Co-infection of Mammalian orthorubulavirus 5 and Mammalian orthoreovirus type-3 in domestic pigs in India

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Abstract

During a routine surveillance for exotic and emerging swine viral diseases in India, five samples (four faecal, one serum) showed cytopathic effects in Vero cells. Transmission electron microscopy of infective cell supernatant revealed the presence of two types of virions. *De novo* metavirome sequencing enabled complete genome assembly of Mammalian orthorubulavirus 5 (MRuV5) and Mammalian orthoreovirus (MRV). The MRuV5 isolates possessed a whole genome of 15246 bp with seven genes (NP, V/P, M, F, SH, HN, L), while the MRV isolates had segmented genome with three large (L1, L2, L3), three medium (M1, M2, M3) and four small (S1, S2, S3, S4) segments. The MRuV5 isolates were genetically grouped with those from various mammalian species reported from South Korea and China. Deduced amino acid sequences of the HN, NP and F gene coding regions of MRuV5 isolates showed the substitutions of three (92L, 111R, 447H), two (86S, 121S) and two (139T, 246T) amino acids, respectively, compared to previously reported strains of the virus. However, they did not reveal any change in predicted amino acid residues at the receptor binding site in HN protein, cleavage site or HN stalk region. S1 gene of the MRV isolates showed the highest nucleotide identity (97.73%) with the MRV3 strain ZJ2013 isolated from pig in China, and these isolates were grouped into MRV type-3. Deduced amino acid sequences of MRV3 S1 gene revealed amino acid residues 198-204NLAIRLP, 249I, 340D, 419E known for sialic acid binding site and neurotropism. We report the co-infection of MRuV5 and MRV3 detected incidentally for the first time in domestic pigs in India. Although MRuV5 and MRV3 develop asymptomatic infections or mild disease in animals and humans, continuous monitoring of evolution and spread of such viruses is important in the current global scenario of increasing threats due to emerging novel pathogens.

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