Spitting images of COPD: The salivary microbiome discriminates between respiratory diseases

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Background:

The microbiome refers to the totality of microorganisms and their collective genetic material present in or on the human body or in another environment. Assessments of microbiomes are based on the use next generation sequencing (NGS) approaches to provide information of microbial genomes extracted from a particular source, without having to isolate and culture them. This allows not only definition of the bacterial population down to that of strains of a bacterial species but also will show how the overall function of the bacterial population is changing.

The microbiome is recognised as contributing to human health, responsiveness to drugs and as an aid in rapid diagnosis of respiratory disease. This could influence anaesthetic strategies in critically ill patients with chronic obstructive pulmonary disease (COPD). Saliva collection is relatively easy, painless and noninvasive. NGS allows subsequent isolation of the salivary microbiome with excellent quality and integrity.

Objective:

Our objective was to analyse the salivary microbiome in order to identify differences between various chronic respiratory diseases to facilitate treatment strategies in patients with COPD during anaesthesia and intensive care.

Materials and Methods:

Following approval by NHS Research Ethics Committee (Wales REC 7) and trial registration (16/WA/0036), 74 patients were enrolled into 3 groups from February to August 2016. Group A comprised 19 healthy controls, Group B of 47 patients diagnosed with COPD and Group C of 8 patients with non-small cell lung cancer (NSCLC). Group B further comprised two groups: B1 (baseline COPD with 40 patients) and B2 (exacerbation of COPD with 7 patients). Saliva samples were collected and total genomic DNA was extracted from 50µl of using the FastDNA Spin Kit. Sequencing of the 16S rRNA gene with PCR amplification of the V3 and V4 region was carried out. Specific “barcode” primers were used for each and sequenced on Illumina MiSeq platform. Derived data were assessed following European Nucleotide Archive (ENA) pipelines for metagenomic analysis to identify bacterial constituents.

Results:

The most remarkable findings were that Staphylococcus levels were relatively low in Groups A, B1 and C but high in Group B2. This is illustrated in the Figure 1. Figure 2 depicts the full pattern of bacterial growth according to disease group. The profile of Group B2 stands out as being significantly different from the other 3 groups. These bacterial changes in microbiome are likely to reflect changes in pathogenic and pro-inflammatory potential and abilities to metabolise drugs.

Discussion:

Results from this preliminary analysis indicate that the salivary microbiome may be useful in stratifying various respiratory disease states. Despite the widespread use of antibiotics in exacerbation of COPD the evidence for their use is surprisingly weak. Antibiotic treatment could bias the microbiome towards the selection of more lethal pathogens.

The results reveal the importance of the salivary microbiome in respiratory disease with possible significant implications in terms of diagnosis and treatment in patients during anaesthesia and intensive care.

Fig. 1 – Heat Map:
Analysis of bacterial concentration in saliva

Fig. 2 – Box and Whisker plot:
Analysis of bacterial concentration in saliva