Evolutionary Plasticity of Zoonotic Porcine Deltacoronavirus (PDCoV): Genetic Characteristics and Geographic Distribution

Amina Nawal Bahoussi[1#], Pei-Hua Wang[1#], Pir Tariq Shah[1#], Hongli Bu[2], Changxin Wu[1,3,4,5] *, Li Xing[1,3,4,5]*

Supplementary Figure 1. The phylogenetic tree based on the full-length genomes of 166 PDCoVs. Multiple sequence alignment was performed using ClustalW. The Maximum Likelihood phylogenetic tree (ML) was constructed in IQ-TREE multicore version 1.6.12 using the best-fit model GTR+F+I+G4 with 1000 bootstraps. The viruses identified in China are indicated with red branches. The viruses reported in China but falling into GI-a and GII-a subgroups are shown in red branches with red circles. The human Haiti PDCoVs are indicated with blue circles. The scale bar in the bottom left represents 0.003 nucleotide substitutions per site. The viruses highlighted with green blocks were included in the genomic similarity analysis in Figure 2. Strains are formatted as GenBank accession number_virus name_country-year of collection_.