Does asthma make COVID-19 worse?

There is active interest in reconciling the tremendous variation observed in COVID-19 outcomes with host immunity. In this preprint, Sajuthi et al. analyse nasal airway epithelial transcriptomes from a large cohort of healthy and asthmatic subjects to distinguish relative contributions of host immune networks to coronavirus susceptibility. They use network co-expression analyses and transcriptomics on mucociliary cultures to show that genes implicated in SARS-CoV-2 infectivity, specifically TMPRSS2 and ACE2, are significantly influenced by type 2 cytokine-driven inflammation and interferon signalling, respectively. Although SARS-CoV-2-specific analysis and experiments are lacking, the study provides a rationale for why type 2 responses, which are aggravated in patients with asthma, might increase susceptibility to severe COVID-19.

ORIGINAL ARTICLE Sajuthi, S. P. et al. Type 2 and interferon inflammation strongly regulate SARS-CoV-2 related gene expression in the airway epithelium. Preprint at bioRxiv https://doi.org/10.1101/2020.04.05.034454 (2020)

Neutralizing antibody response in mild COVID-19

This preprint reports robust induction of SARS-CoV-2-specific neutralizing antibodies in 94% of 175 patients with clinically mild COVID-19 within 2 weeks of symptom onset. Compared with younger patients, middle-aged and older patients in this cohort had higher titres of neutralizing and binding antibodies. As older patients are generally considered at greater risk of severe disease, the robust humoral responses in this cohort may explain their apparent protection. Of note, 10 of 175 patients recovered without developing detectable neutralizing antibody titres, suggesting that antiviral binding antibodies and cellular immune responses can both result in convalescence. Longitudinal observations in addition to stringent clinical and immunological characterization are needed to further assess the specificity and relative contribution to protection of neutralizing antibodies against SARS-CoV-2.

ORIGINAL ARTICLE Wu, F. et al. Neutralizing antibody responses to SARS-CoV-2 in a COVID-19 recovered patient cohort and their implications. Preprint at medRxiv https://doi.org/10.1101/2020.03.30.20047365 (2020)

Cancer therapy tool informs COVID-19 vaccines

T cell vaccines against SARS-CoV-2 are being developed at a rapid pace, but it is imperative that the proteins or peptides they deliver bind to a large variety of HLA haplotypes in the global population. Using a computational tool designed to predict candidate neoantigens for cancer vaccines, this preprint identifies 1,103 unique 9-mer antigens from the SARS-CoV-2 peptidome, each of which binds to a median of 3 of 1,022 HLA class I alleles. This resulted in 6,748 peptide–MHC pairs with high binding affinity. Up to 684 peptides were derived from each viral protein tested. Furthermore, 12 of the identified SARS-CoV-2 epitopes match SARS-CoV epitopes that were previously shown to generate T cell responses ex vivo and in vitro. This publicly available dataset will be an important resource to guide vaccine development.

ORIGINAL ARTICLE Campbell, K. M. et al. Prediction of SARS-CoV-2 epitopes across 9160 HLA class I alleles. Preprint at bioRxiv https://doi.org/10.1101/2020.03.30.016931 (2020)

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