

Porcine sapelovirus in Korea; from epidemiology to pathology

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The porcine sapelovirus (PSV), a species of the novel genus *Sapelovirus* with the family *Picornaviridae*, is known to cause enteritis, pneumonia, polioencephalomyelitis, and reproductive disorders in pigs. However, the prevalence, genetic diversity, structural features of the complete genome, receptor(s) and pathogenesis of PSVs remain largely unknown. By RT-PCR and nested PCR assays, 34% of diarrhea samples tested positive for PSV, and a high proportion of infections occurred along with a variety of other enteric viruses and bacteria. Genomic and phylogenetic analyses of the VP1 genes revealed pronounced genetic diversities between PSVs from Korean and other known strains. The Korean PSV genomes ranged from 7,542 to 7,566 nucleotides excluding the 3'poly(A) tail, and showed the typical picornavirus genome organization; 5'untranslated region (UTR)-L-VP4-VP2-VP3-VP1-2A-2B-2C-3A-3B-3C-3D-3'UTR. Three distinct *cis*-active RNA elements, the internal ribosome entry site (IRES) in the 5'UTR, a *cis*-replication element (*CRE*) in the 2C coding region and 3'UTR were identified and their structures were predicted. Interestingly, the structural features of the *CRE* and 3'UTR were different between PSV strains. Using a variety of approaches including treatment of cells with carbohydrate-destroying chemical, mono- or oligosaccharides, linkage-specific sialidases, lectins, proteases, glucosylceramide synthase inhibitors, we demonstrated that PSV recognized α 2,3-linked sialic acid on GD1a ganglioside. PSV bound to cells from different species but infection was limited to cells of porcine origin. Confirming these observations, *in vivo* studies indicated that PSV induced pathology in piglets but not in chicks, confirming the pathogenicity and host range restriction of PSV. Our data indicated that genetically diverse PSVs induce epidemic infections in Korean pig farms. The availability of these first complete genome sequences for PSV strains will facilitate future investigations of the evolutionary characteristics of PSV. Moreover, our findings will contribute to the understanding of the sapeovirus life cycle and pathogenesis.

Keyword: Porcine sapelovirus, epidemiology, genomic structure, receptor, pathogenesis

Funding Source: This study was supported by Bio-industry Technology Development Program through the Korea Institute of Planning and Evaluation for Technology in Food, Agriculture, Forestry and Fisheries (iPET) funded by the Ministry of Agriculture, Food and Rural Affairs, Republic of Korea.

Disclosure Statement: None of the authors have any conflicts of financial interest to declare.