Description of BQC19 JGH Site Samples

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In total, the JGH Site of the BQC19 has collected samples and/or data from 1428 individuals. Peripheral blood mononuclear cell samples were collected from 890 individuals at different time points (for a total of 1472 samples) and Plasma samples were collected from 1317 individuals at different time points (for a total of 2304 samples). All subjects were tested with SARS-CoV-2 PCR nasal swabs at the JGH.

The characteristics of this data and sample collection are below. Planned and funded analyses are also listed and new proposals that overlap with these planned analyses will not be considered.

BQC19 at the JGH.

Inclusion criteria:

1. Underwent a nasal swab for clinical reasons at a hospital for SARS-CoV-2 testing
2. Cases are those who were PCR positive for SARS-CoV-2. Most patients were admitted.
3. Controls are those who were negative and most were admitted to hospital for other reasons.

Subjects who were SARS-CoV-2 positive represent more severe infection than those discharged, since they were admitted to hospital. Controls, who are those who were negative on all SARS-CoV-2 swabs, but had symptoms, or history, consistent with infection, but no evidence of infection on PCR testing. Approximately half of the sample are cases and half controls. Subjects have been consented for use of ***all data*** captured during their clinical care (including all laboratory, medications, treatment, radiology, viral data etc…), genomics and re-contact for future studies, and sample collection. Samples were collected at day 0, day 2, day 7, day 14 and day 30 for participants remaining in the hospital, when available. Follow-up post-discharged visits on approximately day 30, day 180, and day 365 have started and additional follow-ups on day 730 are planned. Blood samples were collected on day 90, but there is no actual follow up data for this time point.

The data and samples collected to date on Hospitalized subjects include:

- Extensive risk factor measurement, comorbidities & medications through the WHO ISARIC Case Report Form
- Detailed hospitalization and outcome data, including level of respiratory support, laboratory data and interventions through the WHO ISARIC Case Report Form
    - Previous medical history in ICD-10 format
- PBMCs on participants are available at some time points
- Plasma, RNA (PAXGene tubes) on all participants at all available time points
- DNA on all subjects

It is paramount to recognize that samples were collected from COVID19 hot zones. Within these real-world conditions, sample collection was not standardized with regard to meal-times or time of day. We were only permitted to take blood when this was being drawn for clinical purposes. Samples were kept at room temperature until processing, which was often for hours. Samples were not kept on ice or refrigerated prior to processing. Thus, this represents a pragmatic collection. Note that not all individuals had samples taken.

Funded analyses that are underway

- Genome-wide genotyping and Whole-Genome Sequencing (WGS) of the host through the CanCOGeN initiative. DNA is extracted for ~ 1232 samples already and genome-wide genotyping is complete. DNA is being extracted on remaining samples and GWAS and WGS are complete too.
- Serology-based testing (funded by FRQS).
- Viral genome sequencing is being completed on all samples by the Laboratoire Santé Publique du Québec. We are trying to get this data.
- Large-scale proteomics, through measurement of 5,000 circulating proteins through SomaLogic’s SomaScan platform (funded by McGill’s MI4 Program, and the Richards lab). This is done for 800 samples to date.
- Whole-blood transcriptome profiling (funded by FRQS).