

Thanks

Linda

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From: "Liu, Shan-Lu" <liu.6244@osu.edu>

Date: Wednesday, February 12, 2020 12:47 AM

To: Linda Saif <saif.2@osu.edu>

Subject: Re: Commentary for Emerging Microbes & Infections

Hi Linda.

Thanks so much, and your comments are extremely helpful. Please feel free to share with Ralph to get his feedback if possible. We would like to publish this in the next few days.

I will work on reference tomorrow and send you a updated version.

Shan-Lu Liu sent from iPhone

On Feb 11, 2020, at 11:54 PM, Saif, Linda <saif.2@osu.edu> wrote:

Hi Shan-Lu,

I edited this version and added my name as I too feel strongly about denouncing this.

Here are more comments and some refs that I have made in replies to some reporters about this issue if you think any are useful to include. I also wonder if we might share this with Ralph Baric since he is a conspiracy target and maybe he could add additional points, but I know he would not want to be a co-author—not sure if he has time to answer.

The absence of a logical targeted pattern in the new viral sequences and a close relative in a wildlife species (bats) are the most revealing signs that 2019-nCoV evolved by natural evolution. Evolution is stepwise and accrues mutations gradually over time, whereas synthetic constructs would typically use a known backbone and introduce logical or targeted changes instead of randomly occurring mutations.

The closest virus relative to 2019-nCoV is bat CoV RaTG13. There are 4% nt differences between 2019-nCoV and RaTG13, corresponding to >1000 nt based on a genome size of 29k. These changes (SNP) are distributed throughout the genome in a naturally occurring pattern and follow the evolution characteristics typical of CoVs, including the S gene as the most variable region.

(Zhou P, Yang XL, Wang XG, Hu B, Zhang L, Zhang W, Si HR, Zhu Y, Li B, Huang CL, Chen HD, Chen J, Luo Y, Guo H, Jiang RD, Liu MQ, Chen Y, Shen XR, Wang X, Zheng XS, Zhao K, Chen QJ, Deng F, Liu LL, Yan B, Zhan FX, Wang YY, Xiao GF, Shi ZL. 2020. A pneumonia outbreak associated with a new coronavirus of probable bat origin. Nature doi:10.1038/s41586-020-2012-7.

Regarding differences between civet cat SARSr-CoV and SARS-CoV, here is the accurate data: . A total of 202 SNVs with multiple occurrences were identified, among which 200 were in the CDSs. Among the 128 nonsynonymous mutations, 89 led to a predicted radical amino acid changes

Proc Natl Acad Sci U S A. 2005 Feb 15;102(7):2430-5. Epub 2005 Feb 4.

Cross-host evolution of severe acute respiratory syndrome coronavirus in palm civet and human.

Song HD¹, Tu CC, Zhang GW, Wang SY, Zheng K, Lei LC, Chen QX, Gao YW, Zhou HQ, Xiang H, Zheng HJ, Chern SW, Cheng F, Pan CM, Xuan H, Chen SJ, Luo HM, Zhou DH, Liu YF, He JF, Qin PZ, Li LH, Ren YQ, Liang WJ, Yu YD, Anderson L, Wang M, Xu RH, Wu XW, Zheng HY, Chen JD, Liang G, Gao Y, Liao M, Fang L, Jiang LY, Li H, Chen F, Di B, He LJ, Lin JY, Tong S, Kong X, Du L, Hao P, Tang H, Bernini A, Yu XJ, Spiga O, Guo ZM, Pan HY, He WZ, Manuguerra JC, Fontanet A, Danchin A, Niccolai N, Li YX, Wu CI, Zhao GP.