

Evolution of sarbecoviruses

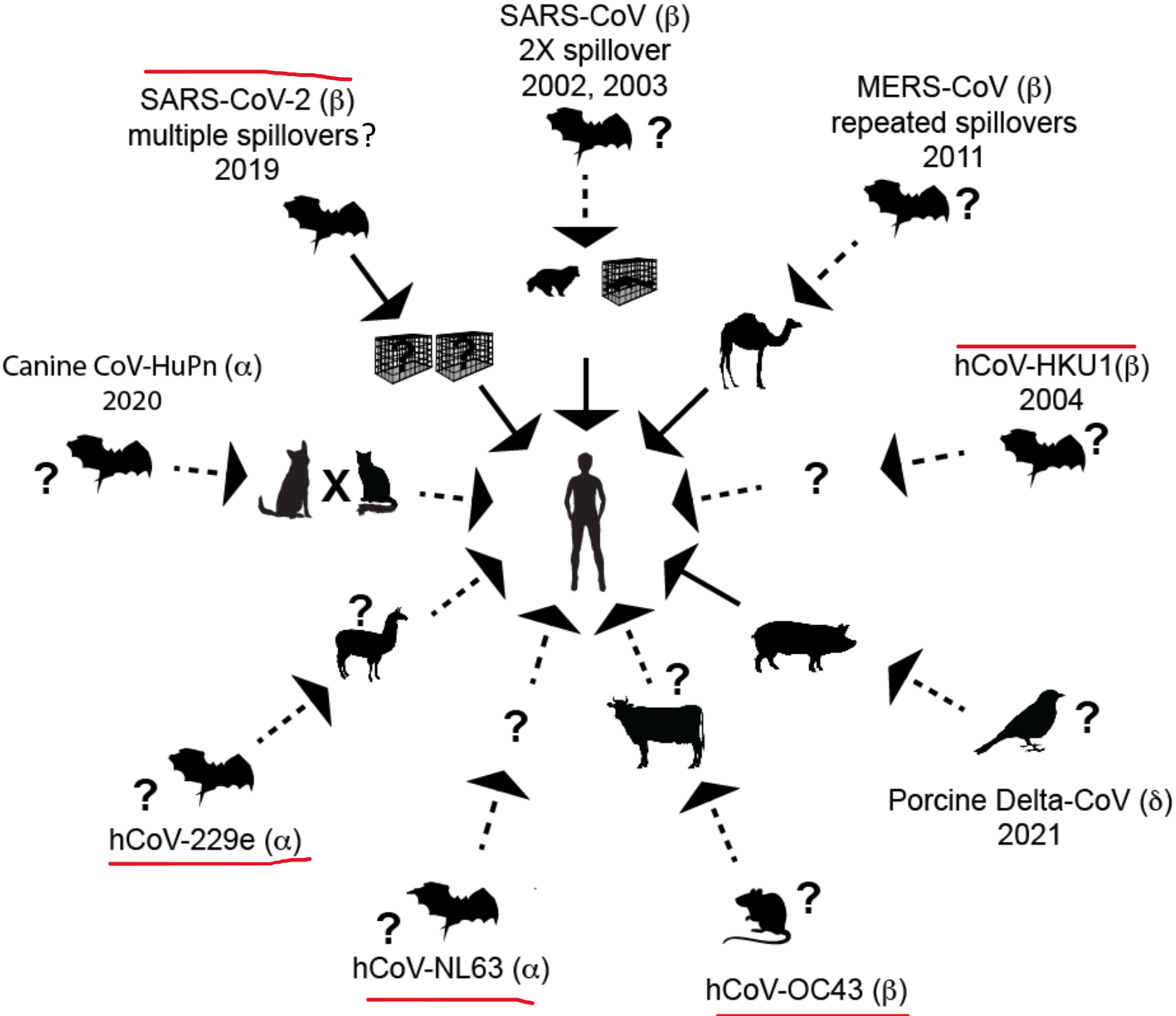
Michael Worobey

Professor and Department Head
Ecology and Evolutionary Biology
University of Arizona

Nine coronaviruses are now known to infect humans

Two new ones since SARS-CoV-2

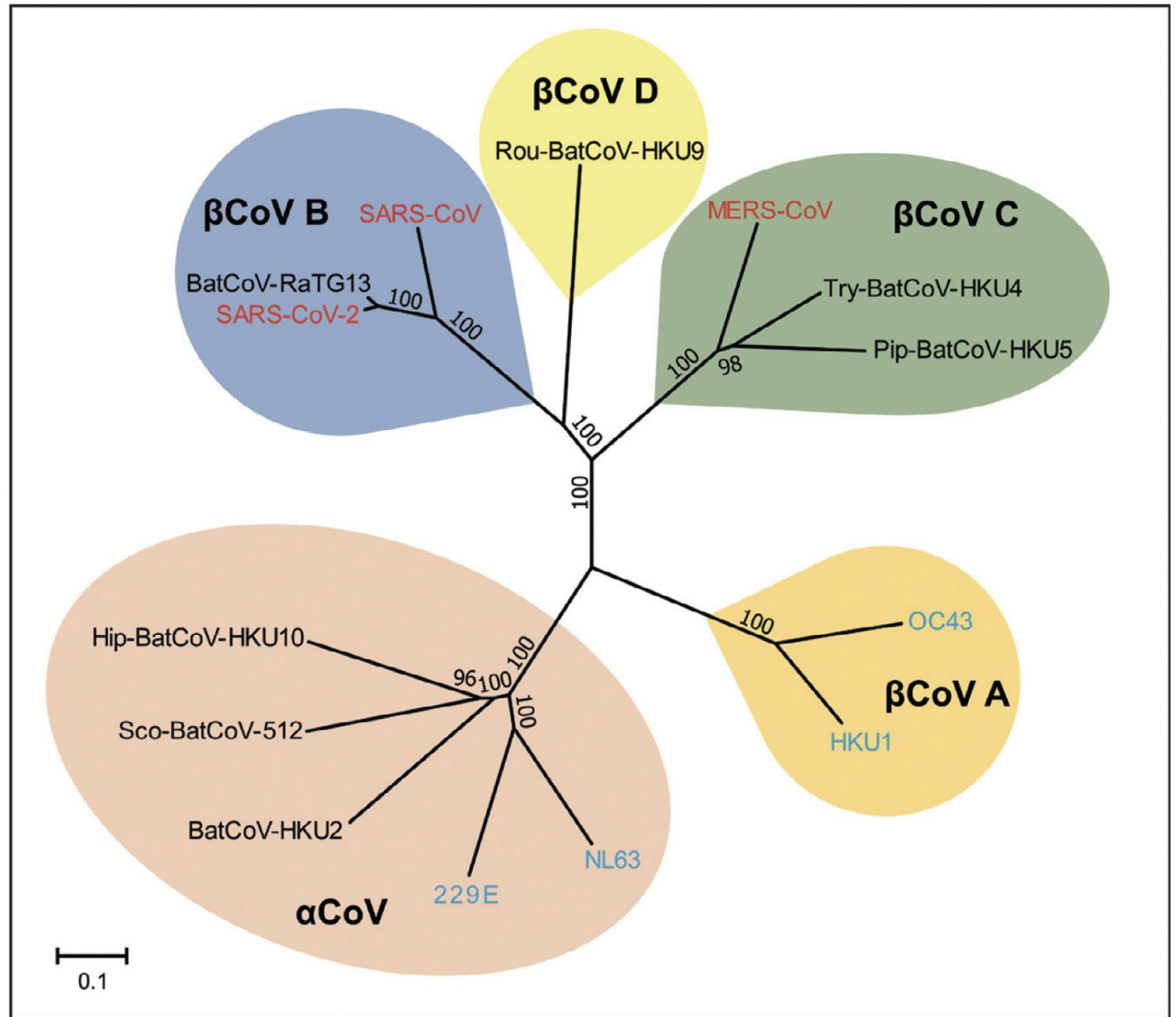
SARS-CoV-2 is in the betacoronavirus genus and the sarbecovirus subgenus



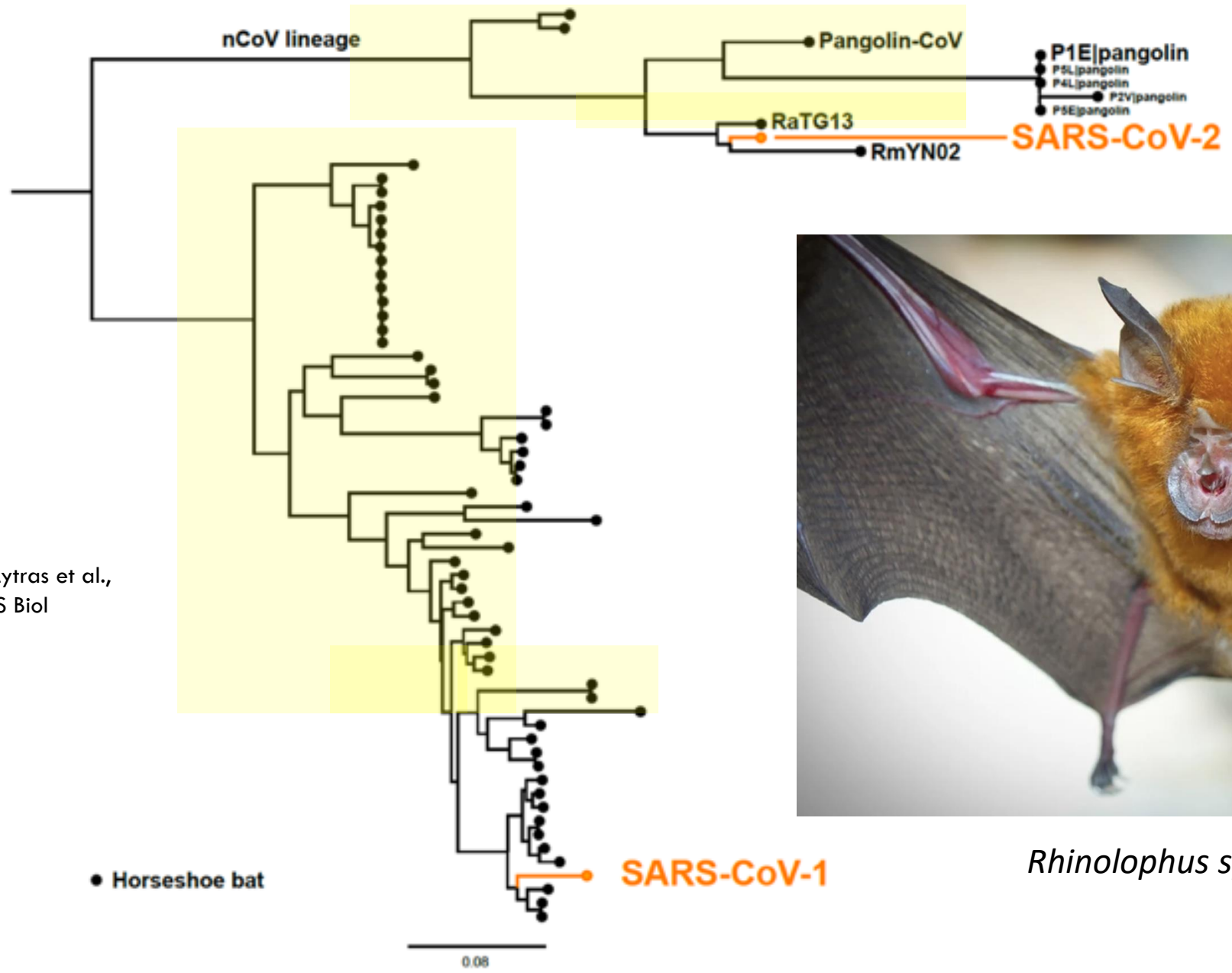
Letter

Does Cross-Neutralization of SARS-CoV-2 Only Relate to High Pathogenic Coronaviruses?

Zhongren Ma,¹ Pengfei Li,² Aqsa Ikram,¹ and Qiuwei Pan^{1,2,*}



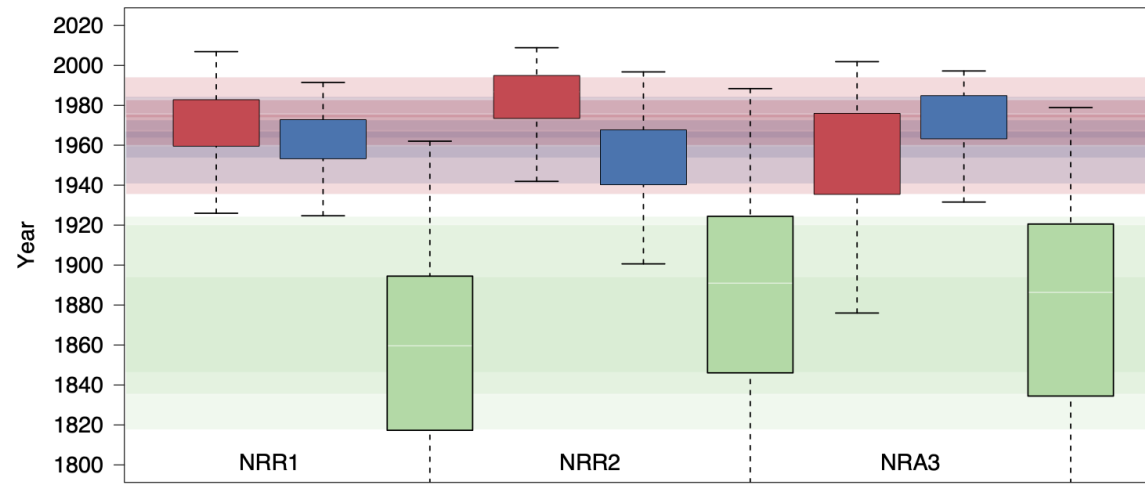
SARS-CoV-2 related to first SARS virus (SARS-CoV)



MacLean/Lytras et al.,
2021, PloS Biol

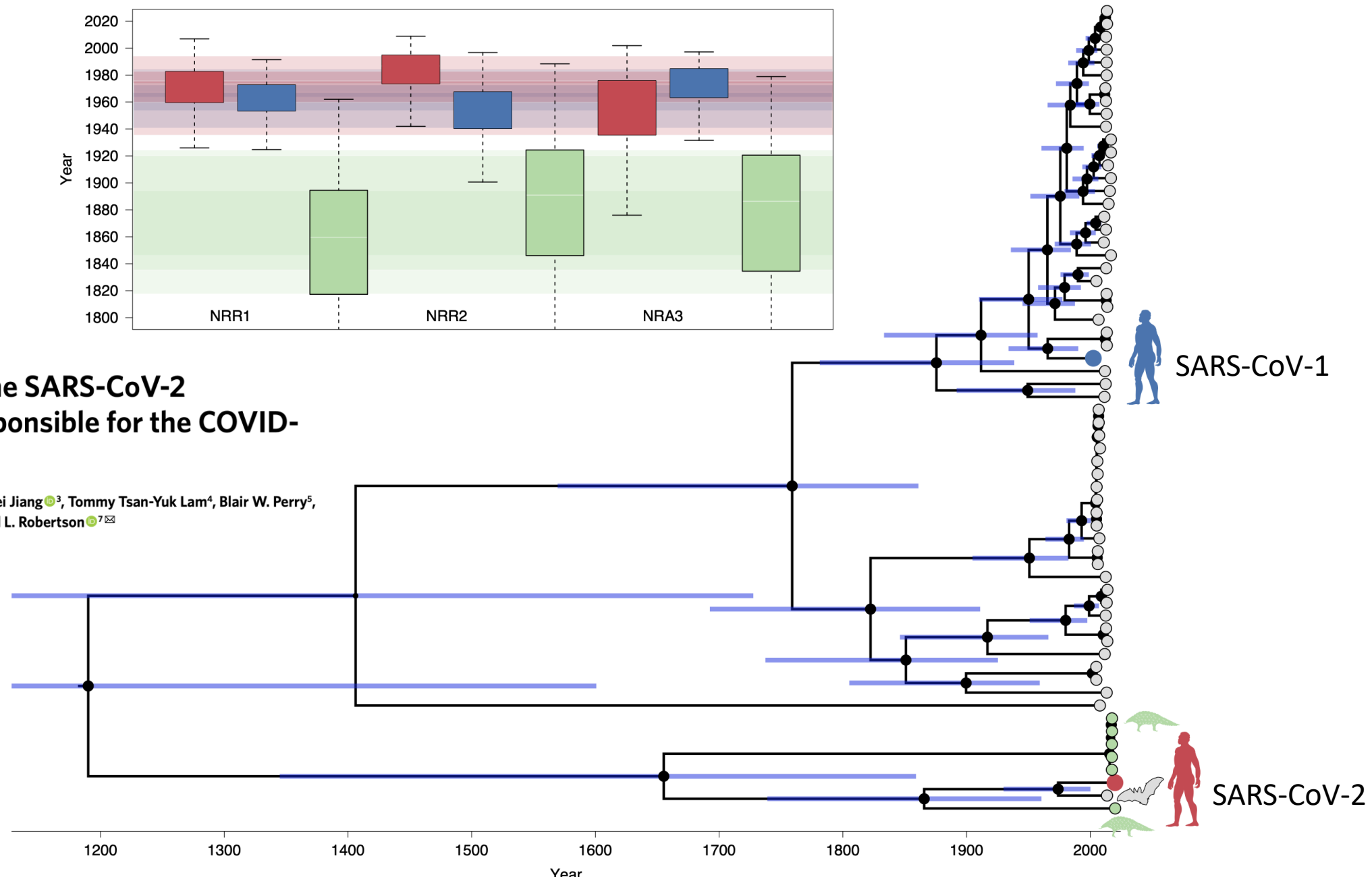


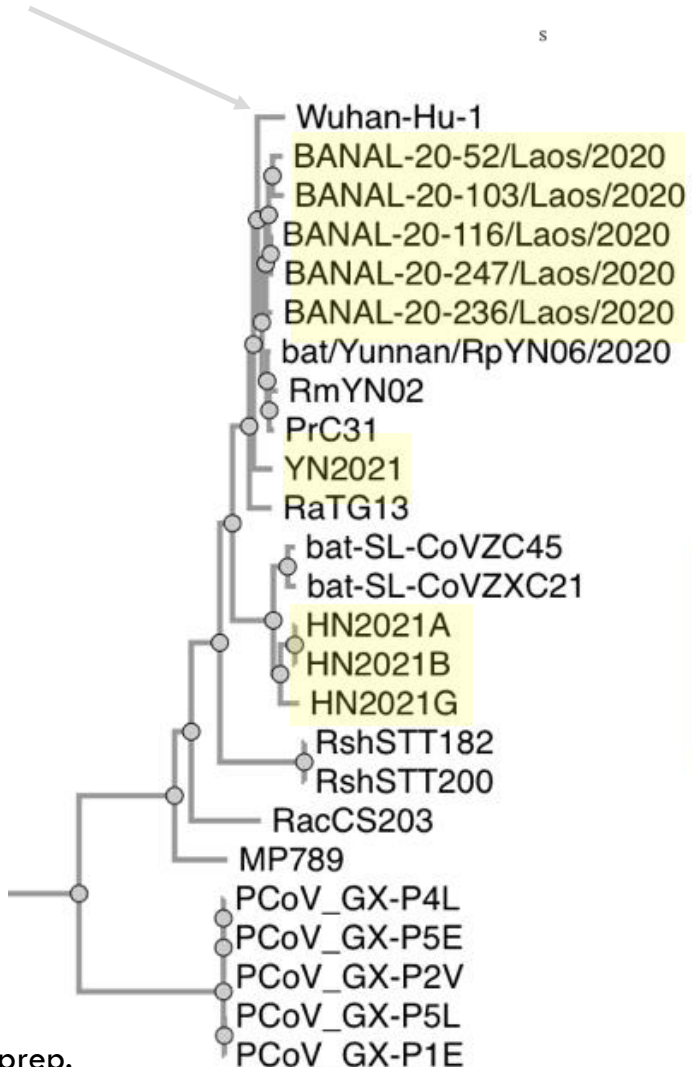
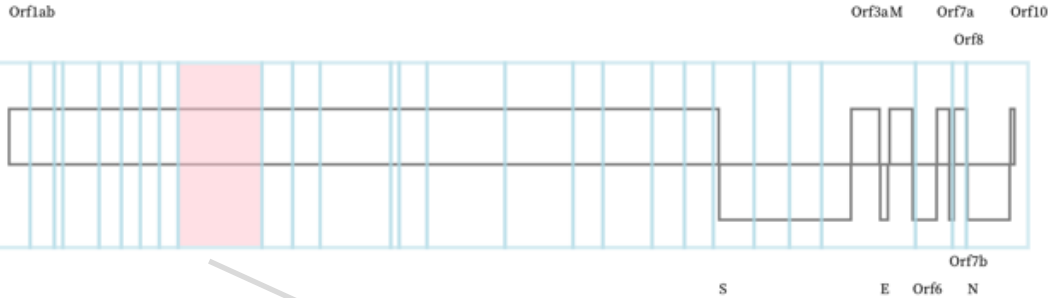
Rhinolophus spp. (horseshoe bats)



Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic

Maciej F. Boni^{1,8}, Philippe Lemey^{2,8}, Xiaowei Jiang³, Tommy Tsan-Yuk Lam⁴, Blair W. Perry⁵, Todd A. Castoe⁵, Andrew Rambaut⁶ and David L. Robertson⁷





BIOLOGICAL SCIENCES - ARTICLE

Coronaviruses with a SARS-CoV-2-like receptor-binding domain allowing ACE2-mediated entry into human cells isolated from bats of Indochinese peninsula

> Sarah Temmam, Khamsing Vongphayloth, Eduard Baquero Salazar, Sandie Munier, Max Bonomi, Béatrice Régault, Bounsavane Douangboubpha, Yasaman Karami, Delphine Chretien, Daosavanh Sanamxay, Vilakhan Xayaphet, Phetphoumin Paphaphanh, Vincent Lacoste, Somphavanh Somlor, Khaithong Lakeomany, Nothasin Phommavanh, Philippe Pérot, Flora Donati, Thomas Bigot, Michael Nilges, Félix Rey, Sylvie van der Werf, Paul Brey, Marc Eloit

DOI: [10.21203/rs.3.rs-871965/v1](https://doi.org/10.21203/rs.3.rs-871965/v1) [Download PDF](#)

BIOLOGICAL SCIENCES - ARTICLE

A comprehensive survey of bat sarbecoviruses across China for the origin tracing of SARS-CoV and SARS-CoV-2

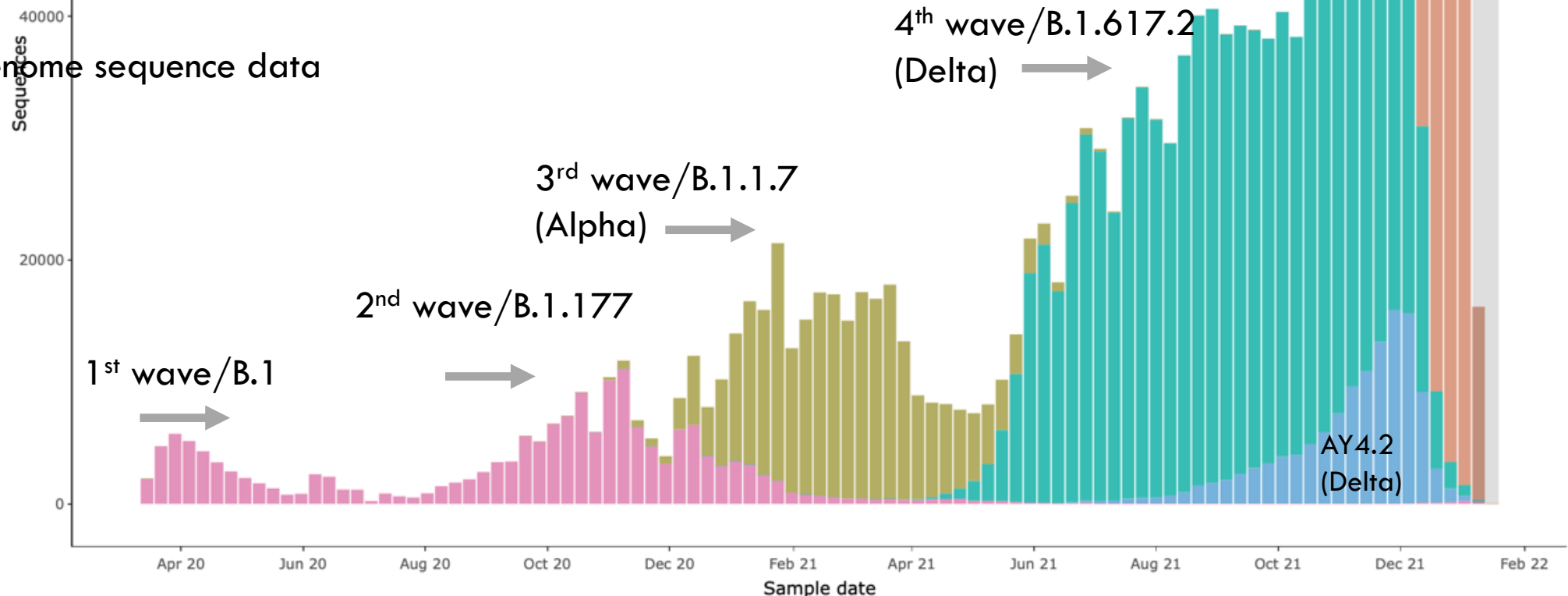
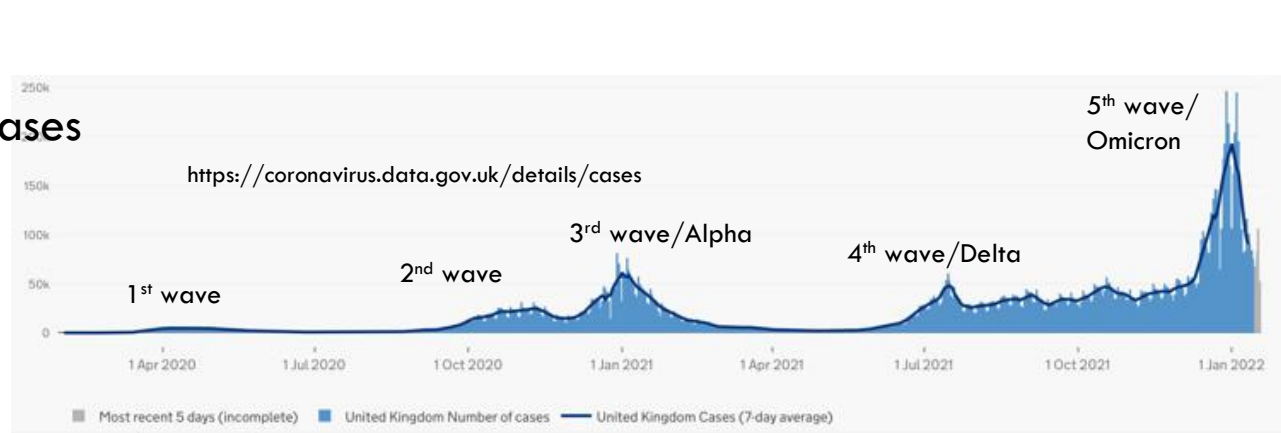
> Zhiqiang Wu, Yelin Han, Yuyang Wang, Bo Liu, Lamei Zhao, Junpeng Zhang, Hao-Xiang Su, Wenliang Zhao, Liguo Liu, Shibin Bai, Jie Dong, Lilian Sun, Yafang Zhu, Siyu Zhou, Yiping Song, Hongtao Sui, Jian Yang, Jianwei Wang, Shuyi Zhang, Zhaohui Qian, Qi Jin

DOI: [10.21203/rs.3.rs-885194/v1](https://doi.org/10.21203/rs.3.rs-885194/v1) [Download PDF](#)

- 🌟 VOCs/VUIs in the UK
- 🛡️ Antigenic Mutations
- 🔗 VOCs/VUIs + Antigenicity
- 🌟 T Cell Epitope Mutations
- ⚙️ Mutation Counts
- 👁️ Mutations by Week
- 📈 Spike Profiles
- 📄 Drug Resistance
- 👂 Ronapreve
- 📄 Geographical Distribution
- 🌟 Omicron and mAb
- 📄 About

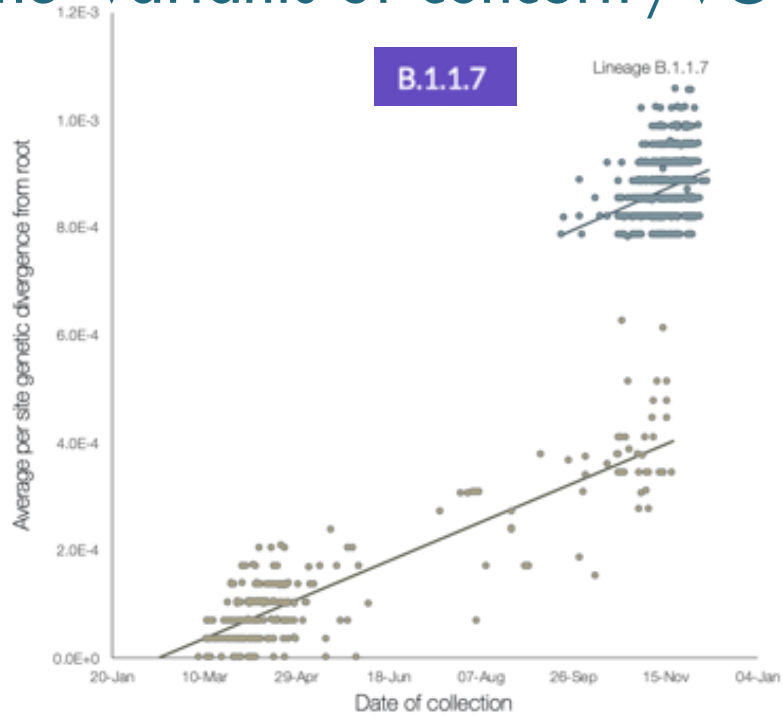
positive cases

genome sequence data



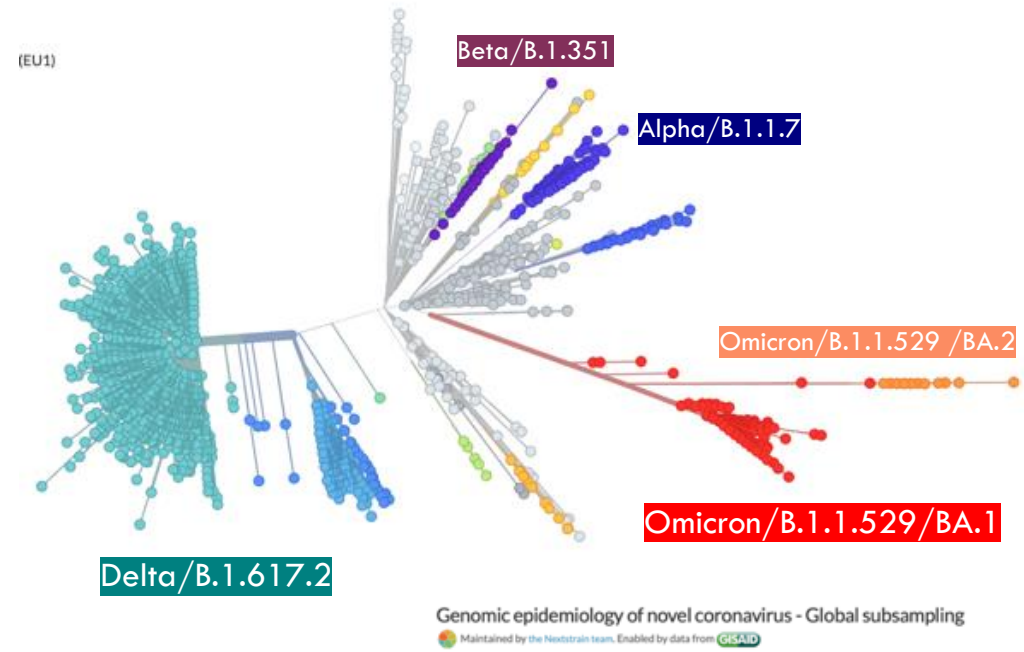
<http://sars2.cvr.gla.ac.uk/cog-uk/>

The 'variants of concern'/VOCs

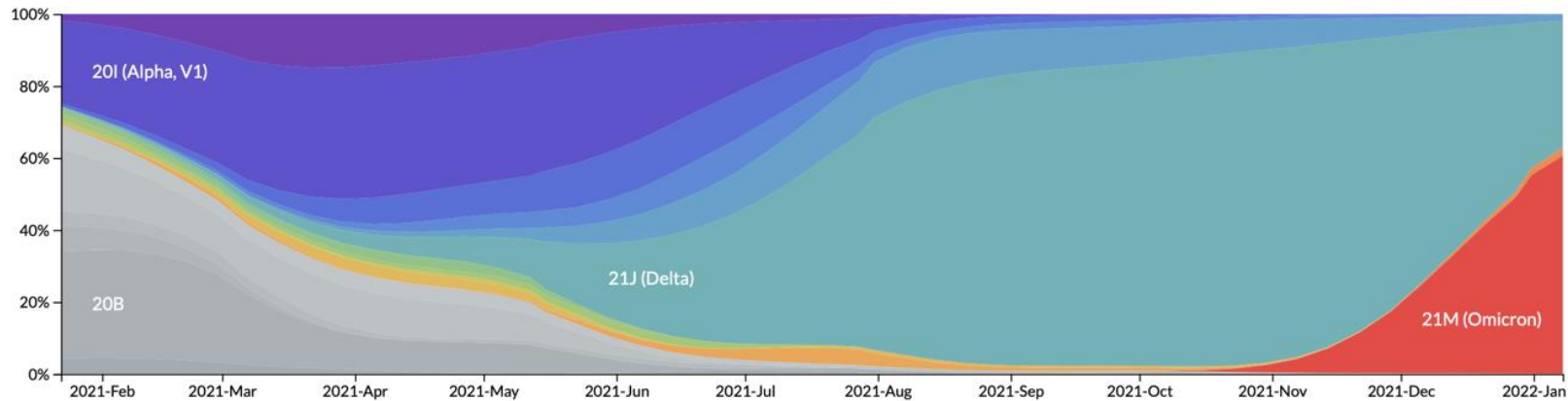


Rambaut et al., 2020,
<https://virological.org/t/563>

Oct 2020 to 17th Jan 2022

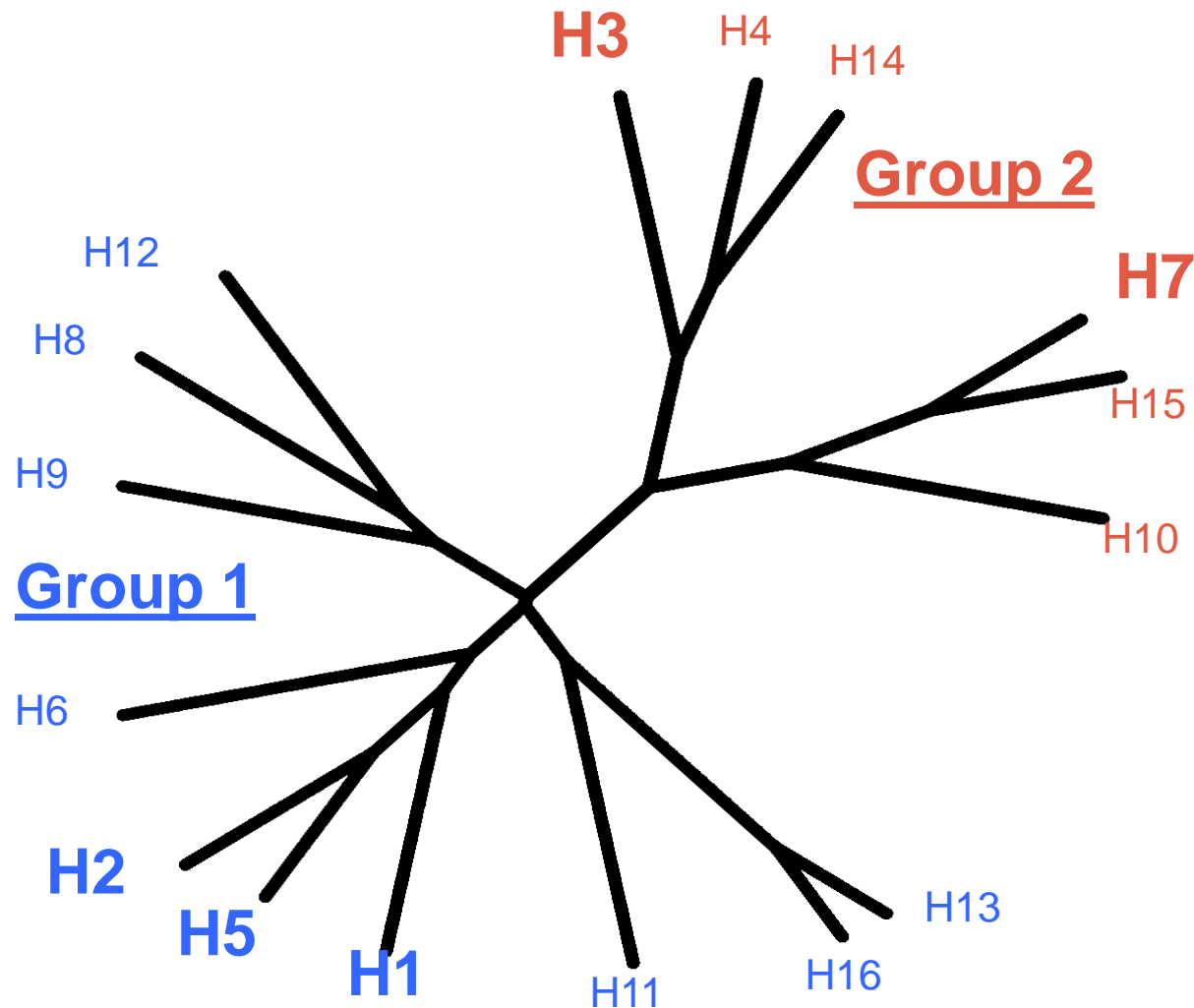


<https://nextstrain.org/ncov>



Influenza A virus: Protection across HA subtypes is possible, but antigenic imprinting an issue

Worobey et al, PNAS 2014



RESEARCH ARTICLE

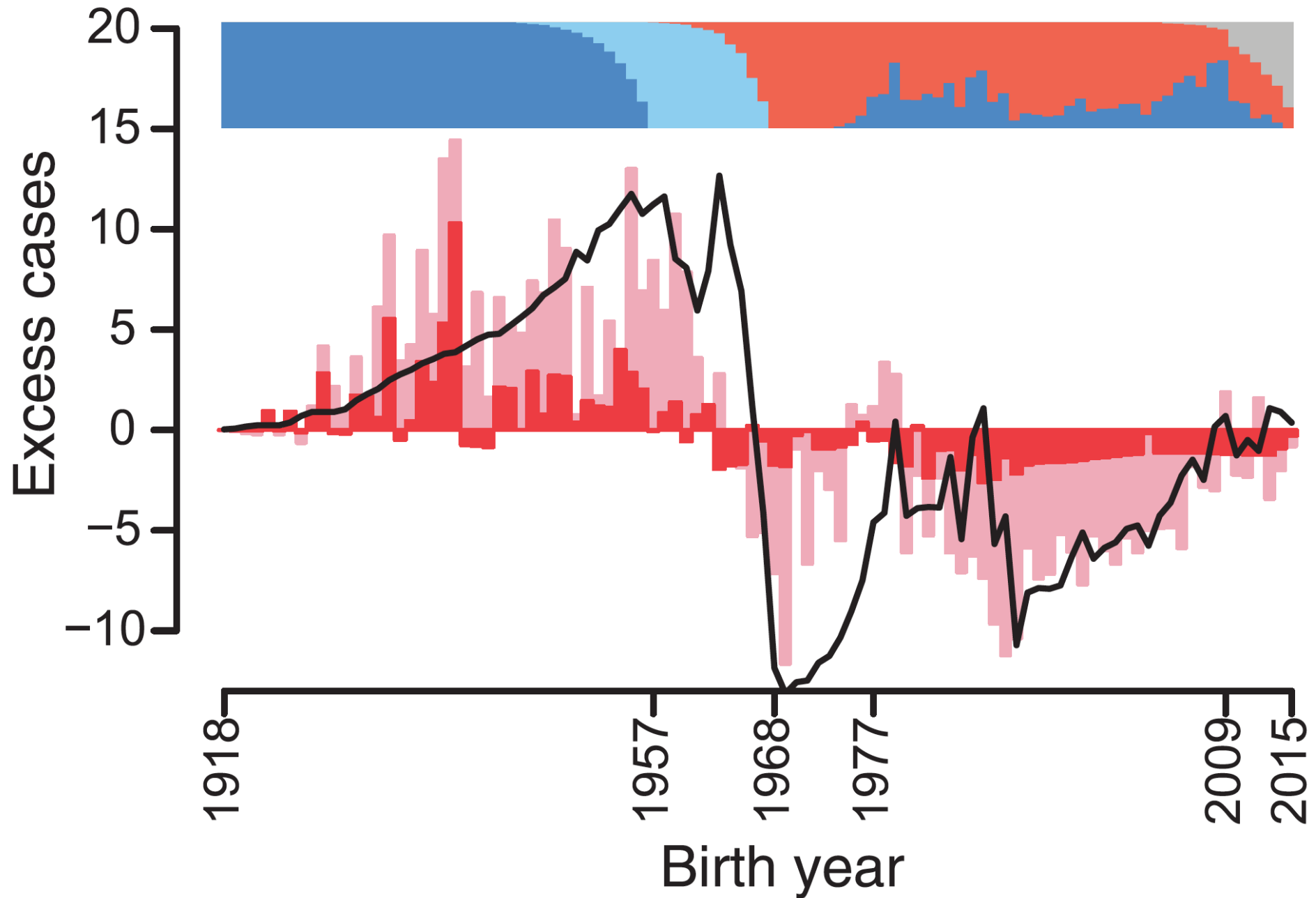
INFLUENZA EPIDEMIOLOGY

Potent protection against H5N1 and H7N9 influenza via childhood hemagglutinin imprinting

Katelyn M. Gostic,¹ Monique Ambrose,¹ Michael Worobey,^{2*} James O. Lloyd-Smith^{1,3*}

Gostic et al (2016) Science

H7N9 cases, corrected for demography



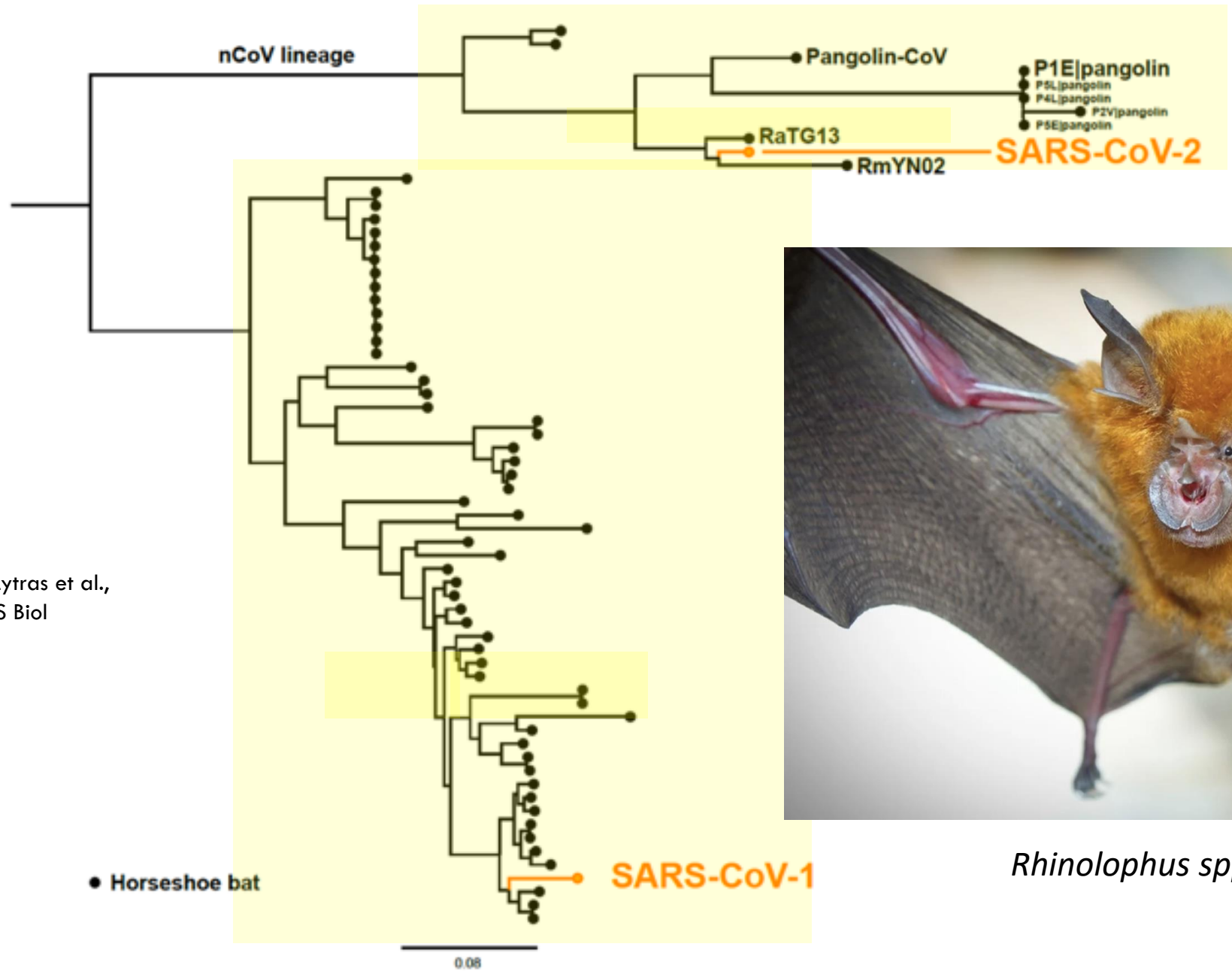
Editor's Note: This article was published on August 18, 2021, at NEJM.org.

ORIGINAL ARTICLE BRIEF REPORT

Pan-Sarbecovirus Neutralizing Antibodies in BNT162b2-Immunized SARS-CoV-1 Survivors

Chee-Wah Tan, Ph.D., Wan-Ni Chia, Ph.D., Barnaby E. Young, M.R.C.P., Feng Zhu, Ph.D., Beng-Lee Lim, M.Sc., Wan-Rong Sia, B.S., Tun-Linn Thein, M.P.H., Mark I.-C. Chen, Ph.D., Yee-Sin Leo, F.R.C.P., David C. Lye, F.R.C.P., and Lin-Fa Wang, Ph.D.

SARS-CoV-2 related to first SARS virus (SARS-CoV)



MacLean/Lytras et al.,
2021, PloS Biol



Rhinolophus spp. (horseshoe bats)

Thanks.