

A phylogenetic tree constructed by using the entire sequence showed that all PorCoV HKU15 strains from the United States clustered together in 1 clade of the genus *Deltacoronavirus* with HKU15-155 and HKU15-44 (online Technical Appendix Figure, panel A, <http://wwwnc.cdc.gov/EID/article/20/9/14-0756-Techapp1.pdf>). This finding indicates that 1 genotype of PorCoV HKU15 is currently circulating in multiple US states. This result was further supported by phylogenetic trees constructed by using the full-length amino acids of spike and nucleocapsid proteins (online Technical Appendix Figure, panels B, C). Because of limitation of the samples received, only a partial genome sequence was determined for strain MN3092 from Minnesota. However, on the basis of the spike and nucleocapsid protein sequence analyses, it is highly likely that the entire genome of the Minnesota strain is genetically identical to that of the other 8 strains (online Technical Appendix Figure, panels B, C).

In addition to the 9 states reported in this study, Iowa has also had a recent detection of PorCoV HKU15 (3). Thus, PorCoV HKU15 has been detected in 10 of the 50 US states, and those 10 states mainly cluster in the midwestern United States (Figure). As with data collected for porcine epidemic diarrhea outbreaks by the US National Animal Health Laboratory Network (<http://www.nahln.org/default/>), data collected on the geographic location and numbers of PorCoV HKU15 cases is also required to be reported weekly.

Earlier reports support avian coronaviruses as the gene source for *Deltacoronavirus* spp. (1,4). To confirm this, surveillance for PorCoV should be carried out among birds. Moreover, effective control strategies, including vaccine development, should be in place for prevention and control of infections caused by PorCoV HKU15.

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Schistosomiasis Haematobium, Corsica, France

To the Editor: In Europe, urinary schistosomiasis (1) has previously been detected only in Portugal, where this focus disappeared during the 1950s (2). However, freshwater snails of the species *Bulinus contortus*, *B. truncatus*, and *Planorbis metidjensis*, which are recognized intermediate hosts for *Schistosoma haematobium* trematodes, have been found in Portugal (3), Spain (4), and Corsica (5,6). This finding suggested that autochthonous schistosomiasis could re-emerge in southern Europe if these mollusks become infected. We report a probable focus for transmission of schistosomiasis haematobium in Corsica, France.

In March 2014, a 4-year-old girl (index case-patient) from France was referred to the Toulouse University Hospital (Toulouse, France), with gross hematuria. Ultrasonography and cystoscopic examination of the bladder detected a polyp. Examination of the polyp for parasites identified bodies that were consistent with schistosome eggs. Parasitologic examination of urine confirmed schistosomiasis by detecting viable *S. haematobium* eggs.

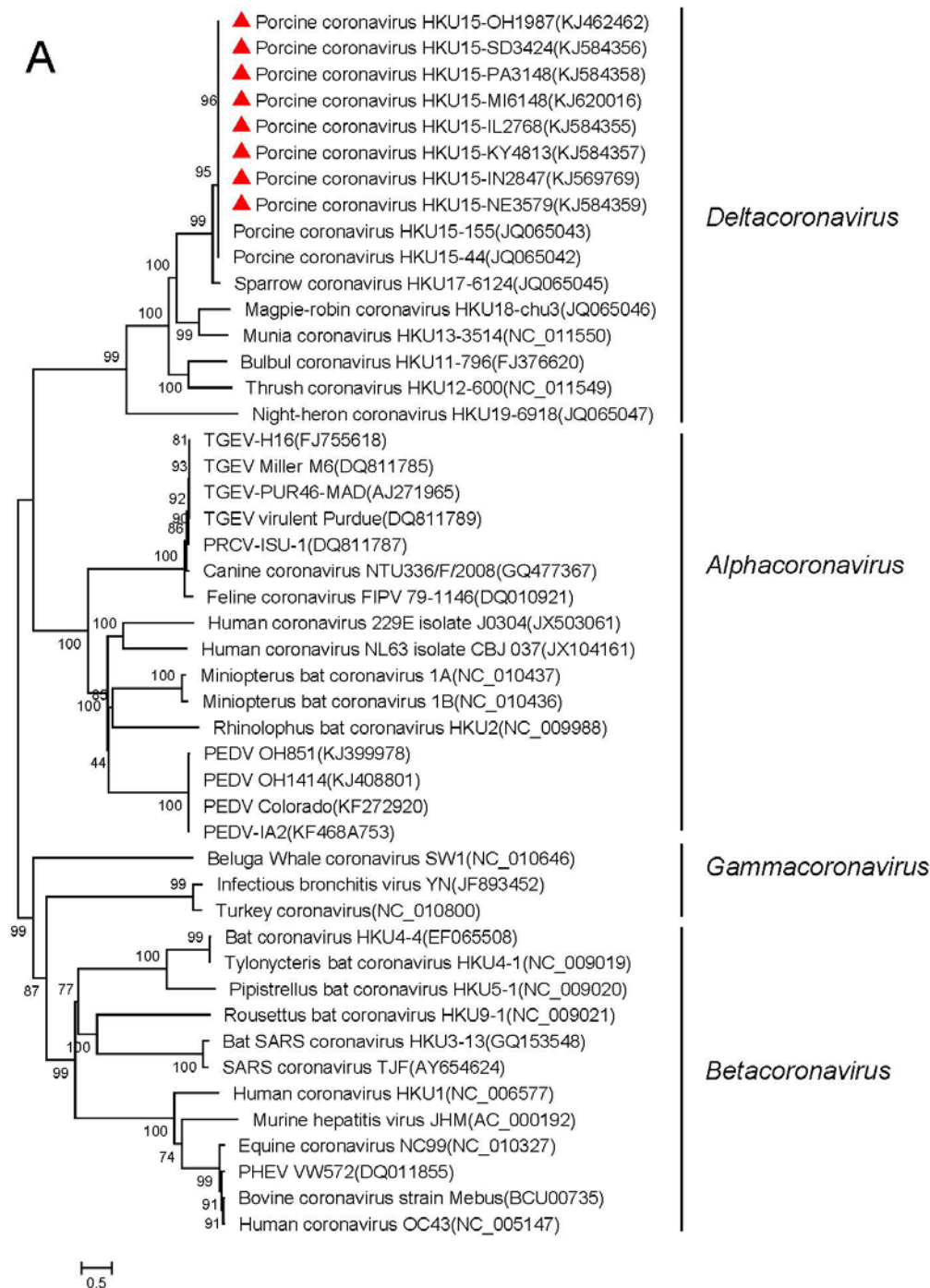
The parents of the girl (family A) did not report any stay or travel in an area to which urinary schistosomiasis was endemic; they reported summer holidays only in Mallorca in the Balearic Islands (Spain) and Corsica. However, her father reported that since 2012, he had experienced gross hematuria that had been evaluated by standard urologic investigations but not by cystoscopy; no etiology was determined. Parasitologic urinalysis in our hospital department showed numerous viable *S. haematobium* eggs in the father's urine.

The parents of the index case-patient also reported that an 8-year-old boy in a friend's family (family B), who shared summer vacations with

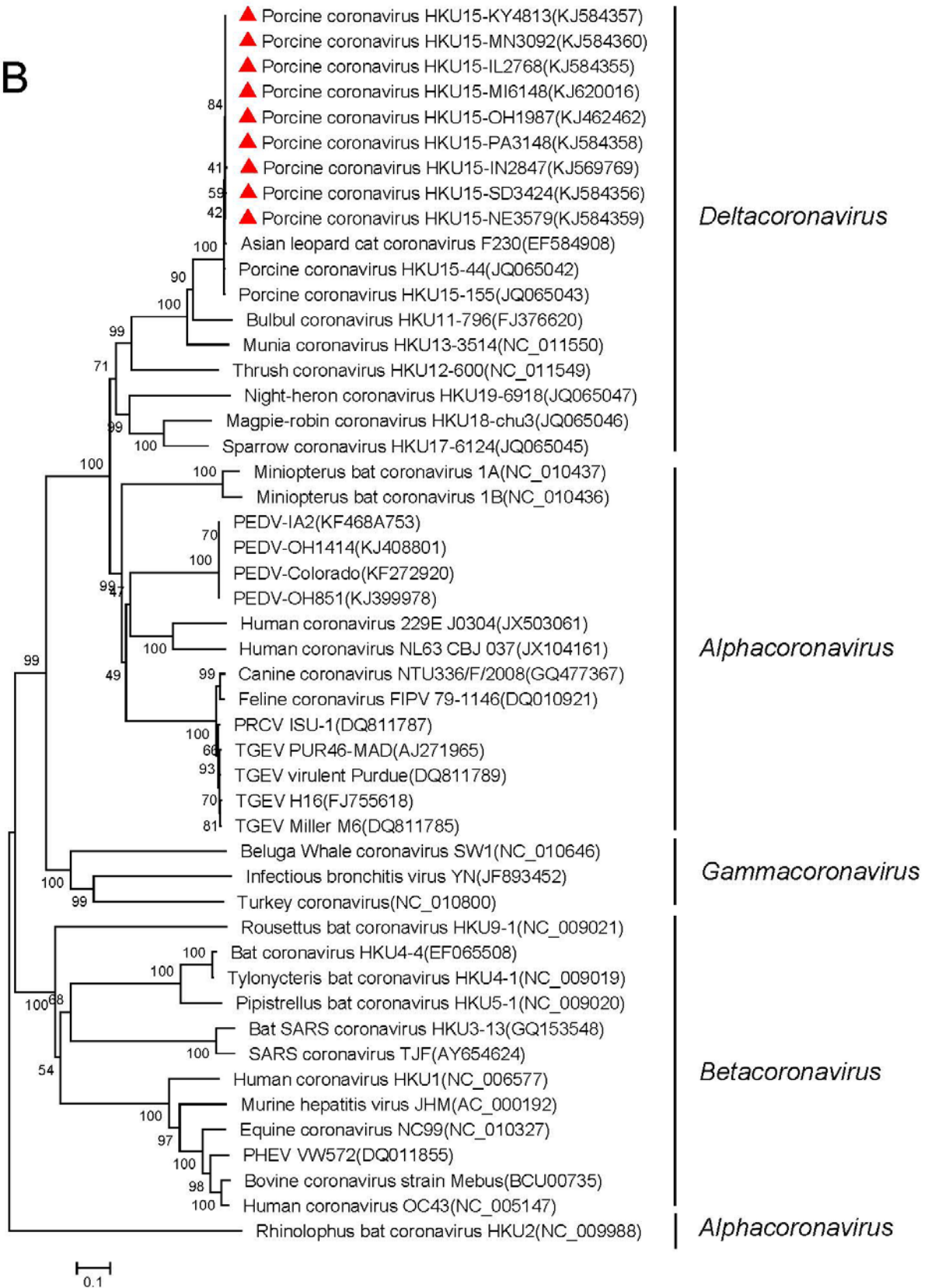
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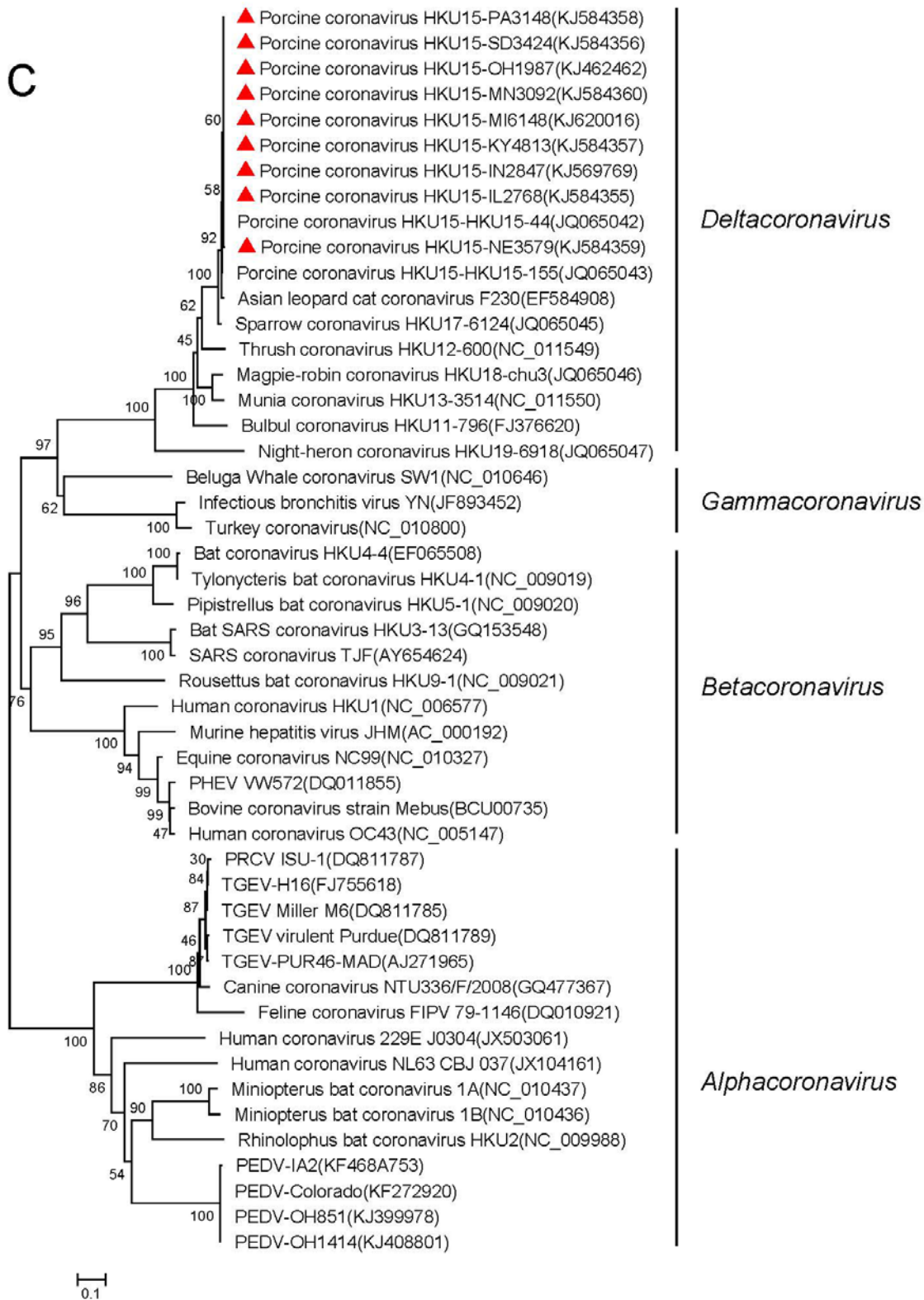
Porcine Coronavirus HKU15 Detected in 9 US States, 2014

Technical Appendix



B





Technical Appendix Figure. Phylogenetic tree constructed on the basis of the whole genome sequences (A), spike protein (B) and nucleocapsid protein (C) of 4 genera of coronaviruses (*Alphacoronavirus*, *Betacoronavirus*, *Gammacoronavirus*, and *Deltacoronavirus*), including the 9 US strains of porcine coronavirus HKU15 (indicated by red triangle). The dendrogram was constructed by using the neighbor-joining method in the MEGA software package, version 6.05 (<http://www.megasoftware.net>). Bootstrap resampling (1,000 replications) was performed, and bootstrap values are indicated for each node. Reference sequences obtained from GenBank are indicated by strain name and accession number. Scale bar represents 0.5 nt (A) or 0.1 aa (B, C) substitutions per site. PEDV, porcine epidemic diarrhea virus; PHEV, porcine hemagglutinating encephalomyelitis virus; PRCV, porcine respiratory coronavirus; TGEV, transmissible gastroenteritis coronavirus; SARS, severe acute respiratory syndrome.