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Published in:
Heliyon

DOI:
10.1016/j.heliyon.2021.e06513

Publication date:
2021

Document version
Publisher's PDF, also known as Version of record

Document license:
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Citation for published version (APA):
Temporal oral microbiome changes with brushing in children with cleft lip and palate

Rita Rodrigues a,b, Ana P. Chung c, Martin S. Mortensen d, Maria H. Fernandes e, António B. Monteiro f, Rowney Furfuro g, Cátia C. Silva b, Maria C. Manso e,h, Søren J. Sørensen d, Paula V. Morais c,*

a Faculty of Dentistry, University of Porto, R. Dr. Manuel Pereira da Silva, 93, 4200-390, Porto, Portugal
b Faculty of Health Sciences, University Fernando Pessoa, Praça 9 de Abril, 349, 4249-004, Porto, Portugal
c University of Coimbra, Centre for Mechanical Engineering, Materials and Processes, Department of Life Sciences, Calçada Martim de Freitas, 3000-456, Coimbra, Portugal
d Department of Biology, University of Copenhagen, Ole Maaløes Vej 5, DK-2200, Copenhagen N, Denmark
e Associated Laboratory for Green Chemistry (LAQV/REQUIMTE), University of Porto, 4051-401, Porto, Portugal
f Lusiadas Hospital, Av. da Boavista 171, 4050-113, Porto, Portugal
g Compor Clinic, R. Aval de Cima 34, 4200-105, Porto, Portugal
h Faculty of Health Sciences, University Fernando Pessoa, Fernando Pessoa Energy, Environment and Health Research Unit (FP-ENAS), Praça de 9 de Abril, 349, 4249-004, Porto, Portugal

ARTICLE INFO

Keywords:
Microbiome
Children and preteen
CLP
Next-generation sequencing
Alloprevotella
Leptotrichia
Rothia

ABSTRACT

This cohort study aimed to characterize the oral microbiome of children with CLP, from two different age groups, and evaluate the effect of supervised or unsupervised toothbrushing on the microbiome of the cleft over time. Swab samples were collected from the cleft area at three different time points (A; no brushing, B; after 15 days and C; after 30 days) and were analyzed using next-generation sequencing to determine the microbial composition and diversity in these time points. Overall, brushing significantly decreased the abundance of the genera Alloprevotella and Leptotrichia in the two age groups examined, and for Alloprevotella this decrease was more evident for children (2–6 years old). In the preteen group (7–12 years old), a significant relative increase of the genus Rothia was observed after brushing. In this study, the systematic brushing over a period of thirty days also resulted in differences at the intra-individual bacterial richness.

1. Introduction

The human oral cavity contains more than 600 different bacterial taxa, most of them are commensal, but a small number are opportunistic pathogens that can cause various oral diseases, as well as systemic diseases (de Castilho et al., 2006; Parapanisiou et al., 2009; Perdikogianni et al., 2009; Edlund et al., 2018). Several factors influence the oral microbiome, including diet, genetics and life style (Lif-Holgerson et al., 2011). Cleft lip and palate (CLP) is the most common congenital orofacial malformation, (prevalence close to 1:700) (Worth et al., 2017) and significantly affects the structure and functions of the oral cavity (Ahluwalia et al., 2004; Gopakumar and Hegde, 2010). Children with CLP suffer from skeletal discrepancies, causing respiratory problems and malocclusion that hinders the removal of bacterial plaque (Shashni et al., 2015; Haza’a et al., 2011; Rivkin et al., 2000; Boloor and Thomas, 2010). Treatment consists of corrective surgery and the use of palatal obturator plates or orthodontic appliances, which may increase microbial colonization due to accumulation of bacterial plaque (Freitas et al., 2013). Furthermore, fear of sanitizing the cleft area (Sundell et al., 2015) leads to a higher plaque index in these children (Parapanisiou et al., 2009; Pisek et al., 2014). Previous studies have shown that children, adolescents, and young adults with CLP have increased risk of developing dental caries and periodontal diseases compared to non-CLP counterparts (Perdikogianni et al., 2009; Rivkin et al., 2000; Howe et al., 2017; Mutarai et al., 2008; Plakwicz et al., 2017). Together this indicates that children with such malformations can be expected to have an unusual oral microbiome. The colonization of the oral cavity commences within the first hours (8–16 h) after birth and this oral microbiome forms the
foundation upon which newer communities develop as new and more niches appear (Mason et al., 2018; Wade, 2013). Moreover, a 24-hour analysis, using metagenomic and metatranscriptomic approaches, of an in vitro oral biofilm assembly and maturation, revealed that the taxonomic composition and functional capacity of mature biofilm is gradually shaped through processes of co-aggregation, competition and production of reactive agents within the microbial community (Edlund et al., 2018). Variations in the microbial composition may be explained by the dynamic development of the oral microbiome that maturates and evolves, following the modifications of the dentition, throughout childhood and adolescence (Kilian et al., 2016; Xu et al., 2015; Grieaard et al., 2011).

Oral health problems may be related to the presence of specific putative periodontal pathogens such as Gram-positive facultative anaerobic bacteria, like Streptococcus mutans and Lactobacillus spp. (Machorowska-Pieniżek et al., 2017; Marsh, 2003), or Gram-negative proteolytic species, from the genera Prevotella, Porphyromonas, Fusobacterium and Treponema (Marsh, 2003). The cleft area is vulnerable to this since it is a site for dental plaque accumulation (Wyrebek et al., 2017; Perdikogianni et al., 2009; Gaggl et al., 1999; Bragger et al., 1985). In dental caries, there is a shift towards community dominance of acidicogenic and acid-tolerant bacteria (S. mutans and Lactobacillus spp.) that demineralize enamel (Marsh, 2003; Wade 2013; Rosier et al., 2018). These bacteria metabolize dietary sugars to acid, creating locally a low pH (5.5); if these acidic conditions persist without sufficient time for remineralization, caries lesions will develop (Rosier et al., 2018). Periodontitis-associated bacteria (e.g. the Gram negative genera previously mentioned) cause tissue damage directly, by the production of proteases such as collagenase or hyaluronidase, however, much of the tissue damage can be caused by activation of the pro-inflammatory pathways and the inflammatory response (Marsh, 2003; Wade 2013).

In children with CLP many factors can inhibit optimal toothbrushing, whether autonomous or parent-assisted. These factors include reticence, due to fear of traumatizing soft tissues or concern with bleeding from whether autonomous or parent-assisted. These factors include reticence, due to fear of traumatizing soft tissues or concern with bleeding from appliance or a CLP surgical intervention, which could significantly change the oral conditions, were excluded from the study.

The children (2–6 years) received parent supervision during oral hygiene, while the preteens (7–12 years), performed their oral hygiene autonomously. Parents of both groups were instructed to maintain the routine oral hygiene. Oral swabs were collected, evaluated and measured at baseline (time point A), without prior brushing, at day 15 (time point B), and day 30 (time point C), after toothbrushing. Of the initial 28 subjects, one child and three preteens were lost to follow-up, which meant that 72 samples were collected, from 13 children and 11 preteens.

2.3. Sample collection

The cleft area was swabbed 3 times, using sterile FLOQSwabs™ (COPAN, USA), spinning the swab along the deepest area of the cleft at a perimeter of 0.5 cm around it. The samples were stored at −20 C until DNA extraction. One investigator collected all samples, thereby ensuring uniform sample collection. After performing the swab, an oral plaque index was evaluated. The adapted plaque index (aPI) was calculated at time point A as described in a different study by Rodrigues et al. (2018).

2.4. DNA extraction

The swab tips were submerged in 1 mL of molecular grade water (W4502, Sigma, UK), and bacteria released by 10s manual agitation. DNA extraction from 200 μl of the water was performed using NucleoSpin® 96 soil kit (740787, Macherey-Nagel, Germany) using an EpMotion 5075v (Eppendorf, USA), following manufacturer instructions, using lysis buffer SL1 with 150 μl Enhancer SX and eluted in 70 μl elution buffer.

2.5. 16S amplicon sequencing and bioinformatics pipeline

The 16S RNA gene amplification procedure was performed using a two-step procedure to amplify the hypervariable V3–V4 region of the 16S rRNA gene, using PCRBIOS HiFi Polymerase (PB10.41, PCRBIO SYSTEMS, UK) in 25 μL reactions (2 μL template, 5 μL reaction buffer, 1 μL forward primer, 1 μl reverse primer, 0.12 μL Polymerase, 15.88 μL molecular grade water (W4502, Sigma, UK). Amplification was performed in 96-well microtiter plates, in a 2720 thermal cycler (Applied Biosystems®, Life Technologies, CA, US) according to the following cycling program: 1 min of denaturation at 95 °C, followed by 30 cycles of 15 s at 95 °C (denaturing), 15 s at 56 °C (annealing) and 30 s at 72 °C (elongation), final extension at 72 °C for 5 min, and storage at 10 °C thereafter. The PCR products from both steps were purified using High Prep™ PCR (AC-60500, MagBio Genomics Inc., USA) PCR Clean Up System, using 0.65:1 beads to amplicon ratio (vol/vol). The first step used 30 amplification cycles and the modified broad range primers Uni341F (‘5’-CTAYGGGRBBGASCAG-3’) and Uni806R (‘5’-GGACTACHVGGGTWTCTAAAT-3’) (Klindworth et al.,...
The second step used 15 amplification cycles and primers developed in-house, which contain sequencing adaptors and unique combinations of forward and reverse indices (Nunes et al., 2016). A negative template-free control and a positive control containing 2.0 µl DNA from a known bacterial mock community (1.0 ng/µl; HM-782D, BEI Resources, VA, US) were included.

Samples were normalized using SequelPrep™ Normalization Plate (96) Kit (Invitrogen, MD, USA), pooled, and concentrated using the DNA Clean and Concentrator™-5 kit (Zymo Research, Irvine, CA, USA). The concentration of the pooled libraries was determined using the Quant-IT™ High-Sensitivity dsDNA Assay Kit (Q33120, Invitrogen, MD, USA) and adjusted to 1.65 ng/µl (4 nM). Amplicon sequencing was performed on the Illumina MiSeq Desktop Sequencer (Illumina Inc., CA, US), with the denatured libraries adjusted to a final concentration of 16 pM. For each run, a 5.0% PhiX internal control was included. All reagents used were from the MiSeq Reagent Kits v2 (Illumina Inc., CA, US). Automated cluster generation and 250 paired-end sequencing with dual-index reads was performed. The sequencing output was as the demultiplexed fastQ-files generated directly on the MiSeq instrument. Up to 192 samples, including controls were sequenced per run.

Sequencing data was analyzed using the QIIME2 (Bolyen et al., 2018) implementation of DADA2 using default parameters (Callahan et al., 2016) producing 2,682,145 high quality merged sequencing reads, representing 3,251 amplicon sequence variants (ASV). Taxonomical classification was performed against SILVA database version 132 (Yilmaz et al., 2014).

### 2.6. Statistical analysis

Statistical analyses and data treatment were performed using the R software platform (R Core Team, 2018). The R package phyloseq was used for data handling (McMurdie and Holmes, 2013), and all plots were created using the ggplot2 package (Wickham, 2016). Based on the rarefaction curves (Figure 1), the single samples with less than 5000 reads were removed from the data set.

The alpha diversity measures, observed richness and Shannon-diversity index (H), were calculated as the mean of 100 separate rarefactions to 6,688 reads per sample (90% of minimum sample depth). Between groups, comparisons of alpha diversity were performed using analysis of variance (anova) (function: ANOVA, package: stats), and correlation with aPI was tested using Spearman, Kendall, and Pearson r correlations (function: ggscatter, package (Kassambara, 2018)). Beta-diversity was calculated using Bray-Curtis dissimilarity index (function: distance, package: phyloseq), and analyzed using Permutational Multivariate Analysis of Variance Using Distance Matrices (PERMANOVA, function: adonis, package (Oksanen et al., 2019)), for aPI we further calculated a PCoA (function: ordinate, package: phyloseq) and correlated aPI with the first 10 axis. To investigate differential abundance of bacteria we used the package DAtest to determine which statistical method to employ (function: testDA, package (Russel et al., 2018)) and then to perform the optimal tests. The relative abundance change (RAC) was calculated for each genus with mean abundance of at least 0.2%, using the formula: $\text{RAC} = \ln(A_1)/\ln(A_0)$, where $A_0$ is the abundance at one time point and $A_1$ is the abundance at a later time point. The significance of between group variance of the RAC were evaluate using anova and Wilcoxon signed rank test, followed by correction for false discovery rates (fdr) ($q = \text{fdr adjusted p-values}$), to identify genera that changed significantly. To test for correlations with aPI we calculated Spearman, Pearson r, and Kendall correlations with the 10 most abundant ASV, species, and genera, based on relative abundance and log transformed relative abundances.

![Figure 1. Rarefaction curves. Rarefaction curves of calculated for observed richness (top) and H (bottom) at 1 to 20000 sequencing reads, separated for child (left) and Tween (right), with samples grouped by timepoint with bars indicating standard deviations.](image)
3. Results

3.1. Characterization of the oral hygiene status

The aPI of both groups of children showed overall insufficient oral hygiene. The aPI were not significantly different between age groups (Mann-Whitney t., p = 0.057), although the children showed a slightly higher median values than the preteens (Me (Q1-Q3): 2.4 (1.8–2.6) vs 1.9 (0.2–2.2), respectively). Moreover, based on the information regarding their brushing habits, their brushing frequencies did not significant differ between groups (Mean (Q1-Q3): 2 (1–2) for children and 1 (1–2) for preteen; p = 0.207).

Figure 2. Phylum level microbiome composition at timepoint A, per patient. Bar plot showing the relative abundance of all phyla with a mean abundance above 1% and remaining phyla group as Other.

Figure 3. Genus level microbiome composition at time point A, per patient. Bar plot showing the relative abundance of all genera with a mean abundance above 4% and remaining genera group as “Other”.

(Mann-Whitney t., p = 0.057), although the children showed a slightly higher median values than the preteens (Me (Q1-Q3): 2.4 (1.8–2.6) vs 1.9 (0.2–2.2), respectively). Moreover, based on the information regarding their brushing habits, their brushing frequencies did not significant differ between groups (Mean (Q1-Q3): 2 (1–2) for children and 1 (1–2) for preteen; p = 0.207).
3.2. The microbiome at baseline (time point A)

At baseline (time point A), in the 24 samples, from 13 children and 11 preteen, the major bacterial phyla present were Firmicutes (54.7%), Proteobacteria (11.6%), Bacteroidetes (11.5%) and Actinobacteria (10.0%) (Figure 2). The five most abundant genera were Streptococcus (37.4%), Leptotrichia (7.6%), Rothia (6.6%), Neisseria (5.3%), and Granulicatella (5.0%) (Figure 3). There were no statistically significant differential abundant phyla or genera between the two groups.

When comparing baseline alpha diversity in the two groups, no significant differences were observed in either observed richness (132 ± 40.6 and 151 ± 48.0, respectively, p = 0.31) or H (3.2 ± 0.54 and 3.3 ± 0.42, respectively, p = 0.47) (Figure 4). The variation in baseline microbiome composition between children and preteen was measured by Bray-Curtis dissimilarity and showed that the age groups significantly explain 6.4% (PERMANOVA, p = 0.04) of the overall variation.

When testing for correlations between the microbiome and aPI at baseline, independent of age group, alpha diversity was not correlated with aPI (p = 0.123 – 0.99). Bray Curtis distances were not correlated with aPI (PERMANOVA, R2 = 0.04, p = 0.61), and when correlating the first 10 axis of a PCoA with aPI only axis 5 showed a significant Kendall correlation with aPI (r2 = -0.35, p = 0.028), but no other axis or type of correlation were significant. Neither of the 10 most abundant ASVs, species, or genera was significantly correlated with aPI.

3.3. Microbiome per group age (child and preteen) after brushing (time point B + C)

The CLP microbiome, after toothbrushing was dominated by the phyla Firmicutes (51.7–52.5%), Actinobacteria (16.4–19.2%), Proteobacteria (12.1–15.1%), Bacteroidetes (8.0–8.4%) and Fusobacteria (6.0–7.2%). At genus level, the dominant bacteria were Streptococcus (32.9–33.6%), Rothia (9.6–12.3%), Gemella (6.0–7.5%), Veillonella (5.3–5.4%), and Haemophilus (4.5–5.4%). Rothia was a major constituent of the oral microbiome in seven preteen and four children, while having a small relative abundance in the other patients. Gemella was a major genus in only one child and one preteen. Neisseria and Veillonella were major genera in two groups of two preteen’s microbiome each. Haemophilus was a major constituent in only one child’s oral microbiome (Figure 5). No
genera were significantly different between the two age groups at either time point (Quasi-Poisson GLM, predictor = group, covariable = Time point) or between time points in either group (DESeq2, predictor = Time point, covariable = Group).

### 3.4. Effect of toothbrushing supervision after 30 days (B + C) compared to the baseline microbiome

To evaluate the impact of the different oral hygiene strategies, the initial microbiome diversity (time point A) was compared with the microbiome diversity of the samples taken after brushing, at day 15 and 30 (time point B and C). Children showed higher observed richness after toothbrushing, at day 15 and initial microbiome diversity (time point A) was compared with the baseline microbiome (Figure 6), and any outliers are indicated as points.

Of the 29 genera tested, four genera changed (RAC different from 0) significantly during initiation (Wilcoxon, q < 0.1 (Figure 6), and three had significantly changed abundance overall.

When comparing between groups, eight genera had a significantly different RAC between groups at one or more of the timespans (ANOVA, q < 0.05). Actinobacillus had significantly positive RAC overall (1.37, q = 0.041), driven by increased abundance during initiation, and no RAC differences between group. Alloprevotella were significantly decreased during initiation (q = 0.042) and especially in the child group, which were significantly lower than the preteen group (q = 0.030), and significantly decreased when seen over the entire period (q = 0.041). Gemella tended to have negative RAC overall, with a significant difference between group during continuation, where RAC were positive for the child group (0.46) and negative for the preteen group (-0.70). Granulicatella did not show any differences between groups, but were found to have significantly negative RAC during initiation (-0.49, q = 0.093). Haemophilus showed a general tendency towards positive RAC over time, with significant differences between group at initiation, which were driven by a significant higher RAC in the child group (1.06 and -0.13, for children and preteen, respectively, q = 0.024). Leptotrichia had a significantly negative RAC during initiation (-0.83, q = 0.004) and overall (-0.93, q = 0.041), with no significant differences during continuation or between groups. Porphyromonas showed a significant lower RAC in the preteen group, when compared overall (q = 0.016) that were driven by a tendency to decreased RAC in the preteen group during initiation and slightly increased RAC in the child group during continuation. Prevotella were significantly different between groups during initiation (q = 0.015) and overall (q = 0.006), with positive RAC in the child group and negative RAC in the preteen group. There was a significant increase of Rothia during initiation (0.76, q = 0.090), with significant differences at continuation (q = 0.025) driving an overall difference between the groups (q = 0.021). Furthermore, in the child group Rothia had a negative RAC (-0.54) during continuation, whereas the preteen group had a steady positive RAC during both in initiation and continuation (0.81 and 0.82, respectively). Streptococcus, the most abundant genus, did not show any great variation in general, but were found to differ significantly between groups during initiation (RAC: -0.27 and 0.21, for child and preteen, respectively, q = 0.014). Lastly, Veillonella had positive RAC in the child group and negative RAC in the preteen group, resulting in significant differences between group seen over the entire project (RAC: 1.08 and -0.73, respectively, q = 0.011).

### 4. Discussion

In this study, we evaluated the oral microbiome of children (2–6 years old) and preteens (7–12 years old) with CLP, using massive high-throughput amplicon sequencing. The data on oral microbiome of CLP patients are scarce and, to our knowledge, this is the first report on the oral microbiome of the cleft area in CLP children and preteens assessed in depth using next generation sequencing. This approach showed that Firmicutes, Proteobacteria, Bacteroidetes, and Actinobacteria were the most abundant phyla in CLP oral microbiome. Additionally, Streptococcus, Leptotrichia, Rothia, Neisseria, and Granulicatella were the dominant genera in the two age groups. This resembles the oral microbiome in non-CLP children, where these taxa have been reported as abundant members, supporting the idea that there is a core oral microbiome (Xu et al., 2015; Grieder et al., 2011).

Other than CLP, all children and preteens included in this study did not have any health problem and presented a health status suitable for their ages. The child group consisted of preschool children with primary dentition and children with mixed dentition (primary and permanent), while the preteen group consisted of children with mixed dentition and pre-adolescents with permanent dentition. The replacement of the primary teeth with a permanent dentition is a striking biological change that would significantly explain the observed age-dependent changes in the oral microbiome. The expansion of biodiversity may be attributable to
both introductions of new species and increase in abundance of the already present organisms. Further explanation includes oral hygiene behavior (Lewis et al., 2017), exposure to external bacteria (Köninnen, 2000) and the development of the immune system (Costello et al., 2012).

We did not observe any correlations between the cleft scar microbiome and the aPI at baseline. Studies have shown that the functional potential in plaque biofilm is more important than the abundance of specific species (Espinoza et al., 2018) and that spatial variation is expected in the oral microbiome (Proctor et al., 2018); it is not surprising that we did not find any correlation between the microbiome of a soft tissue site and the dental surface.

Introduction of the supervised toothbrushing resulted in inter-individual differences in the bacterial composition, without presenting group specific patterns of change, since no genera were significantly different between the two age groups at either time point B or C, or between the two time points in either age group. However, a closer look to the dynamics of the oral microbiome in the cleft area showed relative abundance changes (RAC) of different genera within individual patients. From the beginning to the end of the trial, in which both age groups were requested to brush their teeth, the relative abundances of members of the genera Alloprevotella and Leptotrichia significantly decreased, and the relative abundance of members of the genus Actinobacillus significantly increased. These three genera are naturally occurring members of the microbiome in healthy individuals, but the overabundances of members of the genera Alloprevotella and Leptotrichia have been correlated with oral cancer and periodontitis disease (Zhao et al., 2017; Chen et al., 2018; Li et al., 2014). The RAC of genera Leptotrichia, Granulicatella, Alloprevotella (RAC<0), and Rothia (RAC>0) were significant in the first 15 days of the trial and this change was observed in both groups, with exception of the genus Alloprevotella, where the change occurred mainly in the child group. In addition, the positive RAC of Rothia was evident for the group preteen during the entire trial, while for the child group, the relative abundance of this genus showed a tendency to decrease from time point B to time point C. This group of microorganisms is commonly found associated with both health (core microbiome of children with primary dentition but not in predentate) and oral disease, demonstrating a distinct pathogenic potential of members of this genus (Mason et al., 2018; Crielaard et al., 2011; Zhao et al., 2017). Our data does not enable us to draw any conclusions about the pathogenicity or about the specific species of Rothia present. Members of Streptococcus, Gemella, Haemophilus, Porphyromonas, Prevotella and Veillonella also showed significantly different RAC for the two groups between two or more time points, during the trial. These significant differences between age groups, supports the idea that dynamic changes of the oral microbiome can potentially respond to host development and maturation. Oral bacteria and their metabolites interact with human host cells, both as protective

Figure 7. Boxplots of the relative abundance change (RAC) and abundance of significantly changing genera. A. Boxplot of RAC, per group (child: yellow, preteen blue), for any genus with RAC significantly different from 0 in any of the 3 timespans (Significant change, yes: Black edge, no: green edge), or which differs significantly between groups in any of the timespans (Significant difference, yes: solid fill, no: pale fill). B. Boxplot of the genus abundance of the relevant genera, edge color indicates time point (A (day 0): red, B (day 15): green, C (day 30): blue). Line in box indicates median value, box covers 95% confidence intervals, vertical lines reaches to furthest samples within 1.5 x box height and any outliers are indicated as points.
barriers against pathogen invasion and as causative agents of oral diseases (e.g. caries and periodontal disease). Many oral diseases are being viewed as a consequence of a deleterious shift in the balance of the resident oral microbiome (Willis and Gabaldon, 2020). In dental caries there are changes in the oral microbiome that favors acid-producing (acidogenic) species, from genera such as Streptococcus and Veillonella (Rosier et al., 2018). Members of the genera Porphyromonas and Prevotella have also been strongly associated with caries (Hurley et al., 2019). Periodontal disease, results from an inappropriate inflammatory reaction to the normal microbiome, exacerbated by the presence of some disease-associated bacterial species. Increased abundance of Gram-negative proteolytic species, such Porphyromonas gingivalis and Prevotella spp. have been associated with periodontal diseases (Rosier et al., 2018; Willis and Gabaldon, 2020). However, it is not always clear, whether changes in microbial compositions causes disease or if they are caused by the disease. Some bacterial genera that have been associated with oral disease are commonly found as parts of a healthy oral microbiome, these include Neisseria, Haemophilus, Prevotella, Veillonella, Gemella, Streptococcus, and Porphyromonas (Willis and Gabaldon, 2020). Moreover members of the genus Streptococcus are also well known for their production and secretion of antimicrobial compounds (e.g. hydrogen peroxide, bacteriocins), which can act as defenses against oral pathogens (Edlund et al., 2018).

In the child group, the observed richness was higher after supervised brushing when compared to the initial diversity. An increased diversity of the oral microbiome is generally associated with a healthier oral microbiome; caries-free children have a higher alpha diversity than children with caries (Li et al., 2014; Gross et al., 2010). This indicates that the supervision and guidance by parents promoted a better overall oral hygiene in this group. The supervised toothbrushing affected the composition of the oral microbiome of each individual in this study. Although, these effects were specific to each individual and could not be predicted for the groups in general. The action of toothbrushing, independently of the period of toothbrushing, significantly explained the differences observed in the microbiome of CLP individuals (4.2%). Therefore, preventive intervention (adequate toothbrushing) is of paramount importance to promote a good oral hygiene of CLP children. While the increased risk of dental caries, in individuals with CLP, is still inadequately understood, many of the potential risks factors are related to insufficient cleaning of areas with impeded access.

The consequences of poor oral health are considerable for children and preteens with CLP, since it may affect their candidacy for orthodontic treatment. Furthermore, if good oral hygiene is not maintained during the orthodontic treatment, it can impair future oral health and cleft-related outcomes (Lewis et al., 2017).

This is the first longitudinal study of the oral microbiome of children with CLP. By comparing the oral microbiome over time, we have identified inter-individual differences and changes in the oral microbiome composition, although no general inter group differences were not observed. Nevertheless, we did observe that brushing increased the richness and evenness in the child group and not in the preteen group.

5. Limitations of the study

The strength of this study was limited by the impossibility to ensure a strict and continuous monitoring of the children and their families during the entire study period. The participants were given guidelines for good brushing efficiency (frequency or time of brushing), but the daily brushing was not observed by the study staff and adherence to the guidelines were followed up through a study questionnaire.

We also acknowledge that the NGS data lacked the resolution to identify all bacteria at species level, limiting the transferability of our conclusions to a clinical setting. More research will be needed to clarify the major cause of variation in the oral microbiome of CLP patients.

Declarations

Author contribution statement

Rita Rodrigues: Conceived and designed the experiments; Performed the experiments.
Ana P. Chung: Analyzed and interpreted the data; Wrote the paper.
Martin S. Mortensen: Performed the experiments; Analyzed and interpreted the data; Wrote the paper.
Maria H. Fernandes, António B. Monteiro, Rowney Furfuro, Cátia C. Silva: Performed the experiments.
Maria C. Manso: Conceived and designed the experiments.
Søren J. Sørensen: Contributed reagents, materials, analysis tools or data.
Paula V. Morais: Conceived and designed the experiments; Analyzed and interpreted the data; Contributed reagents, materials, analysis tools or data; Wrote the paper.

Funding statement

This work was supported by FEDER funds within the PT2020 Partnership Agreement and Compete2020-Programma Operacional Factores de Competitividade, by the Portuguese Foundation for Science and Technology (FCT), by the CEMUC strategic program (UID/EMS/00285/2013) and by the research projects PTW PTDC/AAGREC/3839/2014 and Microminer POCI-01-0145-FEDER-031820.

Data availability statement

The sequence data from this study is available in the Sequence Read Archive (SRA) under BioProject ID PRJNA512456.

Competing interest statement

The authors declare no conflict of interest.

Additional information

No additional information is available for this paper.

References


