The COVID-19 MS Coalition—accelerating diagnostics, prognostics, and treatment

Rapid and comprehensive genetic sequencing has shed light on the origin of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and allowed timely implementation of PCR tests to determine the presence of viral RNA. PCR tests for SARS-CoV-2 are some way from being reliably qualitative and will never indicate how the disease might progress in an individual. As COVID-19 becomes endemic, there is a concomitant need for accurate serological assays to detect antibodies to SARS-CoV-2 antigens and ultimately tests for prognostic markers to target treatment options.[1,2] With this considerable genetic insight, and the emerging structural information, comes associated questions regarding the molecular descriptors that contribute to disease progression, especially when we consider spread across different populations. The power of mass spectrometry to generate rapid, precise, and reproducible diagnostic information that complements genomic information and accelerates our understanding of the disease, is now becoming a reality.[3,4]

Mass spectrometry-based analysis can answer questions broadly falling into two categories. The first concerns multi-omic profiling of the host response, correlating prognosis with disease severity. Robust biomarkers will further our understanding of disease mechanisms and the susceptibility of certain clinical groups. The most valuable of these prognostic markers will be those indicating the transition from a beneficial immune response to one that is harmful, ultimately resulting in respiratory distress. Such data will facilitate public health efforts for population screening, defining high-risk patients, tracking disease progression, and identifying sources of vulnerability that will permit treatment stratification and minimise or prevent future coronavirus pandemics.

The second category concerns the SARS-CoV-2 viral spike glycoprotein, which is not only key for host-cell attachment but is also a major target for neutralising antibodies elicited through vaccination. Although RNA sequencing is extraordinarily informative for viral mutation or adaptation via immune selective pressure, it cannot inform on a critical feature of enveloped viruses: viral spike glycosylation. The functional role of SARS-CoV-2 spike glycans, of which there are 66 per trimer,[5] is undetermined yet, along with associated conformational dynamics that shape receptor or antibody binding, a key factor for vaccine design. Investigating spike glycosylation and plasticity with advanced mass spectrometry methods on recombinant preparations and comparing this to wild type viral proteins is crucial to this effort.

The COVID-19 MS Coalition is a collective mass spectrometry effort that will provide molecular level information on SARS-CoV-2 in the human host and reveal pathophysiological and structural information to treat and minimise COVID-19 infection. Collaboration with colleagues at pace involves sharing of optimised methods for sample collection and data generation, processing and formatting for maximal information gain. Open datasets will enable ready access to this valuable information by the computational community to help understand antigen response mechanisms, inform vaccine development, and enable antiviral drug design. As countries across the world increase widespread testing to confirm SARS-CoV-2 exposure and assess immunity, mass spectrometry has a significant role in fighting the disease. Through collaborative actions, and the collective efforts of the COVID-19 MS Coalition, a molecular level quantitative understanding of SARS-CoV-2 and its effect will benefit all.

We declare no competing interests.

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Published **Online**
May 27, 2020
https://doi.org/10.1016/S0140-6736(20)31211-3

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