

TITLE: VIROME OF SERA OF SWINE WITH POST-WEANING MULTISYSTEMIC WASTING SYNDROME (PMWS)

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ABSTRACT:

Porcine circovirus associated disease (PCVAD) is one of the causes of negative economic impact on pig farming systems described worldwide. Losses include expenditures with treatment, increased mortality rates, and decreased productivity. One of the most relevant manifestations of PCVAD is the post-weaning multisystemic wasting syndrome (PMWS). The main pathogen present in PMWS is porcine circovirus type 2 (PCV2). However, observational and experimental studies have shown that other agents may be involved in the pathogenesis and clinical manifestation. In order to contribute to the knowledge of the viruses involved in PMWS, the present study carried out the high-throughput sequencing of swine sera and subsequent analysis of the resulting metavirome. Sixteen serum samples collected in 2008 on a farm in Rio Grande do Sul, from 80 and 100 days old pigs with clinical signs of PMWS, were examined. The sera were pooled, centrifuged, and DNA was extracted by the phenol-chloroform method. Viral DNA was enriched by multiple displacement amplification using phi29 DNA polymerase and sequencing on the Illumina platform. The metagenomic approach was used to data analyze. The viroma of sera revealed the presence of genetic sequences of members of the families of *Parvoviridae* (16,823), *Anelloviridae* (11,434), *Microviridae* (9,265), *Siphoviridae* (38), *Myoviridae* (36), *Podoviridae* (29), *Phycodnaviridae* (3), *Polyomaviridae* (3) and *Circoviridae* (2). PCV2 was detected as the only specie within the family *Circoviridae*. *Porcine parvovirus* (PPV) and *Torque teno sus virus* (TTSuV) were the most frequent species of the families *Parvoviridae* and *Anelloviridae*, respectively. Phages sequenced in the sera of pigs belonged to the families *Microviridae*, *Siphoviridae*, *Myoviridae* and *Podoviridae*. In *Phycodnaviridae*, viruses were identified with similarity to viruses that infect algae (*Paramecium bursaria chlorella virus 1*). In the family *Polyomaviridae*, sequences with similarity to *Chimpanzee polyomavirus*, *Murine pneumotropic virus*, *Orangutan polyomavirus* were identified. PCV2, PPV and TTSuV have already been described as causing the PMWS. However, viruses of the families *Microviridae*, *Siphoviridae*, *Myoviridae*, *Podoviridae*, *Phycodnaviridae* and *Polyomaviridae* had not yet been described in samples from animals affected with PMWS. Characterization of the virome of these animals described herein provides a reference for future studies comparing viral populations in healthy swine.

Keywords: PCV2, Metavirome, high-throughput sequencing, PMWS, PCVAD

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