

Anaerobe 11 (2005) 131-136



www.elsevier.com/locate/anaerobe

### Oral & dental bacteriology & infection—Mini review

## Anaerobes in the upper respiratory tract in infancy

Eija Könönen\*

Department of Microbiology, Anaerobe Reference Laboratory, National Public Health Institute (KTL), Mannerheimintie 166, Fin-00300 Helsinki, Finland

> Received 27 October 2004; accepted 20 November 2004 Available online 26 January 2005

#### Abstract

Development of the indigenous microbiota begins on the surfaces of the human body after birth when infants are exposed to continuous person-to-person and environmental contacts with microbes. Anaerobes constitute a significant part of indigenous bacterial communities at different body sites. Pioneering anaerobic commensals are able to colonize and survive in the oral cavity during the first months of life. After teeth emerge, more attachment sites and potential niches are available for anaerobic bacterial colonization. Specific partner relationships influence the composition and stability of forming multigeneric communities, biofilms, where *Fusobacterium nucleatum* is of specific interest. In infancy, the oral colonization seems to be rather stable at species level, though not at clonal level. The colonization pattern in the nasopharynx is different from that in the oral cavity; anaerobes are absent from healthy nasopharynges but transiently colonize this anatomical site during infection. The most plausible origin for nasopharyngeal anaerobes is the oral cavity and, conceivably, saliva is the most likely transmission vehicle. Whether anaerobic bacteria colonize the nasopharynx just because of ecological changes favoring their growth or whether they could play an active role in the pathogenesis of respiratory infections is not known.

© 2005 Elsevier Ltd. All rights reserved.

Keywords: Anaerobic bacteria; Mouth; Saliva; Nasopharynx; Otitis media

## 1. Background

A newborn is exposed to continuous flow of microbes via other individuals, animals, and the local environment. During the first days of life, the colonization of the host surfaces by various bacteria starts and, gradually, part of them form the indigenous microbiota, which constitutes an integral component of the function of each body site. Distinct habitats harbor different microbial compositions; the microbiota of the mouth is different from that in the lower part of the gastro-intestinal tract. The initial colonization is influenced both by innate and environmental factors which explain the individual composition of the indigenous microbiota at each site. In the oral cavity, the age-related pattern of bacterial colonization is, at least partly, connected with

the development of the primary dentition: first teeth erupt around 6 months of age and the complete dentition is reached around the age of 3 years. Not only interactions between bacteria and their host but also those between different bacteria residing in the same microenvironment influence the composition of the microbiota (or the development of pathologic conditions). Commensal bacteria, i.e. members of the indigenous microbiota, are regarded beneficial to the host by defending against the colonization of invading pathogens; however, some clones may contain characteristics potentially detrimental for the health status of an individual.

The present review deals mainly with data based on culture; most of it originates from a prospective, longitudinal study (a satellite of the Finnish Otitis Media cohort study), where, at baseline, 50 healthy infants were followed from 2 months to 2 years of age on purpose to examine the development of the

<sup>\*</sup>Tel.: +358 9 4744 8242; fax: +358 9 4744 8238. *E-mail address:* eija.kononen@ktl.fi (E. Könönen).

indigenous microbiota in the upper respiratory tract. Saliva and nasopharyngeal swab samples were collected during scheduled routine visits at 2, 6, 12, 18, and 24 months of age. In addition, nasopharyngeal aspirates were collected in a study clinic where otorhinolaryngologic status with pneumatic otoscopy and tympanometry was performed for confirming the diagnosis during suspected acute otitis media (AOM) episodes [1]. A special emphasis was put on adequate sampling, transport, and culture techniques of detecting anaerobic organisms.

#### 2. Establishment of the oral anaerobic microbiota

Adhesion is the initial event in the bacterial colonization, each species having a selective attachment to different oral surfaces [2]. Pioneering anaerobic commensals are able to colonize and survive in the oral cavity during the first months of life [3–5], when only epithelial surfaces with distinct characteristics (smooth buccal and palatal mucosae, rough surfaces of the dorsal tongue) are available. After teeth emerge around the age of 6 months, non-shedding tooth surfaces above and below gingival margin as well as subgingival epithelium become available as new attachment sites for oral bacteria. Gingival crevice forms an especially favorable site for anaerobic bacterial colonization.

Acquisition depends on the supply of suitable bacteria from the surroundings and the successful colonization on the presence of a suitable surface and also a suitable ecosystem. Different periods amenable for the establishment of individual bacterial species in the oral cavity are, most probably, due to specific partner relationships, which determine their succession order. These interbacterial relationships influence the composition and stability of forming oral multi-species communities, biofilms, where Fusobacterium nucleatum is of specific interest as a key species for attachment and survival of more fastidious anaerobes [6,7]. Various microenvironments with different physicochemical properties, among them oxygen tension, are developed within biofilms for residing bacteria [8]. Growth of fastidious anaerobes even in edentulous mouths can be explained by biofilm formation.

As mentioned, there is an age-related succession order of species in anaerobic bacterial colonization of the oral cavity (Table 1), and once established, individual species tend to remain as members of the oral microbiota [5,9–11]. The first species residing the mouth belong to facultative *Streptococcus* and *Actinomyces*, and strictly anaerobic *Veillonella* genera [3–5,10–12]. Besides *Veillonella*, other early-colonizing strict anaerobes, the *Prevotella melaninogenica* group (includes *P. denticola*, *P. loescheii*, and *P. melaninogenica*), *F. nucleatum*, nonpigmented *Prevotella* spp., and *Porphyromonas catoniae* appear in the mouth before tooth eruption, and, from

Table 1 Culture-based isolation frequency (%) of oral anaerobic/microaerophilic bacteria during early childhood (data combined from three studies by Könönen et al. [5,9,13])

|                                 | Age and dental status   |             |         |              |                   |
|---------------------------------|-------------------------|-------------|---------|--------------|-------------------|
|                                 | At 2 months  Predentate | At 6 months |         | At 12 months | Around 3 years    |
|                                 |                         | Predentate  | Dentate | Dentate      | Primary dentition |
| Gram-negative taxa:             |                         |             |         |              |                   |
| Veillonella spp.                | 68                      | 73          | 77      | 80           | 48                |
| Prevotella melaninogenica group | 18                      | 62          | 57      | 75           | 100               |
| Fusobacterium nucleatum         | 9                       | 50          | 61      | 91           | 100               |
| Non-pigmented Prevotella spp.   | 5                       | 37          | 32      | 80           | 96                |
| Porphyromonas catoniae          | 2                       | 49          | 88      | 70           | 100               |
| Leptotrichia spp.               | 2                       | 8           | 25      | 18           | 61                |
| Corroding rods                  | 5                       | 0           | 6       | 34           | 35                |
| Capnocytophaga spp.             | 0                       | 8           | 0       | 20           | 91                |
| Other fusobacteria              | 0                       | 0           | 0       | 11           | 43                |
| Prevotella intermedia group     | 0                       | 0           | 0       | 5            | 52                |
| Selenomonas spp.                | 0                       | 0           | 0       | 2            | 30                |
| Gram-positive taxa:             |                         |             |         |              |                   |
| Actinomyces spp.                | 32                      | 77          | 83      | 91           | NA                |
| Clostridium spp.                | 0                       | 0           | 0       | 9            | NA                |
| Lactobacillus spp.              | 5                       | 0           | 0       | 2            | NA                |
| 'Eubacterium' spp.              | 2                       | 0           | 0       | 2            | NA                |
| 'Peptostreptococci'             | 0                       | 4           | 0       | 0            | NA                |

NA = not available.

#### Download English Version:

# https://daneshyari.com/en/article/9275054

Download Persian Version:

https://daneshyari.com/article/9275054

<u>Daneshyari.com</u>