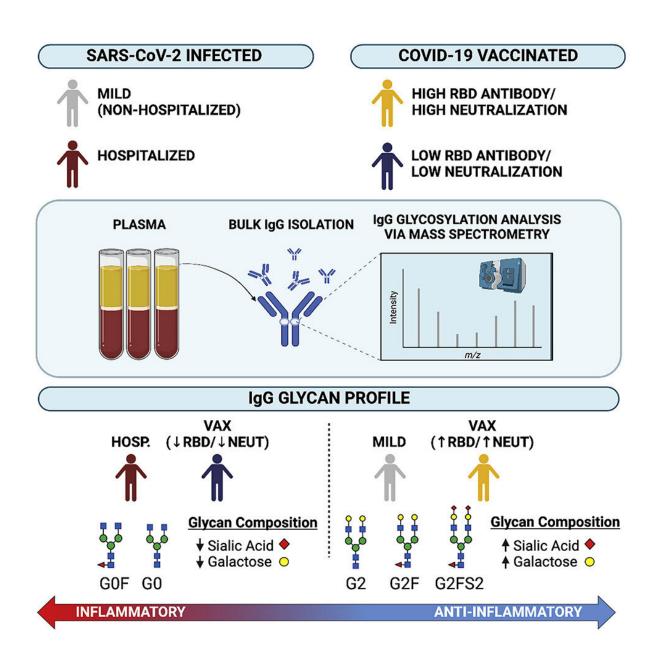


Antibody properties in plasma can predict COVID-19 severity

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Graphical abstract. Credit: *Cell Reports* (2022). DOI: 10.1016/j.celrep.2022.111799

Alterations in the biochemical makeup of bulk plasma IgG, or Fc glycosylation, can predict COVID-19 disease severity and vaccine antibody response, according to a recent study by researchers at RUSH University and Northwestern. The results of the study were recently published in *Cell Reports*.

While efforts to improve COVID-19 vaccines continue, there are still gaps in scientists' understanding of the body's immune response to this novel coronavirus. In partnership with Northwestern, researchers across multiple departments at RUSH University set out to gain insight about the inflammatory state of people infected with SARS-CoV-2 by investigating bulk IgG glycosylation changes in them as well as in vaccinated individuals. The RUSH team included researchers in the Department of Microbial Pathogens and Immunity, Department of Anatomy and Cell Biology and Division of Infectious Diseases.

"Building off data from the HIV and rheumatoid arthritis fields, we knew that characterizing biochemical changes in bulk IgG could be a readout for the inflammatory state in these conditions," said Jeffrey R. Schneider, Ph.D., assistant professor, Department of Microbial Pathogens and Immunity, RUSH Medical College. "Therefore, we set out to profile SARS-CoV-2 infected and vaccinated individuals to identify novel biomarkers for disease severity and vaccine antibody response, respectively."

The investigators reviewed samples of plasma from patient with mild COVID-19 and those hospitalized with the disease, and from vaccinated individuals. They found a correlation between people with increased



inflammatory glycans and COVID-19 disease severity. They also found that people vaccinated against COVID-19 with a low antibody response had a similar <u>glycan</u> profile as patients with severe infections.

The elevated inflammatory glycans in hospitalized COVID-19 patients increased over time, whereas patients with mild COVID-19 were found to have anti-inflammatory glycans that increased over time. One particularly important IgG Fc glycan which was elevated in mild individuals was sialic acid, a critical modulator of the anti-inflammatory response, which also correlated with elevated SARS-COV-2 antibody levels.

These findings are a step forward in COVID-19 severity prediction. The data suggests that the shift in antibody population dynamics, like the glycans reviewed in this study, could be crucial to whether or not an individual develops severe or mild COVID-19.

"We believe our findings can help provide an immunological fingerprint for COVID-19 disease severity and vaccine antibody response, which can be used to better diagnose those who may be pre-disposed to <u>severe</u> <u>disease</u>," Schneider said. "We hope to extrapolate the findings from this study to characterize disease severity in a panel of respiratory viruses such as influenza and <u>respiratory syncytial virus</u>, as well as emerging pathogens to come."

More information: Michelle K. Ash et al, Bulk IgG glycosylation predicts COVID-19 severity and vaccine antibody response, *Cell Reports* (2022). DOI: 10.1016/j.celrep.2022.111799

Provided by Rush University Medical Center



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