

**Daoyu**

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It was forced to use aerosol transmission because only humans wear masks or isolate when an epidemic is reported. In order to be able to still transmit between masked and self isolated humans, the virus is forced to adapt to an aerosol-only transmission mechanism. In contrast,

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Minks and deers neither self isolate nor wear mask, or use any form of prophylaxis efforts—the viral population is eradicated in animals after a population have been fully infected due to the extremely strong protective immunity elicited in animals by SARS-CoV-2 (sterilizing

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Immunity is reported in all species where rechallenge after infection/vaccination have been performed). In addition, population size is important when it comes to viral evolution—the larger the host population size a virus can use the more likely that rare mutations with

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Marginal benefit in transmission would be hit before the virus burn itself out in the host population—SARS-CoV-2 circulation in human hosts is characterized by outbreak after outbreak—very little basal transmission exist other than superspreader events, especially in early

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Circulation. Animal populations are simply not large enough for these rare mutations with enhanced host adaptation to arise before the outbreak have ran it's

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Is circulating to be below 2 weeks—where the human VOCs did not emerge after at least 9 months of circulation with more than a billion hosts sampled. Comparing to animal hosts, where the maximal size of a mink farm population is below 5000 minks per farm, and the maximal size of

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A deer population is <500 deers per herd. [biorxiv.org/content/10.110...](https://doi.org/10.1101/2021.11.10.462110)
In fact, a counterexample of “it mutated less frequently in animals” can be seen in this particular deer isolate, where VOC level of divergence is observed after ~1 year of circulation in a deer population—

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Indicating that host numbers and length of circulation affects viral evolution much greater than “host species effects”.

In fact, rapid initial adaptation characteristic of a novel host is observed in minks—no mink-to-human transmission have been observed without D614G or Y453F.

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Alina Chan 

@Ayjchan



Replying to @Ayjchan

Independent groups of scientists have since analyzed the evolution of SARS-CoV-2 in mink and assessed that there was rapid host adaptation of the virus to mink (new host species) but not in humans.
[biorxiv.org/content/10.110...](https://doi.org/10.1101/2021.11.10.462110)
[biorxiv.org/content/10.110...](https://doi.org/10.1101/2021.11.10.462110)



9:29 PM · Dec 11, 2021 

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As “absence of adaptation from host effects” is at best an incorrect explanation of a phenomenon, and at worst intentionally misleading the public with a biased

explanation effort.

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[ncbi.nlm.nih.gov/pmc/articles/P...](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7685321/)

The same is observed in cats, too. A H655Y mutation is required for transmission between cats—and is fixated within them extremely rapidly. This is also why there have been no evidence that cats can transmit to humans—that being a characteristic that is



<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7685321/>

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Unique to minks and possibly deer (after significant host adaptation to increase titres). In order to begin cat-to-cat transmission it must give up human-to-human transmission.

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Also, all current deer isolates contained mutation D614G, indicating that some level of pre-adaptation to aerosol transmission must happen before spillover to deer can occur. [ncbi.nlm.nih.gov/pmc/articles/P...](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8382122/) WA1 failed to properly infect deer as it rapidly declines to nothing in deer,



<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8382122/>

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While B.1.1.7 is able to thrive.

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May 25

@scotub These are actually not class II MHC epitopes—they are so-called “CTL epitopes” (or MHC class I epitopes) which are in fact dominated by pentapeptide and hexapeptide fragments. The long peptide view only hold for CD4 T cell epitopes, and even with that partial homology still

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May 21

archive.ph/vIPDf archive.ph/QJyQC
archive.ph/SFOKv “Pandemic preparedness” by the WHO mean “more GOF” archive.ph/OG3xv
archive.ph/OtDCN And more parroting of the CCP narrative archive.ph/NqyEo
archive.ph/SNZkm “人不传人，可防可控”

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May 21

It’s not like that the two grants and hundreds of samples didn’t exist and weren’t sent to the WIV during 2018-2019. If they find a QTQTNS genome in it they will use RSVAS to insert ENaC by BLAST.

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May 20

@Biorealism Also RC-O319 is more distant than ZC45, and RahSTT182/200 have A singly deleted RBD making them unrelated to SARS-CoV-2 by the RBD.
drive.google.com/drive/folders/...
And thus incapable of becoming an ancestor (not hACE2-RBD. Variable loop 1 deleted).

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May 19

archive.ph/dyBAJ
independentsciencenews.org/commentaries/d...

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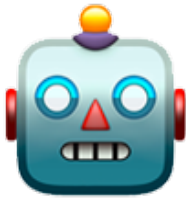


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May 19

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