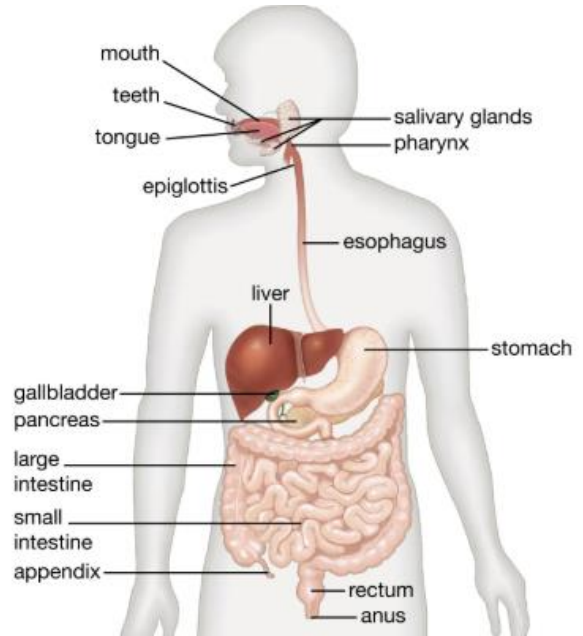


Chapter III: Elements of digestive tract microbiology

The digestive tract should also be viewed as a sequence of habitats in which each anatomical segment imposes its own selective pressures on microorganisms.

These selective pressures include pH, oxygen availability, redox conditions, bile exposure, mucus architecture, digestive enzymes, immune activity, epithelial turnover, and transit time. As a result, the oral cavity, esophagus, stomach, small intestine, and colon do not host the same communities, nor do they allow microorganisms to perform the same functions.

- Microbiota is the set of microorganisms inhabiting a given environment.
- Microbiome is the collective genes, functional capacities, and ecological interactions associated with a microbial community.
- Dysbiosis: an altered ecological state characterized by instability, loss of function, or overrepresentation of opportunistic organisms.



I. Human digestive tract

The digestive tract extends from the mouth to the anus and includes the oral cavity, pharynx, esophagus, stomach, small intestine, large intestine, rectum, and anal canal. Microbial density generally increases from the upper to the lower tract. The upper tract is relatively restrictive because of acidity, oxygen, rapid flow, and digestive secretions, whereas the distal intestine, particularly the colon, supports very dense and mostly anaerobic communities.

• Oral Cavity

The oral cavity includes the teeth, tongue, gingival crevices, buccal mucosa, palate, and saliva. Common genera include *Streptococcus*, *Actinomyces*, *Veillonella*, *Neisseria*, *Haemophilus*, *Prevotella*, and *Fusobacterium*. These organisms coexist in structured multispecies communities rather than as isolated species. The oral microbiota contributes to biofilm organization, metabolism of dietary sugars, and resistance against exogenous microorganisms.

- **Pharynx and Esophagus**

The pharynx and esophagus mainly serve as conduits. The communities detected here frequently resemble oral communities, especially streptococci and other oral-associated taxa. Microbial functions are modest compared with the lower gut. Their main roles involve transient surface colonization and ecological competition

- **Stomach**

The gastric lumen is acidic and mechanically active, and pepsin contributes to the degradation of ingested material. Microbial biomass is low. Acid-tolerant or transient taxa such as *Streptococcus*, *Prevotella*, and *Veillonella* may be found. *Helicobacter pylori* is a well-known specialized gastric colonizer in infected individuals. The main microbiological role of the stomach is selective filtering: It reduces the survival of many ingested organisms .

- **Small intestine**

The small intestine is the major site of digestion and absorption. It receives chyme from the stomach and is exposed to pancreatic enzymes, bile salts, and continuous peristaltic flow. These conditions limit excessive bacterial growth but still permit the presence of selected communities.

The duodenum and jejunum usually contain relatively low densities of microorganisms. Taxa often include *Streptococcus*, *Lactobacillus*, *Enterococcus*, and selected facultative anaerobes. Their functions include modest nutrient conversion, bile interaction, pathogen competition, and signaling with the mucosal immune system.

The ileum is a transition zone between the proximal small intestine and the colon. Transit slows, oxygen decreases, and immune structures such as Peyer's patches are prominent. Microorganisms in this region participate in colonization resistance.

- **Large intestine: Cecum and colon**

The cecum and colon are the principal sites of dense microbial colonization. They provide low oxygen tension, slower transit, a structured mucus layer, and undigested residues arriving from the upper intestine.

The dominant groups are typically Bacillota/Firmicutes and Bacteroidota/Bacteroidetes. Important genera include *Bacteroides*, *Faecalibacterium*, *Roseburia*, *Ruminococcus*, *Blautia*, *Prevotella*, and *Bifidobacterium*.

The colon is the major site of fermentation of nondigestible carbohydrates. Microbes produce short-chain fatty acids such as acetate, propionate, and butyrate. These molecules nourish colonocytes, support epithelial barrier function, regulate inflammation, and contribute to host metabolism. The colonic microbiota also transforms bile acids, synthesizes certain vitamins, metabolizes xenobiotics, and provides strong colonization resistance.

- **Rectum and anal canal**

These distal segments are specialized for storage and elimination of fecal material and are strongly influenced by the distal colonic ecosystem. Most taxa detected in fecal material derive mainly from the distal colon.

Major physicochemical determinants of microbial distribution

The uneven microbial distribution along the digestive tract can be explained by a small number of ecological drivers.

- Low pH strongly restricts microbial survival in the stomach.
- Bile salts inhibit many organisms in the proximal small intestine.
- Slow transit in the colon permits high-density anaerobic growth.
- Mucus-associated niches support specialized taxa such as mucin degraders.
- Host immunity filters which microorganisms persist at each location.

Non-bacterial members of digestive tract microbiology

Although bacteria dominate most descriptions of the digestive microbiota, the tract also contains archaea, fungi, and viruses. Archaea, particularly methanogens such as *Methanobrevibacter smithii*, participate in hydrogen disposal and may influence fermentative efficiency. Fungi are present at lower abundance but may interact with mucosal immunity and bacterial communities. The virome, especially bacteriophages, shapes bacterial population dynamics, gene transfer, and ecosystem stability.

Infant gut microbiota modulation: Factors influencing early colonization

The process is shaped by prenatal, per-partum, and post-partum influences, which determine both the sources of microorganisms and the selective pressures acting on them.

Per-partum factors

- Mode of delivery: vaginal birth promotes exposure to maternal vaginal and fecal microbiota, whereas cesarean birth reduces this route of transmission and increases exposure to skin- and hospital-associated microorganisms.
- Gestational age: preterm infants often show delayed microbial maturation and reduced beneficial anaerobic colonization.
- Intrapartum antibiotherapy: antibiotics administered during labor may reduce transmission of key taxa and can interact with delivery mode in shaping early colonization trajectories.

Post-partum factors

- Type of feeding: breastfeeding is one of the strongest modulators of infant gut microbiota because human milk provides oligosaccharides, immunoglobulins, antimicrobial factors, and microbial inputs that favor *Bifidobacterium*-rich communities.
- Geographic location: geography reflects diet, hygiene, cultural habits, and medical practices, all of which influence microbial exposure and early community assembly.
- Family environment: parents, siblings, caregivers, pets, and household surfaces act as repeated microbial sources that increase reseeding and strain sharing.
- Host–microbe interactions: the infant gut actively selects its microbiota through mucus, immune responses, motility, and physicochemical conditions; colonization is therefore not passive.
- Maternal diet during lactation: maternal nutrition can influence milk composition and indirectly modulate microbial development in the infant.
- Weaning: introduction of solid foods drives a major ecological shift toward a more diverse and adult-like fermentative community.

Roles of the digestive microbiota

Barrier Effect

The intestinal microbiota provides protection against ingested pathogens by forming a biological barrier, commonly referred to as the colonization resistance effect.

- **Competition for nutrients and adhesion sites:** commensal microorganisms compete with pathogenic microorganisms for the same ecological niches, substrates, and epithelial binding sites.
- **Production of inhibitory compounds:** some intestinal bacteria produce organic acids, bacteriocins, and other antimicrobial metabolites that inhibit pathogen growth.
- **Regulation of mucus secretion and reinforcement of the intestinal barrier:** microbial metabolites, particularly short-chain fatty acids, contribute to mucus production and help maintain epithelial integrity.
- **Modulation of host immune responses:** host cell receptors recognize microbial-associated molecular patterns from both pathogenic and non-pathogenic microorganisms, thereby regulating inflammatory and immune responses.

Nutritional and Metabolic Roles

- It contributes to the synthesis of certain vitamins, particularly vitamin K and several B-group vitamins.

- Dietary fibers that cannot be digested by host enzymes are fermented by intestinal bacteria, leading to the production of gases and short-chain fatty acids (SCFAs) such as acetate, propionate, and butyrate.
- These SCFAs can then be absorbed by intestinal cells and used as energy sources, especially by colonocytes in the case of butyrate.
- Likewise, non-absorbed carbohydrates such as starch, pectin, and host-derived glycoproteins can be degraded by intestinal bacteria.

Harmful Effects

- **Carbohydrate-related metabolism:** bacterial enzymes such as β -glucuronidase may release aglycones from glucuronide conjugates; some of these released compounds may have toxic or carcinogenic potential.
- **Nitrogen metabolism:** microbial transformation of nitrogen-containing compounds may contribute, under certain conditions, to the formation of potentially carcinogenic compounds such as nitrosamines.
- **Xenobiotic metabolism:** some intestinal bacteria are able to inactivate drugs, reactivate conjugated compounds, or produce toxic metabolites that may affect host health.

II. Digestive microflora of ruminants

The digestive tract of ruminants is specifically adapted to a herbivorous diet through microbial fermentation in the rumen, which enables these animals to efficiently degrade complex plant fibers and extract nutrients necessary for survival and production. Ruminants are therefore classified as polygastric herbivores because their stomach is divided into four compartments.

Anatomy of the Digestive Tract

- 1. Mouth:** Digestion begins with the ingestion of feed through the mouth. Ruminants use their tongue to grasp grass or forage, which is then cut and crushed by the incisors and molars.
- 2. Esophagus:** After mastication, feed passes through the esophagus, a muscular tube that transports food from the mouth to the stomach.
- 3. Rumen:** The rumen is the first and largest compartment of the ruminant stomach. It functions as a large fermentation chamber in which microorganisms, including bacteria, protozoa, fungi, and archaea, degrade plant material. It can store and ferment large quantities of feed.

4. Reticulum: After initial fermentation in the rumen, part of the digesta passes into the reticulum. This compartment acts as a sorting and filtering structure: small particles and liquids move forward, while larger particles are returned for further rumination and size reduction.

5. Omasum: The omasum is the third stomach compartment. It is mainly involved in the absorption of water, minerals, and certain fermentation products, and also contributes to particle size reduction before digesta enters the final compartment.

6. Abomasum: The abomasum is considered the “true stomach” of ruminants because it resembles the stomach of monogastric animals. It secretes gastric acid and digestive enzymes responsible for the chemical digestion of proteins and other remaining nutrients.

7. Intestines:

- **Small intestine:** After leaving the stomach, digested nutrients are absorbed in the small intestine, which consists of the duodenum, jejunum, and ileum. The duodenum receives secretions from the liver and pancreas, which continue and complete digestion. Carbohydrates, proteins, and lipids are broken down into smaller molecules and absorbed mainly in the jejunum and ileum. The mucosa is lined with villi that increase the absorptive surface area.

- **Large intestine:** The large intestine includes the cecum, colon, and rectum. It is involved in water absorption and the final processing of undigested residues. Feces are formed in the distal part of the tract and eliminated through the anus.

Digestive microflora of the rumen

The rumen contains a highly complex microbial ecosystem composed mainly of bacteria, protozoa, anaerobic fungi, archaea, and bacteriophages. These microorganisms are essential for the digestion of fibrous plant material and for the production of fermentation end-products used by the host.

- **Rumen bacteria:** Rumen bacteria include fibrolytic bacteria, such as *Fibrobacter* and *Ruminococcus*, which attach to plant fibers and produce enzymes that degrade structural carbohydrates, and amylolytic bacteria, such as *Streptococcus* and *Ruminobacter*, which digest starch.

- **Rumen protozoa:** Protozoa contribute to feed digestion and also act as predators of bacteria. They ingest feed particles and microorganisms, secrete digestive enzymes, and participate in nutrient turnover within the rumen ecosystem.

- **Anaerobic rumen fungi:** Rumen fungi, including *Neocallimastix*, *Piromyces*, and *Caecomyces*, are important degraders of plant cell walls. They secrete enzymes involved in the digestion of structural polysaccharides and help disrupt lignocellulosic plant tissues.

• Methanogenic archaea: Methanogenic archaea use hydrogen produced during fermentation to reduce carbon dioxide and generate methane. This process is important for hydrogen disposal in the rumen, although it also contributes to methane emissions from ruminants.



Genera found in the gastrointestinal tract

- | | |
|-------------------------|-----------------------|
| <i>Prevotella</i> | <i>Acetitomaculum</i> |
| <i>Treponema</i> | <i>Mogibacterium</i> |
| <i>Succiniclasticum</i> | <i>Butyrivibrio</i> |
| <i>Ruminococcus</i> | <i>Acinetobacter</i> |

