Blood samples were collected from 10 patients in the ADAPT* study that had long-COVID symptoms two years after their original infection with SARS-CoV2.

An additional 10 blood samples were collected from patients that were also infected but had fully recovered. In each of these groups, we have 5 females and 5 males, age matched. The severity of the original illness was classified based on hospital admission.

Samples are currently being sequenced on the 10X genomics platform. We are using the 5' gene extraction blood protocol and VDJU profiling of B-cell and T-cell receptors.

This will provide transcriptional profiles for each sex and age group. The analysis is useful for evaluating the diversity of an immune system.

Immune profiling of peripheral blood mononuclear cells (PBMCs)

Exploring sex differences of long-COVID-19 at single-cell resolution

Single-cell RNA-seq for cellular resolution of gene expression

Pathway enrichment analysis

Questions to explore:

What genes and pathways are differentially expressed in long-COVID?

Are these the same when we look at sex-specific differential expression?

Are there cell-type differences between cases and those who recover?

What other cellular or gene profiles are associated with long-COVID symptoms?

Interferons
Inflammatory cytokines
Lymphocyte activation and dysregulation
Chronic myeloid cell activation

Autoimmunity
Long-COVID hypotheses
Dysbiosis
Tissue damage

Viral reservoirs or viral remnants

More males die from COVID-19 complications while females suffer more from long-COVID

Death rates are different across sex and age

Long-COVID refers to persistent symptoms beyond 3 months of infection

Interested? Reach out!

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Additional: The immunology and immunopathology of SARS-CoV-2 infection (2022)