Type-2 inflammation reduces SARS-CoV-2 replication in the airway epithelium in allergic asthma through the functional alteration of ciliated epithelial cells

Authors: Naresh Doni Jayavelu, PhD^{1*}, Matthew C. Altman, MD^{1,2*#}, Basilin Benson, MS², Matthew Dufort, PhD¹, Elizabeth R. Vanderwall, BS³, Lucille M. Rich, BS³, Maria P. White, BA³, Patrice M. Becker, MD⁴, Alkis Togias, MD⁴, Daniel J. Jackson, MD^{5**}, Jason S. Debley, MD, MPH^{3,6**}

ONLINE DATA SUPPLEMENT

 Table E1: List of DEGs comparing samples with SARS-CoV-2 virus and with or

 without IL-13 stimulation in allergic asthma and healthy children (excel file).

Table E2: List of genes whose expression is positively correlated with viral load and down-regulated by IL-13 stimulation or genes whose expression is negatively correlated with viral load and up-regulated by IL-13 stimulation identified from bulk and 10X data in allergic asthma children (excel file).

Table E3: List of genes whose expression is positively correlated with viral load and down-regulated by IL-13 stimulation or genes whose expression is negatively correlated with viral load and up-regulated by IL-13 stimulation identified from bulk data in healthy children (excel file).

Table E4: Number of cell counts for cell clusters (cell types) for allergic asthma and healthy children from 10X data (excel file).



Figure E1: (A) ACE2 expression relative to healthy AEC cultures, normalized to GAPDH expression. (B) Therehold cycle (Ct) values for GAPDH expression by AEC cultures from healthy and asthma donors. (D) ACE2 expression relative to healthy AEC cultures, normalized to HPRT expression. (D) ACE2 expression relative to healthy AEC cultures, normalized to PPIA expression. (E) ACE2 expression in uninfected and SARS-CoV-2 infected healthy AEC cultures. (F) ACE2 expression in uninfected and SARS-CoV-2 infected asthma AEC cultures. **p<0.001 (paired ttest); ****p<0.0001 (Wilcoxon matched-pairs signed rank test).

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Figure E2: Plot showing correlation between SARS-CoV-2 viral copy number in infected cultures and ACE2 protein abundance in parallel uninfected cultures from healthy controls (A) and allergic asthma (B). Spearman r and p values are shown on the plots.



Figure E3: Distribution of samples on PCA by batch (A) and condition (B). Samples from the same donor are connected by lines.



PROCH

CD47

CD74

ò

log2(FC)

TRAFD1

CASPa DDX60

5

LPAR6

IFITM1 CIS IFI44L XIXI ELF1 CXCL10 USP18

CMPK2-NCOA7

-5

3

0



(+) IL-13

P = 0.00066

P = 0.000042

(-) (+) IL-13 IL-13

(-) IL-13

(+) IL-13

o log2(Fold Change) -5

Figure E4: (A-F) Examples of ciliated marker genes showing positive association between viral load and expression (scatter plots) and significant differential expression with IL-13 stimulation (box plots). (G) Volcano plot showing the differentially up- and down-regulated genes by IL-13 stimulation. Select interferon type-I genes are highlighted and up-regulated and down-regulated genes are denoted by blue and red color points, respectively. (H) Scatter plot showing the association between viral load and IL-13 induced differential gene expression. The X-axis represents the change in expression due to IL-13 stimulation, and the Y-axis the correlation to viral load. The color of the point shows the statistical significance of differential expression [-log10(adj.P)]. Select interferon type-I genes are highlighted by larger point size.







Figure E5: UMAP clustering and visualization of scRNA-seq data from AECs from two children with allergic asthma separated by stimulated condition (SARS-CoV-2 infection with or without IL-13) (A) and by donor id (B). (C) Dot plot showing expression of key marker genes used for annotation of UMAP clusters to known cell types. Color denotes magnitude of marker genes expression and size of the circle denotes percent of cells expressing the markers. (D-E) Cell type specific viral loads in allergic asthma samples infected with SARS-CoV-2 without and with IL-13 stimulated shown in each cell cluster on the UMAP.



Figure E6: (A) Cell type specific expression of genes showing positive association between viral load and expression and down-regulated by IL-13 stimulation from scRNA-seq data. Expression values are presented as the ratio of expression in the IL-13 stimulated compared to unstimulated condition on a log2 scale shown in each cell cluster on the UMAP. (B) Enriched GO terms for genes showing positive association between viral load and expression and down-regulated by IL-13 stimulation from scRNA-seq data in allergic asthma. The size of each dot denotes the percent of genes and the intensity of color denotes statistical significance as log10(adj.P).



ZTFL1

DNAH5

PH1

4 –2 0 2 Asthma, log2(FC)

CCDC153

4 6 8 -2

-3

-5

-5

SERPIN

-4

Asthma, log10(adj.P)

-1

Ó

В

0

-2

-4 C200

-6

-8

SCGB3A

-6 -4

-8

FAM183A

Α

Figure E7: (A) Examples of select ciliated marker genes association between delta viral load (difference in viral load between IL-13 stimulated and unstimulated) and delta expression (difference in expression between IL-13 stimulated and unstimulated) in allergic asthma and healthy non-sensitized donors. Scatter plots comparing (B) effect sizes (log2FC) and (C) statistical significance (adjusted P.values) due to IL-13 stimulation in allergic asthma and healthy non-sensitized children. Select ciliary and type 2 specific genes are highlighted the same as in Figure 2c and Figure 4c.



Figure E8: (A-B) Cell type specific viral loads in healthy non-sensitized AEC samples infected with SARS-CoV-2 without and with IL-13 stimulated shown in each cell cluster on the UMAP.