

To: [REDACTED] [REDACTED] [REDACTED]@rivm.nl]
From: [REDACTED] [REDACTED] [REDACTED]
Sent: Tue 1/5/2021 9:09:59 PM
Subject: Fwd: Delta 69/70 mutations and infectivity
Received: Tue 1/5/2021 9:11:11 PM
[Kemp - 6970 deletion variant.pdf](#)
[ATT00001.htm](#)

Sent by iPhone

Begin forwarded message:

From: " [REDACTED] [REDACTED] [REDACTED] " < [REDACTED]@amsterdamumc.nl >
To: " [REDACTED] [REDACTED] [REDACTED] " < [REDACTED]@amsterdamumc.nl >, " [REDACTED] [REDACTED] [REDACTED] " < [REDACTED]@amsterdamumc.nl >, " [REDACTED] [REDACTED] [REDACTED] " < [REDACTED]@amsterdamumc.nl >, " [REDACTED] [REDACTED] [REDACTED] " < [REDACTED]@amsterdamumc.nl >
Subject: FW: Delta 69/70 mutations and infectivity

Van: [REDACTED] [REDACTED] [REDACTED]@med.cornell.edu >
Verzonden: dinsdag 5 januari 2021 08:39
Aan: [REDACTED] [REDACTED] [REDACTED] < [REDACTED]@amsterdamumc.nl >
Onderwerp: Fw: Delta 69/70 mutations and infectivity

From: [REDACTED] [REDACTED]@med.cornell.edu >
Sent: Monday, January 4, 2021 5:30 PM
To: Korber, [REDACTED] [REDACTED]@lanl.gov >; [REDACTED] [REDACTED]@pennmedicine.upenn.edu >; [REDACTED] [REDACTED]@duke.edu >; [REDACTED] [REDACTED]@scripps.edu >; Dean, Natalie E < [REDACTED]@ufl.edu >; [REDACTED] [REDACTED]@yale.edu >; [REDACTED] [REDACTED]@scripps.edu >; [REDACTED] [REDACTED]@med.cornell.edu >
Subject: Delta 69/70 mutations and infectivity

I think [REDACTED] sent this round? Here's what I think... Solid but narrow in scope.

[Kemp SA, ... Gupta RK. 2020. Recurrent emergence and transmission of a SARS-CoV-2 spike deletion deltaH69/V70. bioRxiv preprint.](#)

This is a solid study of the effects of deleting residues 69 and 79 from the NTD of the S-protein. These sequence changes arise in the B117 UK, and other, problematic lineages, although not without other accompanying changes. The first part of the paper presents phylogenetic tree and geographic distribution data, before depicting where this deletion and other linked changes are located on the S-protein structure. The final figure is new. It illustrates the infectivity for 293T and HeLa-ACE2 cells of PVs based on the 614G sequence within and without the 69/70 deletions. For both cell types, the deletions confer an infectivity gain of 2-fold. That increase seems less (in previous papers, not this one) than is seen when D614G is compared with the original Wuhan strain. However, it's reasonable to think that the other mutations that co-segregate with the 69/70 deletion may confer additional infectivity boosts.