New PEDV Strains detected in US Swine
1-30-2014

Iowa State University Veterinary Diagnostic Laboratory (ISU VDL) is offering PEDV S1 (first 2.2 kb portion of the spike gene) sequencing to the clientele to help determine the genetic relatedness and molecular epidemiology of PEDV in US swine. During the time periods of January 24 – January 29, 2014, PEDV S1 sequencing was performed on 15 PEDV cases at ISU VDL. Among them, PEDV S1 sequences from 10 cases (ISU cases 6-15) are similar to each other and to the PEDV strains identified in US swine since April 2013 (99.1-100% nucleotide identities). In distinct contrast, the PEDV S1 sequences from the other 5 cases (ISU cases 1-5) only have 93.9-94.6% nucleotide identities to the PEDV strains previously identified in US swine. However, these 5 PEDV cases shared 99.6-100% nucleotide identities to each other based on the S1 sequences.

Phylogenetic analysis based on the S1 sequences demonstrated that aforementioned 10 PEDV cases clustered together with PEDV strains identified in US since April 2013. However, the aforementioned 5 PEDV cases clustered very differently from the PEDV strains previously identified in US swine (Figure 1, Page 2). Sequence alignment showed that the S1 sequences of these 5 PEDV cases had some deletions and insertions compared to PEDV viruses previously identified in US.

Based on the data currently available, it appears unlikely that this strain is a mutant evolved from PEDV previously identified in US swine. Determination of the entire genome sequences of these new PEDVs are in progress and will help determine the origin of the viruses.

The PEDV real-time RT-PCR offered at ISU VDL is targeting the nucleocapsid (N) gene. The N-gene is known to be a conserved portion of the PEDV genome. Thus far, the PEDV N-gene real-time RT-PCR being conducted at the ISU VDL seems to be readily detecting these new PEDVs. The full-length N gene sequences of the new PEDVs have been determined and were similar to the PEDVs previously identified in the US.
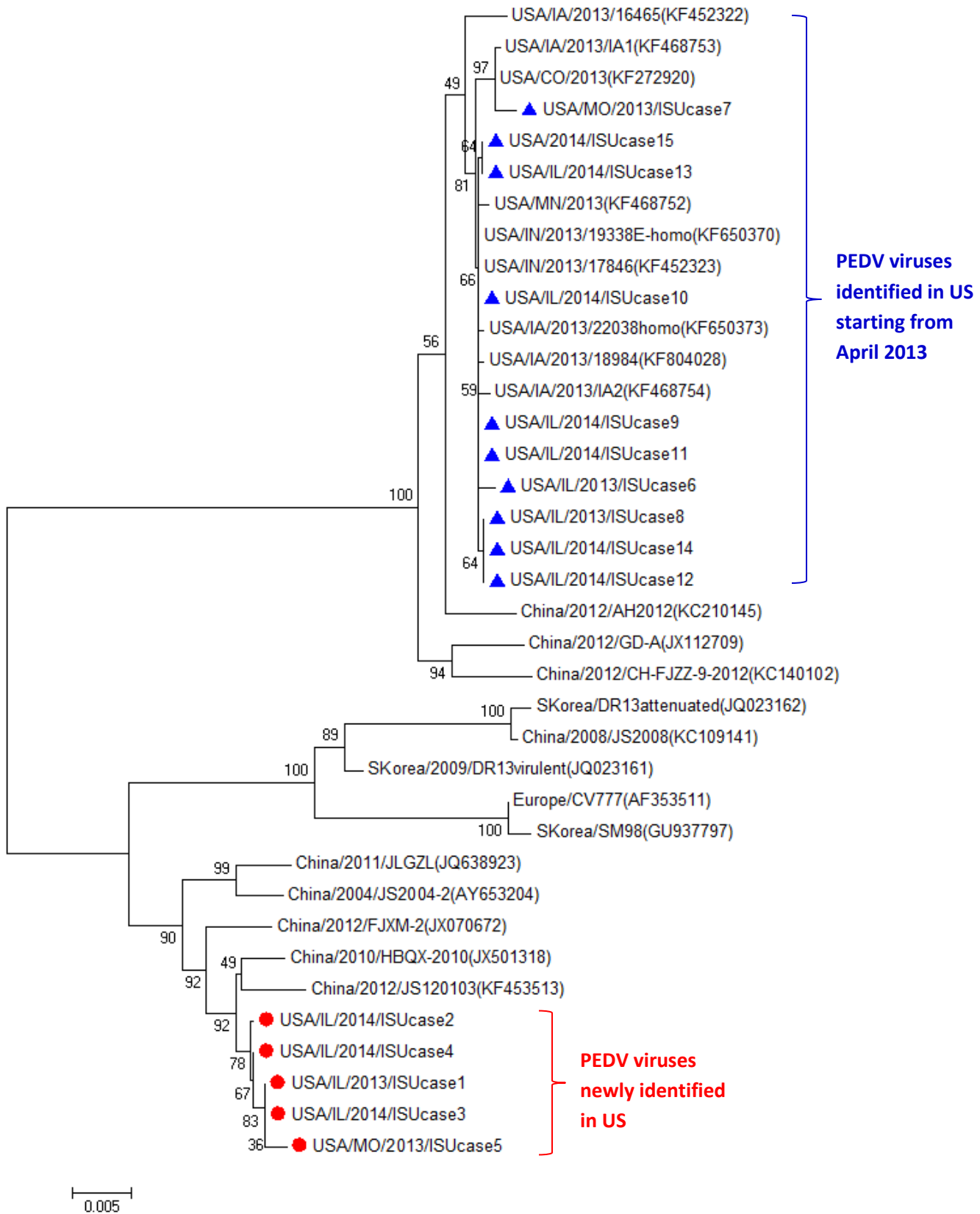
For more information, please contact ISU VDL.

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.