

# Identification and Analysis of Porcine Circovirus in Fur Animals

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## Introduction

The porcine circovirus (PCV) is a single-stranded, non-enveloped, small circular DNA virus that belongs to the genus *Circovirus* and the family *Circoviridae*. It has a genome that is about 1.7 kilobytes long. There are two major open reading frames (ORFs) in the PCV genome, ORF1 and ORF2. The replicase (Rep) protein is encoded by ORF1, and the capsid (Cap) protein is encoded by ORF2. ORF2 is frequently utilized for genetic variation analysis because it exhibits more genetic variation. In pigs, PCV1, PCV2, and PCV3 are currently known to exist. PCV1 was first found to be a contaminant in cell cultures, and it was found to not be pathogenic for pigs. Postweaning multisystemic wasting syndrome (PMWS), porcine dermatitis and nephropathy syndrome (PDNS), and reproductive disorders are all associated with PCV-associated diseases caused by PCV2. One of the most significant pathogens threatening the global swine industry is PCV2. Through metagenomic sequencing in 2016, PCV3, which was found in pigs with PCV systemic disease and cardiac pathology, was identified as a new porcine circovirus. Although its pathogenicity is unknown, cloned PCV3 has been reported to potentially cause pig diseases similar to PDNS [1].

## Description

In 2019, a brand-new porcine circovirus known as porcine circovirus type 4 (PCV4) was discovered for the first time in Hunan province, followed by Henan province, Shanxi province, and Jiangsu province. The virus was then found in Guangxi, Jiangxi, Inner Mongolia, and other Chinese and South Korean provinces. The complete PCV4 genome sequence is currently known to be 1770 base pairs long and to contain two main ORFs that, respectively, encode the 296-amino-acid Rep protein and 228-amino-acid Cap protein. According to the findings of a recent retrospective study, PCV4 could be detected in 2008-collected sera, indicating that PCV4 has been present in China for at least 14 years. Although PCV4 has not yet been successfully isolated, recent research has shown that rescued PCV4 can cause disease in piglets. In conclusion, PCV4 has spread widely in China and may be a serious threat to the pork industry.

In pigs, PCV4 is linked to respiratory, enteric, diarrhea, and PDNS. Although several reports suggested that PCV2 and PCV3 were detected in non-porcine species, its mechanism of cross-species transmission remains unknown. In general, pigs are the natural reservoirs of PCV. However, little is known about PCV4 transmission between species. A recent study found that dairy cows can be infected with PCV4, with a positive rate of 2.22 percent and negative rates for PCV2 and PCV3. In addition, genetic studies demonstrate

that PCV4 and the Mink circovirus share the highest genomic identity. We all know that China has grown to become one of the most important producers of fur animals. In addition to fox and raccoon dogs, mink is a significant domestic fur animal species in China [2-5].

The small-scale family breeding model of breeding fur animals, which are frequently mixed with other domestic animals like pigs, is the predominant breeding model in China. The cross-species transmission of porcine viruses to fur animals has thrived in this breeding mode. PCV2 was found in reproductively unable farmed foxes and raccoon dogs in a previous study. As a result, the circumstances of PCV4 transmission between pigs and fur animals were the focus of our research. We found PCV4 in mink, fox, and raccoon dogs in this area. This is the first study to report PCV4 genetic characteristics and detect PCV4 in fur animals, expanding our knowledge of PCV4's molecular epidemiology. The cross-species transmission of PCV4 was supported by this new study. This indicated that PCV2 may pose a threat to the breeding of fur animals. We speculated that the PCV2 infection in fur animals was caused by the current breeding method of fur animals in light of the retrospective prevalence of PCV2 in fur animals. Due to the close proximity of pig and fur animal farms or mixed breeding, China's dominant breeding model for fur animals was the small-scale family model. Circoviruses were more likely to spread between species as a result of this breeding method. 220 sera samples from pig farms near fur animal farms were submitted to our laboratory for the purpose of tracing the origin of these PCV4 strains from fox and raccoon. We obtained six complete genomes of PCV4 strains and found a PCV4 prevalence of 20.45% in sera samples from nearby pig farms. The homology alignment revealed that the genome sequences of six fur animal-origin PCV4 strains and those of pig-origin PCV4 strains shared 99.7 to 99.9% nucleotide identities, suggesting the possibility of PCV4 transmission across species. Horizontal transmission of PCV4 between infectious and susceptible individuals was found to be the most effective method, but the initial host of PCV4 and the path of transmission remain unknown.

## Conclusion

The genetic evolution and epidemiology of fur animal-origin PCV4 can be better understood through the genetic analysis and epidemiological investigation of these PCV4 strains. Additionally, it provides the foundation for future PCV4 prevention and management. However, the traditional mixed feeding model of fur animals with other species poses a serious threat to the fur animal breeding industry, and aggressive measures should be taken to stop PCV4 cross-species transmission as soon as possible.

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