

Origin and evolution of pathogenic coronaviruses

Jie Cui, Fang Li and Zheng-Li Shi

<https://doi.org/10.1038/s41579-018-0118-9>

Supplementary information

Fig. S1. Phylogenetic analysis of SARS-related coronaviruses and MERS-related

coronaviruses. (A) The SARS-related phylogeny based on the complete RdRp coding sequences was constructed using the maximum likelihood (ML) method under the GTR+I+ Γ model of nucleotide substitution. The strain Zhejiang2013 (GenBank No. KF636752) was used as a root of this tree. Only bootstrap values $\geq 70\%$ are shown.

All strains here were named using abbreviations of bat species, sample ID and sampling provinces in China: YN, Yunnan; GZ, Guizhou; GX, Guangxi; GD, Guangdong; HK, Hong Kong; SAX, Shaanxi; HuB, Hubei; SX, Shanxi; HeN, Henan; HeB, Hebei; ZJ, Zhejiang; JL, Jilin; SK, South Korea (Asian country); BG, Bulgaria (European country).

Three major viral lineages were shown and colored as L1 (denoting lineage 1) - L3. (B)

The MERS-related phylogeny using a full-genome alignment of all of the coding regions was reconstructed. HKU4-1 (EF065505) and HKU5-1 (EF065509) was regarded as the root. Only bootstrap values $\geq 70\%$ are shown. All strains here were

named using abbreviations of host species, sample ID and sampling locations: IT, Italy; CN, China; SA, South Africa; ET, Ethiopia; MA, Morocco; BF, Burkina Faso; NG, Nigeria; UAE, The United Arab Emirates; KSA, Kingdom of Saudi Arabia; OM, Oman; JO, Jordan; TH, Thailand. Two major lineages were shown as L1 and L2 and two small clusters were also exhibited as B1 and B2.

A



