

Medical Microbiology

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Medical Microbiology

TENTH EDITION

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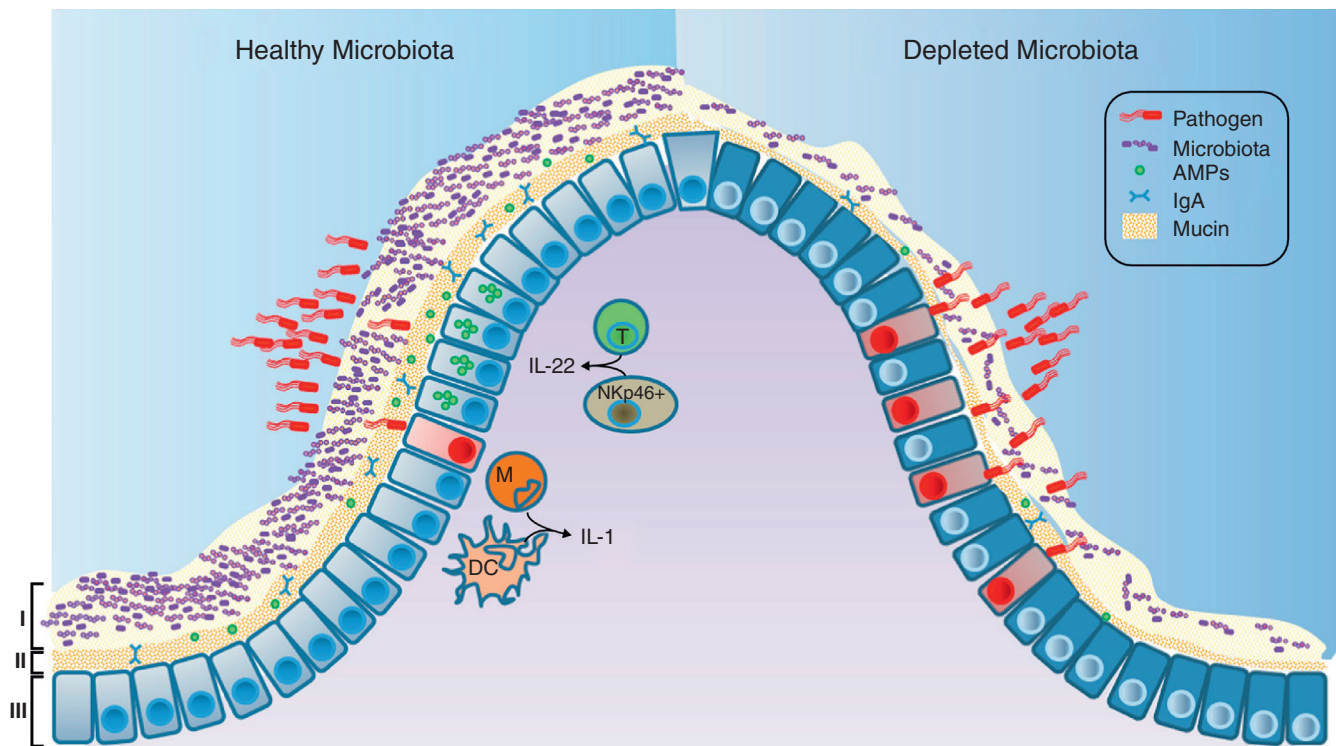


Fig. 2.2 Intestinal microbiota protection against enteric infections. (I) Saturation of colonization sites and consumption of nutrients limit pathogen access to host tissues; (II) the microbiota prime innate immunity by stimulating mucin production, immunoglobulin (IgA), and antimicrobial peptides (AMPs); and (III) the microbiota stimulate interleukin (IL)-22 expression, which increases epithelial resistance, and IL-1 β production, which promotes recruitment of inflammatory cells. (From Khosravi, A., Mazmanian, S., 2013. Disruption of the gut microbiome as a risk factor for microbial infections. *Curr. Opin. Microbiol.* 16, 221–227.)

Evolution of the Microbiome and Normal Flora

The **normal flora** or microbial population of a particular site of the body consists of a unique community of core and secondary microbiota that evolved through a symbiotic relationship with the host and a competitive relationship with other species. The host provides a place to colonize, nutrients, and some protection from unwanted species (innate immune responses). The microbes provide needed metabolic functions, stimulate innate and regulatory immunity, and prevent colonization with unwanted pathogens (Fig. 2.2). The ability to tolerate the amount of oxygen or lack thereof (redox state) and the pH and salt concentration, as well as to scavenge essential minerals and harvest and metabolize the available nutrients, determines the numbers and nature of the species that populate a site of the body. Anaerobic or facultative anaerobic bacteria colonize most of the sites of the body because of the lack of oxygen in sites such as the mouth, intestine, and genitourinary tract.

The composition of the microbiota is influenced by personal hygiene (e.g., use of soap, deodorants, mouthwash, skin peels, enemas, vaginal douches), diet, water source, medicines (especially antibiotics), and exposure to environmental toxins. Drinking well water versus chlorinated city water or a diet consisting of fiber, sugar, or fats can select for different intestinal bacteria based on their ability to use the essential minerals (e.g., iron) and nutrients. Alteration

of the environment with foods or medicines can also alter the microbiota (Fig. 2.3). These changes can be acceptable if the core microbiome and critical functional properties of the microbiome are maintained but can result in disease if these functions are lost. Historically, the greatest concern with the use of broad-spectrum antibiotics was the selection of resistant bacteria; however, a greater concern should be the disruption of the microbiome and loss of essential functions. Because antibiotics are not completely selective for the targeted pathogen, the use of antibiotics is always associated with some degree of toxicity.

Of the more than 150 species of bacteria that colonize the gut of a healthy adult individual, most are members of Bacteroidetes (e.g., *Bacteroides*) and Firmicutes (e.g., *Clostridium*, *Ruminococcus*, *Faecalibacterium*, *Lactobacillus*), with Actinobacteria (e.g., *Bifidobacterium*) present in smaller numbers. Interestingly, the importance of many of these bacteria was not appreciated before gene sequencing was used to identify and quantitate the gut microbiota. Within the colon, some bacteria establish their niche by waging interspecies warfare with bacteriocins (e.g., colicins produced by *Escherichia coli*), other antibacterial proteins, and metabolites that deter other species from growing. These molecules also benefit the host by eliminating invading bacteria including *Salmonella*, *Shigella*, *Clostridioides difficile*, *Bacillus cereus*, and other pathogens. The bacteria must also resist antimicrobial peptides and immunoglobulin (Ig) A produced by the host and released into the bowel.

Metabolism of nutrients plays a major role in the symbiotic relationship between the human host and microbe.

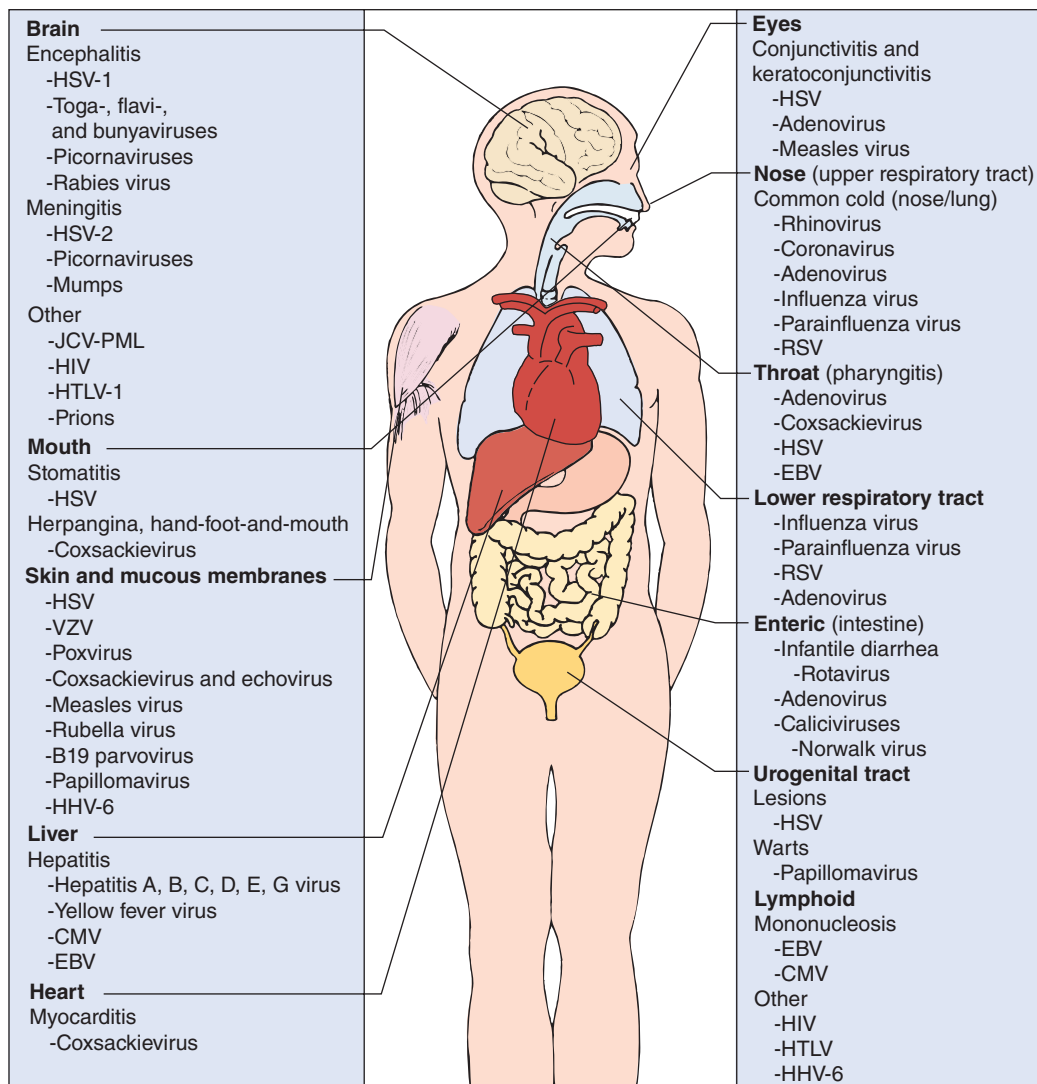


Fig. 37.1 Major target tissues of viral disease. *CMV*, Cytomegalovirus; *EBV*, Epstein-Barr virus; *HHV-6*, human herpesvirus 6; *HIV*, human immunodeficiency virus; *HSV*, herpes simplex virus; *HTLV*, human T-cell lymphotropic virus; *JCV-PML*, JC virus induction of progressive multifocal leukoencephalopathy; *RSV*, respiratory syncytial virus; *VZV*, varicella-zoster virus.

Although enteroviruses (picornaviruses) are spread by the fecal-oral route, they usually cause only mild or no gastrointestinal symptoms. Instead, these viruses establish a viremia, spread to other target organs, and then cause clinical disease.

Enveloped viruses, including CMV and HIV, may infect the colon from the blood stream or by anal sex.

SKIN INFECTIONS AND MANIFESTATIONS

Skin is a barrier to virus infection but small cuts or abrasions in the skin allow infection by direct contact with lesions or contaminated fluids (HSV) or fomites (e.g., towels). Oral and genitourinary mucopithelium are prominent targets of viruses. Most of these infections present at the site of infection (e.g., papillomaviruses, HSV, molluscum contagiosum). Many skin infections and the rashes that result from virus infections result from systemic spread

of the virus to the skin or hypersensitivity reactions elicited by the infection.

INFECTIONS OF OTHER ORGANS AND TISSUES

Viremic spread, either free in blood or cell associated in monocytes, brings viruses to the liver where the immunotolerance and hepatocyte biosynthetic machinery foster viral replication. The liver is often a source for a secondary viremia but can also be damaged by the infection. Cell-mediated immunity is necessary to control liver infections by hepatitis A, B, D, C, G, and E viruses and yellow fever virus but also causes the symptoms of hepatitis.

The heart and other muscles are also susceptible to viral infection and damage causing myocarditis or pericarditis. Infection of secretory glands, accessory sexual organs, and mammary glands by CMV generates virus to spread the virus and the inflammatory response to **mumps** causes the