

Porcine circovirus type 3 in free-living wild boars in Brazil

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Introduction

Porcine circovirus type 3 (PCV3) was firstly identified in domestic swine in the US (4,5) and subsequently in several countries, including Brazil (1,7). PCV3 is detected in both sick (4,5) and healthy pigs (1). Domestic swine and wild boars are susceptible to infection with similar viral and bacterial pathogens. Although PCV3 has been detected in wild boars in Germany (6), Italy (1) and Spain (3), information about PCV3 circulation in wild boars worldwide is scarce. The aim of this study was to investigate PCV3 occurrence in free-living wild boars in Brazil.

Materials and Methods

Serum and/or lung samples from 70 wild boars were collected between January of 2017 and June of 2019 in four cities (Castro, $n = 40$; Carambeí, $n = 6$; Ponta Grossa, $n = 15$; and Teixeira Soares, $n = 9$) located in Paraná state, Brazil. Sampling collection was performed by officially authorized exotic wildlife controller agents, according to IN 03/2013 of IBAMA (2). Viral DNA was extracted from sera ($n = 70$) and lung tissue ($n = 7$) using DNeasy Blood & Tissue Kit (Qiagen®). PCR assays for diagnostic and sequencing were performed using specific primers for PCV3 (4). The PCR products were gel-purified using BigDye X Terminator Purification Kit (Qiagen) and nucleotide sequences were determined using an ABI3130xl Genetic Analyzer. The obtained sequences were analyzed and assembled with the Phred/Phrap/Consed software. Phylogenetic analyses were performed using Neighbor Joining (NJ) method in MEGA 6.0 software. ORF2 nucleotide (nt) sequences were compared with other ORF2/PCV3 sequences available in GenBank.

Results

PCV3 was detected in 7 out of 70 (10%) sera and in 5 out of 7 lungs. PCV3 positive samples were from wild boars sampled in Castro and in Ponta Grossa, between 2017 and 2018. The three obtained sequences were grouped in PCV3c genotype cluster and the ORF2 sequences presented a 100% of similarity among them (Figure 1). The nt similarities between the PCV3 sequences presented here and those available on GenBank are 98.7-99.8% for Brazilian commercial pigs, and 98.6-99.2% for wild boar samples worldwide.

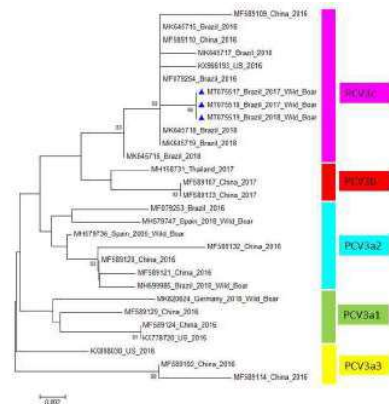


Figure 1. Phylogenetic tree of ORF2 sequences using the NJ method. The three Brazilian PCV3 sequences are labeled with a solid blue triangle.

Conclusions and Discussion

This is the first report of PCV3 in free-living wild boars in Brazil. The identity matrix revealed a high similarity between the three PCV3 sequences from this study and other sequences available in GenBank. As previously reported, wild boars are susceptible to PCV3 infection (6) and the virus has been detected in pig herds in Brazil (7). Previous studies have suggested that occurrence of PCV3 infection in commercial pigs is higher than in wild boars (1,3) implying the role of pig management in PCV3 transmission and survival. Currently, there is no evidence that PCV3 causes disease in wild boars. However, PCV3 prevalence in wild boars should be evaluated to establish the viral dynamic in these pig population.

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