Proceedings of the

23rd International Pig Veterinary Society (IPVS) Congress

VOLUME II

23rd IPVS CONGRESS
MEXICO 2014

June 8 – 11, 2014
Cancun, Quintana Roo, Mexico

Proceedings of the 23rd International Pig Veterinary Society (IPVS) Congress

Volume 2

Poster presentations

June 8 – 11, 2014
Cancun, Quintana Roo, Mexico

P.549

Investigation of CaCV-1 in swine herds in Brazil

EL Zanella[1]; CH Okino[2]; JPH Sato[3], DESN Barcellos[3], JR Ciacci-Zanella[2].
[1] *College of Agronomy and Veterinary Medicine, University of Passo Fundo, Passo Fundo- RS, Brazil;*
[2]*Embrapa Swine and Poultry Research Center, Animal Health Laboratory, Concórdia, Brazil*[2]
[3]*Veterinary Medicine School, Federal University of Rio Grande do Sul/UFRGS, Porto Alegre, Brazil*[1],
janice.zanella@embrapa.br

Introduction

Circoviridae family comprises of the Circovirus genus whose member species are known to infect only birds and pigs, the Gyrovirus genus, including the Chicken anemia virus (CAV) and the proposed genus Cyclovirus (4, 9). In the past, only porcine circovirus was known to infect mammals and cause economic impact (4). Porcine circovirus type 2 (PCV2) is an important infectious agent affecting both domestic and wild pigs (8). PCV2 disease (PCVD) has been characterized in Brazil as well as in many pork-producing countries worldwide (1, 9). Studies have discovered single stranded DNA viruses co-infections as cause of reproductive problems in pigs in Brazil. Those analyses identified by PCR sequences of single stranded DNA viruses (ssDNA): PCV2, porcine circovirus type 1 (PCV1), torque-teno sus virus (TTSuV1 and TTV2 of the family *Anelloviridae*) and porcine parvovirus (PPV) in fetuses. Recently, a circovirus was isolated from dogs (CaCV-1) and associated with the death or injury in these animals (2, 5). In view of the frequent association and co-infection between PCV2 and other ssDNA viruses, the aim of this study was to investigate the presence of PCV2 and CaCV-1 in domestic and in captive wild boars in Brazil.

Materials and Methods

Samples used in this study included 56 samples of domestic pigs and 129 samples of captive wild boars. For domestic pigs, were analyzed 43 sera samples, pool of organs of 2 aborted fetuses, of 1 mummified piglet and of 1 stillborn piglet. In addition, lungs of 3 nursery pigs and lymph nodes of 6 nursery pigs from PCVD suspect cases were also analyzed. Bronchial and mesenteric lymph nodes of 129 captive wild boars from two farms were collected at slaughter. Captive wild boars were slaughtered with seven months old and 32kg in average. Viral DNA was extracted from pools of lymph nodes using DNeasy Blood & Tissue Kit (Qiagen). The PCV2 nested PCR (3) or PCV2 quantitative real time PCR (qPCR) (6, 7) and CaCV-1 real time PCR (5) were performed using specific primers and probes.

Results

Fifty-five out of 185 (29.7%) total samples (sera, pools of lymph nodes or lungs) were positive for PCV2 by nested and/or qPCR (Table 1). Twelve out of 43 sera samples of domestic pigs and 3 out of 6 lymph nodes of domestic pigs as well were positive for PCV2. In addition, one lung sample and pool of organs of a mummified pig was also positive for PCV2. For captive wild boars, 38 out of 129 lymph node pool of bronchial and mesenteric lymph nodes were positive for PCV2.
All 185 samples used in this study were negative for CaCV-1.

Table 1. qPCR results of 185 porcine samples tested for PCV2 and CaCV-1

Samples	qPCR results	
	PCV2	CaCV-1
Domestic pig		
Total of Samples	56	56
Positive Sera /Total	12/43	0/43
Positive LN / Total	3/6	0/6
Positive Lung / Total	1/3	0/3
Positive AF/ Total	0/2	0/2
Positive MP / Total	1/1	0/1
Positive SB / Total	0/1	0/1
Captive wild pig		
Total of Samples	129	129
Positive LN / Total	38/129	0/129
Total Positive Samples	55/185 (29.7%)	0/185 (0%)

LN: pool of bronchial and mesenteric lymph nodes
AF: pool of organs of aborted fetuses
MP: pool of organs of mummified piglet
SB: pool of organs of stillborn piglet

Conclusions and Discussion

Although all analyzed samples were negative for CaCV-1, this is the first description of molecular diagnostic of CaCV-1 in swine tissues, fetuses or sera in Brazil for both domestic and captive wild boars. This diagnostic tool is important to be accessible for studies of the pathogenesis and epidemiology of ssDNA viruses co-infections in economically important species such as swine.

Acknowledgement

The authors thank Neide Simon for technical support. This work was funded by Embrapa Swine and Poultry, CNPq (578102/2008-0) and UFRGS. JRC Zanella is a fellow of the National Council for Scientific and Technological Development (CNPq).

References

1. Ciacci-Zanella et al.: 2006, Ciên Rural 36:1480-1485.
2. Kapoor, et al., 2012. J Virology, 86(12), p.7018.
3. Kim et al.: 2001, J Virol Methods 92:105-111.
4. Li et al. 2010, J Virol 84(4): 1674-1682.
5. Li et al.: 2013, Emer Inf Diseases 19:534-541.
6. Olvera et al.: 2007, Virology 357:175-185.
7. Opriessnig et al.: 2003, Vet Pathol 40:521–529.
8. Segales et al.: 2013, Vet Microbiol 165:13-20.
9. Smits, et al. 2013. Emer Inf Diseases 19:1511-1513.