Microevolution of Middle East Respiratory Syndrome–Coronavirus during an Outbreak, South Korea, 2015

Technical Appendix

Technical Appendix Table 1. Clinical description of the patient included in this study

| Case ID	Sex	Age, y	Outcome*	Exposure history	Underlying disease
#14	M	35	Discharged	Inpatient	None
#35	M	38	Hospitalized	Healthcare worker	Fatty liver, cough-variant asthma
#168	M	36	Discharged	Healthcare worker	None
#163	F	52	Discharged	Healthcare worker	None

*Outcome status November 1, 2015

Technical Appendix Table 2. Variants identified within the eight strains

Nucleotide position Hu/Riyadh KSA_2959_2015	Gene	Nucleotide mutation compared with Hu/Riyadh KSA_2959_2015	Predicted amino acid change	#14	#35	#168	#163
2917	ORF1ab	2639A>G	Asn880Ser	A	A	G	A
5852	ORF1ab	5574G>A	Synonymous	G	G	G	A
7933	ORF1ab	7655C>T	Ser2552Phe	C	C	C	T
10089	ORF1ab	9811A>G	Ser3271Gly	A	G	A	A
11257	ORF1ab	10979C>T	Ala3660Val	T	T	C	C
18916	ORF1ab	18639G>A	Synonymous	G/A*	G	G	G
21726	Spike	271C>T	His91Tyr	C	C	T	C
22984	Spike	1529A>G	Asp510Gly	A	A	G	A
23041	Spike	1586T>C	Ile529Thr	C	C	T	T
24622	Spike	3167A>G	Gln1056Arg	A	A	A	G

Nucleotide position Hu/Riyadh KSA_2959_2015	Gene	Nucleotide mutation compared with Hu/Riyadh KSA_2959_2015	Predicted amino acid change	#14	#35	#168	#163
25495	Spike	4040C>T	Pro1347Leu	C	C	C/T*	C
25903	ORF4a	52C>T	Pro18Ser	C	C	T	C
26979	ORF5	140T>C	Val47Ala	T	C	T	T

*These nucleotide changes (G to A and C to T) appear during the course of infection.
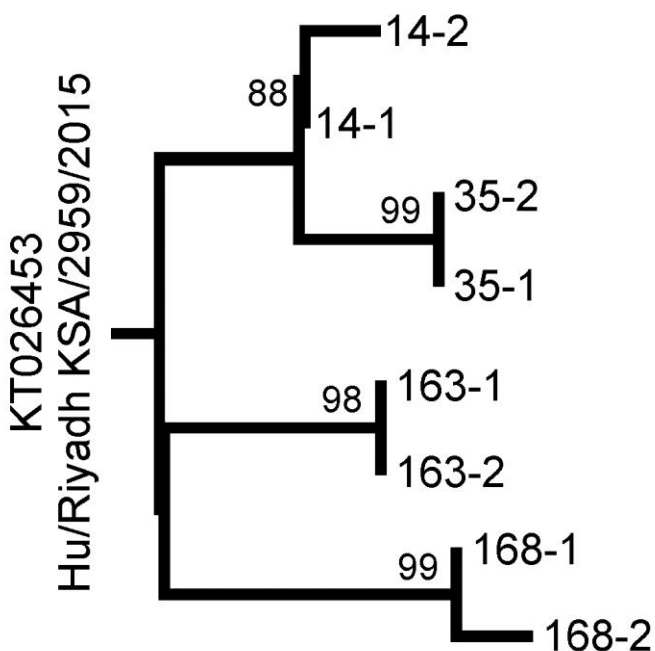
Technical Appendix Figure. Phylogenetic analysis based on variant sites using maximum likelihood (PhyML) with a general time reversible substitution model. A total of 1,000 bootstrapped phylogeny reconstructions were performed. The tree is rooted to a MERS-CoV sequence obtained from a recent outbreak in Riyadh/KSA (GenBank accession no. KT026453), which was found to constitute the closest phylogenetic neighbor to the viruses shown here (strain reference shown at the tree root).