Preliminary analysis of Middle East respiratory syndrome coronavirus (MERS-CoV) sequences from Korea and China

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Prepared by members of the WHO-convened "Laboratory Experts for MERS-CoV" with additional data from several research groups (see complete contributors listing in Appendix).

Recent Middle East respiratory syndrome (MERS) cases in Korea and China are thought to have originated from a virus carried by a traveller returning from the Middle East after visits to the Kingdom of Saudi Arabia (KSA), Bahrain, the United Arabic Emirates and Qatar. A MERS-CoV sequence from a patient in Guangdong has been produced by the Chinese CDC (GenBank KT006149) and the MERS-CoV sequence from a patient in Korea (MERS-CoV/KOR/KNIH/002_05_2015, *submitted to GenBank*) has been produced by the Korea National Institute of Health and ChunLab, Inc.

A preliminary analysis of the two viral genomes supports the following conclusions:

1. A strict consensus of the Korean and Chinese MERS-CoV sequences clusters closest with viruses obtained from a recent outbreak in Riyadh in February-March 2015 (1) (Figure 1). The Chinese and Korean viruses are however divergent enough from the Riyadh 2015 cluster to potentially be derived from a separate zoonotic event in the Arabian Peninsula. Given the travel history of the Korean index patient (2) to other countries with recent MERS-CoV cases, the originating country cannot be determined with certainty. From these data the new MERS-CoVs are unlikely to be phenotypically different from the MERS-CoV currently circulating in the Arabian Peninsula and are unlikely to present different virulence or transmission properties. However, further clinical, epidemiological and virus genetic data will be required to be certain of these preliminary conclusions. In addition, there is an urgency to increase sequencing efforts in all countries where MERS-CoV is circulating. This will increase our knowledge of transmission patterns and inform public health measures required to prevent transmission.

2. The two currently available sequences from Korea and China are from patients with a direct epidemiological link and as such are not expected to show many nucleotide differences. However, it is important to note that the Korean sequence was obtained from a cell culture passaged virus while the Chinese sequence was obtained by direct sequencing of patient swab material. In addition, different error rates and profiles for the sequencing platforms used (Sanger and Ion Torrent for the Chinese sequence versus Illumina for the Korean sequence) and differences in the assembly methods could be a factor. We therefore assume that most of the differences between the Korean and Chinese sequences are the result of these technical issues. Further sequencing will clarify this. These considerations led us to use a strict consensus sequence in the analyses above.

3. No shared amino changes in the encoded spike were observed between the Korean and Chinese sequences. If there was a more transmissible virus emerging in Korea/China and this was due to a new spike variant, then one would expect the changes to be shared by the two sequences. This was not observed. Additional sequencing of patient samples in Korea will help to resolve the sequence diversity within this cluster.

References

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Figure Legend

Figure 1. Phylogenetic reconstruction of 171 available MERS CoV sequences. A strict consensus was created between the Korean and Chinese sequences (marked in red with asterisk), recent virus sequences from Riyadh (Riyadh KKUH 2015) are from (1) and viruses sequences from camels are shown in orange. Colored boxes indicate previously-defined clades or lineages. The Al-Hasa hospital outbreak is collapsed for clarity. Clade support is shown where the bootstrap support values were greater than 75%. The scale bar is in units of substitutions/site. A maximum-likelihood phylogeny was constructed from the alignment of 171 MERS CoV sequences using RAxML version 7.8.6 under a GTR+G substitution model. Clade support was assessed by bootstrapping with 1000 pseudo-replicates.

Appendix. This summary was prepared with contributions from the following (in alphabetical order):

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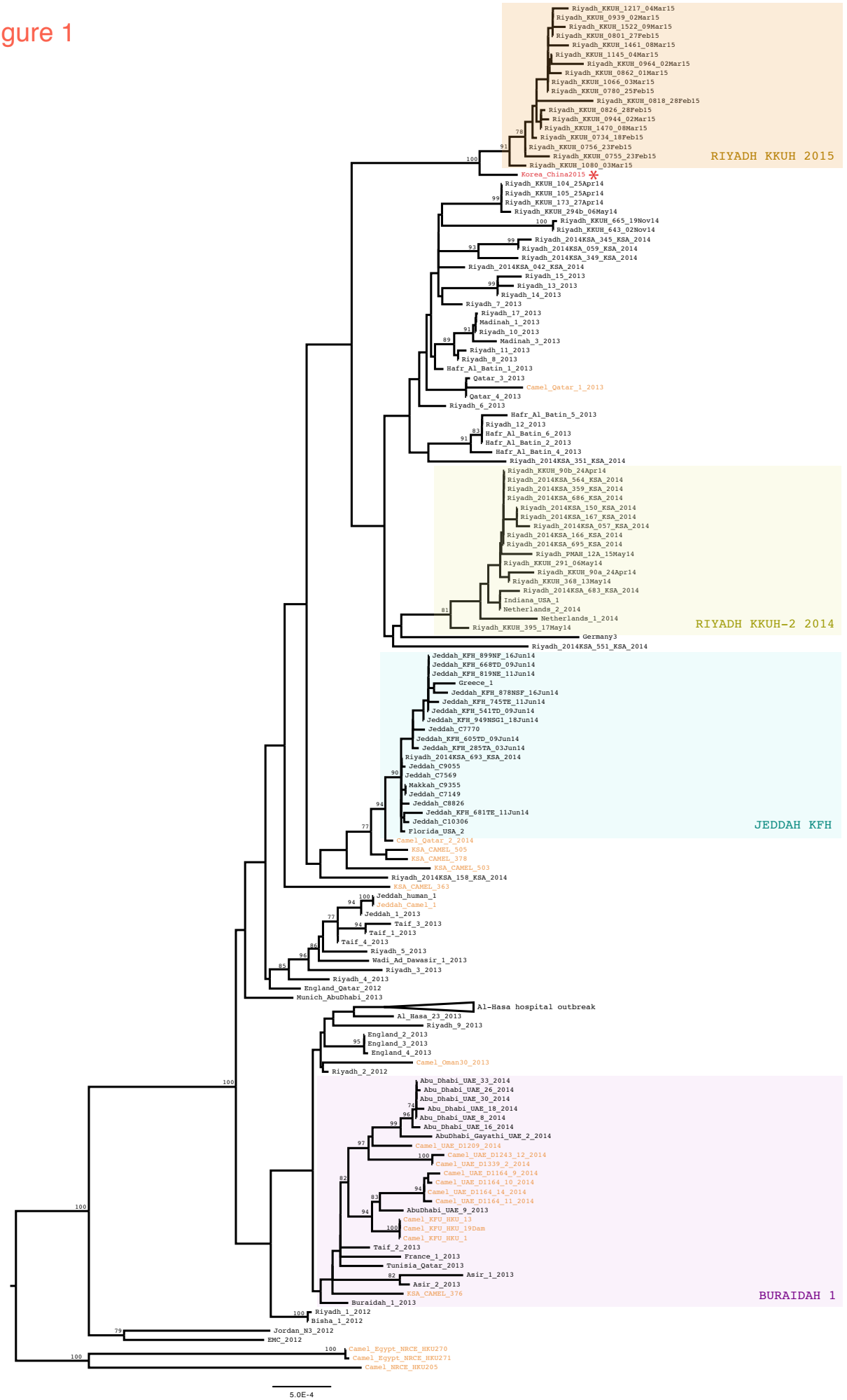
Figure 1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