Changes of Oral Pathogens in Children with Respiratory Disease

Takafumi Ooka

Abstract

Respiratory disease occurs frequently in children. The nasal cavity, trachea, and oral cavity are considered the primary routes of infection. We aimed to investigate the types of microbial pathogens present in the oral cavities of children with respiratory disease. In addition, we compared the detection rates of different pathogens between the oral cavity and the nasopharynx according to Hellman dental age.

We included 32 children who were hospitalized for respiratory disease and classified them according to Hellman dental age. Specimens were collected using 2 palate swabs: one taken at hospital admission and the other at discharge. The culture results of the samples were compared with those of nasopharyngeal cultures.

The following 6 bacterial strains were detected in both the palate and nasopharynx: α-Streptococcus, Corynebacterium, Haemophilus influenzae, Haemophilus parainfluenzae, MRSA, and Neisseria.

In the comparison of the detection rates, Neisseria were significantly more frequently detected in the palate. MRSA was detected at a significantly higher rate in the nasopharynx. When the detection rates of different bacteria were compared according to Hellman dental age, significant differences were observed in the detection rates of α-Streptococcus in stage IA and Neisseria in stages IC and IIA.

We noted that the bacterial load of specific bacteria in the palate increased with Hellman dental age.

Keywords: Respiratory disease; Oral pathogens; Nasopharynx; pathogen; Dental age; Childhood

Description

The objective of oral hygiene management is to not only improve oral cleanliness, but also reduce the number of microorganisms in the oral cavity and pharynx to prevent respiratory infection. It has been reported that oral hygiene management decreases the number of microorganisms in these regions, and high-concentration chlorhexidine gluconate reduces the number [1]. For childhood, mortality due to pneumonia and acute bronchitis has decreased over time in Japan. In 1950, the childhood mortality rates for pneumonia and acute bronchitis were 17.0% and 5.0%, respectively, whereas in 1990, these rates had declined to 2.4% and 0.2%, respectively. The childhood mortality rate for pneumonia had further declined to 1.6%, and that for acute bronchitis had remained at 0.2% in 2011 [1]. However, despite the large overall decline in mortality due to respiratory diseases, they continue to occur relatively frequently in children [2]. Respiratory infections are particularly common in neonates and infants who have little immunity. In such cases, the nasal cavity and the trachea are considered as the primary routes of infection. Bacteria that colonize the nasopharynx are known to have similar characteristics as pathogens that cause respiratory tract infections [3]. Japanese healthcare guidelines therefore stipulate the identification of pathogenic bacteria through sputum or nasopharyngeal cultures and the administration of effective antibacterial agents [4]. However, although the oral cavity is also considered as an important route of infection for respiratory infections, few currently published studies have been conducted to compare the microbial pathogens present in the oral and nasal cavities.

The oral cavity is the entrance to the respiratory tract and is thus considered a route of entry for respiratory disease virulence factors. A relationship between oral bacteria and respiratory disease has also been suggested, of which ventilator-associated pneumonia is considered a typical example [5]. Colonization of the oral cavity by microbial pathogens has been reported to cause disease onset; studies have also reported the influx of oral secretion below the glottis through the outer surface of the tracheal intubation tube and similar observations [6].

Recently, we carried out the study to assess oral care methods in children with respiratory disease by examining the relationship between nasopharyngeal bacterial flora and the types and numbers of oral microbial pathogens in children with respiratory disease [7].

The subjects were thirty-two children (22 boys and 10 girls; hereinafter referred to as “respiratory disease group”) who were admitted to the pediatric ward of Showa University Hospital for respiratory disease between July and November 2013 were recruited to the study. The age of the children in the respiratory disease group ranged from 1 month to 6 years 1 month, with a mean age of 1 year 10 months. The respiratory disease group was classified according to
Hellman dental age as follows: Hellman stage IA (pre-dental period), 8 children (mean age, 3 months); Hellman stage IC (primary tooth eruption), 16 children (1 year 6 months); and Hellman stage IIA (completion of primary dentition), 8 children (4 years 3 months). The control group was classified according to Hellman dental stage as follows: Hellman stage IA, 8 children (mean age, 3 months); Hellman stage IC, 16 children (1 year 6 months); and Hellman stage IIA, 8 children (4 years 3 months). The respiratory diseases under investigation were pneumonia, bronchial asthma, bronchiolitis, bronchitis, respiratory syncytial virus infection with respiratory symptoms, and asthmas. Children with congenital diseases or underlying diseases were excluded from the study. The duration of hospitalization ranged from 3 to 14 days, with a mean of 6.8 days.

Specimens were collected using a sterile cotton swab. The subjects’ deep palates were scraped with a dedicated sterile swab under fixed pressure for approximately 10 seconds; these were then used as specimens [25,26]. From these specimens, species of Staphylococcus, Streptococcus, and Enterococcus were classified as gram-positive cocci. Neisseria species were classified as gram-negative cocci. Intestinal bacteria, fungi non-fermented, Vibrio species, and Haemophilus species were classified as gram-negative bacilli. Corynebacterium species were classified as gram-positive bacilli. Then, after the classification, colonies were identified for each species. Specimens in which a colony was detected during that period were considered as positive, whereas specimens in which no colony was detected during the period were considered as negative. These species were chosen as objectives because the detection rate was relatively high and had a relation with respiratory diseases.

Specimens were collected twice, that is, once at hospital admission (within 24 hours after admission) and once at discharge (within 24 hours before discharge). The results obtained from these specimens were also compared with the results (obtained from medical records) of bacterial cultures of specimens taken from the posterior wall of the nasopharynx that were performed by a pediatrician during the same period.

As a result, a total of 25 bacterial strains were isolated from the palates of the respiratory disease and control groups, respectively. A total of 14 bacterial strains were isolated from the nasopharynges of the respiratory disease group, of which 6 strains were detected in both the palate and nasopharynx.

In the palates of the respiratory disease group, the most frequently detected bacteria were α-Streptococcus spp., which were detected in all the subjects (100%). The second most frequently isolated bacteria were Neisseria spp. (75%), followed by γ-Streptococcus spp. (53%). In the palates of the control group, the most frequently detected bacteria were α-streptococcus species (100%), followed by γ-Streptococcus (69%) and Neisseria spp. (59%). In the respiratory disease group, the most frequently detected bacterial strain in the nasopharynx was Streptococcus pneumoniae (56%), followed by Moraxella catarrhalis (47%) and Corynebacterium spp. (44%). The 6 bacterial species detected in both the palate and nasopharynx were α-Streptococcus, Corynebacterium, Haemophilus influenzae, Haemophilus parainfluenzae, MRSA, and Neisseria spp. For the 6 bacterial species, subjects were classified according to Hellman dental age to compare the following: (1) detection rates in the palates of the respiratory disease group at admission and discharge and the control group; (2) detection rates in the nasopharynges of the respiratory disease group at admission and discharge; (3) changes in the microbial pathogens detected between admission and discharge in the palate and nasopharynx in the respiratory disease group.

We compared the detection rates in the palate by bacterial species for each of the 6 species detected in both the palate and nasopharynx.

The statistical analysis for each of the 6 bacterial species showed no significant differences in Hellman dental stages between the patients in the respiratory disease group at admission and discharge, and in the control group.

In addition, the comparison of the patients at different Hellman dental ages in the respiratory disease group at admission and discharge, and the control group showed no significant differences in the detection rates of α-Streptococcus spp., Corynebacterium spp., H. influenzae, H. parainfluenzae, or MRSA. Regarding the detection rate of Neisseria spp., significant differences were observed between the following: patients in the respiratory disease group at Hellman dental stages IA and IC at admission, patients in the respiratory disease group at Hellman dental stages IA and IIA, patients in the control group at Hellman dental stages IA and IC, and patients in the control group at Hellman dental stages IA and IIA (p<0.01). In the respiratory disease group, the detection rate at admission was 12.5% among the patients at Hellman dental stage IA, 87.5% among the patients at Hellman dental stage IC, and 100% among the patients at Hellman dental stage IIA. In the control group, the detection rate was 0% among the patients at Hellman dental stage IA, 75.0% among the patients at Hellman dental stage IC, and 87.5% among the patients at Hellman dental stage IIA.

We compared the detection rates in the nasopharynx by bacterial strain for each of the 6 strains detected in both the palate and nasopharynx. As a result, no significant differences in the detection rates of the 6 bacterial species were observed between admission and discharge in the respiratory disease group. In addition, as with the palate, we compared detection rates between the patients at different Hellman dental ages. A significant difference in the detection rate of MRSA was observed at admission between the patients at Hellman dental stages IA and IC, as well as between the patients at Hellman dental stages IA and IIA (p<0.05). The detection rates of α-streptococcus and Neisseria spp., though high in the palate, were low in the nasopharynx.

Finally, we compared and examined the changes in bacterial detection rates in the palate and nasopharynx between admission and discharge in respiratory disease patients. Assessments were classified into 3 categories as follows: “no detection,” cases in which bacteria were not detected at admission or discharge; “reduction,” cases in which the bacterial count was lower at discharge than at admission; and “no change/increase,” cases in which the bacterial count was unchanged or higher at discharge than at admission. Moreover, no significant differences in changes in detection rates between the palate and nasopharynx were observed for Corynebacterium species, H. influenzae, H. parainfluenzae, and MRSA in any of the patients in the respiratory disease group.

A significant difference in changes in detection rates between admission and discharge for α-Streptococcus species was observed between the palate and nasopharynx of patients at Hellman dental stage IA (p<0.01). Of the subjects, 12.5% showed a decrease in detection rate in the palate, while 87.5% demonstrated no change/increase. Of the subjects, 50.0% showed a decrease in detection rate in the nasopharynx, while none of the subjects demonstrated any change/increase.
Significant differences in changes in detection rates at admission and discharge were observed between the palate and nasopharynx for *Neisseria* species among the patients at Hellman dental stage stages IC and IIA ($p<0.01$). Of the patients at Hellman dental stage IC, 56.3% demonstrated a decrease in detection rate in the palate, while 37.5% showed no change/increase. Of the subjects, 6.3% showed a decrease in detection rates in the nasopharynx, while 12.5% showed no change/increase. Of the patients at Hellman dental stage IIA, 25.0% showed a decrease in detection rates in the palate, while 75.0% showed no change/increase. Of the subjects, 25.0% showed a decrease in detection rates in the nasopharynx, while none showed any change/increase.

Among the 6 strains detected in both the palate and nasopharynx, no significant differences in detection rates were observed between the respiratory disease group at admission and discharge, and the control group. The fact that no differences were observed between the respiratory disease and control groups suggests that no oral microbial pathogens unique to the respiratory disease group were observed.

Detection rates of *Neisseria* species increased significantly with increasing Hellman dental age. So, we suggest that the detection rates of *Neisseria* species increased as the subjects’ teeth erupted.

In the study, comparisons between the detection rates of the 6 bacterial species detected in both the palate and nasopharynx showed no significant differences between admission and discharge in the respiratory disease group.

MRSA was frequently observed in the patients at Hellman stage IA, while detection rates were significantly lower among patients at Hellman stages IC and IIA. Neonates who acquire *a-Streptococcus* species or upper respiratory tract indigenous bacteria are reported to be significantly less likely to carry MRSA [8], and the MRSA bacterial load is considered to decrease owing to colonization by other strains. In the present study, the ages of the patients at Hellman stage IA, those at Hellman stage IC, and those at Hellman stage IIA ranged from 1 to 6 months, from 7 months to 2 years 6 months, and from 3 years 1 month to 6 years, respectively. Thus, MRSA prevalence may have decreased owing to the subjects of higher dental ages also being of higher chronological ages.

In the comparison between changes in bacterial load in the palate and nasopharynx, significant differences in bacterial load were observed for *a-Streptococcus* species among the patients at Hellman dental stage IA and for *Neisseria* spp. among the patients at Hellman dental stages IC and IIA. The detection rates of *Neisseria* species, despite significant differences in bacterial load between the patients at Hellman dental stages IC and IIA, did not demonstrate a constant trend.

Previous studies described limited relationship between age and microbial changes on oral and pharyngeal mucosa. Therefore, these results are new findings that show the relevance of tooth eruption and detection of specific bacterial strain. In conclusion, among the 6 strains detected in both the palate and nasopharynx, no clear associations were observed in rates of increase or decrease in bacterial load between the 2 locations. However, in the upper respiratory tract (nasal cavity, pharynx, and larynx), the indigenous flora comprised microbes of species such as *Staphylococcus, Streptococcus, Haemophilus, Neisseria, and Corynebacterium*; these are reported to be partially similar to the flora in the oral cavity [9]. Additionally, some microbial floras of the species have relationship of teeth eruption in childhood. Therewith, further studies and further examine would be considerable to reveal the association between the aforementioned bacteria and the development of respiratory diseases.

References