Microbial Composition in the Nasopharynx of Children with and without Viruses during Asthma Exacerbations.

Caitlin R Murphy, MBBS1; Michael S Robeson II, PhD1; Darrell L Dinwiddie, PhD2; Joshua L Kennedy, MD1, 2

1University of Arkansas for Medical Sciences; 2Arkansas Children’s Research Institute, Little Rock, AR

Abstract

Introduction

The years, microbiome research has attempted to elucidate the role of microbial composition to respiratory tract that is

Methods

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Results

Viral Genomes

Microbiome

Figure 1. Methods. DNA was harvested using the Zymo Microbiomes kit. Amplification of 16S rRNA genes 12-25 was conducted using primer sets that targeted regions of the gene and generating fast read Illumina bar code adapter sequences. A record high eight-fold PCR was conducted to add the Illumina bar code adapter sequences to each sample. Sequencing was performed on Illumina HiSeq 2500 at each sample. Analysis was conducted using the mothur pipeline. A total of 16,298 OTU (SILVA 138) was obtained and were analyzed using V.43.01 pipeline. Data were clustered by weighted UniFrac and LDA discriminator to identify differences in microbial composition between the communities. The communities were clustered into three groups: controls, virus-only, and asthma-only.

Figure 2. Prevalence of Viral infections in the population.

Isolate DNA/RNA

Table 1. Demographics.

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