

Our July focus is an article in JVDI's upcoming September issue: "SARS-CoV2 spike protein gene variants with N501T and G142D mutation–dominated infections in mink in the United States," by Hugh Y. Cai, Allison Cai.

J Vet Diagn Invest 2021;33(5). <https://doi.org/10.1177/10406387211023481>

Abstract. Large numbers of mink have been infected with SARS-CoV2 containing the spike protein Y453F mutation in Europe, causing zoonosis concerns. To evaluate the genetic characteristics of the U.S. and Canadian mink–derived SARS-CoV2 sequences, we analyzed all animal-derived (977) and all Canadian (19,529) and U.S. (173,277) SARS-CoV2 sequences deposited in GISAID from December 2019 to March 12, 2021, and identified 2 dominant novel variants, the N501T-G142D variant and N501T-G142D-F486L variant, in the U.S. mink–derived SARS-CoV2 sequences. These variants were not found in mink from Canada or other countries. The Y453F mutation was not identified in the mink-derived sequences in the United States and Canada. The N501T mutation occurred 2 mo earlier in humans than in mink in the United States, and the novel N501T-G142D and N501T-G142D-F486L variants were found in humans prior to mink. Our results suggest that the novel SARS-CoV2 variants may have evolved during human infection and were then transmitted to mink populations in the United States.

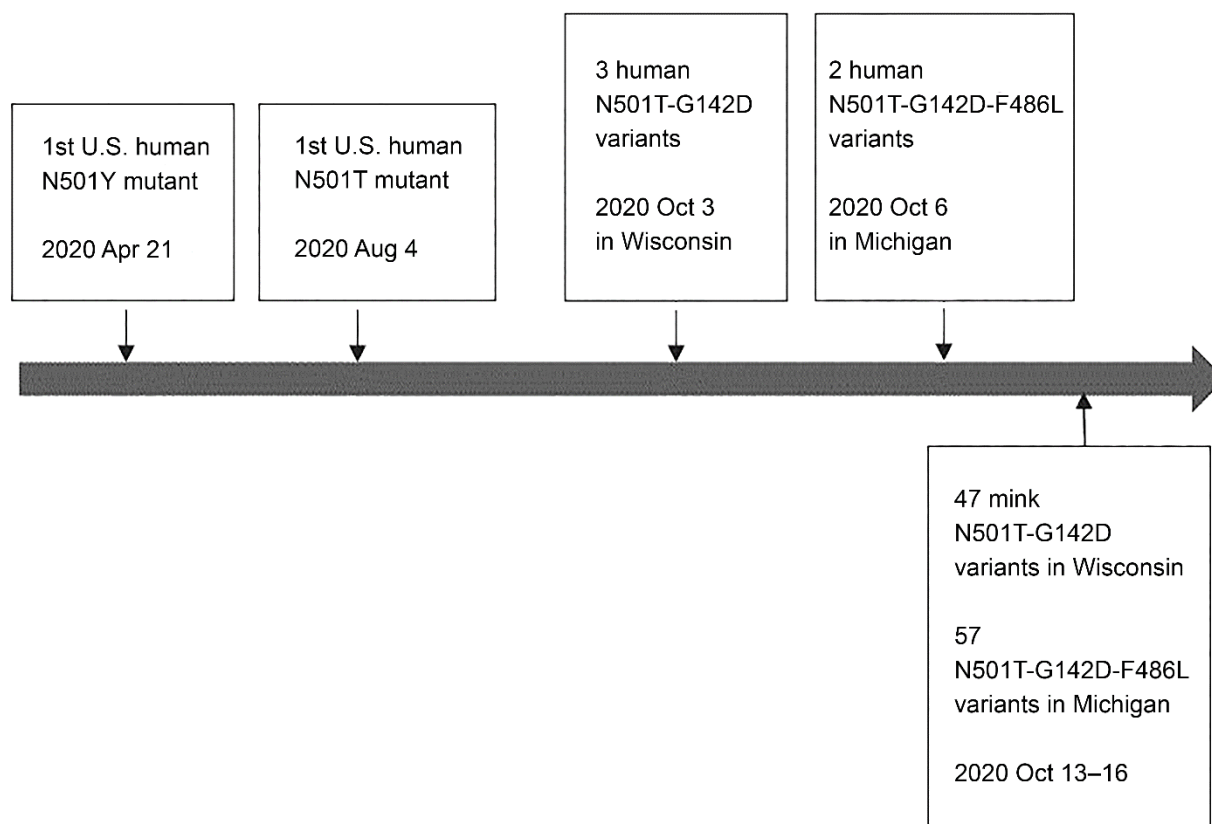


Figure 1. Timeline of emergence of human-derived (above the timeline) and mink-derived (below the timeline) SARS-CoV2 spike protein N501T-G142D and N501T-G142D-F486L variants in the United States. Timeline scale is not proportional.

JVDI News

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