

Veillonella

type 1 and type 2, *Veillonella montpellierensis*, *Eggerthella* spp.

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Clinical Bacteriology

Jeffrey K. Actor PhD, in [Elsevier's Integrated Review Immunology and Microbiology \(Second Edition\)](#), 2012

Veillonella

Veillonella spp. are nonmotile, gram-negative diplococci that are the anaerobic counterpart of Neisseria. *Veillonella* is part of the normal flora of the mouth and gastrointestinal tract and may be found in the vagina as well. Although of limited pathogenicity, *Veillonella* is often mistaken for the more serious gonococcal infection. *Veillonella* spp. are often regarded as contaminants; they are often associated with oral infections; bite wounds; head, neck, and various soft tissue infections; and they have also been implicated as pathogens in infections of the sinuses, lungs, heart, bone, and CNS. Recent reports have also indicated their isolation in pure culture in septic arthritis and meningitis.

Pathology

Pus and Abscess Formation

An accumulation of pus in an enclosed tissue space is known as an *abscess*. Pus, a whitish-yellow substance, is found in regions of bacterial infection including superficial infections such as pimples. Pus consists of macrophages and neutrophils,

bacterial debris, dead and dying cells, and necrotic tissue. Necrosis is caused by released lysosomes, including lipases, carbohydrases, proteases, and nucleases.

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Anaerobic Cocci and Anaerobic Gram-Positive Nonsporulating Bacilli

Eija Könönen, in [Mandell, Douglas, and Bennett's Principles and Practice of Infectious Diseases \(Eighth Edition\)](#), 2015

Members of the Commensal Microbiota

Among gram-negative anaerobic cocci, Veillonella species are common and considered mainly harmless, or even beneficial, colonizers of the mouth from the early years of life onward,³¹ whereas Acidaminococcus and Megasphaera spp. reside in the human intestine and genitourinary tract, respectively.^{21,32,33}

Also, gram-positive anaerobic cocci—GPAC, as they are often called in the current literature—are commonly present as part of the human microbiota, residing in the mouth, intestines, and both the female and male genital tract as well as skin.^{1,34,35} Only limited knowledge, however, exists about their role as commensal organisms, whereas they are frequently connected to various infections at or close to their colonization sites.

Anaerobic gram-positive nonsporulating bacilli belong to the commensal microbiota of the digestive tract, and some members are part of the microbiota of the urogenital tract and skin. Bifidobacteria and Collinsella are important bacteria in the development of the gut microbiota.³⁶ In the elderly, a decrease in the levels of intestinal Bifidobacterium populations is seen with aging.³⁷ Lactobacilli form an important component of the mucosal microbiota of the gastrointestinal tract, the most prevalent species being Lactobacillus rhamnosus, *L. paracasei*, *L. plantarum*, and *L. salivarius*.³⁸ In the female genital tract and the rectum, the predominant lactobacilli are *L. crispatus* and *L. iners*, in particular, and *L. gasseri* and *L. jensenii*.^{32,33,39,40} Hydrogen peroxide production by these species, except for *L. iners*, may help to control the overgrowth of bacterial vaginosis-associated organisms and to protect from obstetric infections during pregnancy.³⁹ Because of their beneficial characteristics, a variety of *Lactobacillus* and *Bifidobacterium* strains are increasingly used as probiotics, aiming to alter the composition of the microbiota.⁴¹

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Metabolism, Central (Intermediary)

M.P. Spector, in [Encyclopedia of Microbiology \(Third Edition\)](#), 2009

Propionic acid-producing fermentations

Members of *Propionibacterium*, *Bacteroides*, *Bifidobacterium*, and *Veillonella*, as well as some species of *Clostridium* and *Corynebacterium*, produce propionate, acetate, and CO₂ as the major end products of glucose, lactate, and glycerol fermentation. In these bacteria, pyruvate is carboxylated to form OAA in a reaction mediated by methylmalonyl-CoA–oxaloacetate transcarboxylase using biotin and coenzyme/vitamin B₁₂ as cofactors. This reaction also yields propionyl-CoA. In the next series of reactions, OAA is first reduced to malate by NADH/H⁺ through the action of malate dehydrogenase. A water molecule is then removed from malate to form fumarate via the action of malate dehydratase/fumarase. Fumarate is then reduced to succinate by FADH₂ in a reaction catalyzed by *fumarate reductase*. Succinate is converted to succinyl-CoA, which is then converted to methylmalonyl-CoA by the coenzyme/vitamin B₁₂-containing methylmalonyl-CoA mutase. The enzyme activity catalyzing the succinate to succinyl-CoA conversion is propionyl-CoA:succinate:CoA transferase. In this reaction, the CoA from propionyl-CoA is transferred to succinate, yielding both succinyl-CoA and propionate (**Figure 9**). These bacteria can also decarboxylate pyruvate to form acetate and CO₂, yielding one ATP and one NADH/H⁺ in the process. Thus, the formation of acetate plus CO₂ from pyruvate allows for the generation of an additional ATP from sugar *catabolism* while the conversion of pyruvate to propionate allows for the regeneration of NAD⁺ helping to maintain O–R balance in the cell.

In addition to forming propionate, acetate, and CO₂ from sugar fermentation, propionic acid bacteria ferment lactate to acetate, CO₂, and propionate. The overall process produces two propionate, one acetate, and one CO₂ from three lactate molecules with the additional yield of one ATP. *Clostridium propionicum*, *Bacteroides ruminicola*, *Peptostreptococcus* species, and others are able to convert lactate to lactyl-CoA and then to acrylyl-CoA by the removal of a water molecule; the latter step is catalyzed by lactyl-CoA dehydratase. Acrylyl-CoA is then reduced by NADH/H⁺ to propionyl-CoA by the enzyme acrylyl-CoA reductase. Propionyl-CoA is then converted to propionate. The fermentation properties of propionic acid bacteria make them important in the manufacture of Swiss cheese with propionate and acetate contributing to the unusual flavor and CO₂ production causing the wholes characteristic of these cheeses.

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The Gastric Microbiome in Benign and Malignant Diseases

Thais Fernanda Bartelli, ... Emmanuel Dias-Neto, in [Microbiome and Metabolome in Diagnosis, Therapy, and other Strategic Applications](#), 2019

General Dysbiosis in Gastric Cancer

Other taxa enriched in gastric cancer patients are Lactococcus, Veillonella, Fusobacterium, and Leptotrichia. Analysis of microbial metabolic output in those patients identified an increase in lactic acid-producing bacteria, enrichment of short-chain fatty acid production pathways, and enrichment of proinflammatory oral bacterial species [31].

Dysbiosis in intestinal metaplasia and gastric cancer subjects has been characterized, as compared to superficial or atrophic gastritis. Additionally, oral bacteria, such as Peptostreptococcus stomatis and Dialister pneumosintes, had significantly higher abundance in gastric cancer as compared to the other stages analyzed, and together with Streptococcus anginosus, Parvimonas micra and Slackia exigua, could differentiate gastric cancer patients from superficial gastritis cases [32].

Whether the gastric mucosal dysbiosis is the causative agent or a consequence of altered mucosal physiology/tumor microenvironment is yet to be fully uncovered. Controlled in vivo experiments, through the introduction of specific known bacteria, will be required to elucidate their role [33]. Nonetheless, gastric cancer has been subdivided into four molecular subtypes by the TCGA (The Cancer Genome Atlas) [34], one of them defined according to the presence of EBV. Future studies might well consider the results of gastric microbiome analysis [33].

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Industrial Biotechnology and Commodity Products

Z. Xu, ... L. Jiang, in [Comprehensive Biotechnology \(Second Edition\)](#), 2011

3.18.3.6.2 Strains

Propionibacteria and several other genera of anaerobic bacteria such as Veillonella, Selenomonas, and Clostridium, especially Clostridium propionicum, produce pro-

propionic acid as a main fermentation product. *Propionibacteria* are Gram-positive, non-spore-forming, nonmotile, anaerobic, and rod-shaped bacteria. Other genera can utilize more limited sugars; for example, *Veillonella parvula* can use lactate, pyruvate, and succinate only [16]. Therefore, *Propionibacterium* species have been most extensively studied and applied for propionic acid production and granted generally recognized as safe (GRAS) status by the United States Food and Drug Administration (FDA).

Propionibacteria have been used in the production of Swiss cheeses, vitamin B₁₂, probiotics, and propionic acid. In Swiss-type cheeses, *Propionibacteria* consume lactate and produce propionic acid, acetic acid, and CO₂. The produced acids, accumulated praline, and metabolites from amino acid catabolism are responsible for development of the cheese flavor. Moreover, the ‘eyes’ or holes in the Swiss cheese body are formed as a result of CO₂ produced from *Propionibacteria*. *Propionibacteria* such as *P. acidipropionici*, *P. shermanii*, *P. freudenreichii*, *P. freudenreichii* subsp. *shermanii*, and *P. freudenreichii* subsp. *freudenreichii* are commonly used for propionic acid production. However, *P. acidipropionici* has been the most used species for industrial propionic acid production.

Propionibacteria are Gram-positive, nonmotile, non-sporulating, short rod-shaped, mesophilic anaerobes. As *Propionibacteria* play an important role in a variety of industrial applications, their nutrient requirements, growth conditions, and properties of their metabolism have been extensively studied [16]. All essential nutrients including carbon, nitrogen, and trace elements for cell growth, product formation, and cellular maintenance are required in the fermentation medium, and Mg²⁺ and Mn²⁺ in the medium have a major role in the conversion efficiency of cell metabolism [17]. In *Propionibacterium arabinosum*, the decarboxylation of succinate, the first half of the last couple of reactions in the propionate formation pathway catalyzed by CoA transferase finally leading to propionic acid formation, is accelerated by the presence of metallic cations such as Mg²⁺ and Mn²⁺ in the medium. The optimal growth conditions are a pH range of 6–7 and a temperature range of 30–32 °C under anaerobic conditions. If the pH is below 4.5, no growth and cell activity were observed [16].

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The Human Microbiome

Jacquelyn S. Meisel, Elizabeth A. Grice, in [Genomic and Precision Medicine \(Third Edition\)](#), 2017

Oral Microbiome

Streptococcus dominates the oral cavity, but other abundant genera include *Veillonella*, *Gamella*, *Rothia*, *Fusobacterium*, and *Neisseria* [31,32]. A recent study that used statistical models to partition human microbiome data into body-site specific community types identified a significant association between gut and oral community types, despite their strong taxonomic differences [33]. One potential explanation for this connection is that oral bacterial populations seed the gut, thereby giving rise to distinct gut community types.

The majority of human oral viruses are bacteriophage, individual-specific, and persist over time [34]. Genome-encoded clustered regularly interspaced short palindromic repeats (CRISPRs) are a form bacterial defense mechanism against mobile genetic elements like bacteriophage and provide a genomic record of phage–bacteria interactions. Streptococcal CRISPR sequences in the oral cavity revealed great diversity within individuals, suggesting that each individual was exposed to unique viral populations [35].

The oral microbiome has been linked to both dental caries (cavities) and periodontitis (gum disease). The complex microbial communities of caries are taxonomically and functionally different from those colonizing healthy oral cavities [36]. In periodontitis, *Porphyromonas gingivalis* is the suspected etiological agent. Small quantities of this bacterium were shown to induce changes in the oral microbiota by exploiting the complement cascade to cause periodontal bone loss [37]. Epidemiological studies have suggested a correlation between periodontitis and atherosclerosis. These two seemingly unrelated diseases may be linked by microbiota, as the types and abundance of bacteria in atherosclerotic plaques correlated with the abundance of those same bacteria in the oral cavity [38]. These studies indicate the potential utility of the microbiome as a clinical biomarker.

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Infections Caused by Anaerobic Microorganisms

Fernando Cobo, in [Reference Module in Biomedical Sciences](#), 2021

Gram-negative anaerobic cocci

From the three described genera of Gram-negative anaerobic cocci, *Veillonella*, *Acidaminococcus* and *Megasphaera*, the first of them is that it has epidemiological rel-

evance. Its clinical meaning is unknown and they are considered microorganisms of low virulence. The most relevant species are *V. parvula*, *V. atypica* and *V. dispar*, which are part of the microbiota of the oral cavity and the intestinal and genitourinary tract. They are mainly isolated within polymicrobial infections, although in some circumstances such as malignancies may cause bacteremia (Cobo et al., 2020a, b).

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INFECTIONS WITH SPECIFIC MICROORGANISMS

Steven C. Buckingham, in [Feigin and Cherry's Textbook of Pediatric Infectious Diseases \(Sixth Edition\)](#), 2009

GRAM-NEGATIVE COCCI

The three genera of anaerobic gram-negative cocci, *Acidaminococcus*, *Megasphaera*, and *Veillonella*, are normal fecal flora that rarely cause disease in humans. *Veillonella* spp. also are part of the normal oral flora. In children, *Veillonella* spp. occasionally have been associated with abscesses, aspiration pneumonia, and chronic sinusitis.³⁶

With the exception of a single described isolate of β -lactamase-producing *Acidaminococcus fermentans*, strains of *Acidaminococcus* and *Megasphaera* are susceptible to penicillin and to cephalosporins.⁶⁷ Although *Veillonella* spp. do not produce β -lactamase, they commonly are resistant to penicillin, perhaps because of alterations in penicillin-binding proteins.⁹⁴ *Veillonella* spp. nonetheless remain susceptible to ampicillin, amoxicillin-clavulanate, cefoxitin, and third-generation cephalosporins.^{101,104}

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The Esophageal Microbiome

Prapti Shrestha BMedSc(Hons), ... Guy D. Eslick DrPH, PhD, FACE, FFPH, in [Gastrointestinal Diseases and their Associated Infections](#), 2019

Infective Esophagitis

The normal flora of the healthy esophagus typically contains species of Streptococcus, Neisseria, Veillonella, Fusobacterium, Bacteroides, Lactobacillus, Staphylococcus, Prevotella, Enterobacteriaceae, and yeasts.¹ Infectious esophagitis is rare in

those who are not immunocompromised, although some cases of infection with herpes simplex and *Candida albicans* occur on occasion. In the immunosuppressed, often for organ transplantation, chronic inflammatory diseases, or chemotherapy, as well as sufferers of acquired immune deficiency syndrome (AIDS), infective esophagitis becomes more common.² It may be caused by cytomegalovirus, herpesvirus, *Candida* species, and others. The typical symptoms of infectious esophagitis are odynophagia, dysphagia, and bleeding. Choice of treatment depends on the particular pathogen implicated.

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Oral Bacteria Transmissible by Saliva and Kissing

Jacobo Limeres Posse, ... Crispian Scully, in [Saliva Protection and Transmissible Diseases](#), 2017

2.2 The Adult Salivary Microbiome

By adulthood, Actinomyces, Fusobacterium, Haemophilus, Neisseria, Oribacterium, Rothia, Treponema, and Veillonella, predominate, along with Firmicutes, Proteobacteria, Actinobacteria, and other Fusobacteria.¹² The oral microbiome of systemically healthy adults may include Actinomyces, Capnocytophaga, Escherichia, Gemella, Granulicatella, Haemophilus, Neisseria, Oribacterium, Peptostreptococcus, Prevotella, Streptococcus, Veillonella—and nonculturable bacteria.¹³ Human Oral Microbe Identification Microarray assays show that Streptococcus and Veillonella are the most predominant genera identified, and that age, gender, diet, alcohol consumption, and body mass index have minimal effect on the bacterial profile, but smoking and socioeconomic status can affect the flora.¹⁴ Various cocci, mycobacteria, and treponemes may also be found in saliva, in quantities possibly sufficient to infect other individuals.¹⁵

The salivary microbiome thus becomes complex and composed of bacteria from different oral surfaces.¹⁶ Cariogenic and periodontopathogenic bacterial flora habitually colonize the human mouth and this literature is well reviewed elsewhere.¹⁷

There is little or no variation in microbial profiles over time¹⁸ and similarity between siblings seems to be retained,¹⁹ but oral hygiene affects the bacterial diversity in saliva,¹³ as does oral disease.²⁰

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