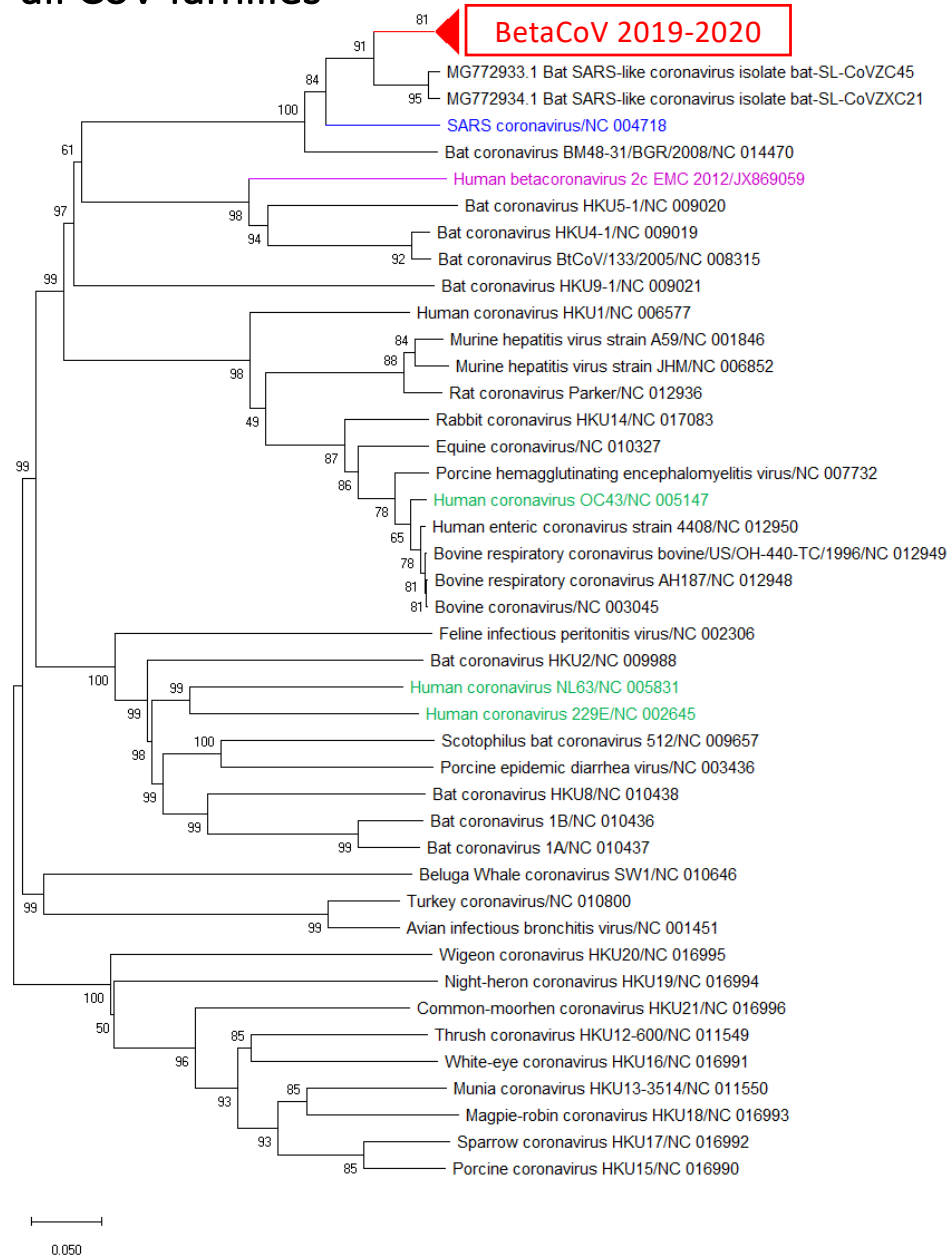


Full genome NJ tree all CoV families



- Phylogenetic tree shows virus is not close to common cold coronaviruses and only distantly related to SARS-CoV;
- The available sequence also informs diagnostics efforts.

Red ... BetaCoV 2019-2020

Blue ... SARS CoV

Purple ... MERS CoV

Green ... common cold CoV

We gratefully acknowledge the Originating and Submitting laboratories of sequence data in alphabetic order:

P.R. China: Hubei Provincial CDC

Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College

National Institute for Viral Disease Control and Prevention,

at the Chinese Center for Disease Control and Prevention

Wuhan Institute of Virology, Chinese Academy of Sciences

Wuhan Jinyintan Hospital

Japan: Department of Virology III, National Institute of Infectious Diseases;

Thailand: Bamrasnaradura Hospital, Nonthaburi

Department of Disease Control, Ministry of Public Health

Department of Medical Sciences, Ministry of Public Health

Thai Red Cross Emerging Infectious Diseases - Health Science Centre.

Phylogenetic tree of Wuhan CoV full genome sequences in context of representatives of all CoV families (whole genome Neighbor Joining, Maximum Composite Likelihood, uniform rates, 500 bootstrap, MegaX)



by BII, A*STAR Singapore

Maximum likelihood tree of all outbreak sequences with **orf1a region** 2020-01-20



0.020

Phylogenetic tree created with RAXML-NG (Maximum Likelihood tree search, 10 randomized parsimony starting trees, GTR model, Gamma distributed rates, 500 bootstrap) and visualized in MegaX

All outbreak sequences so far are very closely related, including BetaCov/Kanagawa/1/2020, BetaCov/Nonthaburi/74/2020 and BetaCov/Nonthaburi/62/2020 from **Japanese** and **Thai** patients, respectively.

We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data as follows:

P.R. China: Wenjie Tan, Xiang Zhao, Wenling Wang, Xuejun Ma, Yongzhong Jiang, Roujian Lu, Ji Wang, Weimin Zhou, Peihua Niu, Peipei Liu, Faxian Zhan, Weifeng Shi, Baoying Huang, Jun Liu, Li Zhao, Yao Meng, Xiaozhou He, Fei Ye, Na Zhu, Yang Li, Jing Chen, Wenbo Xu, George F. Gao, Guizhen Wu;

Peng Zhou, Xing-Lou Yang, Ding-Yu Zhang, Lei Zhang, Yan Zhu, Hao-Rui Si, Zhengli Shi;

Lili Ren, Jianwei Wang, Qi Jin, Zichun Xiang, Yongjun Li, Zhiqiang Wu, Chao Wu, Yiwei Liu

Bin Fang, Xiang Li, Xiao Yu, Linlin Liu, Bo Yang, Faxian Zhan, Guojun Ye, Xixiang Huo, Junqiang Xu, Bo Yu, Kun Cai, Jing Li, Yongzhong Jiang;

Japan: Naganori Nao, Kazuya Shirato, Shutoku Matsuyama, Makoto Takeda;

Thailand: Pilailuk Okada, Siripaporn Phuygun, Thanutsapa Thanadachakul, Supaporn Wacharapluesadee, Sittiporn Parnmen, Warawan Wongboot, Sunthareeya Waicharoen, Rome Buathong, Malinee Chittaganpitch, Nanthawan Mekha.



by BII, A*STAR Singapore

Maximum likelihood tree of all outbreak sequences with **full genome** 2020-01-20



0.000050

Phylogenetic tree created with RAXML-NG (Maximum Likelihood tree search, 10 randomized parsimony starting trees, GTR model, Gamma distributed rates, 500 bootstrap) and visualized in MegaX

- Outbreak structure not yet significantly discernible (bootstrap support <60)
- sequence variation is low;
- Long branches may reflect sequencing quality issues.

We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data as follows:

P.R. China: Wenjie Tan, Xiang Zhao, Wenling Wang, Xuejun Ma, Yongzhong Jiang, Roujian Lu, Ji Wang, Weimin Zhou, Peihua Niu, Peipei Liu, Faxian Zhan, Weifeng Shi, Baoying Huang, Jun Liu, Li Zhao, Yao Meng, Xiaozhou He, Fei Ye, Na Zhu, Yang Li, Jing Chen, Wenbo Xu, George F. Gao, Guizhen Wu;

Peng Zhou, Xing-Lou Yang, Ding-Yu Zhang, Lei Zhang, Yan Zhu, Hao-Rui Si, Zhengli Shi;

Lili Ren, Jianwei Wang, Qi Jin, Zichun Xiang, Yongjun Li, Zhiqiang Wu, Chao Wu, Yiwei Liu

Bin Fang, Xiang Li, Xiao Yu, Linlin Liu, Bo Yang, Faxian Zhan, Guojun Ye, Xixiang Huo, Junqiang Xu, Bo Yu, Kun Cai, Jing Li, Yongzhong Jiang;

Japan: Naganori Nao, Kazuya Shirato, Shutoku Matsuyama, Makoto Takeda;

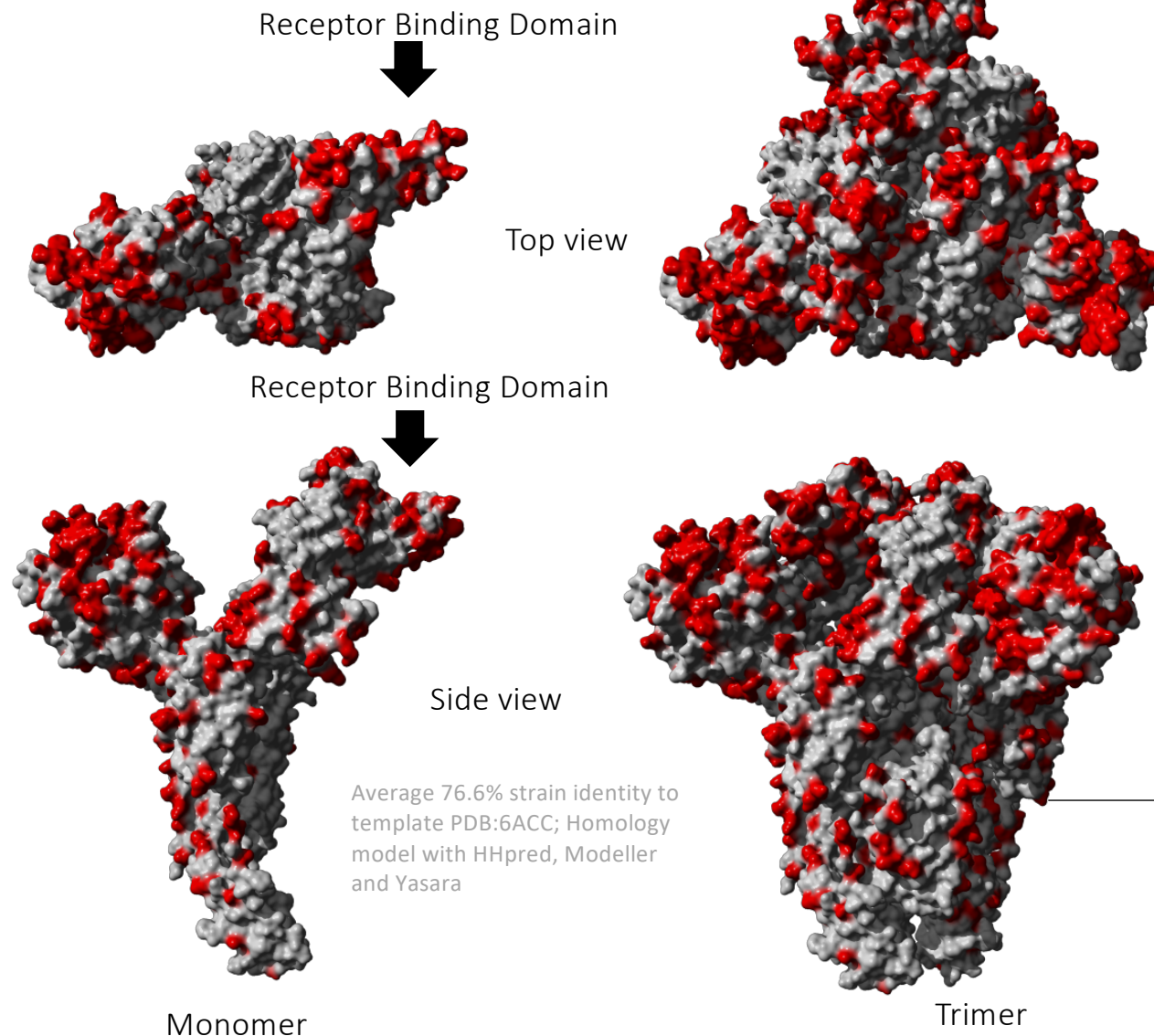
Thailand: Pilailuk Okada, Siripaporn Phuygun, Thanutsapa Thanadachakul, Supaporn Wacharapluesadee, Sittiporn Parnmen, Warawan Wongboot, Sunthareeya Waicharoen, Rome Buathong, Malinee Chittaganpitch, Nanthawan Mekha.



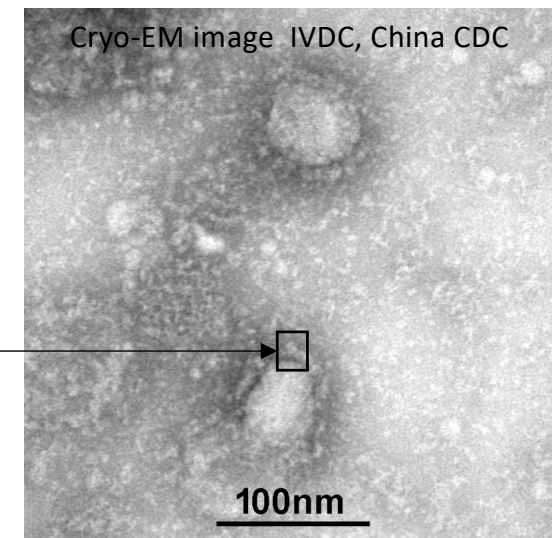
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Spike glycoprotein BetaCoV vs SARS

Red ... consensus differences (surface mutations)



- Although related to SARS-CoV the newly discovered BetaCoV is quite different at the critical surface epitopes and the receptor binding domain;
- Transmissibility and severity cannot be predicted but needs to be measured;
- SARS-CoV candidate vaccines predicted to NOT yield cross-reactive immune responses against this virus.



We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.

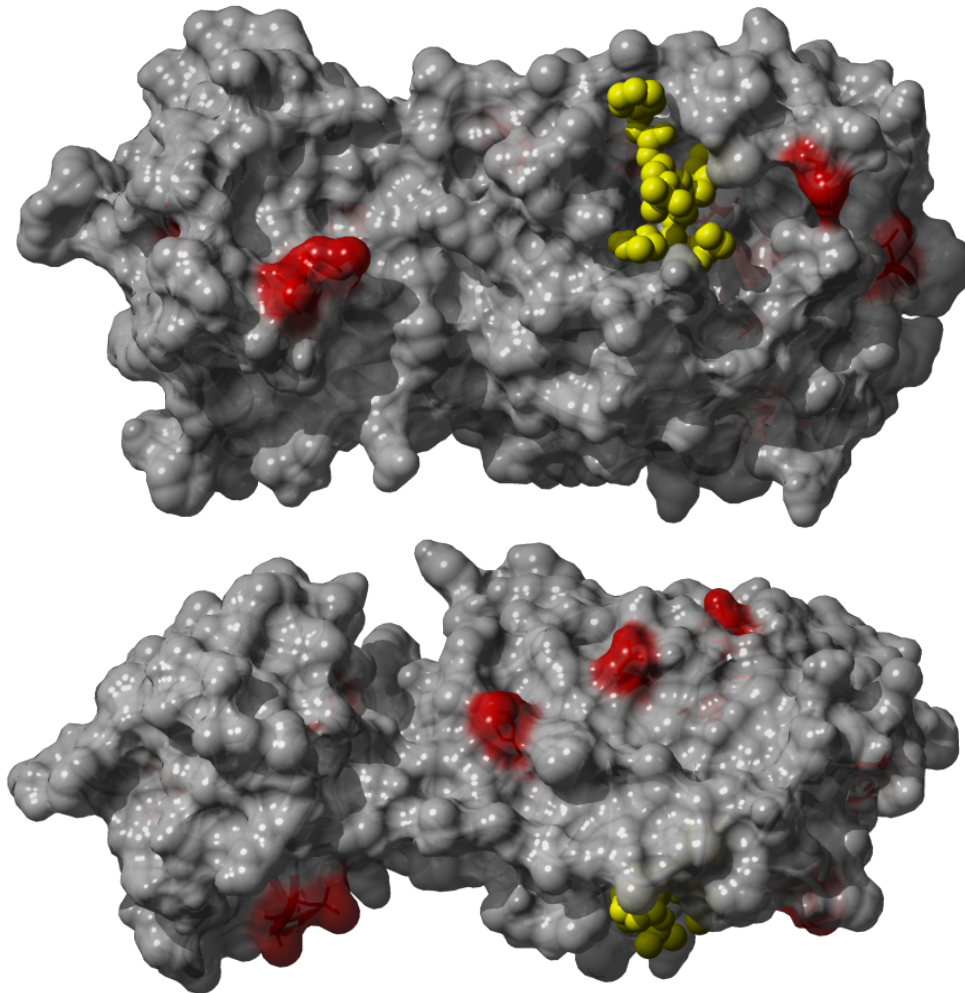
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Main protease BetaCoV vs SARS

Red ... consensus differences (surface mutations)

Yellow ... substrate analogue/inhibitor



- The main protease which is a potential drug target is highly conserved between BetaCoV and SARS with 96% overall identity
- Substrate and inhibitor binding pocket is 100% conserved
- Inhibitors developed against the SARS-CoV main protease have good potential to bind similarly to BetaCoV

Template PDB:3TNT; Homology model with HHpred, Modeller and Yasara

We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.

by BII, A*STAR Singapore

