

Transcriptional profiling of immune and inflammatory responses in the context of SARS-CoV-2 fungal superinfection in a human airway epithelial model

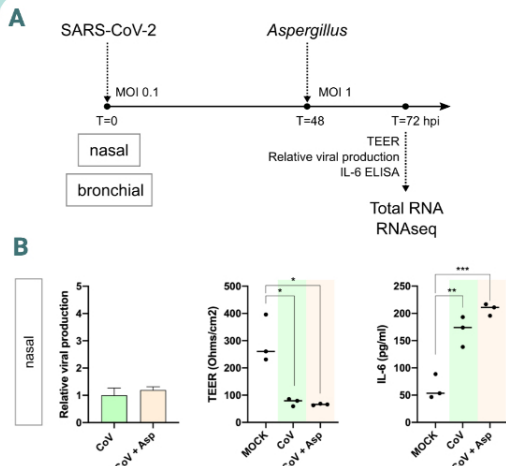
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Context

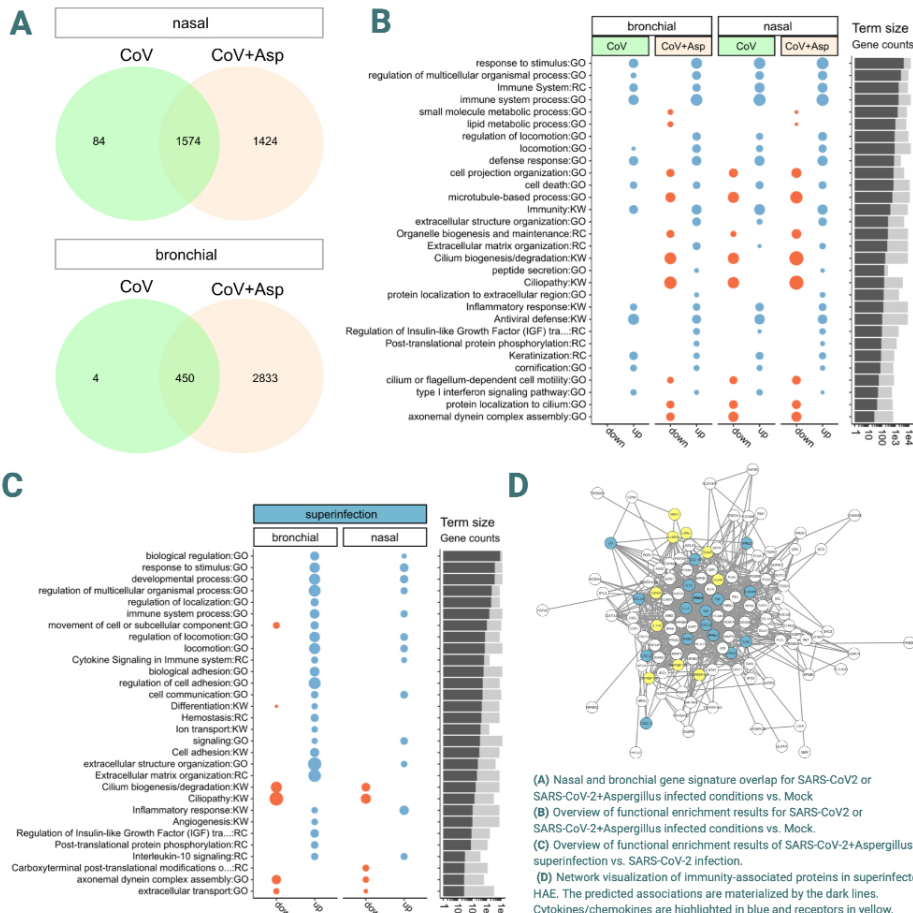
- Fungal superinfections can affect the course and severity of respiratory viral infections
- Several reports indicating high prevalence of *Aspergillus* superinfections associated with COVID-19
- => **Reasons for increased vulnerability to *Aspergillus* in COVID-19 patients?**
- => **Contribution of *Aspergillus* to SARS-CoV-2 related lung inflammation and COVID-19 pathophysiology?**

Experimental strategy



(A) Overview of experimental strategy (B) At 72h post-infection, for both nasal and bronchial HAE model, the relative viral production (intracellular) was determined using RTqPCR, and the impact of infection on epithelium integrity was monitored by measure of the transepithelial resistance (TEER Ohms/cm2). IL-6 was measured at the apical using a specific ELISA assay.

Results

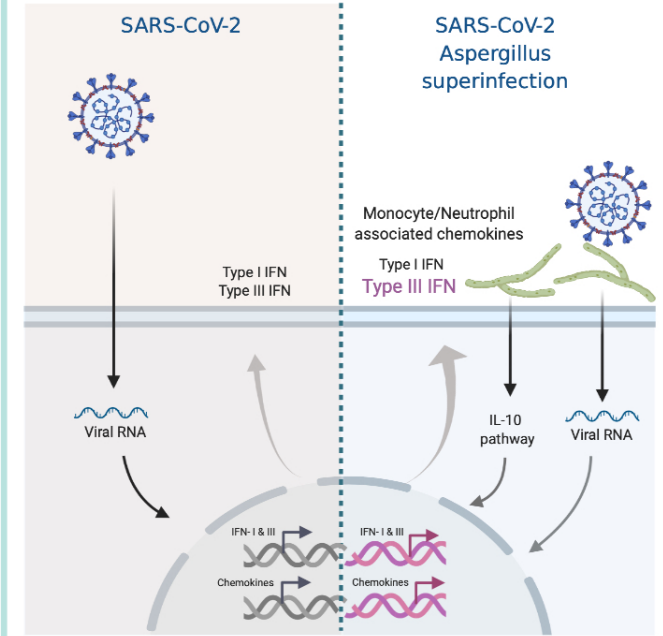


C

D

Key findings

- Unique transcriptional footprints of superinfection**
 - imbalanced type I/type III IFN
 - monocyte and neutrophil associated chemokines
- SARS-CoV-2 -induced immunomodulation**
 - => Favorable context for severe forms of Aspergillosis
- Treatments targeting COVID-19 inflammatory response**
 - => Counter-productive for the management of Aspergillosis?



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The authors declare that they have no conflict of interest.
Preprint available: <https://www.biorxiv.org/content/10.1101/2020.05.19.103630v1>