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Metagenomic Profiling and Characterisation of the Upper Respiratory Tract Virome in a Longitudinal Cohort of Asthmatic Patients and Healthy Volunteers

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Asthma is a heterogeneous chronic inflammatory disorder that affects millions of people worldwide, posing a significant societal and economic burden. Scientific findings suggest that distinct microbial and viral communities of the respiratory tract characterize each individual, similarly to what is known about the gut microbiome. However, the virome of asthma patients appears to be more variable compared with healthy individuals as it has been demonstrated that children with asthma have a characteristic virome that correlates to disease severity and control. This project is part of the CURE (Construction a Eubiosis Reinstatement Therapy for Asthma) program that has the long-term ambition to develop phage-based treatments for patients with asthma.

Here, we present the analysis of 201 respiratory tract DNA samples of 11 asthmatic patients (cases) and 7 healthy volunteers (controls) from Greece, taken at regular intervals within a period of 12 months. We perform a taxonomical profiling of the samples using up to date databases (NCBI BLAST-Nr database, 2022). We describe the key characteristics of each patient including the most abundant species/genera/families, species richness and alpha diversity. In total we identify 267 distinct viral species out of which 37 (13.86%) belong to the family of *Anelloviridae*, 34 (12.73%) to the family of *Retroviridae* and 25 (9.36%) to the family of *Papillomaviridae*. Nonetheless the majority of the viral species identified (125 – 46.8%) belong to the order of *Caudovirales* indicating the importance of bacteriophages in the human virome.

Focusing on the virome of each individual, we present an annotated phylogenetic tree indicating the species present in each patient and identify differentially expressed viral species in health and disease, using a generalised linear model (glm) approach with the aim of using lung virome characteristics as potential biomarkers of severity and exacerbation prediction. Initial results indicate that 22 viral species are associated with either asthmatic patients or healthy volunteers. Out of these species, 11 (50%) are bacteriophages.