Identification and complete genome analysis of novel picornavirus in bovine in Japan - DTU Orbit (07/12/2018)

Identification and complete genome analysis of novel picornavirus in bovine in Japan

We identified novel viruses in feces from cattle with diarrhea collected in 2009 in Hokkaido Prefecture, Japan, by using a metagenomics approach and determined the (near) complete sequences of the virus. Sequence analyses revealed that they had a standard picornavirus genome organization, i.e. 5’ untranslated region (UTR) - L- P1 (VP4- VP3- VP2- VP1) - P2 (2A- 2B- 2C) - P3 (3A- 3B- 3C-3D) - 3’UTR- poly(A). They are closely related to other unclassified Chinese picornaviruses; bat picornaviruses group 1-3, feline picornavirus, and canine picornavirus, sharing 45.4-51.4% (P1), 38.0-44.9% (P2), and 49.6-53.3% (P3) amino acid identities, respectively. The phylogenetic analyses and detailed genome characterization showed that they, together with the unclassified Chinese picornaviruses, grouped as a cluster for the P1, P2, 3C and VP1 coding regions. These viruses had conserved features (e.g. predicted protein cleavage sites, presence of a leader protein, 2A, 2C, 3C, and 3D functional domains), suggesting they have a common ancestor. Reverse-transcription-PCR assays, using specific primers designed from the 5’UTR sequence of these viruses, showed that 23.0% (20/87) of fecal samples from cattle with diarrhea were positive, indicating the prevalence of these picornavirus in the Japanese cattle population in Hokkaido Prefecture. However, further studies are needed to investigate the pathogenic potential and etiological role of these viruses in cattle.

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