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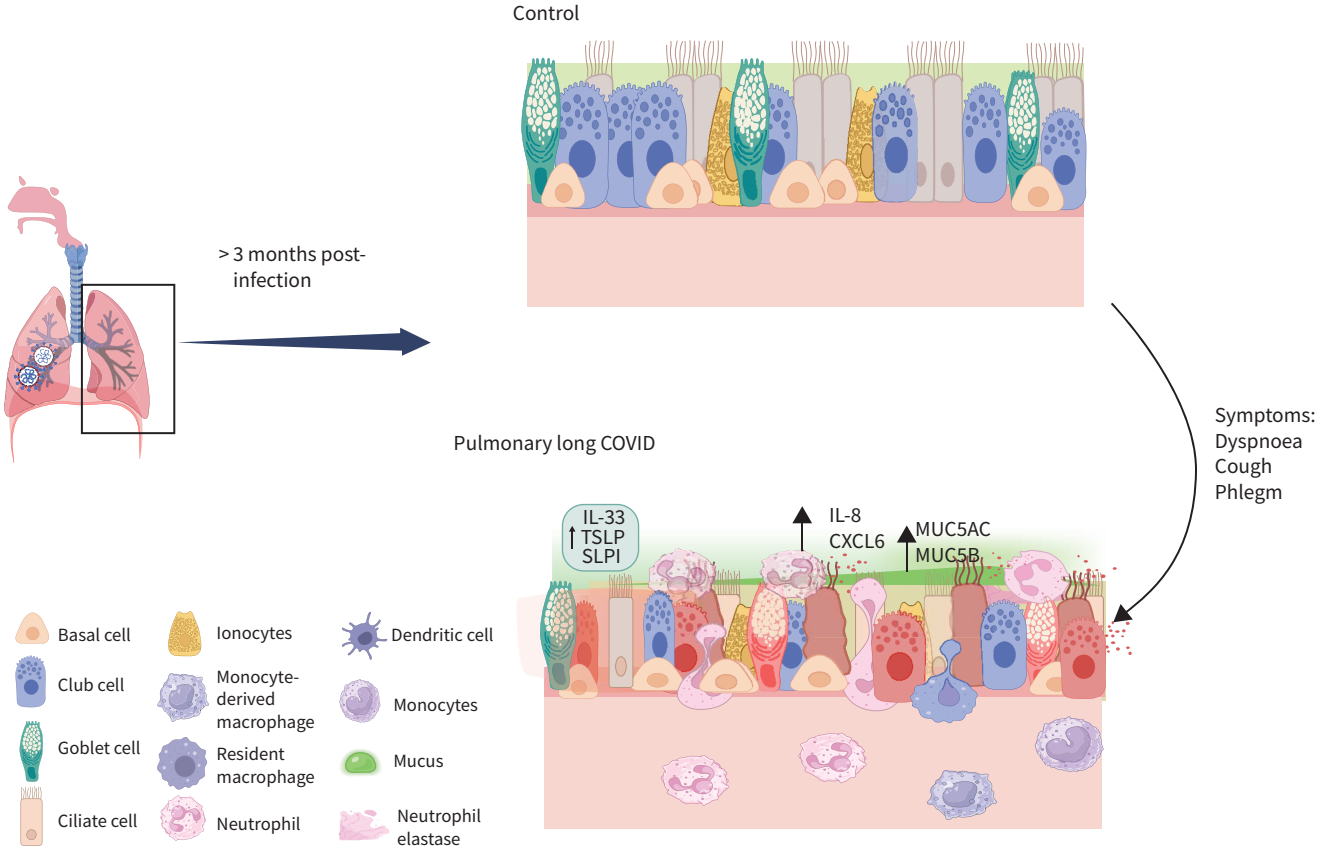

GRAPHICAL ABSTRACT Overview of the study. IL: interleukin; TSLP: thymic stromal lymphopoietin; SLPI: secretory leukocyte protease inhibitor.

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Shareable abstract (@ERSpublications)
Single-cell profiling shows infiltration of neutrophils with upregulation of inflammatory chemokines and mucin genes in the airway mucosa of patients with pulmonary long COVID, indicating persistent small airway inflammation in pulmonary long COVID https://bit.ly/3XieXQN

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Abstract

Aim To elucidate the important cellular and molecular drivers of pulmonary long COVID, we generated a single-cell transcriptomic map of the airway mucosa using bronchial brushings from patients with long COVID who reported persistent pulmonary symptoms.

Method Adults with and without long COVID were recruited from the general community in Greater Vancouver, Canada. The cohort was divided into those with pulmonary long COVID, which was defined as persons with new or worsening respiratory symptoms following ⩾12 weeks from their initial acute severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection (n=9); and control subjects defined as SARS-CoV-2 infected persons whose acute respiratory symptoms had fully resolved or individuals who had no history of acute coronavirus disease 2019 (COVID-19) (n=9). These participants underwent bronchoscopy from which a single cell suspension was created from bronchial brush samples and then sequenced.

Results A total of 56 906 cells were recovered for the downstream analysis, with 34 840 cells belonging to the pulmonary long COVID group, which strikingly showed a unique cluster of neutrophils in the pulmonary long COVID group ($p<0.05$). Ingenuity Pathway Analysis revealed that the neutrophil degranulation pathway was enriched across epithelial cell clusters. Differential gene expression analysis between the pulmonary long COVID and control groups demonstrated upregulation of inflammatory chemokines and epithelial barrier dysfunction across epithelial cell clusters, as well as over-expression of mucin genes across secretory cell clusters.

Conclusion A single-cell transcriptomic landscape of the small airways suggest that neutrophils may play a significant role in mediating the chronic small airway inflammation driving pulmonary symptoms of long COVID.

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