Figure 1. Phylogenetic analysis of the PEDV S1 portion nucleotide sequences. The tree was constructed using the distance-based neighbor-joining method of the software MEGA5.2. Bootstrap analysis was carried out on 1,000 replicate data sets, and values are indicated adjacent to the branching points. The recent cases with sequences (ISU cases 1-5) different from PEDV identified in US in 2013 are indicated with solid circles. The recent cases (ISU cases 6-15) with sequences similar to PEDV identified in US in 2013 are indicated with triangles.