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DIFFERENCES IN THE LOWER AIRWAY MICROBIOTA OF INFANTS WITH AND WITHOUT CYSTIC FIBROSIS

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Abstract

Background—Cystic fibrosis (CF) lung disease commences in infancy, and understanding the role of the microbiota in disease pathogenesis is critical. This study examined and compared the

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AUTHORS' CONTRIBUTIONS

KBF performed the literature search and data analysis, wrote the first draft of the manuscript and prepared the figures. KMW assisted with data analysis. DSA, RC and KG were authors of the previous studies of this birth cohort and were responsible for the initial study design, recruitment, data collection and analysis. SCR was responsible for the design of this study. TWF, GAS and KMW performed the 16S rRNA gene sequencing of the BAL samples. All authors were involved in data interpretation and contributed to the editing of subsequent manuscript drafts.

CONFLICT OF INTEREST STATEMENT

The authors have no conflicts of interest.

lower airway microbiota of infants with and without CF and its relationship to airway inflammation in the first months of life.

Methods—Infants newly-diagnosed with CF were recruited into a single-centre study in Melbourne, Australia from 1992–2001. Bronchoalveolar lavage was performed at study entry. Healthy infants undergoing bronchoscopy to investigate chronic stridor acted as controls. Quantitative microbiological culture was performed and inflammatory markers were measured contemporaneously. 16S ribosomal RNA gene analysis was performed on stored samples.

Results—Thirteen bronchoalveolar samples from infants with CF and nine from control infants, collected at median ages of 1.8-months (25^{th}-75^{th} percentile 1.5 to 3.1-months) and 5-months (25^{th}-75^{th} percentile 2.9 to 8.2-months) respectively, provided 16S rRNA gene data. Bacterial biomass was positively associated with inflammation. Alpha diversity was reduced in infants with CF and between-group compositional differences were apparent. These differences were driven by increased *Staphylococcus* and decreased *Fusobacterium* and were most apparent in symptomatic infants with CF.

Conclusion—In CF lung disease, differences in lower airway microbial community composition and structure are established by age 6-months.

Summary

Differences in the composition and structure of the lower airway microbiota of infants with and without cystic fibrosis are established in the first six months of life, and are most apparent in symptomatic infants.

Keywords

Cystic fibrosis; microbiota; 16S ribosomal RNA; bronchoalveolar lavage fluid; inflammation; infant

INTRODUCTION

Over the past two decades, the widespread application of molecular analysis techniques, including 16S ribosomal RNA (16S rRNA) gene sequencing, has changed our understanding of the human microbiome. In health, the lungs are not sterile, and the host-microbiota relationship is likely to have an important role in the development and modulation of the immune response, and therefore, in the early pathogenesis of disease [1, 2].

Unfortunately, the “healthy” or “typical” lower airway microbiota in infancy and early childhood remains unknown [3]. Lower airway samples from infants and young children can only be reliably obtained via bronchoscopy, requiring general anaesthesia. Consequently, the lower airway microbiota in this important population has not been described.

Cystic fibrosis (CF) lung disease begins in infancy [4]. Culture-based studies suggest that lower airway infection is a key trigger for inflammation, however elevated inflammatory markers have been reported in the setting of negative culture results [5–7]. There are significant differences between the nasopharyngeal microbiota of infants with CF and healthy controls at the time of diagnosis by newborn screening and before antibiotic

exposure, most notably an increased prevalence of *Staphylococcus* species [8, 9]. However, these observations cannot be inferred to represent the lower airway microbiota [10–12]. Similarly, microbiota composition changes and diversity decreases with age and advancing disease [13], and findings from sputum samples of older children and adults with CF cannot be extrapolated to infants.

We have previously explored the development of the lower airway microbiota over time in a birth cohort of infants and young children with CF [14]. In order to explore the role of the lower airway microbiota in the earliest pathogenesis of CF lung disease, we now present a subset of this study population, infants who had lower airway samples obtained at younger than age 6-months. We compare the composition and structure of their lower airway microbiota to that of a control group of infants without lung disease, who had lower airway samples obtained during the same time period. We hypothesised that there would be differences in microbiota composition in infants with CF, and that these differences would be most pronounced in infants with respiratory symptoms.

METHODS

Participants

Infants newly diagnosed with CF, either following newborn screening or presentation with meconium ileus and sweat chloride concentrations >60mmol/L were recruited into a single-centre study in Melbourne, Australia, from 1992–2001. Otherwise healthy infants, undergoing bronchoscopy for investigation of congenital stridor during the same time period, who were free of other symptoms and not taking antibiotics in the previous 14-days, were recruited as controls. Bronchoscopy and bronchoalveolar lavage (BAL) were performed at study entry. Samples collected from infants with CF aged <6-months and from control infants aged <12-months were included in this analysis. Infants with CF were not routinely prescribed prophylactic antibiotics.

BAL samples were obtained from the right middle lobe and lingula, and except for a small subset of infants with CF [15], pooled at the time of collection, as previously reported [5, 14, 16] and described in the Online Supplement. Inflammatory markers, interleukin-8 (IL-8) and neutrophil elastase (NE), were measured and quantitative bacterial cultures were performed contemporaneously. Whole BAL samples were stored at −70°C and 16S rRNA gene sequencing analysis was performed on available samples. The Royal Children's Hospital Melbourne Human Research Ethics Committee approved this study. Written informed consent was obtained from parents/guardians.

16S ribosomal RNA gene sequencing

16S rRNA gene sequences were generated on the Roche 454 platform, using V1–3 variable regions, following Human Microbiome Project protocols [17], as reported previously [14] and detailed in the Online Supplement. Reads passing through quality control were classified using Ribosomal Database Project naïve Bayesian classifier [18], V2.2 with training set 6. Sequences were classified to the lowest taxonomic level that could be assigned with confidence values >0.5.

Statistical analysis

Statistical analysis was performed using 'R' [19], packages 'vegan' [20] and 'metagenomeSeq' [21]. BAL samples from infants with CF were designated as "unwell" or "stable" based on the presence or absence of respiratory symptoms and/or antibiotic use at the time of collection.

NE values below the assay detection limit of 5 mcg/mL were assigned a value of 2.5 mcg/mL. IL-8 and NE values were logarithmically transformed for analysis. Chi square tests, t-tests and Mann-Whitney tests were used to compare categorical, and parametric and non-parametric continuous variables respectively.

BAL samples that returned a minimum of 1000 reads were included for analysis of microbiota diversity and composition (Figure E1). Sequences not classified to genus level were removed prior to analysis. Alpha-diversity was assessed with Shannon Diversity Index (SDI), richness and Pielou's evenness index.

The data were rarefied to 1000 reads per sample for analysis of beta-diversity, using the Bray-Curtis dissimilarity index and principal coordinate analysis [20]. Permutational multivariate analysis of variance, multivariate homogeneity of groups dispersion and Tukey's Honest Significant Difference methods were used to compare beta-diversity between subject groups [20]. Constrained ordination using redundancy analysis with analysis of variance testing was utilised to explore the impact of disease status on microbiota composition [20].

Data were normalised using 'MetagenomeSeq' to account for sparse high-throughput data from low volume and potentially low concentration samples [21]. Relative abundance of genera in individual samples, odds ratios for presence of individual genera and logarithmic fold changes in their prevalence between infants with CF and controls were calculated. P-values were adjusted using the Benjamini-Hochberg correction.

RESULTS

Participants

Twenty-one BAL samples from 21 infants with CF and ten samples from ten control infants, collected at median ages of 1.8-months (25^{th}-75^{th} percentile 1.5 to 2.5-months) and 5.6-months (2.9–8.6-months) respectively underwent 16S rRNA gene sequencing, including 13 samples from infants with CF (62%) and nine samples from controls (90%) that yielded greater than 1000 reads (Table 1; Figure E2 and Table E1). Control infants were diagnosed with laryngeal or subglottic pathology based on bronchoscopic findings [laryngomalacia, n=9 (90%); stridor not otherwise specified, n=1 (10%)]. Of the infants with CF whose BAL samples yielded above 1000 reads, eight (62%) were stable and five (38%) were unwell (with respiratory symptoms and/or antibiotic use) at the time of BAL. There were no differences in age or cystic fibrosis transmembrane regulator genotype between these groups, although more of the unwell infants with CF had prior antibiotic exposure (4/5 [80%] compared with 3/8 [38%] stable infants, p=0.36). There were no significant

differences in the clinical characteristics of infants with CF whose BAL samples yielded above or below 1000 reads.

Quantitative culture and airway inflammation

BAL samples yielding fewer than 1000 reads had reduced bacterial growth on quantitative culture compared with the samples yielding greater than 1000 reads (median 790 colony forming units (CFU)/mL (25^{th}-75^{th} percentile 1–2340 CFU/mL) versus 36765 CFU/mL (6301–223300 CFU/mL) respectively, p=0.004); Figure E3).

BAL samples yielding fewer than 1000 16S rRNA gene reads, suggestive of lower bacterial biomass, had reduced IL-8 compared to samples yielding greater than 1000 reads (median pg/mL (25^{th}-75^{th} percentile 26.3–35 pg/mL) versus 66.4 pg/mL (41.1–195.3 pg/mL respectively, t-test ($\log_{10}$ IL-8): p=0.03), although there was no difference in NE concentration between the groups (median 5.9 mcg/mL (2.5–7.8 mcg/mL) versus 2.5 mcg/mL (2.5–12.1 mcg/mL) respectively, t-test ($\log_{10}$ NE): p=0.6; Figure E4).

Alpha-diversity

Microbial richness was reduced in the lower airway samples of infants with CF compared with controls regardless of clinical status at the time of BAL (95% confidence interval (CI) of difference between infants with CF and controls: 1.13 – 11.83, p=0.02). There were no differences in either Shannon diversity index or Pielou's evenness between the groups overall (Shannon index: 95% CI of difference −0.21 – 1.0, p=0.19; Pielou's evenness: 95% CI of difference −0.1 – 0.29, p=0.31). Although there were reductions in both indices in unwell infants with CF, these were not statistically significant (Figure 1). Alpha-diversity indices were not correlated with lower airway inflammatory markers (Figure E5).

Beta-diversity

The Bray-Curtis dissimilarity index and principal coordinate analysis were used to quantify compositional differences in the microbiota of individual BAL samples (Figure 2A). Permutational multivariate analysis of variance using distance matrices demonstrated significant differences between the subject groups (p=0.01).

Constrained ordination was then performed using redundancy analysis to assess the compositional variation in lower airway microbiota attributable to disease status (CF stable, CF unwell and control; ANOVA, p=0.04). Results are shown in Figure 2B.

Average dispersion from the centroid was increased in BAL samples from unwell infants with CF (0.56) compared with controls (0.39; 95% CI of difference between means: −0.34 – 0.01, p=0.07), indicating greater inter-individual differences amongst the former group. There were no differences in the beta-diversity of lower airway samples of control infants compared to stable infants with CF (0.47; 95% CI of difference between means: −0.23 – 0.08, p=0.43), or between unwell and stable infants with CF (95% CI of difference between means: −0.09 – 0.27, p=0.43; Figure E6).

Microbiota composition

Normalisation methods to account for sparse high-throughput data were employed to enable comparison of both the relative abundance of genera within individual BAL samples and the differential abundance of individual genera in BAL samples of infants with CF and controls (Figure 3).

In a linear fit model assessing the differential abundance of individual genera in BAL samples from infants with CF and control infants, *Staphylococcus, Ralstonia* and *Methylobacterium* were increased in the former with logarithmic (log_2) fold increases of 3.7, 3.2 and 2.2 respectively. *Fusobacterium, Neisseria* and *Escherichia/Shigella* were the most increased genera in the lower airway samples of control infants with logarithmic (log_2) fold increases of 3.3, 2.9 and 2.4 respectively; Figure 4; Table E2).

Differences in median relative abundance of individual genera in the three subject groups are further highlighted in Supplementary Figure E7. Differences in the composition of the lower airway microbiota in infants with CF were most pronounced in those who were unwell at the time of BAL, with the greatest increase in *Staphylococcus* and decrease in *Streptococcus* in this group.

Antibiotic exposure

In infants with CF, previous or current exposure to treatment antibiotics had no impact on bacterial load in quantitative culture, 16S rRNA gene sequence reads, alpha-diversity or beta-diversity indices when compared to BAL samples collected from antibiotic-naïve infants (Table E3; Figure E8).

DISCUSSION

This study revealed substantial differences between the early lower airway microbiota of infants with and without CF that were most marked in symptomatic infants. Both structural and compositional differences were apparent in the first months of life: richness was reduced in infants with CF; *Staphylococcus* was increased and *Fusobacterium* was decreased. In the presence of active respiratory disease, the relative abundance of recognised CF pathogens increased at the expense of a diverse range of typical bacteria. We also found a relationship between lower airway bacterial biomass and inflammation, such that those BAL samples which failed to amplify to 1000 16S rRNA gene sequence reads had less bacterial growth in quantitative culture and lower IL-8 concentrations compared with the BAL samples that yielded greater than 1000 sequence reads.

This study provides the first description of the lower airway microbiota of infants without significant lung pathology. By comparing such “healthy” lower airway microbiota to that of very young infants with CF, diagnosed predominantly by newborn screening, not prescribed anti-staphylococcal prophylaxis and managed in a single CF centre with minimal treatment variation, this study offers unique insights into the microbiological origins of CF lung disease. As has been reported in the nasopharynx [8, 9], the most substantial difference between the airway microbiota of infants with CF and controls was the increased prevalence of *Staphylococcus* in the former. It has long been established that *S. aureus* is a major

pathogen in early CF lung disease. Its detection using classical culture methodology is associated with increased neutrophilic inflammation, earlier onset of structural lung disease and poorer lung function outcomes [4–6, 16, 22–25]. Using molecular analysis techniques its prevalence has now been confirmed in both the upper and lower airways in the first months of life, soon after diagnosis by newborn screening, and prior to antibiotic exposure [8, 9, 14]. This study highlighted both the relative absence of *Staphylococcus* from the lower airways of healthy infants and its dominance in symptomatic infants with CF, thus emphasising its central and early role in the pathogenesis of CF lung disease.

This study provides further evidence that CF lung disease begins early, with profound differences in the lower airway microbiota driven by disease state and established by age 6-months. We previously demonstrated that in infants and young children with CF not prescribed antibiotic prophylaxis, both reduced alpha-diversity in the lower airway microbiota and dominance of recognised CF pathogens were associated with increased lower airway inflammatory markers [14], which are risk factors for the earlier development of structural lung disease. In that longitudinal study, including the CF BAL samples presented in this analysis, microbial community composition was dynamic, with considerable changes in its composition over the first years of life.

Age-related changes in the lower airway microbiota of preschool children with CF have been further described in two recent studies. The first, involving 136 children (median age 11-years (range 0.2–20-years) undergoing clinically indicated bronchoscopy at 13 North American CF centres, reported that in participants younger than 2-years, non-traditional taxa, particularly *Streptococcus*, comprised approximately half of the lower airway microbiota, while in those older than 6-years, the microbiota was frequently dominated by traditional pathogenic taxa [13]. Similarly, in a contemporary Australian cohort of 46 preschool children (median age 1.95-years (25^{th}-75^{th} percentile 1.13–4.06-years) routinely prescribed antibiotic prophylaxis until age 2-years, a distinct progression of the lower airway microbiota was described; from relative sterility in infancy, to dominance of bacterial sequences common to the oropharynx by age 2-years and dominance of traditional CF pathogens in participants older than 4-years [26]. Our data in infants not prescribed routine antibiotic prophylaxis identified a different, likely pathogenic microbiota even in the first six months of life in infants with CF.

The influence of prophylactic antibiotics on the early lower airway microbiota is highlighted in our recent comparison of BAL samples from 17 Australian infants prescribed antibiotic prophylaxis (age 3.5±0.9-months) and 15 North American infants (age 6±1.6-months) [27]. In that study, alpha-diversity was lower in the youngest infants and in those prescribed anti-staphylococcal prophylaxis, and decreased alpha-diversity was associated with decreased airway inflammation. Neither alpha-diversity nor microbiota composition was influenced by intermittent use of treatment antibiotics. Unlike the current study however, these studies lacked non-CF controls.

The present study systematically described the lower airway microbiota of non-CF infants without significant lower airway pathology. Not unexpectedly, the composition of the lower airway microbiota differed substantially from previous descriptions of the healthy upper

airway microbiota [28–30]. The most prevalent genera in the lower airways of infants without CF were *Streptococcus* and *Neisseria*, with relative absence of the skin flora typically encountered in the nasopharynx, specifically *Staphylococcus, Dolosigranulum* and *Corynebacterium*. *Moraxella* and *Haemophilus*, which are also commonly reported in upper airway samples, had a median relative abundance of 0.2% and 0.09% respectively in control BAL samples. While these BAL samples were obtained from infants with stridor, without evidence of concomitant infection, they emphasise the significant distinctions between the upper and lower airway microbiological communities in health.

This study has a number of important limitations. Firstly, it involved the retrospective analysis of BAL samples collected approximately 20-years earlier and is limited by small sample size, including of antibiotic-naïve CF infants, and a 3.2-month difference in median age between the CF and control populations. If the lung microbiota follows a similar ontogeny to that of the human gut, with increase in bacterial diversity and changes in response to weaning and diet, then the older age of the subjects without CF may have favoured a more diverse lung microbiota. However, maturation of the human lung microbiota during infancy has not been studied.

Samples were subject to strict storage conditions and analysis criteria to minimise the impact of time on the quality of 16S rRNA gene data. We have previously demonstrated that these data correlated both with culture results obtained contemporaneously on the same BAL samples [14] and with descriptions of the lower airway microbiota in older participants, suggesting that they accurately reflect the lower airway microbiota. We have been unable to differentiate 16S rRNA gene reads corresponding to the *Staphylococcus* genus to a species level, however our earlier analysis demonstrated correlation between the detection of *Staphylococcus* by molecular analysis and the finding of *S. aureus* in the corresponding BAL culture and the presence of pulmonary inflammation [14]. While quantitative PCR was not performed, normalisation techniques were employed to minimise bias in analysis of differential abundance of individual genera in these small volume, low bacterial load samples [21].

16S rRNA gene analysis of eight BAL samples from infants with CF returned fewer than 1000 reads and could not be included for analysis of microbiota composition. While potential differences in dilution were not controlled for, the sequences obtained from these BAL samples more closely represent the negative laboratory controls than the BAL samples of control infants, suggesting low bacterial biomass as a likely explanation for the low reads. Consistent with this, these BAL samples had lower total bacteria in quantitative culture and reduced IL-8, raising the possibility that the resident lower airway microbiota of “healthier” infants with CF had not yet become established, and emphasising that infection is indeed an important trigger for inflammation in early CF lung disease.

Lastly, this study included BAL samples from a control population of infants with stridor, primarily laryngomalacia, who were older than the study group of infants with CF. Obtaining lavage samples from healthy infants not otherwise requiring anaesthesia is ethically unjustifiable. We hypothesise that the lower airway microbiota of infants with laryngeal or subglottic pathology would potentially be more similar to that of infants with

CF than would be that of completely healthy infants and thus, the differences in lower airway microbiota between our infant cohorts highlight the significant alterations in the lower airway microbiota present early in CF lung disease.

This study provides further evidence that CF lung disease begins very early in life, with substantial differences in the lower airway microbiota established soon after birth, and most pronounced in symptomatic infants. The lower airway microbiota is dynamic and there is increasing evidence that age and/or disease progression and antibiotic prophylaxis influence its composition. It will be important to determine how the earliest changes in the lower airway microbiota described in this study are associated, or even implicated, with the development of lung damage in CF. It is also possible that altering the lower airway microbiota in CF infants to have a similar composition and structure to that of the healthy infant's lower respiratory tract could be a potential therapeutic strategy to prevent progression of early lung disease. Further longitudinal studies, including long-term outcome measures in both infants with CF and age-matched controls are required to better understand the clinical significance of these changes.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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ABBREVIATIONS

16S rRNA	16S ribosomal RNA
BAL	Bronchoalveolar lavage
CF	Cystic fibrosis
IL-8	Interleukin 8
NE	Neutrophil elastase

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HIGHLIGHTS

- The lower airway microbiota is altered substantially in infants with cystic fibrosis
- Differences appear within the first six months of life
- Differences are most apparent in symptomatic infants with cystic fibrosis
- Airway inflammation is associated with bacterial biomass

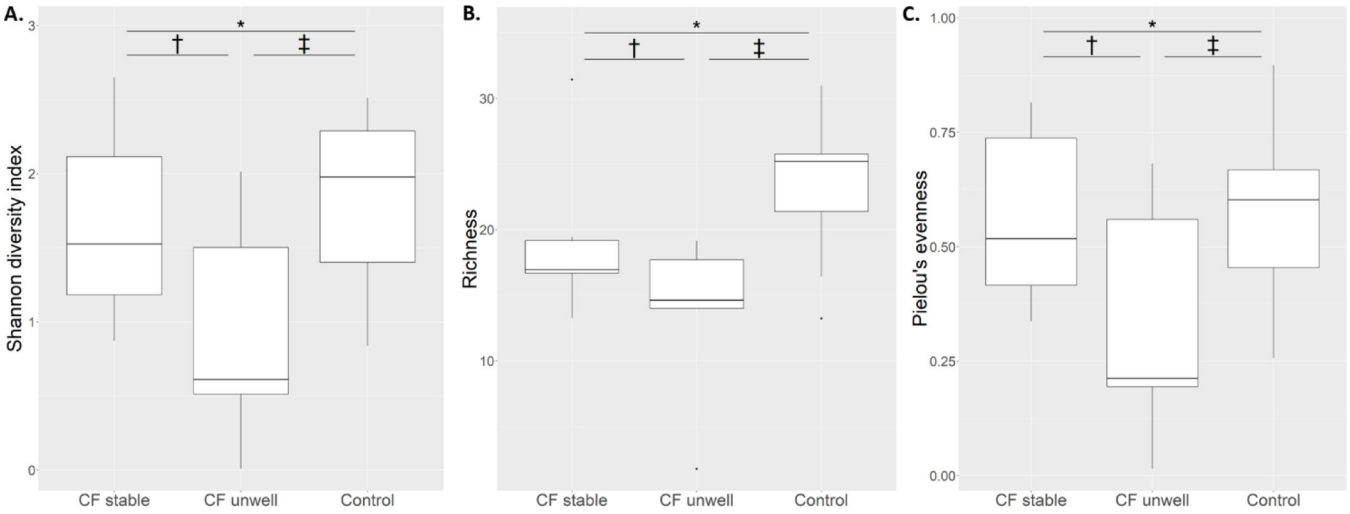

Figure 1: Alpha-diversity indices in bronchoalveolar lavage samples of stable infants with cystic fibrosis, unwell infants with cystic fibrosis and control infants.

1A: Shannon diversity index. *95% confidence interval (CI) of difference −0.53 – 0.76, p = 0.7; †95% CI of difference −0.3 – 1.72, p = 0.14 ; ‡95% CI of difference −0.16 – 1.82, p = 0.09. **1B: Microbial richness.** *95% CI of difference −1.26 – 10.17, p = 0.12; †95% CI of difference −3.18 – 13.9, p = 0.18; ‡95% CI of difference 1.32 – 18.31, p = 0.03; **1C: Pielou's evenness:** *95% CI of difference - 0.19 – 0.21, p = 0.91; †95% CI of difference −0.12 – 0.57, p = 0.16; ‡95% CI of difference −0.1 – 0.56, p = 0.14.

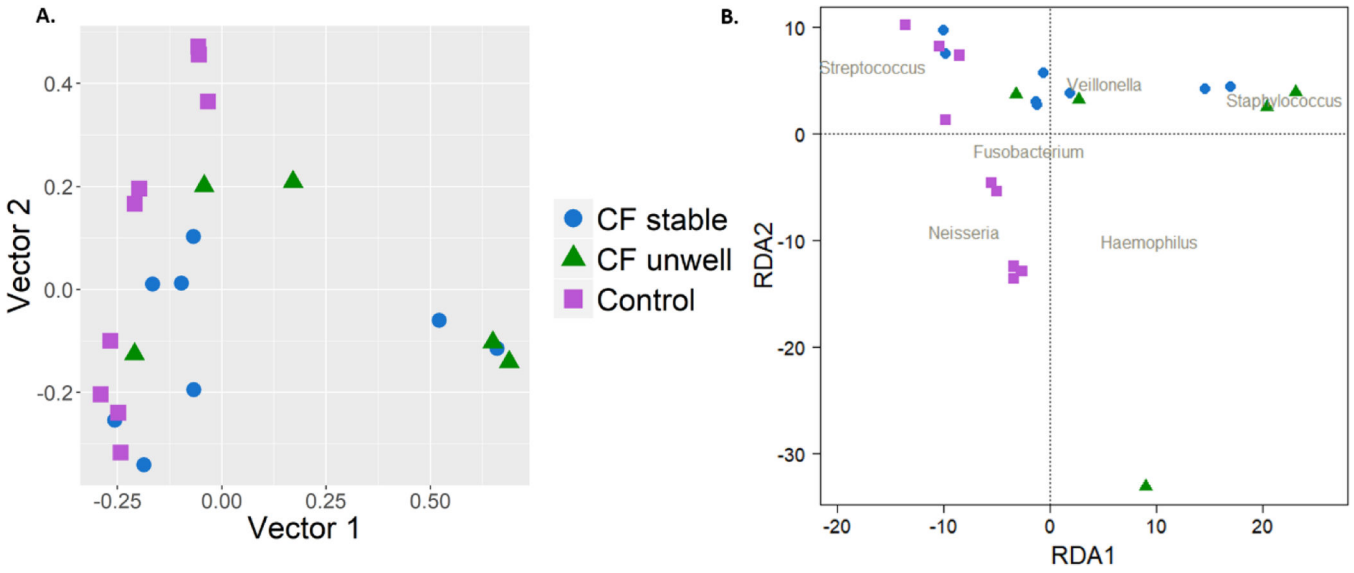

Figure 2:

Beta diversity of individual bronchoalveolar lavage samples. 2A: Principal coordinate analysis of bronchoalveolar lavage samples from stable and unwell infants with cystic fibrosis and control infants. 2B: Redundancy analysis plot of bronchoalveolar lavage samples, constrained by disease status.

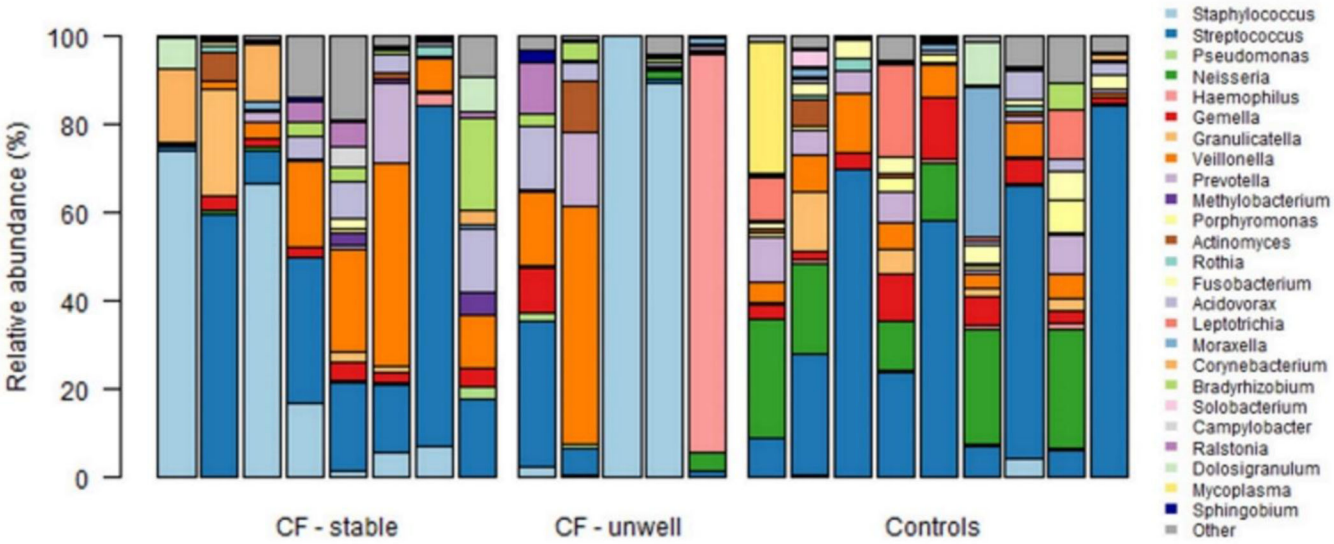

Figure 3: Composition of the lower airway microbiota of individual stable infants with cystic fibrosis, unwell infants with cystic fibrosis and control infants.

Each column represents a single bronchoalveolar lavage sample. The relative abundance of the individual genera, calculated from normalized data, is displayed in the stacked column graphs (range 0–100%), with each colour representing an individual genus. Genera with a mean relative abundance > 0.5% in any of the three subject groups are shown (see legend).

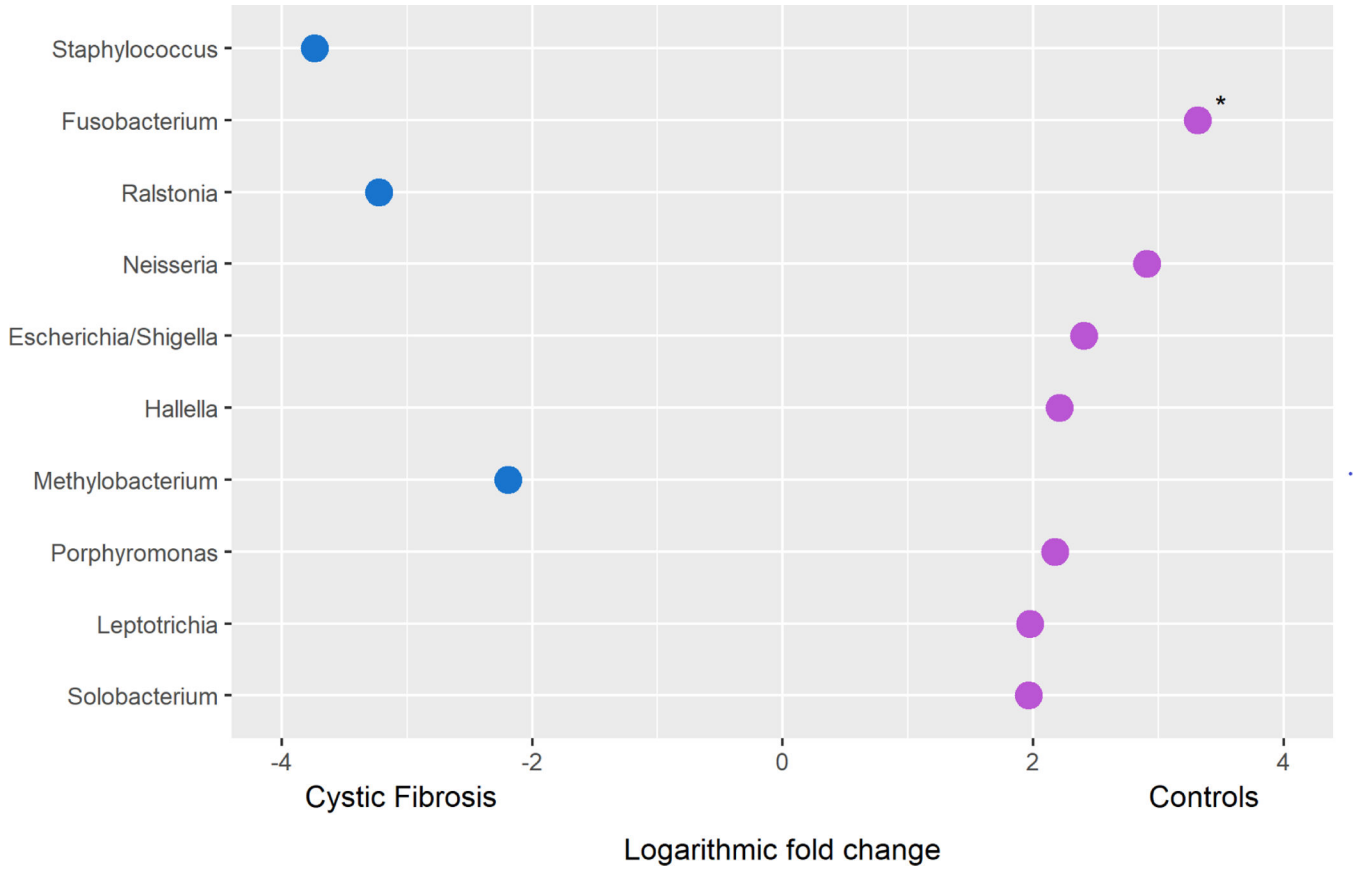

Figure 4: The differential abundance of individual genera in the lower airways of infants with cystic fibrosis compared to control infants.

The logarithmic (log_2) fold change of the top 10 ranked genera in a linear model fit assessing between-group differences of bronchoalveolar lavage samples is presented. Genera with increased relative abundance in infants with cystic fibrosis and controls are indicated in blue (●) and purple (●) respectively. * $p < 0.05$.

TABLE 1:

Subjects' clinical and bronchoalveolar lavage characteristics.

	Infants with CF* whose BAL samples yielded > 1000 16S rRNA gene reads (n=13)	Infants with CF whose BAL samples yielded < 1000 16S rRNA gene reads (n = 8)	p†	Control infants whose BAL samples yielded > 1000 16S rRNA gene reads (n=9)	p‡
Clinical characteristics					
Male, n (%)	7 (54%)	4 (50%)	1	7 (78%)	0.57
Age (months), median (25^{th}-75^{th} ile)	1.8 (1.5–3.1)	2.0 (1.7–2.4)	0.54	5.0 (2.9 – 8.2)	0.007
P.Phe508del homozygous, n (%)	11 (85%)	5 (63%)	0.53	-	-
Diagnosis by newborn screening, n (%)	11 (85%)	6 (75%)	1	-	-
Prior antibiotic exposure, n (%)	7 (54%)	4 (50%)	1	-	-
Respiratory symptoms at BAL, n (%)	5 (38%)	1 (13%)	0.43		
Antibiotics at BAL, n (%)	4 (31%)	0	0.24		
Bronchoalveolar lavage features					
Bacterial colony forming units/mL, median (25^{th} – 75^{th} ile)	1.94×10^4 (6×10^3 – 6.3×10^5)	645 (0.75–1635)	0.008	5.83×10^4 (1.11×10^4 — 2.02×10^5)	0.9
Interleukin-8 (pg/mL), median (25^{th} – 75^{th} ile)	79 (56–195.6)	30 (25–36) §	0.03	41 (22.1–71) §	0.21
Neutrophil elastase (mcg/mL), median (25^{th} – 75^{th} ile)	6.2 (2.5–16.1)	4.2(2.5–8.6) **	0.37	2.5 (2.5–5.1) §	0.33

*CF: Cystic fibrosis

†Comparison between infants with CF whose bronchoalveolar lavage samples yielded greater than or fewer than 1000 16S rRNA gene sequence reads respectively. Chi-square test for categorical variables; t-test for parametric continuous variables; Whitney test for non-parametric continuous variables

‡Comparison between infants with CF and control infants whose bronchoalveolar lavage samples yielded greater than 1000 16S rRNA gene sequence reads. Chi-squared test for comparison of categorical variables; Mann Whitney test for comparison of continuous variables

§Missing data from three participants
Missing data from one participant

**Missing data from two participants