Links for the references mentioned in the text (many of which occur multiple times):

Diaz et al. 2006

https://doi.org/10.1128/AEM.72.4.2837-2848.2006

Dige et al. 2009

https://doi.org/10.1099/mic.0.027706-0

Eisenberg et al. 2020

doi: 10.1099/ijsem.0.004024

Eren et al. 2014

https://www.pnas.org/content/111/28/E2875

Friskopp & Hammarström 1980

doi: 10.1902/jop.1980.51.10.553

García López and Martín-Galiano 2020

https://www.frontiersin.org/articles/10.3389/fmicb.2020.00524/full

Hezel and Weitzberg 2013

https://doi.org/10.1111/odi.12157

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https://www.nature.com/articles/nrmicro2381

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Mark Welch et al. 2020

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Nouioui et al. 2018

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Periasamy & Kolenbrander 2010

https://doi.org/10.1146/annurev-micro-090817-062503

Rosier et al. 2020

https://doi.org/10.1038/s41598-020-69931-x

Segata et al. 2012

https://doi.org/10.1186/gb-2012-13-6-r42

Socransky et al. 1998

https://onlinelibrary.wiley.com/doi/10.1111/j.1600-051X.1998.tb02419.x

van Dijk et al. 1998

https://doi.org/10.1007/s002239900443

Wilbert et al. 2020

https://doi.org/10.1016/j.celrep.2020.02.097

*Streptococcus*

**Overview:** Streptococci are among the most abundant bacteria in the mouth, making up 30-60% of the bacteria on the buccal mucosa and 15-30% of the bacteria on the tongue dorsum and in supragingival plaque.

**Ecological role/importance in health and disease:** The 37 species of *Streptococcus* listed in HOMD include many members of the healthy commensal microbiota as well as several that are pathogens and one that is used to produce yogurt (*S. thermophilus*).Streptococci such as*S. mitis* and *S. gordonii* are among the first bacteria to colonize the tooth surface after it is cleaned, where they begin the process of ecological succession (Diaz et al. 2006). *S. salivarius* is abundant on the tongue dorsum and can carry out nitrate reduction to nitrite, thereby participating in the physiology of its human host (Hezel and Weitzberg 2013). Other streptococci that are usually rare in the healthy mouth can cause disease, such as *S. mutans,* which is associated with dental caries, *S. pyogenes*, which causes strep throat, and *S. pneumoniae*, which can cause pneumonia. In the subgingival plaque biofilm, most streptococci are grouped into the “yellow complex,” but *S. constellatus* is a member of the “orange complex” marking part of the ecological succession from health toward periodontitis (Socransky et al. 1998).

*Neisseria*

**Overview:** Bacteria of the genus *Neisseria* are abundant in the mouth, making up 2-10% of the bacteria at most oral sites.

**Ecological role/importance in health and disease:** Several of the 20 species of *Neisseria* in HOMD are common members of the normal oral microflora. For example, *N. flavescens*, *N. perflava*, and *N. subflava* are abundant on the tongue dorsum and *N. elongata*, *N. mucosa*, and *N. oralis* in dental plaque. Other species, such as *N. meningitidis* and *N. gonorrhoeae*, are human pathogens included in HOMD as reference sequences even though they are not generally detected in the mouth.

*Rothia*

**Overview:** Bacteria of the genus *Rothia* are abundant in the healthy oral microbiome, making up 3-10% of the bacteria in dental plaque and 1-5% of the bacteria at sites such as the tongue dorsum and buccal mucosa.

**Ecological role/importance in health and disease:** Three species of genus *Rothia* are abundant in the oral cavity: *R. aeria, R. dentocariosa*, and *R. mucilaginosa*. *R. aeria* and *R. dentocariosa* are found predominantly in dental plaque. *R. mucilaginosa* is abundant on the tongue, where it forms large patches (Wilbert et al. 2020). All three species are capable of nitrate reduction to nitrite and therefore may participate in human nitric oxide homeostasis (Hezel and Weitzberg 2015, Rosier et al. 2020). They can also act as opportunistic pathogens.

*Veillonella*

**Overview**: Bacteria of the genus *Veillonella* are among the most abundant bacteria in the healthy mouth. They make up approximately 10% of the bacterial community on the tongue, tonsils, and throat and 2-4% in dental plaque and on the cheeks and gums.

**Ecological role/importance in health and disease:** Veillonella spp. consume lactate and thrive adjacent to lactate-producing streptococci (Perisamy & Kolenbrander 2010). Veillonellae such as *Veillonella parvula* are early colonizers of teeth; they cannot grow by themselves on saliva but they are abundant in the biofilm that forms during the first 4 hours on enamel in the mouth (Diaz et al. 2006, Periasamy and Kolenbrander 2010). Other species – *V. dispar*, *V. rogosae*, and *V. atypica* – are members of the tongue dorsum biofilm (Wilbert et al. 2020, Mark Welch et al. 2019). The as-yet unnamed *Veillonella* sp. HMT 780 is abundant on the gums. *V. parvula* is a member of the “purple complex” in the subgingival biofilm together with *Schaalia odontolytica* (Socransky et al. 1998).

*Actinomyces*

**Overview:** Bacteria of the genus *Actinomyces* are abundant in the healthy oral microbiome, making up 5-10% of the cells in dental plaque. In 2018 some species formerly considered to be *Actinomyces* were reclassified into genus *Schaalia*, including several species abundant on the tongue (Nouioui et al. 2018). Twelve oral species remain in the genus *Actinomyces* include *A. naeslundii*, *A. oris*, and *A. graevenitzii*.

**Ecological role/importance in health and disease:** *A. naeslundii* and its relatives are early colonizers in the dental plaque biofilm (Diaz et al. 2006, Dige et al. 2009). *A. graevenitzii* is abundant in the biofilm on the tongue. Some species, particularly *A. israelii* and *A. gerencseriae*, are in lower abundance in the healthy microbiome but can cause opportunistic infections known as actinomycosis.

*Schaalia*

**Overview:** Bacteria of the genus *Schaalia* are abundant in the healthy mouth, particularly on the tongue dorsum, tonsils, and throat where they make up 3 to 6% of the oral microbial community. They were formerly considered to be in genus *Actinomyces* and were reclassified into genus *Schaalia*in 2018 (Nouioui et al. 2018).

**Ecological role/importance in health and disease:** There are 9 species of *Schaalia* in the mouth, including 5 named species (*S. cardiffensis*, *S. georgiae*, *S. lingnae* [Not Validly Published], *S. meyeri*, and *S. odontolytica*, as well as 4 taxa that are currently unnamed (*Schaalia* *spp.* HMT 172, 178, 180, and 877). Most of the *Schaalia* spp. detected in the healthy mouth in Human Microbiome Project data are members of the unnamed taxa *S. sp.* HMT 172 and *S. sp.* HMT 180 (Eren et al. 2014). *S. odontolytica* (formerly *A. odontolyticus*) is a member of the “purple complex” in subgingival plaque together with *Veillonella parvula* (Socransky et al. 1998).

*Prevotella*

**Overview:** The genus *Prevotella* is species-rich, with 51 species recognized in HOMD. Some of these species are found primarily in dental plaque and buccal mucosa, others primarily on the tongue, tonsils, hard palate, and throat.

**Ecological role/importance in health and disease:** As they are anaerobic, dental plaque *Prevotella* are more abundant in subgingival than supragingival plaque; major species include *P. oris* and *P. nigrescens*. On the tongue dorsum, *P. melaninogenica* has both high prevalence and high abundance, and an additional 5 or more *Prevotella* species also have >70% prevalence, making the tongue dorsum *Prevotella* community both abundant and complex. Two species, *P. intermedia* and *P. nigrescens*, are considered part of the “orange complex” in subgingival plaque marking part of the ecological succession from health toward periodontitis (Socransky et al. 1998).

*Capnocytophaga*

**Overview:** *Capnocytophaga* are abundant in dental plaque, making up 10% of the community in supra- and sub-gingival dental plaque sampled from healthy people (Eren et al. 2014). They make up 1-2% of the community on tonsils and throat, and lower amounts at other oral sites. There are 22 species of *Capnocytophaga* in the human oral microbiome, many of which have not yet been formally named.

**Ecological role/importance in health and disease:** *Capnocytophaga* are capnophilic, requiring high concentrations of carbon dioxide for growth; they therefore are often located adjacent to other bacteria such as *Streptococcus* spp. that produce CO2. The most abundant *Capnocytophaga* in dental plaque are *C. gingivalis/C. granulosa*, *C. leadbetteri*, and *C. sputigena*, each of which has >2% mean abundance and >85% prevalence in both supra- and sub-gingival plaque (Eren et al. 2014). Other, currently unnamed taxa can be sporadically abundant but with lower prevalence. In the subgingival plaque microbiome, *C. gingivalis*, *C. ochracea*, and *C. spuigena* formed part of the “green complex” together with *Eikenella corrodens*, *Campylobacter concisus*, and *Aggregatibacter actinomycetemcomitans* (Socransky et al. 1998).

*Gemella*

**Overview:** There are five species of *Gemella* in the human oral microbiome: *G. bergeri*, *G. haemolysans*, *G. morbillorum*, *G. sanguinis*, and G. sp. HMT 928.

**Ecological role/importance in health and disease:** *Gemella* species reach their highest relative abundance on the buccal mucosa and keratinized gingiva, where *G. haemolysan*s makes up 5-8% of the community. *G. sanguinis* makes up about 1% of the tongue dorsum microbiota and *G. haemolysans* and *G. morbillorum* together make up 0.5-1% of dental plaque in healthy individuals. *Gemella* species can be opportunistic pathogens; *G. morbillorum* and, less frequently, *G. haemolysans* are detected in endocarditis and other opportunistic infections (García López and Martín-Galiano 2020).

*Porphyromonas*

**Overview:** The genus *Porphyromonas* is abundant in the healthy mouth, making up between 2% and 5% of the community at each site within the mouth (Segata et al. 2012).

**Ecological role/importance in health and disease:** Among the 12 oral species, *P. pasteri* has the broadest distribution, making up 1-4% of the total community at each oral site (Eren et al. 2014). The unnamed *Porphyromonas* sp. HMT 930 dominates on the keratinized gingiva and is also abundant on the buccal mucosa. The widely studied taxa *P. gingivalis* and *P. endodontalis* are detected with low abundance in subgingival plaque in healthy individuals but become more prominent in periodontitis. *P. gingivalis*, together with *Treponema denticola* and *Tannerella forsythia*, is part of the “red complex” of subgingival taxa associated with periodontitis (Socransky et al. 1998).

*Corynebacterium*

**Overview:** Oral members of genus *Corynebacterium* (*C. matruchotii* and *C. durum*) are prominent in dental plaque, where they make up 5 to 9% of the community; they are a minor component (<0.5%) of the community at other sites in the healthy mouth. Other corynebacteria are abundant in the skin microbiome and are included in eHOMD for their potential importance in the nasal microbiome.

**Ecological role/importance in health and disease:** *C. matruchotii* is not among the earliest colonizers of the tooth surface but enters the dental plaque biofilm after about 24 hours of biofilm growth and maturation (Mark Welch et al. 2016). The membranes of *C. matruchotii* nucleate the precipitation of calcium from saliva (van Dijk et al. 1998), which may contribute to the observation that dental plaque that is rich in filaments forms calculus more readily than does plaque rich in cocci (Friskopp & Hammarström 1980). *Corynebacterium* spp. are the foundational taxa in hedgehog structures (Mark Welch et al. 2016), creating a spatial structure inhabited by other members of the plaque biofilm. Corynebacteria are occasionally reported as opportunistic pathogens in immunocompromised individuals.

*Haemophilus*

**Overview:** Bacteria of the genus *Haemophilus* are abundant in the mouth, making up several percent of the bacteria at most oral sites (Segata et al. 2012, Eren et al. 2014). Members of the genera *Haemophilus* and *Aggregatibacter* are closely related and not always cleanly distinguished using short fragments of the 16S ribosomal RNA gene.

**Ecological role/importance in health and disease:** Of the twelve species recognized in HOMD, one, *H. parainfluenzae*, is by far the most abundant at most sites within the mouth. Several others, including *H. haemolyticus* and an unnamed H. sp. HMT 036, are primarily detected on the keratinized gingiva. The opportunistic pathogen *H. influenzae* is detected with low prevalence in healthy individuals. Other pathogens such as *H. aegyptius* and *H. ducreyi* are included in HOMD as reference strains although they are not generally detected in the healthy oral microbiome. The taxon “*Terrahaemophilus aromaticivorans*”, formerly included in HOMD, is now considered a synonym for *H. parainfluenzae*.

*Aggregatibacter*

**Overview:** Bacteria of genus *Aggregatibacter* are moderately abundant in the mouth, making up 2% or less at most oral sites except for the tongue dorsum where they are in very low abundance. Members of the genera *Haemophilus* and *Aggregatibacter* are closely related and not always cleanly distinguished using short fragments of the 16S ribosomal RNA gene.

**Ecological role/importance in health and disease:** The *Aggregatibacter* species most abundant in the healthy mouth are *A. aphrophilus*, *A. paraphrophilus*, *A. segnis*, and the unnamed A. sp. HMT 458. The species *A. actinomycetemcomitans* is associated with periodontitis, including aggressive periodontitis, and was part of the “green complex” of Socransky et al. (1998).

*Fusobacterium*

**Overview:** Bacteria of genus *Fusobacterium* are abundant in the mouth, particularly in subgingival plaque, where they make up approximately 10% of the community, as well as in supragingival plaque and in samples from the palatine tonsils, tongue dorsum, throat, and saliva. Three subspecies of *F. nucleatum*, subspecies *animalis*, *polymorphum*, and *vincentii,* are abundant in dental plaque and the palatine tonsils, while *F. periodonticum* is abundant in samples from the tongue dorsum and from the tonsils, throat, and saliva.

**Ecological role/importance in health and disease:**

In the dental plaque model of Kolenbrander and colleagues, *F. nucleatum* is considered the taxon that forms a bridge between early colonizers and later-colonizing periodontal pathogens (Kolenbrander & London 1993, Kolenbrander et al. 2010), although imaging-based evidence for its role as a physical bridge is lacking (Mark Welch et al. 2020). *F. periodonticum* and several subspecies of *F. nucleatum* (*F. nucleatum* subspecies *nucleatum*, *polymorphum*, and *vincentii*) are considered part of the “orange complex” in subgingival plaque marking part of the ecological succession from health toward periodontitis (Socransky et al. 1998).

*Leptotrichia*

**Overview:** Bacteria of genus *Leptotrichia* are abundant in the healthy mouth, making up 3% or more of the bacteria in dental plaque and on the tongue, tonsils, and throat. Many of the species recognized in HOMD are as yet unnamed. The unnamed taxa L. sp. HMT 215 is abundant on the tongue dorsum whereas *L. buccalis*, *L. hongkongensis*, and the unnamed L. spp. HMT 212 and 392 are abundant in dental plaque. Some species, including HMT 221 which is abundant on the tongue dorsum, were reclassified into the genus *Pseudoleptotrichia* in 2020 (Eisenberg et al. 2020).

**Ecological role/importance in health and disease:** *Leptotrichia* spp. are anaerobic or microaerophilic. In the “hedgehog” structure of dental plaque, together with *Fusobacterium* spp. they occupy a presumably anoxic zone in the interior of the structure (Mark Welch et al. 2016). *Leptotrichia* spp. may also cause opportunistic infections.

*Pseudoleptotrichia*

**Overview:** Bacteria of genus *Pseudoleptotrichia* are abundant in the healthy mouth, making up about 1% of the bacteria on the tongue, tonsils, and throat. The genus was split from *Leptotrichia* in 2020 (Eisenberg et al. 2020) and contains one named species, *P. goodfellowii*, and two unnamed taxa, HMT 219 and 221. Of these three taxa, HMT 221 is the most abundant in the mouth.

*Campylobacter*

**Overview:** Bacteria of genus *Campylobacter* make up approximately 1 to 3% of the microbiota at most sites within the mouth. There are seven named and one unnamed species recognized in the HOMD.

**Ecological role/importance in health and disease:** Unlike many members of the oral microbiome, *Campylobacter* species are motile by means of flagella. *C. gracilis* is detected primarily in dental plaque, while *C. concisus* and *C. rectus* are more broadly distributed in the mouth. Three species, *C. gracilis*, *C. rectus,* and *C. showae*, are considered part of the “orange complex” in subgingival plaque marking part of the ecological succession from health toward periodontitis (Socransky et al. 1998). Some species of *Campylobacter* cause infections known as campylobacterosis, but these species are not members of the oral microbiome.

*Tannerella*

**Overview:** Members of the genus *Tannerella* are moderately abundant in the oral microbiome, making up less than 0.5% on average of the microbiome at any oral site. They are close relatives of the genus *Porphyromonas* and are classified with them into the family Porphyromonadaceae.

**Ecological role/importance in health and disease:** *Tannerella* spp. are found primarily in sub- and supragingival dental plaque and in samples from the tonsils and throat. *Tannerella forsythia* (formerly *T. forsythensis*), together with *Porphyromonas gingivalis* and *Treponema denticola*, is part of the “red complex” of subgingival taxa associated with periodontitis (Socransky et al. 1998). The other members of genus *Tannerella* in HOMD have not yet been named.

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For the following provisionally named genera, could you construct text in the following form?

[Name of genus] is a provisionally named genus constructed to provide a stably named reference for a currently unnamed taxon represented by a set of 16S rRNA clones. It contains [x] species, [list them here].

For example

Bacteroidaceae [G-1] is a provisionally named genus constructed to provide a stably named reference for a currently unnamed taxon represented by a set of 16S rRNA clones. It contains one species, Bacteroidaceae [G-1] bacterium HMT 272.

Absconditabacteria (SR1) [G-1]

Anaerolineae [G-1]

Bacteroidales [G-2]

Bacteroidetes [G-3]

Bacteroidetes [G-4]

Bacteroidetes [G-5]

Bacteroidetes [G-7]

Clostridiales [F-1][G-1]

Clostridiales [F-1][G-2]

Clostridiales [F-3][G-1]

Erysipelotrichaceae [G-1]

Gracilibacteria (GN02) [G-1]

Gracilibacteria (GN02) [G-2]

Gracilibacteria (GN02) [G-3]

Gracilibacteria (GN02) [G-4]

Lachnospiraceae [G-10]

Lachnospiraceae [G-2]

Lachnospiraceae [G-3]

Lachnospiraceae [G-7]

Lachnospiraceae [G-8]

Lachnospiraceae [G-9]

Mollicutes [G-1]

Mollicutes [G-2]

Neisseriaceae [G-1]

Peptoniphilaceae [G-1]

Peptoniphilaceae [G-2]

Peptoniphilaceae [G-3]

Peptostreptococcaceae [G-1]

Peptostreptococcaceae [G-2]

Peptostreptococcaceae [G-3]

Peptostreptococcaceae [G-4]

Peptostreptococcaceae [G-5]

Peptostreptococcaceae [G-6]

Peptostreptococcaceae [G-7]

Peptostreptococcaceae [G-8]

Peptostreptococcaceae [G-9]

Propionibacteriaceae [G-1]

Propionibacteriaceae [G-2]

Ruminococcaceae [G-1]

Ruminococcaceae [G-2]

Ruminococcaceae [G-3]

Saccharibacteria (TM7) [G-1]

Saccharibacteria (TM7) [G-2]

Saccharibacteria (TM7) [G-3]

Saccharibacteria (TM7) [G-4]

Saccharibacteria (TM7) [G-5]

Saccharibacteria (TM7) [G-6]

Saccharibacteria (TM7) [G-7]

Saccharibacteria (TM7) [G-8]

Syntrophomonadaceae\_[VIII][G-1]

Veillonellaceae [G-1]