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China owns Nature Magazine’s ass

Debunking claims from the article **“The proximal origin of SARS-CoV-2” arguing that COVID-19 definitely wasn’t engineered in a lab** way back in March 2020

Harvard2TheBigHouse

Apr 19, 2022

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*From the co-author* [Dan Sirotkin] [*of the first peer-reviewed paper examining a laboratory origin for SARS-CoV-2*](https://email.mg2.substack.com/c/eJwlkMtqxSAQhp_muAw6mhgXLkqhu0LfIHgZE2ligpoT8vb19MAwV36G_3Om4rznWx97qeSVpnofqBNeZcVaMZOzYJ6i1wBKjpIPxGvh2diPJJYpZMTNxFXXfCI5TrtGZ2rc00she6kEWbT3BgEDdYMDxlXAMLAQnA2y70cp6fuvOX3E5FDjE_O9JySrXmo9yoN_POCrxXVdXXI2dmnduhSXbt6fbX1srmWTa3Qrltb-fH9KwXuhoA0kaqAAVDAFlHPBO96NljGrHCgIygovH4JuM3TltKUa99u5fSNZB7eYgu02vxz-L5vBqdXtTLHeEyZjV_Rv7_WN8J_GNGPC3ND6yVTNhp4KSgUoxuHttcHpQahRsIG0r35vqqQXk58me6gL2jgveyP_B_L0iyI)*, as well as its addendum, which formally linked the*[*H1N1 Spanish Flu pandemic strain release of 1977*](https://email.mg2.substack.com/c/eJwlkMmOhCAQhp-mORo2FQ4c5jKvQVhKJYNgALvj2w-2SaXWVFX-z5kGay6XOnJt6Ha6XQeoBJ8aoTUo6KxQdPCKUjmLmU3IK-6JGAUKVS8FYDchqlZOQMdpY3CmhZzujXmcJUebmolgTGBjxDj11kIMd-CtEX7kQozy-WtOHyA5UPCGcuUEKKqttaO-2M-L_nbLKYYEMdhiyjV8QoRrcHnvE59D9wQPBGPaMxugDhTTXmIyo6B6TjEnkmLGOBvYICwhVjoq6SIt9_OL432lQz1tbcb93XdRUYvbTIU-W2-R32bXqHvczxTapSEZG8E_8ttD8QtEr5CgdLpem6bINGKOMaeSMPrI7XxGyqXgZEL9q899K6nNlLcpnrYNbFi33OH_A77rilY)*to gain-of-function research.*

*Way back over two years ago when I’d* [Dan Sirotkin] *only been looking into all this stuff for about six weeks, Nature Magazine published their much-ballyhooed*[The proximal origin of SARS-CoV-2](https://email.mg2.substack.com/c/eJwlkM2OhSAMhZ_msrsGCqgsWMxmXsPwU5WMogG8xrcfvCbNadOmbc7nTMFpS5fet1zILUO5dtQRz7xgKZjIkTENwWsA1fUdb4nXwrNe9iTkYUyIqwmLLulAsh92Cc6UsMV7o5OdEmTWbSu4dNi1fQdgVcsls8i5YRJHLjx9_prDB4wONX4wXVtEsui5lD2_-M8Lfmuc59lEU46EjdvW2jCpBLdgrmUWTCr2pkDftK-iSNBAAahgCijngje86S1jVjlQMCorfPcSdJ2gyYfNxbi_-ypJenSzyVhn0-3s26zGhprXI4ZyDRiNXdA_nsuD7kthmDBiqkj9YIpmraSCUgGKcXg8VigShOoFa0n96re6FfVs0sckD2VGG6Z5q8T_AZUZhpU) *on March 17, 2020,* *which has since been cited by over 2,000 news outlets and been accessed nearly six-million times.*

[*Two days later I’d respond with the article below*](https://email.mg2.substack.com/c/eJxNkc2u4yAMhZ-m7Kj4SwkLFnczrxEZcBJ0E4iAtNN5-iG3sxgJ2QJj--g7HhouubztkWsjV5ja-0Cb8FU3bA0LOSuWKQYrhNGjlg8SrAp8HEYS6zQXxB3iZls5kRyn26KHFnO6OvSgjSKrlUw5g0LoMGo9hAdTMIIe5lEbwwchP3vhDBGTR4tPLO-ckGx2be2oN_l1E7_6WaE8oYSW24ouLmvu0u4-770kmGA9MdkDNz34NSag-ZUqTdDOgnSHBf7EhJVCrTSgO9N3TAvtw-hR8u-4w0ZziUtMNM-0QqnU5ycV1G8Q9-trv8ZAuaEvqKnRueSdAt3A9YUk2i5CMMWNYFIqeZf30XHujBdGzMapoG-K7Yu419PVBv770k6Knf0KFXttuUj-PHaQU8_7mWJ7T5jAbRg-jNvHqh_q04IJS7cwTNAsfwxMMaaE4VJ8mHYTBqHMqPiD9K0h965k_3EU_2H8CxTrr-Q)*, which thoroughly eviscerates the idiotic assertions put forth by that article, none of which hold up to even the slightest bit of logical or scientific scrutiny. This article was transparent propaganda from the very start, and yet it’s gone nearly untouched in the press and the academic literature, as the only thing that’s allowed to the surface is the limited hangouts pretending to argue about technical minutiae from over two years ago.*

*If a scientific outsider and untrained journalist* [me, Dan Sirotkin]*was able to almost instantly point all of this out over two years ago after he’d just been studying all this stuff for a few weeks, to zero in on serial passage as a vital part of the puzzle and tear apart the façade presented by Kristian Andersen, how come the rest of the media - making their six-figure salaries and getting all their fancy awards - has gone along with their charade and is still suppressing the two peer-reviewed papers linked above?*

*Because after two years the media and our governments are still determined to pour poison into your ears, since the billionaires who own them all aren’t ever going to admit their roll in the worst crime against humanity in our shared history.*

Maybe you shouldn’t blindly believe everything you read? Even if the source has a pretty solid reputation? [- Dan Sirotkin]

[*Nature* magazine has censored over 1,000 articles](https://email.mg2.substack.com/c/eJwlUcuurCAQ_Jphh8EGVBYszub-huHRKjkOGMBj_PuLMwmpSrrpVKXKmYpryrc-UqnkgbneB-qIV9mxVszkLJjn4DWAGqeRD8Rr4ftJTiSUecmIbxN2XfOJ5DjtHpypIcXnYpSjEmTTYCRKCyMHGCRatkg-cOuNQaekWoavrjl9wOhQ4x_mO0Uku95qPcqL_7zgX3vXdXUhluBxC-uGGX3n0rstHreNgPVTo541YLyBTemXfkyV9r3Qw-RKL3MXWo4c4oqZRlPPjDQ1TepSk8-xUGPTWanDWFIuWzio20I0JGhgAEz0Chjngne8m2zfW-VAwaKs8ONLsPcKXTltqcb9Pv5I1ovbTMG2W5-sPsPmam78PmOo94zR2B39N8X6LeOT67xixNxK8rOpuh8kE4wJUD2Hb2otZglCTaIfSFP1qV1FvZn8Z7KHuqFtUaXW4X-bX6dM) at the request of the Chinese government over the past several years, and [runs columns sponsored by outside interests](https://email.mg2.substack.com/c/eJwtkcuO6yAMhp-m7FJxS0MWLGZzXiPi4iZoUojAzChvf5x2JGSMsf1bn4NDWEs97VEasssseB5gM_y2HRChst6gLilaKefJTOrBotVRmNGw1JZnBXi5tFusHdjR_Z6Cw1TyVTGN06zZZo0an5MXmutZqBBnI41y4yMYI4AbpT-6rscEOYCFH6hnycB2uyEe7aa-bvIfnQpYXbi6_zoM2z2UF0Ull5wuPl2-IuM6bqUOf9ltyA57hYGyX5DR1XMopEBvEqu5Dc6XjkODd-c2tINsqW1LBzVjyZKA5FrMkiul1V3djRfCz0HO8jl7Haeb5q9V3lv3DV34vuZi1T7D5hrQ33oBegeJz3KN0XPCc4Hs_A7xgw4_G3jDXFbIUGkzcXFoxWPkmnMtCZ78oCK2o9Sz0eLBSDUWqsp2c_XH1ShxA5_WrdDi_gMQuKJ_). And it seems pretty clear that their recent article, [“The proximal origin of SARS-CoV-2”](https://email.mg2.substack.com/c/eJwlkM2OhSAMhZ_msrsGCqgsWMxmXsPwU5WMogG8xrcfvCbNadOmbc7nTMFpS5fet1zILUO5dtQRz7xgKZjIkTENwWsA1fUdb4nXwrNe9iTkYUyIqwmLLulAsh92Cc6UsMV7o5OdEmTWbSu4dNi1fQdgVcsls8i5YRJHLjx9_prDB4wONX4wXVtEsui5lD2_-M8Lfmuc59lEU46EjdvW2jCpBLdgrmUWTCr2pkDftK-iSNBAAahgCijngje86S1jVjlQMCorfPcSdJ2gyYfNxbi_-ypJenSzyVhn0-3s26zGhprXI4ZyDRiNXdA_nsuD7kthmDBiqkj9YIpmraSCUgGKcXg8VigShOoFa0n96re6FfVs0sckD2VGG6Z5q8T_AZUZhpU) is just one more example of their influence. China bought off the head of Harvard’s chemistry department, you don’t think they could buy off run-of-the-mill research scientists scrambling for tenure and funding and publication? It’s absolutely horrific that so many scientists and researchers are taking part in what’s really clearly a disinformation campaign orchestrated by the Chinese Communist Party, and willfully spreading a smokescreen about something that’s already killed thousands and is projected to kill millions more across the planet.

And while the mainstream corporate media mindless regurgitates claims from the Chinese government that are falsifiable with the simplest of google searches, allowing the public to be lulled into a false sense of security and complacency, and Reddit rapidly censors and moderates anything that might indicate that this virus leaked from a Chinese lab and so the Chinese government is to blame for this pandemic  – sites like [ZeroHedge](https://email.mg2.substack.com/c/eJwlkM2OhSAMhZ_msjRQUGTBYjbzGoafqmS8YACvcZ5-cEyaNjnNSfsdZyouKV96T6WSu0312lFHPMuGtWImR8E8Ba8BlBwlH4jXwrOxH0ko05wR3yZsuuYDyX7YLThTQ4q3Q_ZSCbJqNijejxIGKntn2eglMkN7O3s3z87Q5645fMDoUOMH85Uikk2vte7lxb9e8N3qPM_uF3Na0S_YufRuGgkaKAAVTAHlXPCOd6NlzCoHCmZlhZcvQd8LdOWwpRr3cztJ1rNbTcG2W26Af7H9P7X5PmKo14TR2A39g1afhP5hpwUj5pacn0xtdD0VlApQjMOD0th7EGoUbCDtqk_NFfVq8sdkD3VFG5Y1tWD_ANV8gPc" \t "_blank), that have been at the forefront of keeping the lines of investigation open, have been banished from Twitter and marginalized.

1. **Below is a takedown of that article**, and the good news is
2. a much more nuanced and honest look at the origins of COVID-19, the Wuhan Strain of coronavirus [is just a click away](https://email.mg2.substack.com/c/eJxNkU2OwyAMhU9Tdqn4awMLFrOZa0QOOAmaFCpwWuX2Q9pqNBJ6lrHsZ332QDjnsrt7rsQOGWi_o0v4rCsSYWFbxTLE4KS0venVlQWngzAXw2IdpoJ4g7g6Khuy-zau0QPFnI6O_tJbzRYXcDJXMJL3BozhXmEwEnAaRQhC9_j2hS1ETB4dPrDsOSFb3UJ0ryf1dZLf7S1QHlACZVpwjPOS22pnn2-tJLnkLXDRRB2y5jlWasusHaTQEfolfTJY9xprl6euzelyiXNMf-lzWyB1Ppec4BHLVjvJhe2Sz482lUXXnCTXwkqulFZndTajEKP10srJjjr0J81vszzXbawE_udYkBU3-QUqttp84Hp9NlpDi7ctRdoHTDCuGN4g6X2PF9phxoSl3SkMQE5cL1xzrqUVSr7BNdIXqa3R4sqaa8itK7kPLPmP1S9b76eA).

[Nature Magazine:] Thus, the high-affinity binding of the SARS-CoV-2 spike protein to human ACE2 is most likely the result of natural selection on a human or human-like ACE2 that permits another optimal binding solution to arise. This is strong evidence that SARS-CoV-2 is not the product of purposeful manipulation.

* [Dan Sirotkin:] As our report mentions [right at the start](https://email.mg2.substack.com/c/eJxNkU2OwyAMhU9Tdqn4awMLFrOZa0QOOAmaFCpwWuX2Q9pqNBJ6lrHsZ332QDjnsrt7rsQOGWi_o0v4rCsSYWFbxTLE4KS0venVlQWngzAXw2IdpoJ4g7g6Khuy-zau0QPFnI6O_tJbzRYXcDJXMJL3BozhXmEwEnAaRQhC9_j2hS1ETB4dPrDsOSFb3UJ0ryf1dZLf7S1QHlACZVpwjPOS22pnn2-tJLnkLXDRRB2y5jlWasusHaTQEfolfTJY9xprl6euzelyiXNMf-lzWyB1Ppec4BHLVjvJhe2Sz482lUXXnCTXwkqulFZndTajEKP10srJjjr0J81vszzXbawE_udYkBU3-QUqttp84Hp9NlpDi7ctRdoHTDCuGN4g6X2PF9phxoSl3SkMQE5cL1xzrqUVSr7BNdIXqa3R4sqaa8itK7kPLPmP1S9b76eA), scientists passed the H5N1 Bird Flu through a series of ferret hosts until it gained ACE2 affinity and then became incredibly virulent, which is what’s seen with COVID-19 since its affinity to ACE2 is orders of magnitude higher than SARS.  It’s also the process used on the H1N1 Bird Flu that either leaked out of a Soviet lab in the 70’s or was introduced as part of a vaccine trial gone awry, it’s considered the product of laboratory manipulation since it was very similar to strains of H1N1 that hadn’t been in circulation for decades, and seemed to be the product of [“sequential passage in an animal reservoir”](https://email.mg2.substack.com/c/eJwlkMluxCAMhp9muDUCQxYOHHrpa0QsToKaQATOVHn7MjOSd8uy_s9bwjWX25y5EnuFme4TTcK_uiMRFnZVLHMMBkCP0ygHFowKYuonFuu8FMTDxt1QuZCdl9ujtxRzel2M_agV2wz0OPVSjFqrsFg9-cVLz-0kHQQxhPD5a68QMXk0-MRy54RsNxvRWR_y-wE_zQ4Xc2fr0eWyttbnRJioVUNz1Ry54EJ-iZ5FAxyAK6GBS6lkJ7vJCeG0Bw2LdiqMD8WPFbp6uUrW_3Y-H6yYxW-2YtutL1nvYVM1t3xcKdI9Y7Jux_ARTB9ubwTziglL4xlmS0YMPVecK9BCwkdgI9KD0pMSA2tfQ25XyWy2PG0JQBu6uG654f4HgNiF-w) which was determined by its vast genetic distance from any other present strain of flu, just like COVID-19 which also appears so distant from any related coronavirus that [it’s been placed in its own clade](https://email.mg2.substack.com/c/eJwlkMuOhSAMhp_msDsGCl5YsJjNvIapUJWMogE8xrcfPCZNr2mb_7OYadriZfYtZXa7Pl87mUBnWihniuxIFHvvDIBuu1Y2zBnlRFd3zKd-jEQr-sXkeBDbj2HxFrPfwr3R1q1WbDZoR-yUGkcBSBY1ylpCW6oRqXXN8PzFw3kKlgx9KF5bILaYOec9veTPC36LnedZBcxHpMpua2lgzN4ulEqalKgb9ebA37zpuvfFvAEOwJXQwKVUspJVNwgxaAsaRj0o174UXyeo0jGkjPbvvsqiGe2MicpsupV9m0VYX-J6BJ-vngIOC7lHc37QfSn0EwWKBanrMRvR1FxxrkALCY_GAqUGpTslGla-uq1sBTNj_GB0kGca_DRvhfg_f2iIVw), an isolated branch way out on its own in the viral family tree – meaning it’s the lone example of its kind, and doesn’t clump together with all the other known coronaviruses. That process of sequential passage through animal hosts leaves a genome that appears “natural” and not purposeful as well since it wouldn’t leave a genomic smoking gun and would simply appear to be the result of “natural” selection. So this is either exquisitely lazy research or dissimulation, the authors are either unaware of the Bird Flu study, which was well covered, [especially by the scientific press](https://email.mg2.substack.com/c/eJwlkUmOhDAMRU9T2YEyMWSRRW_6GiiDgaghKSWmSty-A0jWt-RB33p2BmFJ-dTvVJBcMuH5Bh3hWzZAhEyOAnkKXnOuhnEQPfFaejZ2IwllmjPAbsKmMR9A3ofdgjMYUrw2hm5QkqxaOjULS7vZubkfemndyJS5hAowcnx8zeEDRAcaPpDPFIFsekV8l5f4efHfGt_vty3uHtrN0qa81OJ1aU2cMlbTLfcMhoKlsdk4aHbwwTQFU94bk9MRfeNSxJyqUwlma-btqO3rgEKC5pRzKpniVAgpWtGOljGrHFd8Vlb64SXpvvC2HLagcX-tSzvJenarKVB7y0XkLlYgU837EQOeE0RjN_APK3yQ3_SmBSLk-go_GdSs76ikVHLFBH_YVJgdl2qUrCfV1ae6FfVq8sdkz3EFG5Y11U_9A-Xxnio), or are willfully ignoring it.

Given the level of genetic variation in the spike, it is likely that SARS-CoV-2-like viruses with partial or full polybasic cleavage sites will be discovered in other species.

* This seems like pretty intentional dissimulation. It’s “likely” that other viruses with this cleavage site will be found? What? How likely? 1 in 10? 1 in 10 million? Is it likely that if my aunt grew balls she’d become my uncle? Is it “likely” that a natural intermediate animal vector will be found? Well… likely or not, until it happens it seems incredibly disingenuous to state that “likely” means a damn thing here.

The functional consequence of the polybasic cleavage site in SARS-CoV-2 is unknown, and it will be important to determine its impact on transmissibility and pathogenesis in animal models. Experiments with SARS-CoV have shown that insertion of a furin cleavage site at the S1–S2 junction enhances cell–cell fusion without affecting viral entry.[14](https://email.mg2.substack.com/c/eJwlkF2KhTAMhVdj3660af3pQx-GgVnAbED6E7WMVmnrFXc_9QrhJCSEw_mszjht8VL7ljK5ZcjXjirgmRbMGSM5EsbBOwUgu77jLXFKONY3PfFpGCPiqv2icjyQ7IdZvNXZb-H-6JpOCjIrzp2W7Ugbq0eHvaFdbw3TmnYCeGvx8dWH8xgsKnxjvLaAZFFzznuq-FcFP6XO86yDzkfE2m5rWeiYvV0wlTEJ1kj2okBftC8iK-ARx9f3LxPEK6AAVDAJlHPBa173hjEjLUgYpRGuqwRdJ6jTYVLW9u82IFGNdtYJy226Q36WJeNQ-noEn68BgzYLuid-fih-gAwTBoyFrht0VqxtqKBUgGQcnriFTwNC9oK1pLi6rXwFNev41tFBntH4ad4K_H8z6YqW)

* This doesn’t seem to address the virus’s provenance at all, but just as an aside it seems like a lot of the viruses with furin cleavage sites engage in ADE, which COVID-19 appears to be doing from a clinical perspective: neurological damage, the second infection is worse, and areas like Wuhan with extended infections have much higher CFRs as infections overlap.

The acquisition of polybasic cleavage sites by HA has also been observed after repeated passage in cell culture or through animals.[17](https://email.mg2.substack.com/c/eJwlkNuKhTAMRb_Gvh3pzUsf-jAMzAfMD0gvUctolTYe8e-nHiHshISw2csZhGlLl963jOSWAa8ddIQzL4AIiRwZ0hC85lx1fSda4rX0rG96EvIwJoDVhEVjOoDsh12CMxi2eH90TackmfUoPHDKJfMN7ZX3ljWjGxW1vW8ts-7xNYcPEB1oeEO6tghk0TPinivxVfGfUud51tHgkaB221oWJmFwC-QyZskaxV6U0xfti6iKiwTj6_uXdSToYs-pZIpTIaSoRd1bxqxyXPFRWem7StJ14nU-bEbj_m4DkvToZpOh3KY75GdZMg6lr0cMeA0QjV3AP_HxofgBMkwQIRW6fjCoWdtQSankign-xC18Gi5VL1lLiqvfylfUs0lvkzzHGWyY5q3A_wcyNIqb)

* Exactly. Passage through a series of ferret hosts in a lab may have given COVID-19 this distinct cleavage site, if it wasn’t simply spliced directly in. Further support for possibility that serial passage through lab animals played a role in the creation of COVID-19 [comes from an April 2020 pre-print](https://email.mg2.substack.com/c/eJwlkduOhCAMhp9muCSAIHLBxe7FvobhUJWsgsHq7Lz9MmPStE0Paf6vwSHMpb7sXg4kbzfiaweb4XmsgAiVnAfUMUUrhNGD7noSrYx8UANJxzhVgM2l1WI9geynX1NwmEp-b2iljSSL7aN0RjGpFRjOtVZcSYDQKe-Zdozdd90ZE-QAFi6or5KBrHZB3I9H9_UQP82ezyf1qdS_dNFS51YJJSNkbBlnlHPGWyaYYJTJjwnFBnZxOp3rSvc4PcT3gttKkm1TgkluBOs62dGODp5zb4IwYjJeRv2QbJsFPU5_oAu_NJSNVDuFxR3QevNb9afYRI8tbmdO-BohO79CvHngjfVDaJwhQ2244-jQ8r7xYEwKwztx62_AlJBmkLwn7WosbSvbxdXL1ShwAZ_mpbRv_AO3w46M), which found that coronaviruses that target the ACE2 receptor bind with ferrets cells more tightly than any other species except the tree shrew, which only scored about 2% higher. Tree shrews have also been used for serial viral passage, and [were promoted in a 2018 paper out of China](https://email.mg2.substack.com/c/eJwlkMtqxSAQhp_muAzeYuLCRSl0V-gbBC-TRJpoUHNC3r5zekDGcWT4-T5vGyy53ObItZFXmdp9gElw1Q1ag0LOCmWKwXCuh3EQigQjAxv7kcQ6zQVgt3EzrZxAjtNt0dsWc3ptDP2gJVmNYj1QKmdurZ1nR1WQlPNZeq7VKLx659ozREgeDDyh3DkB2cza2lEf4uPBv_Bc19Ul72KXtr1Lce2W_MTxsXustrToN6jY_nx_KjYMkjF8kGg4plHJNKdCSNGJbnSMOY3xfNZOhuEh6b7wrp6uNut_O593UszsV1sB_5YX4f8QASe89zPFdk-QrNsgvNnbW-G_jWmBBAXVhsk2w1RPJfJzzQR_s6Kcnks9SqYIpoaMW8mstjxtCbyt4OKyZjT_B-beikE) as a preferable host for laboratory serial passage since they’re cheaper, smaller, easier to handle, and closer to humans evolutionarily and physiologically than ferrets.  Pangolins however, formed a much weaker bond than either, and were clustered way down on the list along with a handful of other much more unlikely intermediate animal hosts.

It is improbable that SARS-CoV-2 emerged through laboratory manipulation of a related SARS-CoV-like coronavirus. As noted above, the RBD of SARS-CoV-2 is optimized for binding to human ACE2 with an efficient solution different from those previously predicted.[7](https://email.mg2.substack.com/c/eJwlkE2OwyAMhU9Tdo3AEAgLFqOR5gBzgYgfJ0GTkApIq9x-SCtZz5Yt23qftxXnPZ_msZdKLhnr-UCT8FVWrBUzOQrmMQYDoNWguCTBiMCGfiCxjFNG3GxcTc0Hksfh1uhtjXu6NlSvtCCLcU75KUjdS82lkmC951yyAbSX3Cv9-WuPEDF5NPjEfO4JyWqWWh_lxr9u8NPi9Xp1ydYjY-f3rTVsrtGvWFpZBOs1u1Ogdzo00TfgGaf7968i0QAFoIJpoJwL3vFucIw57UHDpJ0I6iboNkNXDleq9X_XfZLN5BdbsM3my-O72SyOLW9HivUcMVm3Yvi4rx-Ibx7jjAlzgxtGWw2TPRWUCtCMw8dtw9OD0INgkrSvYW9bySw2P20OUBd0cV72xv4f2HOJmg),[11](https://email.mg2.substack.com/c/eJwlkF2KhTAMhVdj3660af3pQx-GgVnAbED6E7WMVmnrFXc_9QrhJCSEw_mszjht8VL7ljK5ZcjXjirgmRbMGSM5EsbBOwUgu77jLXFKONY3PfFpGCPiqv2icjyQ7IdZvNXZb-H-6JpOCjIrOsLI275rnOSsEbZHMAyspo3sBTXj46sP5zFYVPjGeG0ByaLmnPdU8a8Kfkqd51kHnY-Itd3WstAxe7tgKmMSrJHsRYG-aF9EVsAjjq_vX8aIV0ABqGASKOeC17zuDWNGWpAwSiNcVwm6TlCnw6Ss7d9tQKIa7awTltt0h_wsS8ah9PUIPl8DBm0WdE_8_FD8ABkmDBgLXTforFjbUEGpAMk4PHELnwZEAcBaUlzdVr6CmnV86-ggz2j8NG8F_j8fHImu" \t "_blank).

* Yes, again we aren’t arguing that this thing was built nucleotide-by-nucleotide as the perfect bespoke bio-weapon. This efficient solution is exactly the kind of thing that would be selected for after passage through animals in lab, which was already done to the Bird Flu that created a horrifically virulent strain. Isn’t it funny that no one’s mentioning that experiment? Or Baric’s work at UNC? How come every single public-facing virologist seems to be leaving these studies out? Are they really unaware of them? That seems exceedingly hard to believe when I was able to find them on the front page of a single google search. Seems a lot more likely everyone’s just covering each other’s asses since they realize the magnitude of what’s happening and how deep into the cover-up they already are.

Furthermore, if genetic manipulation had been performed, one of the several reverse-genetic systems available for betacoronaviruses would probably have been used.[19](https://email.mg2.substack.com/c/eJwlkN2KhDAMhZ_G3o20abX2ohfLwj7AvoD0J2pZrdLWEd9-OzMQknBCOJzPmYLznm597LmQVxvLfaCOeOUVS8FEzoxpDF4DKDlI3hOvhWdDN5CQxykhbiasuqQTyXHaNThTwh5fH7KTSpBFG8sHqjhXnWVSmslbaaWjVVC9dQI_vub0AaNDjU9M9x6RrHop5cgN_2rgp9Z1XW005UzYun2rgkkluBVzXbNgnWIPCvRBh9pUAzzh9Pj-ZYoEDRSACqagugre8nawjFnlQMGkrPCyEXSboc2nzcW4v5cBSXpyi8lYb_Mr5FusGcc6tzOGco8YjV3Rf-KXD8U3kHHGiKnS9aMpmvUdFZQKUIzDJ27l04FQg2A9qa5-r19RLyY9TfJQFrRhXvYK_x-c54oc)

* This is an utterly vacuous statement. Probably doesn’t mean a damn thing in science. “Okay folks, we probably won’t get an earthquake anytime soon, so no reason to prepare for one or try and detect one coming!” Seriously?

Instead, we propose two scenarios that can plausibly explain the origin of SARS-CoV-2: (i) natural selection in an animal host before zoonotic transfer; and (ii) natural selection in humans following zoonotic transfer.

* As we’ve explained before, there was no trace of this virus before November 2019, and full zoonotic jumps don’t just magically happen, especially not of a virus that’s so incredibly adapted to humans and able to infect us undetected and spread undetected, and then kill us after more than enough time has passed to find multiple new hosts. It’s funny so many virologists are throwing out the book of how zoonotic jumps happen… all that money in dual-use gain-of-function research must be quite blinding. Kind of amazing they don’t care how many thousands of people are dying. As far as the intermediate animal host goes: It might as well be a unicorn at this point. Until someone finds it, it’s just conjecture.

Malayan pangolins (*Manis javanica*) illegally imported into Guangdong province contain coronaviruses similar to SARS-CoV-2.[21](https://email.mg2.substack.com/c/eJwlkFGOhSAMRVcjf89ARYUPPiaTzAJmAwakKBlFA_iMux98Js1t06a5uWfUGactXmrfUia3DPnaUQU804I5YyRHwjh4qwBkL_qmI1Zxy0QriE-Di4ir9ovK8UCyH2bxo85-C_dH3_aSk1lZwygVHRVMMwNOi6bhruPOuVZwzdrHVx_WYxhR4RvjtQUki5pz3lPVfFXwU-o8zzrofESsx20tCx2zHxdMZUyctZK9KNAXFUVkBU1E9_r-BUa8AgpAOZNAi3dTN7UwjBk5ggQnDbd9xek6QZ0Ok7Ie_24DEpUbZ52w3KY75GdZMg6lr0fw-RowaLOgfeLnh-IHyDBhwFjo2kFnxbqWcko5SNbAE7fwaYFLwVlHiqvdyldQs45vHS3kGY2f5q3A_wdMp4nU) Although the RaTG13 bat virus remains the closest to SARS-CoV-2 across the genome[1](https://email.mg2.substack.com/c/eJwlkE2OgzAMhU_T7IoSJxSyyGI00hxgLoDyYyAaCFViWnH7CUWyni1btvU-bwmnLR_muRVipwx0PNEkfJcFiTCzvWAeYjAAuus7-WDBqCD6tmexDGNGXG1cDOUd2XN3S_SW4pbOja7ttGKz8aNH1ynNpeYdD9ZJC0IrLnh7irz-2j1ETB4NvjAfW0K2mJnoWW7y6wY_Nd7vd5Ms7Rkbv621YTNFv2CpZVGi1eLOgd95X0XfQGYc79-_gkUDHIAroYFLqWQjm94J4bQHDaN2KnQ3xdcJmrK7Qtb_nfdZNqOfbcE6m06Pn2a1ONS87inSMWCybsFwuacL4ofHMGHCXOGGwZIRj5YrzhVoIeFyW_G0oHSvxIPVr2GrW8nMNr9sDkAzujjNW2X_D2LPiS4), some pangolin coronaviruses exhibit strong similarity to SARS-CoV-2 in the RBD, including all six key RBD residues.[21](https://email.mg2.substack.com/c/eJwlkFGOhSAMRVcjf89ARYUPPiaTzAJmAwakKBlFA_iMux98Js1t06a5uWfUGactXmrfUia3DPnaUQU804I5YyRHwjh4qwBkL_qmI1Zxy0QriE-Di4ir9ovK8UCyH2bxo85-C_dH3_aSk1lZwygVHRVMMwNOi6bhruPOuVZwzdrHVx_WYxhR4RvjtQUki5pz3lPVfFXwU-o8zzrofESsx20tCx2zHxdMZUyctZK9KNAXFUVkBU1E9_r-BUa8AgpAOZNAi3dTN7UwjBk5ggQnDbd9xek6QZ0Ok7Ie_24DEpUbZ52w3KY75GdZMg6lr0fw-RowaLOgfeLnh-IHyDBhwFjo2kFnxbqWcko5SNbAE7fwaYFLwVlHiqvdyldQs45vHS3kGY2f5q3A_wdMp4nU) (Fig. [1](https://email.mg2.substack.com/c/eJwlkMGOhCAMhp9muK2BggoHDnuZ1zAIVckqGqgzmbdfHJPmb9Ombf7PO8J5zx977IXYJQN9DrQJ32VFIszsLJiHGCyA6XUvOxasCkK3msUyTBlxc3G1lE9kxzmu0TuKe7o2-rY3ii3WgZ6U5J4rqblsQz-ZTkmnneQTTq69_7ozREweLb4wf_aEbLUL0VEe8vcBzxrv97tJjs6Mjd-32nCZol-x1LIo0Rrxw4H_cF3FPEA-4yxYtMABuBIGuJRKNrLRoxCj8WBgMqMK_UPxbYamnGMh5_-u4yzbyS-uYJ3Nl8Fvs_obat7OFOkzYHLjiuG2TjfBL4xhxoS5kg2DIyu6livOFRgh4bZa2bSgjFaiY_Vr2OtWsovLL5cD0IJjnJe9gv8HUV6Ivw)). This clearly shows that the SARS-CoV-2 spike protein optimized for binding to human-like ACE2 is the result of natural selection.

* The most recent study, covered in our article, that examines the neutral sites that are assumed to best show heritage found that pangolins are “very unlikely” to have served as a host at all. Their assertion that *natural*natural selection is clearly shown is raw steamy bullshit. Serial passage through ferrets or tree shrews fits the overall big picture far better than this pangolin crap.

For a precursor virus to acquire both the polybasic cleavage site and mutations in the spike protein suitable for binding to human ACE2, an animal host would probably have to have a high population density (to allow natural selection to proceed efficiently) and an ACE2-encoding gene that is similar to the human ortholog.

* *WAIT WAIT WAIT!!* You mean exactly like a bunch of ferrets or tree shrews, both of which have the same ACE2 receptor as humans, all jammed into a bunch of cages together and then infected over and over again in a lab?! That’s crazy talk!! Other than the fact it was exactly the process used to make the Bird Flu into something that [“could make the 1918 pandemic look like a pesky cold.”](https://email.mg2.substack.com/c/eJwlUctuxCAM_JrllohXNuHAoZf-RsTDSVBZiIBslH59na6EjG0YzXjsTIM1l0vvuTZyh7ldO-gEZ43QGhRyVChz8JpzNU6jeBKvpWfTMJFQ56UAvEyIupUDyH7YGJxpIacbMQ6jkmTTi2BPrww4JbgdgA5OUjECtXYQanHuw2sOHyA50PCGcuUEJOqttb0-xNeDf-M5z7P3JkZTb3m9yy9s5j0k5MMM6xekZsqFBaeM4cU4BnFnzpTY_Qb8Urq65SP6rjokbKG22lWIS-cg1Vy6tkEo3TYk1hWoYIrbEE-C5pRzKpniVAgpetFPljGrHFd8UVb68SHpa-V9PWxtxv3cCknRi9tMBXxbb6f-m2jUfMs9UmjXDMnYCP7jYfus4t_VeYUEBVfkZ9M0ew5UUiq5YoJ_PEOTBy7VJNmTIKvPiEp6M-Vtiuc4iA0rzlrhD4UtpVg)

It is possible that a progenitor of SARS-CoV-2 jumped into humans, acquiring the genomic features described above through adaptation during undetected human-to-human transmission. Once acquired, these adaptations would enable the pandemic to take off and produce a sufficiently large cluster of cases to trigger the surveillance system that detected it.[1](https://email.mg2.substack.com/c/eJwlkE2OgzAMhU_T7IoSJxSyyGI00hxgLoDyYyAaCFViWnH7CUWyni1btvU-bwmnLR_muRVipwx0PNEkfJcFiTCzvWAeYjAAuus7-WDBqCD6tmexDGNGXG1cDOUd2XN3S_SW4pbOja7ttGKz8aNH1ynNpeYdD9ZJC0IrLnh7irz-2j1ETB4NvjAfW0K2mJnoWW7y6wY_Nd7vd5Ms7Rkbv621YTNFv2CpZVGi1eLOgd95X0XfQGYc79-_gkUDHIAroYFLqWQjm94J4bQHDaN2KnQ3xdcJmrK7Qtb_nfdZNqOfbcE6m06Pn2a1ONS87inSMWCybsFwuacL4ofHMGHCXOGGwZIRj5YrzhVoIeFyW_G0oHSvxIPVr2GrW8nMNr9sDkAzujjNW2X_D2LPiS4),[2](https://email.mg2.substack.com/c/eJwlkFuKhTAMhldj3460ab30oQ_DwCxgNiC9RC2jVdp6xN1PPUL4ExKS8H9WZ5y2eKl9S5ncMuRrRxXwTAvmjJEcCePgnQKQXd_xljglHOubnvg0jBFx1X5ROR5I9sMs3urst3BvdE0nBZkVCG1H1rVUIzaUAWusoWOHutfctCCfv_pwHoNFhW-M1xaQLGrOeU8V_6rgp8R5nnXQ-YhY220tDR2ztwumUibBGsleFOiL9kVkBTzi-Pr-BeIVUAAqmATKueA1r3vDmJEWJIzSCNdVgq4T1OkwKWv7d98nUY121gnLbLo9fprF4lDyegSfrwGDNgu6x31-IH54DBMGjAWuG3RWrG2ooFSAZBwetwVPA0L2grWkfHVb2Qpq1vGto4M8o_HTvBX2_0VDifo)

Hence, this scenario presumes a period of unrecognized transmission in humans between the initial zoonotic event and the acquisition of the polybasic cleavage site. Sufficient opportunity could have arisen if there had been many prior zoonotic events that produced short chains of human-to-human transmission over an extended period.

* Sure this would be plausible… other than the fact that, [as we cover in our report](https://email.mg2.substack.com/c/eJxNkU2OwyAMhU9Tdqn4awMLFrOZa0QOOAmaFCpwWuX2Q9pqNBJ6lrHsZ332QDjnsrt7rsQOGWi_o0v4rCsSYWFbxTLE4KS0venVlQWngzAXw2IdpoJ4g7g6Khuy-zau0QPFnI6O_tJbzRYXcDJXMJL3BozhXmEwEnAaRQhC9_j2hS1ETB4dPrDsOSFb3UJ0ryf1dZLf7S1QHlACZVpwjPOS22pnn2-tJLnkLXDRRB2y5jlWasusHaTQEfolfTJY9xprl6euzelyiXNMf-lzWyB1Ppec4BHLVjvJhe2Sz482lUXXnCTXwkqulFZndTajEKP10srJjjr0J81vszzXbawE_udYkBU3-QUqttp84Hp9NlpDi7ctRdoHTDCuGN4g6X2PF9phxoSl3SkMQE5cL1xzrqUVSr7BNdIXqa3R4sqaa8itK7kPLPmP1S9b76eA), that statistical analysis shows that this thing didn’t hit humans until November of 2019, which this article agrees with. But zoonotic jumps only occur after a genomic trial-and-error process where the virus jumps to one host, spreads to a few new hosts, and then fizzles out. There is absolutely no evidence anywhere of this occurring. Every single data points to this thing hitting humans in November and being immediately adapted and dangerous. There is no trace whatsoever of it creating small clusters of infections and dying out – stating there could have been doesn’t mean it’s been seen. It hasn’t. And as our report covers, this would require sustained interaction with the intermediate host – how does that happen in the middle of a massive modern urban metropolis the size of NYC? And where is this intermediate host anyways? If an intermediate host isn’t needed, is it some magical sleep-flying bat that decided not to hibernate and fight crime in Wuhan when its buddies were all hibernating, creating the sustained interactions with humans as it fought for Justice? Because that’s about as plausible as what’s being proposed here.

The presence in pangolins of an RBD very similar to that of SARS-CoV-2 means that we can infer this was also probably in the virus that jumped to humans.

* Again, [analysis of the neutral sites](https://email.mg2.substack.com/c/eJw9kUGOwyAMRU9TdhOBISQsWMxmrhE54CZoEoiAtOrth7TSSMhY33x9-eGw0pLyyx6pVHaVqb4OspGeZaNaKbOzUJ6CtwBmGAepmbfKi7EfWSjTPRPtGDZb80nsOOctOKwhxcsx9INRbLUSvXRyFG7WqAE0qGFET0pxfXdCmk8unj5QdGTpQfmVIrHNrrUe5Sa_b_DTDrrm2oPr0nl0Lu1NiiVfA__A5vzCXIPbqCk-hVYF7wQ38v9dfCJyqVvXD0OvtGTBAgfgShjgUirZyW6chZiNAwN3Mys_3BTfF-jKOZeK7vcKZtne3YqF2my51n-Lbfup3fsZQ31NFHHeyH_A1A_fN6ppoUi5cfcTVit0zxXnCoyQ8AHRyPWgzKiEZi3Vp-aKdsX8wOyhrjSHZU3tW_4ABSGSbg) shows that pangolins were almost certainly not in play.

Furthermore, a hypothetical generation of SARS-CoV-2 by cell culture or animal passage would have required prior isolation of a progenitor virus with very high genetic similarity, which has not been described

* This means nothing. There is no open-source shared database of viruses. No one has any idea what viruses are in China’s BSL-4 lab, where they’ve been collecting these viruses for years. As mentioned, one of our persons-of-interest was the very first person to isolate a coronavirus from a bat that uses the ACE2 receptor. He also worked at UNC in Baric’s lab making the hyper-virulent bat coronavirus in 2015. It should also be noted that several years prior to tinkering directly with bat coronavirus spike-proteins, Baric orchestrated research that involved isolating a coronavirus from civets and then [passing it through mammalian ACE2 receptor cells](https://email.mg2.substack.com/c/eJwlkMtqxSAQhp_muBQdzcWFi1LortA3CF4miTTRoOaEvH09PTDMlZ_h_5ypuKR86yOVSl5pqveBOuJVNqwVMzkL5il4DaCGcRA98Vp6PnYjCWWaM-JuwqZrPpEcp92CMzWk-FIM3aAkWTUo7KwVM1MoFJOG9wPvpDGzkMyjdO-_5vQBo0ONT8x3ikg2vdZ6lIf4eMBXi-u6aHQ20LjtNIaVLunZ1sfuWja5Brdhae3P9yd0XPU9awMJGhgAk1wBE0IKKuhoObfKgYJZWemHh2T7ArSctlTjfqlLO8l6dqsp2G7Ly-H_shmcWt3PGOo9YTR2Q__2Xt8I_2lMC0bMDa2fTNW875hkTILiAt5eG5wOpBol70n76lNTRb2a_DTZQ13RhmVNjfwf61aKSQ) that were grown in the lab from kidney and brain samples – serial passage through host cell lines instead of entire hosts, which imparted a strong affinity for ACE2, and presumably created an airborne strain of coronavirus. And if cells derived from kidneys and brains were used for the serial passage development of COVID-19, that might help explain its affinity for attacking [the kidneys](https://email.mg2.substack.com/c/eJwlkcuOwyAMRb-m7BrxyoMFi9nMb0QGnARNChU4jfL3Q1vJAnSRfXWPPRCuuVz2mSux9zHT9USb8Kw7EmFhR8Uyx2ClNOM0qoEFq4OY-onFOi8F8QFxt1QOZM_D7dEDxZzeHWM_Gs02i4tww7KoxbnAJ8c56MkMEAIINcK4fH3hCBGTR4svLFdOyHa7ET3rTf3c5G-r8zy7Nn3bwYW4YqXO50fTfU6EidoLCt7_Ykh41TtBWZEw3FN-4X73ueQEr1iOyqKVXEquhZFcKa061U1OCGe8NHIxTofxpvljlV09XCXwf28nVuziN6jY_tZ36I_YMs_tfhwp0jVjArdj-OKgL9UPoHnFhKXRDjOQFUPPNedaGqHkN37j1UttJi0G1lxDbl3JblBeUIKkDV1ct9yW8Q9WspXu) [and brains](https://email.mg2.substack.com/c/eJwlkcuOhCAURL-m2Wl4-WDBYjbzG4bHVckoGMA2_v1cuxNCXSCVqhycqbCkfOsjlUqebar3ATrCVTaoFTI5C-QpeM25GsZB9MRr6dnYjSSUac4AuwmbrvkEcpx2C87UkOLjGLpBSbJqA7PtJJOy78XMjBDKjBRG2bl-pE7231xz-gDRgYY35DtFIJteaz3KS_y8-C-u67raC-zuW5d2PG9nXFCeriicckol5TiG2JS0Q-NMgdK49A6-YarZzd2sJu9NXaGx2YT44oKRoNHKqWSKUyGkaEU7WsasclzxWVnph5ek-8LbctpSjft78knWs1sxAN-WB8HnEglMqPsZQ70niMZu4L9w6pfxB9e0QISM7P1kqmZ9h8Wp5IoJ_oWB9Dou1ShZTzDVJ3RFjeXfJnuO_W1Y1oRf8w8kJ5UJ) of its human hosts.

Subsequent generation of a polybasic cleavage site would have then required repeated passage in cell culture or animals with ACE2 receptors similar to those of humans, but such work has also not previously been described.

* The fuck it hasn’t.

Retrospective serological studies could also be informative, and a few such studies have been conducted showing low-level exposures to SARS-CoV-like coronaviruses in certain areas of China.[26](https://email.mg2.substack.com/c/eJwlkN2KxCAMhZ-m3k3RqK1eeLEs7APsCxR_0la2tYPaGebt15lCOAkJ4XA-bysuR36Z-1EqectUX3c0CZ9lw1oxk7NgnmIwAHpUIx9IMCIwJRWJZZoz4m7jZmo-kdxPt0VvazzS-2OUoxZkNYPz6JWbhbM0cCrRMw0oqAc5K6Xl5WvPEDF5NPjA_DoSks2std5Lx786-Gn1fD77ZOuZsffH3hY21-g3LG0sgknNbhTojaomugOecb59_8JAogEKQEWzpZwL3vNeOcac9qBh1k6EsRN0X6AvpyvV-r-3Aclm9qst2G7LO-Rn2TJOre9nivU1YbJuw3DFrxfFD5BpwYS50Q2TrYYNkgpKBWjG4Yrb-EgQWgk2kOYajvaVzGrzw-YAdUUXl_Vo8P8BEdyKcw) Further serological studies should be conducted to determine the extent of prior human exposure to SARS-CoV-2.

* Beyond the statistical analysis that indicates it only hit humans in November in 2019, is the fact that the version of COVID-19 found in the first few dozen hosts was exactly the same – there aren’t any variants whatsoever, just one version. This is not what would be found with the genomic trial-and-error of a full zoonotic jump, which requires sustained human-to-human transmission as different variants of the virus try and fail to adapt to human biology. Here, only one variant was found in all the initial infected humans, instead of the multiple variants that would be expected. But does fit what would happen if a virus that already had high affinity to the ACE2 receptor, which is the comparable in humans, ferrets, and tree shrews, leaked out of a lab. But addressing this point in particular, oh weird, [the study they cite from March of 2018](https://email.mg2.substack.com/c/eJwlkN2OhCAMhZ9G7sZAwQEuuNibeQ3DT1WyDhrA2fj2i2PStM1pmpPzeVtx3vJp9q1UcrWxnjuahH9lxVoxk6NgHmMwAFoqyZ8kGBGYGhSJZZwy4tvG1dR8INkPt0Zva9zS9SEHqQVZDPcDyokryxV7DhK1n0KYmHLSIacUb197hIjJo8EP5nNLSFaz1LqXjv908Gq1xvTblz3HNGPu_fZums01-hXbxmjPKJUdDPAqDGCgD8rUg1IGD0miAQpABdNAORe8571yjDntQcOknQiyE_Q9Q18OV6r1v5cByWbyiy3YbvOV8yu2mGOb7yPFeo6YrFsx3ATqDfLLZJwxYW6Aw2iracmpoFSAZhzuxA3RAEIrwZ6kuYatfSWz2PyxOUBd0MV52Rr_fwFKio4) was done mostly *on people who live in villages barely a kilometer away from bat caves.*A far cry from a massive urban city bout the size of NYC.Oh, and how many of these villagers, who live about a kilometer or less from bat caves, had antibodies indicating exposure to bat coronaviruses? Two-point-seven percent. (There is hand-waving about how long antibodies persist in humans, but I’m pretty sure it’s more than long enough.) That study actually sampled people living in Wuhan too and found… no evidence whatsoever of exposure to “SARS-CoV-like coronaviruses.”  So are these peer-reviewers just straight chugging lead paint, or are they on the take too?

The finding of SARS-CoV-like coronaviruses from pangolins with nearly identical RBDs, however, provides a much stronger and more parsimonious explanation of how SARS-CoV-2 acquired these via recombination or mutation.[1](https://email.mg2.substack.com/c/eJwlkN2KhDAMhZ_G3o20abX2ohfLwj7AvoD0J2pZrdLWEd9-OzMQknBCOJzPmYLznm597LmQVxvLfaCOeOUVS8FEzoxpDF4DKDlI3hOvhWdDN5CQxykhbiasuqQTyXHaNThTwh5fH7KTSpBFG8sHqjhXnWVSmslbaaWjVVC9dQI_vub0AaNDjU9M9x6RrHop5cgN_2rgp9Z1XW005UzYun2rgkkluBVzXbNgnWIPCvRBh9pUAzzh9Pj-ZYoEDRSACqagugre8nawjFnlQMGkrPCyEXSboc2nzcW4v5cBSXpyi8lYb_Mr5FusGcc6tzOGco8YjV3Rf-KXD8U3kHHGiKnS9aMpmvUdFZQKUIzDJ27l04FQg2A9qa5-r19RLyY9TfJQFrRhXvYK_x-c54oc)

* Again, just demonstrably false.

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