



**Phylogenetic dendrogram of cattle viral diarrhea (mucosal disease) causative agents BVDV-1 and BVDV-2 identified in Siberian farms (2006-2017).** Dendrogram is based on sequence analysis of the 5'-non-translated region (5'-UTR). The ClustalW-based alignment of sequences. The topology of the tree is constructed by the neighbor-joining method. The genetic distance matrix is calculated using the minimal evolution method. The external group is the sequence of the virus BVDV-3. Near each node of the dendrogram, bootstrap support is indicated. Investigated isolates are underlined. For reference strains, the name and number in the database GenBank (NCBI) are indicated.