

From: [Regular Faculty in the Department of Medicine](#) on behalf of [Schwartz, David](#)
To: [dom-regularfaculty](#)
Subject: DOM Covid Communication
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Dear Friends and Colleagues.

I hope you and your families are doing well, and that you, like me, share the optimism associated with the marked decline in cases, new and better therapeutic options for our patients who develop SARS-CoV-2 infection, and the successful vaccination campaign. In addition, our clinical operations are beginning to return to normal, and steps are being taken to safely return our campus to more normal operations.

While lots of indicators are moving in the right direction, there are a couple of elements of uncertainty that justify consideration.

- Genetic variants of SARS-CoV-2 remain an issue, and will be the subject of Medical Grand Rounds (MGRs) this week - Eric Poeschla will present "Emerging SARS-CoV-2 Variants: Implications for the Pandemic, the Vaccines and our Patients" (Wednesday, 3/10 at noon). Dr. Poeschla heads up our division of Infectious Diseases and is an internationally recognized authority on RNA viruses. MGRs will prove to be an incredibly informative lecture and discussion, so try to make the time to attend. However, in advance of Dr. Poeschla's lecture, Eric and I would like you to know a few key points about the genetic variants of SARS-CoV-2:
 - The three main variants of concern remain B.1.1.7 (1st identified in the UK), B.1.351 (1st identified in South Africa) and P.1 (1st identified in Brazil).
 - B.1.1.7 and B.1.351 are known to be present in the US, but only B.1.1.7 has been detected in Colorado so far.
 - Colorado has reported about 190 cases of B.1.1.7, but the degree of sampling is low, here and nationally, so our knowledge is limited and it's likely cases are being underrepresented.
 - New variants of interest -- in California and New York -- have been reported in news media and a few non-peer-reviewed preprints, but the data are few and the importance and impact of these variants are not clear at present.
 - There is no evidence that variant B.1.1.7 significantly evades natural or vaccine-induced immunity. Some limited, early data from the U.K. suggest that B.1.17 could possibly be slightly more pathogenic, but this has not been verified. B.1.1. 7 does appear to be more transmissible, which is added reason to double down on our mitigation measures (masking, social distancing, etc).
- Covid-19 remains a disease that is heterogeneously distributed across our population and throughout the U.S.
 - Covid-19 is deeply rooted in healthcare disparity. When we examine those who have developed Covid, those who have died from Covid, and those who are receiving vaccines to prevent SARS-CoV-2 infection, it is clear that this disease has

- been disproportionately affected by race, ethnicity, and socioeconomics.
- Covid-19 is unevenly distributed across the U.S.
 - States, such as NY, New Jersey, Rhode Island, had a high incidence and are staying high
 - States, such as South Carolina, Georgia, and Kentucky, had a high incidence and are going down
 - States, such as Nebraska, Louisiana, and Maine, had a low incidence and are going up
 - States, such as Iowa, Idaho, and Ohio, had a low incidence and are staying low
 - While deaths nationally are going down, deaths in Virginia, Texas, Mississippi, Kentucky, D.C., Montana, Oregon, and Alaska are increasing
 - While some of this epidemiological heterogeneity can be explained on the basis of healthcare disparity, required social distancing, or vaccine distribution, some of this heterogeneity may reflect the biology of the virus. My point is that while we've learned a great deal, there remains unexplained patterns of disease, and we still have a great deal to learn. For example, we need to understand the seasonality of this virus, the expected baseline persistence of infections in our population, and the long-term sequelae of those who have been infected with SARS-CoV-2.
 - Bottom line, let's stick with what works – social distancing has to remain a priority.

I've drawn your attention to both the genetic variants of SARS-CoV-2 and the persistent heterogeneity of Covid-19 to alert you to the possibility that we may be faced with yet another surge of Covid-19 patients. Given how much we've learned about preventing transmission of SARS-CoV-2, caring for patients with this disease, how well we've mobilized and readjusted our medical teams, and how well we've worked together, I'm confident that we'll be able to address this challenge and other challenges that emerge from the pandemic.

I want to close by thanking all of you for everything you've done over the past year. I can't be more proud of our faculty, trainees, and staff. You are the reason for our success over the past year. Please let me know if you have questions or concerns. My very best wishes to you, your families, and your friends.

David

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