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Perspectives on the evolution of porcine parvovirus

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Porcine parvovirus (PPV) is a major cause for reproductive failure in swine. Although PPV infections were highly prevalent in South Korea, widespread use of the vaccine has dramatically reduced the infection rate. To our knowledge, there has been neither an investigation into the epidemiology nor a phylogenetic analysis of PPV strains in South Korea. This study focused on the phylogeny of PPV strains in South Korea via nucleic acid analysis using lung samples collected from 2013 to 2016. Only one sample (T142_South Korea, 2016) was tested positive for the detection. We focused on nucleotide changes found in the T142 South Korea strain. However, our analysis revealed that the *VP1* and *VP2* genes of T142 South Korea are identical to those in the Kresse strain isolated in the USA in 1985. Next, we focused on the evolution of PPV and compared strains isolated from the 20th century to those from the 21st century. Although PPV's nucleotide substitution rate is as high as that in RNA viruses, we found that the average number of mutations in the variant regions was reduced compared to that of strains isolated in the 20th century. The *VP1* phylogenetic data revealed four distinct genetic lineages, two from Europe and one from Asia, which evolved independently from the European lineages. From an evolutionary point of view, the amino acid substitutions of both lineages are clearly different.

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