur when the harmonious relationship between the host and the host's microbiota is disrupted. Any site in the body is susceptible to infection with these indigenous organisms when a mucosal barrier or the skin is compromised by surgery, trauma, tumor, ischemia, or necrosis, all of which can reduce local tissue redox potentials. Because the sites that are colonized by anaerobes contain many species of bacteria, disruption of anatomic barriers allows contamination of normally sterile sites by many organisms, resulting in mixed infections involving multiple species of anaerobes in combination with synergistically acting facultative or microaerophilic organisms.

Severe mixed infections of the head and neck may arise from an abscessed tooth infected with commensal microbiota of the mouth. Examples of infections arising from an oral source are chronic sinusitis, chronic otitis media, Ludwig's angina, and periodontal abscesses. Brain abscesses and subdural empyema are also commonly associated with the oral microbiota. Oral anaerobes are usually responsible for pleuropulmonary diseases such as aspiration pneumonia, necrotizing pneumonia, lung abscess, and empyema.

Anaerobes from the intestine play an important role in various intraabdominal infections, such as peritonitis and intraabdominal abscesses (Chap. 159). Colonic contents are the source of microorganisms in the case of these infections, which usually follow disruption of intestinal continuity and contamination of the peritoneal cavity. Anaerobic bacteria are isolated frequently in female genital tract infections, such as salpingitis, pelvic peritonitis, tuboovarian abscess, vulvovaginal abscess, septic abortion, and endometritis (Chap. 163). In addition, these bacteria are often found in bacteremia and in infections of the skin, soft tissues, and bones.

Predominant among the anaerobic gram-positive cocci that produce disease are the peptostreptococci; the species of this genus that are most commonly involved in infections are *P. micros*, *P. magnus*, *P. asaccharolyticus*, *P. anaerobius*, and *P. prevotii*. Clostridia (Chap. 179) are anaerobic spore-forming gram-positive rods that are isolated from wounds, abscesses, sites of abdominal infection, and blood. Gram-positive anaerobic non-spore-forming bacilli are uncommon as etiologic agents of human infection. *P. acnes*, a component of the skin microbiota and a rare cause of foreign-body infections, is one of the few nonclostridial gram-positive rods associated with infections. The principal anaerobic gram-negative bacilli found in human infections belong to the *B. fragilis* group and to *Fusobacterium*, *Prevotella*, and *Porphyromonas* species.

The most important potential anaerobic pathogens found in the upper airways and isolated from clinical specimens of oral and