Coronavirus in Bats shows Relationship to Appalachian Ridge and Porcine Epidemic Diarrhea Viruses, Brazil

Technical Appendix

Figure: Phylogenetic trees obtained with the Maximum likelihood (using FastTree 2.1.7 software) A) and Neighbor-Joining (using MEGA v6.0) B) methods for the partial RdRp gene (144 bp). The sequences of this study are highlighted in blue with the name UNICAMP_bat_BR_14 (submitted to GenBank under the
code KM514667). The GenBank no. accession sequences retrieved are described in order as shown in the trees: AlphaCoV Eptesicus fuscus (JX537914.1), PEDV (Porcine Epidemic Diarrhea Coronavirus, AF353511); UNICAMP_bat_BR_14; AlphaCoV Perimyotis subflavus ARCoV.2 MCA IT (JX537913.1); Human CoV NL63 (AY567487); Miniopterus bat CoV 61 (AY864196); Miniopterus bat CoV HKU8 (DQ249228); TGEV CoV virulent purdue (Transmissible Gastroenteritis Coronavirus, DQ811789); Human CoV 229E (AF304460); IBV (Avian Infectious Bronchitis Virus, FJ904722); Turkey CoV (EU095850); SARS CoV (Human Severe Acute Respiratory Syndrome CoV, JF292915); MERS CoV (Middle East Respiratory Syndrome, KJ741000.1); Human CoV HKU1 (AY597011); Murine CoV MHV-A59 (FJ647225); Human CoV OC43 (AY903460); Thrush CoV HKU12-600 (FJ376621); Asian Leopard cat CoV (EF584908); Munia CoV HKU13-3514 (FJ376622). No. branches represent the support values. Scale bars indicate no. nuclear substitutions per site.